

Association and Path Coefficient Analysis in Rice Germplasm for Panicle Architectural and Yield Attributing Traits

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ABSTRACT: Rice is known as a prime food for more than half of the global population. Due to the expanding population on world, it is essential to increase productivity and production of rice. Therefore, increasing the grain yield has become one of the main goals for the breeders. Improving the panicle architecture and yield attributing traits has been the leading target domain in high-yield breeding in rice. Hence, to develop an economically viable variety, plant breeders need to employ an effective selection technique that takes into account the link between yield and the contributing characteristics i.e., panicle architecture traits. The present study is being carried out to examine the phenotypic, genotypic correlation, and path coefficient analysis of 69 genotypes of rice. Single plant yield, spikelet fertility, the number of filled grains per panicle, and panicle weight were found to be significantly positively correlated with the panicle architecture and yield-attributing traits. Thus, choosing individuals with these traits can increase yield. According to path coefficient analysis the traits namely, the number of productive tillers, number of filled grains, and 1000 grain weight were found to have a direct positive impact on yield. Hence, choosing this character could increase yield and yield components.

Keywords: Rice, Panicle architecture, Phenotypic correlation, Genotypic correlation, Path analysis.

INTRODUCTION

Rice, commonly known as 'Arisi' and 'Nel' in Tamil Nadu, is not only a basic food crop of the state, nevertheless it is an essential cereal crop for more than half of the world's human population. According to recent studies, there will be a 12% growth in the global population. Thus, an improvement in the productivity of crops by at least 13% and an increase in rice grain output of 500 million metric tonnes are required to satisfy the demand for rice from the growing population (Al-daej *et al.*, 2023). The development of rice cultivars with increased production potential is a desired outcome of the rice breeding program (Shrestha *et al.*, 2021). This can support to fulfill the raising demand for rice due to population growth. Additionally, improved rice cultivars can contribute to food security and poverty reduction in many nations where rice is a dominant food. The Green Revolution enabled a symbolic rise in rice production that enabled self-sufficiency and even a surplus for exports; however, in recent years, a reduction is seen in development and crop yield from Green Revolution technologies (Dhurai *et al.*, 2014). Panicle architecture traits are a leading target domain for breeding next-generation high-

yielding varieties in rice (Han *et al.*, 2014; Agata *et al.*, 2020). Hence, to develop an economically viable variety, plant breeders need to employ an effective selection technique that takes into account the link between yield and the contributing characteristics i.e., panicle architecture traits (Devi *et al.*, 2016).

The rachis, primary branches, and secondary branches, along with other elements like the number of seeds per panicle, the number of seeds per primary and the number of seeds per secondary branches, the length of the primary and secondary branches, and the length of the panicle, make up the panicle architecture (Agata *et al.*, 2020). It has been discovered and functionally characterized that several genes regulate panicle architecture. The yield potential of crops is greatly influenced by these genes. Knowing how they work will make it easier to create new varieties with better panicle architecture and greater grain yields. The Grain Number 1 a (*Gn1a*), the Grain Number Per Panicle 1 (*GNP1*) (Zhai *et al.*, 2020; Wang *et al.*, 2020), Grain Length and Awn Development (*GAD1*) (Jin *et al.*, 2016), Awn 1 (*An1*) (Luo *et al.*, 2013), and Plant Architecture and Yield 1 (*PAY1*) genes all increase the number of grains per panicle (Wei *et al.*, 2022). Grain number and grain shape are regulated by the gene

Regulator of Grain Number 1 (*RGNI*) (Li *et al.*, 2021). Since the yield has a complicated nature and the multi-dimensional influence of each component, combining the link between the yield and its component features is vital (Parimala *et al.*, 2020).

Association and path coefficient analysis is used to find out the amount of connection between yield and its component parts. The relative significance of their direct and indirect effects is also highlighted by this process and clarifies how they relate to grain production. Furthermore, this type of analysis can assist plant breeders in creating their selection techniques to increase grain yield (Moosavi *et al.*, 2015; Babu *et al.*, 2012; Sarangi *et al.*, 2022). This study aims to understand the relationship between panicle architecture traits and yield-attributing traits and to identify traits to break the yield barrier in future breeding programs.

MATERIALS AND METHODS

Genetic Material. This research comprised of 69 germplasm lines from various regions of southern India and these lines include both landraces and varieties (Table 1).

Field trial. The experimental study was conducted in 2022 during the *Kharif* and *Rabi* seasons at the South Farm of the Karunya Institute of Technology and Sciences in Coimbatore. A randomized block design (RBD) with a 20 × 20 centimeter spacing was used to grow the genotypes in three replications. The crop was raised normally by adhering to the suggested crop management techniques, which included irrigation, fertilizer application, and pesticide application.

Phenotyping of the germplasm lines. All the accession were phenotyped manually, figure 1 shows different types of panicles in this study. The plants were labeled after being randomly selected. The 13 quantitative morphological traits that are linked to panicle architecture, such as days to 50% flowering (days), plant height (cm), number of productive tillers (Nos), panicle length (cm), number of primary branches (Nos), number of secondary branches (Nos), number of seeds per primary branch (Nos), number of seeds per secondary branch (Nos), panicle weight (g), number of filled grains (Nos), spikelet fertility percentage (%), and 1000 grain weight (g), single plant yield (g) were phenotyped.

Statistical analysis. The data were statistically analyzed for the aforementioned character using the correlation coefficient method developed by Singh and Chaudhary (1995) and the path analysis method developed by Dewey and Lu (1959). R package (<https://cran.r-project.org/>) version 4.2.2 was used for phenotypic correlation, genotypic correlation, and path coefficient analysis.

RESULTS AND DISCUSSION

Phenotypic and Genotypic Association. Acquiring the main traits that may be used to enhance crops through an effective breeding program, requires careful selection based on an understanding of the area and aspect of the relationship between yield and its qualities

(Babu *et al.*, 2012; Vengatesh and Govindarasu 2018). The phenotypic correlation (Fig. 2 and Table 2) and genotypic correlation (Fig. 3 and Table 3) for the thirteen panicle architecture traits and yield attributing traits *viz.*, days to 50% flowering (days), plant height (cm), number of productive tillers (Nos), panicle length (cm), number of primary branches (Nos), number of secondary branches (Nos), number of seeds per primary branch (Nos), number of seeds per secondary branch (Nos), panicle weight (g), number of filled grains (Nos), spikelet fertility percentage (%), and 1000 grain weight (g), single plant yield (g) were studied. The findings showed that for the majority of the studied characters, estimates of genotypic correlation coefficients were found to be higher than phenotypic correlation coefficients, so this shows a strong inherent association among the characters that may be caused by the environment's masking or moderating effects (Nikhil *et al.*, 2014). The phenotypic correlation shows that the traits *viz.*, number of productive tillers (0.475**), panicle length (0.171*), seeds per primary branch (0.145*), panicle weight (0.292**), the number of filled grains per panicle (0.211**), and 1000-grain weight (0.475**) are highly positively correlated with single plant yield. While the genotypic correlation reveals that single plant yield is highly significantly correlated with the number of productive tillers (0.636**), panicle weight (0.578**), number of filled grains (0.250*), and 1000 grain weight (0.513**). Similar findings were also reported by Manivelan *et al.* (2022); Babu *et al.* (2012); Lakshmi *et al.* (2014); Saha *et al.* (2019). A common phenotypic and genotypic correlation was observed between the number of productive tillers, panicle weight, number of filled grains, and 1000-grain weight towards yield.

Path Coefficient analysis. The Dewey and Lu's (1959) path coefficient analysis, which further divides the correlation coefficients into the direct and indirect effects of characters, provides insight into how relationships are linked (Shrestha *et al.*, 2021). The result of the genotypic path was given in (Fig. 4 and Table 4) and the phenotypic path analysis was given in (Fig. 5 and Table 5), the phenotypic path analysis showed that the traits *viz.*, 1000 grain weight (0.551), spikelet fertility percentage (0.103), number of filled grains (0.213), panicle weight (0.124) and number of productive tillers (0.617) exhibited very high positive direct effects toward single plant yield. Similar results were reported by (Bagudam *et al.*, 2018; Shrestha *et al.*, 2021; Gupta *et al.*, 2020). Whereas genotypic path analysis showed the trait's number of productive tillers (0.953), number of filled grains per panicle (0.747), and 1000-grain weight (0.704) exhibited very high direct positive effects towards single plant yield. In the genotypic path, the panicle weight (-0.148) and spikelet fertility percentage (-0.107) showed a high negative direct effect on the single plant yield.

Hence, these traits were observed to have a major relationship with yield, distinctively the traits number of productive tillers, number of filled grains per panicle, and 1000-grain weight could be used as major selection indices in future breeding programs.

Table 1: List of 69 rice genotypes used in this study.

Sr. No.	Genotypes	Landraces/varieties	Area
1.	CO 51	Variety	Tamil Nadu
2.	BABTLA	Variety	Kanchipuram, TN
3.	KARUPUKAVUNI	Landraces	AC and RI, Madurai
4.	SUPER PONNI 43	Variety	Kanchipuram
5.	IR50	Variety	Kanchipuram
6.	GUNDU	Variety	Kanchipuram
7.	RLR	Variety	Kanchipuram
8.	LLR	Variety	Kanchipuram
9.	CHINNAR	Landrace	Tamil Nadu
10.	KRG 13	Variety	West Bengal
11.	KRG 12	Landrace	Tamil Nadu
12.	KRG 9	-	-
13.	KRG 7	Landrace	Tamil Nadu
14.	KRG 4	Landrace	Tamil Nadu
15.	KRG 3	Landrace	Tamil Nadu
16.	KRG 10	Variety	Uttarakhand
17.	KRG 11	-	-
18.	KRG 2	Landrace	Tamil Nadu
19.	KRG 5	Variety	Bangladesh
20.	KRG 16	Landrace	Tamil Nadu
21.	KRG 15	Variety	West Bengal
22.	KRG 14	Variety	Orissa
23.	KRG 17	-	-
24.	KRG 6	Landrace	Tamil Nadu
25.	KRG 1	-	Tamil Nadu
26.	KRG 62	-	-
27.	KRG 65	-	-
28.	KRG 60	-	-
29.	KRG 19	-	-
30.	KRG 20	-	-
31.	KRG 64	Variety	West Bengal
32.	KRG 63	-	-
33.	KRG 61	-	-
34.	KRG 50	Variety	-
35.	KRG 45	-	-
36.	KRG 24	Landrace	Tamil Nadu
37.	KRG 21	-	-
38.	KRG 29	Landrace	Tamil Nadu
39.	KRG 22	-	-
40.	KRG 30	Landrace	Tamil Nadu
41.	KRG 66	-	-
42.	KARTHIKA	Variety	Kerala
43.	PUNCHAKAYMA	Landrace	Kerala
44.	PRATHYASA	Variety	Kerala
45.	PISINI	Variety	Kanchipuram
46.	RENJINI	Variety	Kerala
47.	PAVITHRA	Variety	Kerala
48.	MAKOM	Landrace	Kerala
49.	MYSORE MALLI	Landrace	Thanjavur
50.	THOYAMALLI	Landrace	Thanjavur
51.	VALLAN SAMBA	Landrace	Thanjavur
52.	ILLUPAIPOO SAMBA	Landrace	Thanjavur
53.	THANGA SAMBA	Landrace	Thanjavur
54.	KULLAKAR	Landrace	AC and RI, Madurai
55.	MILAGU SAMBA	Landrace	AC and RI, Madurai
56.	KOTHAMALI SAMBA	Landrace	AC and RI, Madurai
57.	ASD 16	Variety	TNAU, Coimbatore
58.	TPS 3	Variety	TNAU, Coimbatore
59.	CO 53 TFL	Variety	TNAU, Coimbatore
60.	KEERAI SAMBA	Landrace	Kanniyakumari
61.	ADT 45	Variety	TNAU, Coimbatore
62.	POONGAR	Landrace	AC and RI, Madurai
63.	AMMAN PONNI	Variety	AC and RI, Madurai
64.	SITHIRAIKAR	Landrace	AC and RI, Madurai
65.	KARUMKURUVAI	Landrace	State seed farm, Kanniyakumari
66.	JCL NEL	Variety	Madurai
67.	RAKTHASALI	Landrace	-
68.	KALASAR NEL	Landrace	Kottaram
69.	KOTTARAM SAMBA	Landrace	Kottaram

Table 2: Estimates of phenotypic correlation among the panicle architecture and yield attributing traits.

	DTF	PH	PT	PL	PB	SB	SPB	SSB	PW	FG	SF	1000GW	SPY
DTF	1												
PH	0.066	1											
PT	0.017	-0.187**	1										
PL	0.014	0.425**	-0.099	1									
PB	0.121	0.023	-0.026	0.084	1								
SB	0.022	0.160*	-0.118	0.160*	0.302**	1							
SPB	0.030	0.132	-0.064	0.074	0.097	0.546**	1						
SSB	-0.003	-0.001	0.051	0.034	0.127	-0.482**	-0.001	1					
PW	-0.045	0.292**	-0.005	0.331**	0.078	0.096**	0.122	0.008	1				
FG	0.089	0.366**	-0.197**	0.497**	0.246**	0.255	0.196**	0.064	0.334**	1			
SF	0.144*	0.251**	-0.180**	0.233**	0.142*	-0.028**	0.014	0.283**	0.140*	0.571**	1		
1000GW	-0.149*	0.179**	-0.134	0.037	0.045	0.105	0.113	-0.066	0.133	-0.013	-0.126	1	
SPY	-0.049	0.121	0.475**	0.171*	0.084	0.127	0.145*	0.006	0.292**	0.211**	0.058	0.475**	1

** significance at 5%, *** significance at 1%

Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Table 3: Estimates of genotypic correlation among the panicle architecture and yield attributing traits.

	DTF	PH	PT	PL	PB	SB	SPB	SSB	PW	FG	SF	1000GW	SPY
DTF	1												
PH	0.072	1											
PT	0.015	-0.286*	1										
PL	0.025	0.498**	-0.151	1									
PB	0.205	0.071	-0.113	0.094	1								
SB	0.025	0.178	-0.166	0.197	0.475**	1							
SPB	0.040	0.180	-0.087	0.103	0.160	0.706**	1						
SSB	-0.004	-0.011	0.057	0.034	0.197	-0.546**	-0.005	1					
PW	-0.061	0.532**	-0.032	0.634**	0.134	0.285*	0.162	0.010	1				
FG	0.095	0.450**	-0.286*	0.611**	0.459**	0.317**	0.297*	0.095	0.801**	1			
SF	0.155	0.271*	-0.204	0.267*	0.240*	-0.037	0.025	0.299*	0.254*	0.672**	1		
1000GW	-0.156	0.189	-0.169	0.038	0.068	0.116	0.117	-0.063	0.252*	-0.022	-0.122	1	
SPY	-0.049	0.128	0.636**	0.206	0.194	0.139	0.214	-0.001	0.578**	0.250*	0.061	0.513**	1

** significance at 5%, *** significance at 1%

Note: PH- plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield

Table 4: Estimates of direct and indirect effects of genotypic path analysis between panicle architecture and yield attributing traits.

	DTF	PH	PT	PL	PB	SB	SPB	SSB	PW	FG	SF	1000GW
DTF	-0.007	0.004	0.014	-0.001	-0.014	0.002	-0.001	0.000	0.009	0.071	-0.017	-0.110
PH	0.000	0.059	-0.273	-0.022	-0.005	0.011	-0.003	0.000	-0.079	0.336	-0.029	0.133
PT	0.000	-0.017	0.953	0.007	0.008	-0.010	0.002	0.000	0.005	-0.214	0.022	-0.119
PL	0.000	0.029	-0.144	-0.043	-0.006	0.012	-0.002	0.000	-0.094	0.457	-0.029	0.027
PB	-0.001	0.004	-0.108	-0.004	-0.068	0.029	-0.003	0.000	-0.020	0.343	-0.026	0.048
SB	0.000	0.010	-0.158	-0.009	-0.032	0.061	-0.013	0.000	-0.042	0.237	0.004	0.082
SPB	0.000	0.011	-0.083	-0.004	-0.011	0.043	-0.019	0.000	-0.024	0.222	-0.003	0.083
SSB	0.000	-0.001	0.054	-0.001	-0.013	-0.033	0.000	0.000	-0.001	0.071	-0.032	-0.044
PW	0.000	0.031	-0.030	-0.028	-0.009	0.017	-0.003	0.000	-0.149	0.598	-0.027	0.177
FG	-0.001	0.026	-0.273	-0.027	-0.031	0.019	-0.006	0.000	-0.119	0.747	-0.072	-0.015
SF	-0.001	0.016	-0.194	-0.012	-0.016	-0.002	0.000	0.000	-0.038	0.502	-0.107	-0.086
1000GW	0.001	0.011	-0.161	-0.002	-0.005	0.007	-0.002	0.000	-0.038	-0.016	0.013	0.704

(Diagonal bolded values are direct effects)

Residual effect -0.052

Note: PH- plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Table 5: Estimates of direct and indirect effects of Phenotypic path analysis between panicle architecture and yield attributing traits.

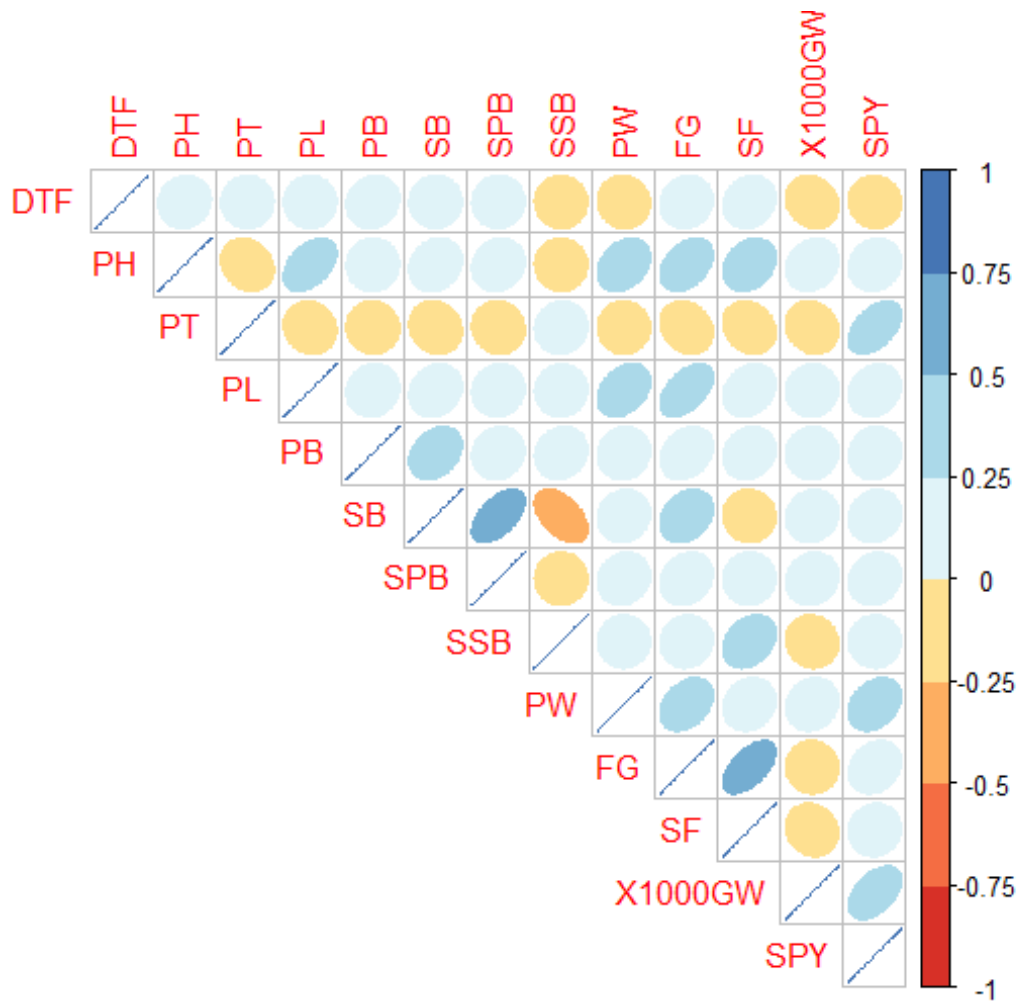
	DTF	PH	PT	PL	PB	SB	SPB	SSB	PW	FG	SF	1000GW
DTF	-0.003	-0.002	0.011	0.001	-0.004	0.002	0.001	0.000	-0.006	0.019	0.015	-0.082
PH	0.000	-0.036	-0.116	0.019	-0.001	0.011	0.004	0.000	0.036	0.078	0.026	0.099
PT	0.000	0.007	0.617	-0.004	0.001	-0.008	-0.002	0.000	-0.001	-0.042	-0.019	-0.074
PL	0.000	-0.015	-0.061	0.045	-0.002	0.011	0.002	0.000	0.041	0.106	0.024	0.021
PB	0.000	-0.001	-0.016	0.004	-0.029	0.021	0.003	0.000	0.010	0.052	0.015	0.025
SB	0.000	-0.006	-0.073	0.007	-0.009	0.070	0.016	-0.001	0.012	0.054	-0.003	0.058
SPB	0.000	-0.005	-0.039	0.003	-0.003	0.038	0.029	0.000	0.015	0.042	0.001	0.062
SSB	0.000	0.000	0.032	0.002	-0.004	-0.034	0.000	0.003	0.001	0.014	0.029	-0.037
PW	0.000	-0.011	-0.003	0.015	-0.002	0.007	0.004	0.000	0.124	0.071	0.015	0.073
FG	0.000	-0.013	-0.122	0.022	-0.007	0.018	0.006	0.000	0.041	0.213	0.059	-0.007
SF	0.000	-0.009	-0.111	0.010	-0.004	-0.002	0.000	0.001	0.017	0.122	0.104	-0.070
1000GW	0.000	-0.006	-0.083	0.002	-0.001	0.007	0.003	0.000	0.016	-0.003	-0.013	0.552

(Diagonal bolded values are direct effects)

Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

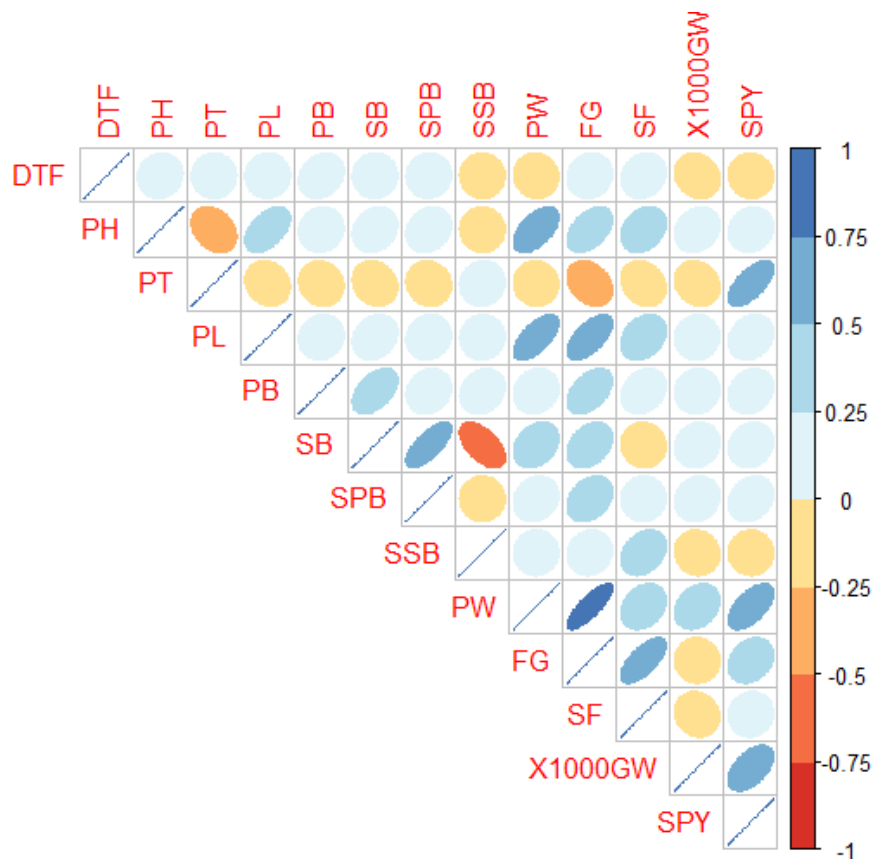


Fig. 1. Panicle architecture variations observed in A) KRG 3- Open panicle B) BABATLA- Compact panicle C) MAKOM – Intermediate panicle D) KRG 10- Intermediate panicle.



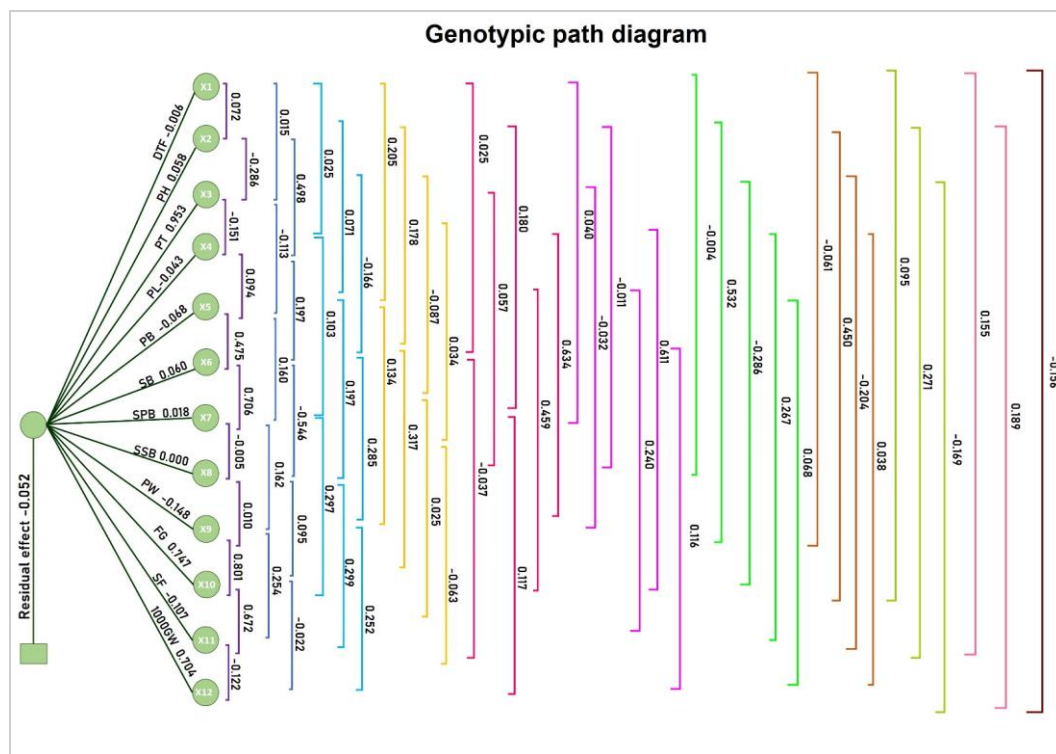
Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Fig. 2. Estimates of phenotypic correlation coefficients between panicle architecture traits and yield attributing traits.



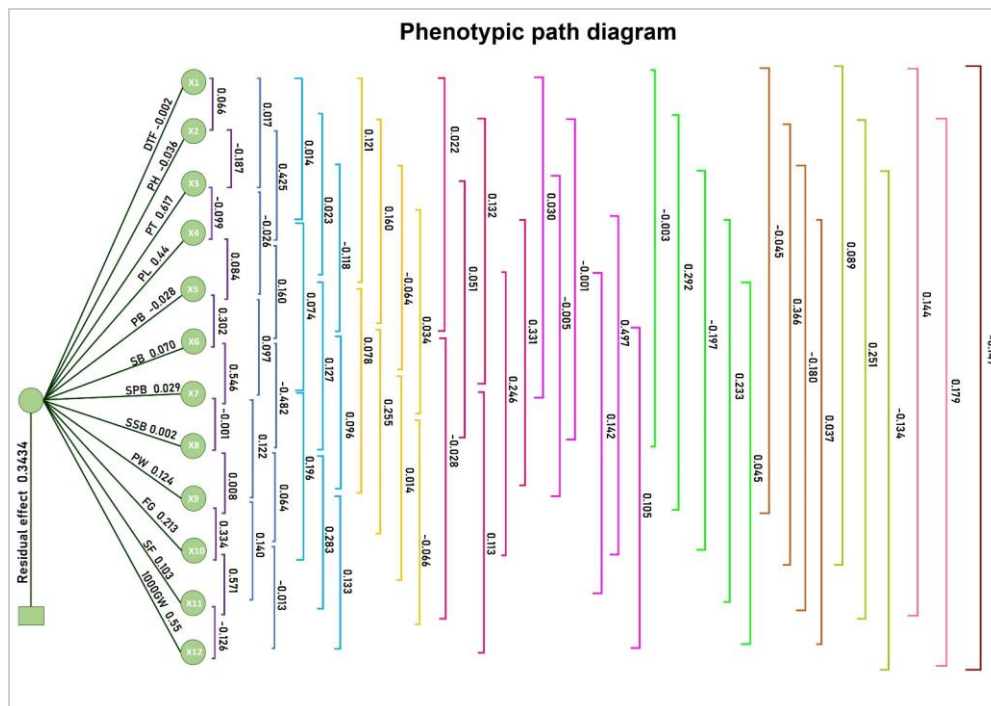
Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Fig. 3. Estimates of Genotypic correlation coefficients between panicle architecture traits and yield attributing traits.



Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Fig. 4. Genotypic path diagram displaying cause and effect relationships among quantitative traits and single plant yield.



Note: PH- Plant height, PT- Number of productive tillers, PL- Panicle length, PB- Number of primary branches, SB- Number of secondary branches, SPB- Seeds per primary branch, SSB- Seeds per secondary branch, PW- Panicle weight, FG- Number of filled grains per panicle, SF- Spikelet fertility, 1000GW- 1000 grain weight, SPY- Single plant yield.

Fig. 5. Phenotypic path diagram displaying cause and effect relationships among quantitative traits and single plant yield.

CONCLUSIONS

Concisely, the rice landraces and varieties under study have the potential to include several significant and beneficial traits. According to the path analysis and assessment of phenotypic and genotypic correlation, the most trustworthy variables for increasing rice production were the number of productive tillers, the number of filled grains per panicle, and 1000grain weight. So, when choosing to improve rice productivity, the highest priority should be given to these characteristics.

FUTURE SCOPE

Future research can focus on breeding high-yielding rice varieties by prioritizing traits such as the number of productive tillers, Number of filled grains, and 1000 grain weight. Further investigation of the underlying genes and genetic mechanisms responsible for the identified traits can provide valuable insights.

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Conflict of Interest. Authors have no conflict of interest.

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