Original Research Article

Genetic studies for selected agronomic traits in 19 maintainer genotypes of rice (*Oryza sativa* L.)

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ABSTRACT

The current study was performed at MARDI Seberang Perai, Penang, Malaysia during the Off Season 2020. This study aims to analyze genetic parameters, correlation and path coefficient for 11 agronomic traits in 19 maintainer rice genotypes.All experimental units were laid out in RCBD with three replications.Observations were recorded for days to 50% flowering, plant height, culm height, panicle length, total panicle per plant, total spikelet per panicle, spikelet fertility, thousand grain weight, grain length, grain width, and grain yield per plant.The ANOVA revealed significant differences of genotype factor for all assessed traits. The total spikelet per panicle trait exhibited the highest phenotypic and genotypic variance. Moreover, this trait simultaneously had high broad-sense heritability and high genetic advance as percent of mean. Total panicle per plant recorded the highest value of phenotypic and genotypic coefficient of variation among traits under study and were classified as high and moderate, respectively. The traits association study revealed significant positive correlation between grain yield per plant and two traits viz. total panicle per plant and spikelet fertility. Path analysis revealed a very high direct effect of plant height, culm height, and panicle length on grain yield per plant. This study contributes essential knowledge for the strategic design of effective breeding programs.

Keywords: agronomic traits, genetic parameters, correlation, path analysis

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world besides maize and wheat. It is mainly cultivated and produced in Asia, accounting for about 90% of global rice production. For instance, China was the largest producer of global milled rice (148.30 million metric tons) followed by India (120.00 million metric tons), Bangladesh (35.30 million metric tons), Indonesia (34.90 million metric tons), and Vietnam (27.10 million metric tons) for 2023/2024 [1]. Rice is also a staple food for Malaysian and plays significant roles in the national's food security, socio-economy and culture. In 2021, Malaysia produced about 1.68 million metric tons of milled rice and imported about 1.06 million metric tons of milled rice where the self-sufficient level (SSL) accounted for 61.3% [2]. In many rice growing countries, population growth, urbanization, climate change, and pest outbreaks often threaten rice production. Hybrid rice technology is one of the alternative approaches to increase rice productivity by exploiting heterosis. Hybrid rice has the potential to increase yield about 15 to 20% over the inbred varieties cultivation [3].

Evaluating hybrid parental genotypes is a prerequisite for hybrid rice breeding program. Phenotypic characterization is a simple, fast, and low-cost method that is commonly used in breeding programs by assessing important agronomic traits such as yield, maturation, and other yield contributing traits. According to Singh *et al.*[4], genetic variation is a key for genetic improvement. Thus, estimating genetic parameters to reveal the genetic structure of desirable traits in a set of germplasm collections is imperative for breeders to design the breeding program. Moreover, the information on the relationship between characters is important for selection in breeding and could be achieved through the correlation and path coefficient analysis. The first explains the relationship between two traits. The latter on the other hand, explains the direct and indirect effects of independent traits on the dependent trait. This was initially suggested by Wright [5] and discussed by Dewey and Lu [6]. Therefore, this study was carried out to analyze genetic parameters, character association, and direct and indirect effects of selected agronomic traits on yield.

2. MATERIAL AND METHODS

A total of 19 maintainer rice genotypes were used for this study (Table 1). These materials consisted of breeding lines from the Breeding Programme, Paddy and Rice Research Centre, Malaysian Agricultural Research and Development Institute (MARDI), Malaysia and varieties acquired from materials sharing program under the Hybrid Rice Development Consortium (HRDC), International Rice Research Institute (IRRI), Philippines. A pot study was carried out in a greenhouse at MARDI Seberang Perai, Penang, Malaysia (N 5° 32' 27.73''E 100° 28' 10.844'') in the Off Season 2020 (April – September 2020).

All rice entries were grown in a total of six fiberglass pots (inner dimension 2.2 m length x 1.0 m width x 0.3 m height). Each pot was filled with farm soil collected from the paddy field at MARDI Seberang Perai. All experimental units were arranged in a randomized complete block design (RCBD) with three replications. Initially, all rice entries were raised in four-gallon plastic pots containing farm soil until rice seedlings reached 21 days old (after sowing). Each entry was transplanted in a row with a single seedling. Each row consisted of five plants by which a total of 10 rows can be occupied in each experiment pot. Rice seedlings were transplanted at an 18 cm x 20 cm distance. Crop management such as nutrient supply and pest control were done according to the rice technology manual of MARDI [7].

All rice genotypes under investigation were characterized for 11 agronomic traits namely days to 50% flowering (DFF), plant height in cm (PHT), culm height in cm (CHT), panicle length in cm (PLT), total panicle per plant (TPP), total spikelet per panicle (TSP), spikelet fertility in % (SFT), thousand grain weight in gram (TGW), grain length in mm (GLT), grain width in mm (GWD), and grain yield per plant in gram (YPP)(Table 2). Data for all traits were recorded according to the Standard Evaluation System for Rice (SES) of IRRI [8]. Data were collected digitally using the Field Book software version 5.3.0 [9].

The analysis of variance (ANOVA) was performed for all 11 agronomic traits of maintainer rice genotypes using the Statistical Tool for Agricultural Research (STAR) software version 2.0.1. In addition, correlation analysis, path analysis, genetic parameters viz. phenotypic variance (V_p), genotypic variance (V_g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (H^2), genetic advance as percent of mean (GAPM) were computed using the ‘variability’ package in the R Studio software version 2023.03.0 [10]. The computation of V_p and V_g were done according to the method explained by Johnson *et al.*[11]. The calculation of PCV and GCV followed the method suggested by Burton and Vane [12]. Further, the classification of PCV and GCV were according to the following scale: 0-10% (low), 10-20% (moderate) and >20% (high) [13].

The calculation of H^2 followed the formula proposed by Allard [14] while the H^2 scale was classified as follows: <40% (low), 40-60% (moderate), and >60% (high) [15]. The GAPM value was calculated according to the method suggested by Johnson *et al.*[11]. Likewise, the classification of GAPM was based on the following scale: <10% (low), 10-20% (moderate), and >20% (high) [11]. The phenotypic correlation coefficients of selected traits were calculated according to the method suggested by Miller *et al.*[16] and the correlation significance were tested as per described by Fisher and Yates [17]. The path coefficients were computed according to the technique given by Goulden [18] and classified according to Lenka and Mishra [19] with the following categories: 0.00 – 0.09 (negligible), 0.10 – 0.19 (low), 0.20 – 0.29 (moderate), 0.30 – 0.99 (high), and >1.00 (very high).

Table 1. List of maintainer rice genotypes used in the experiment

No.	Genotype	Source	No.	Genotype	Source
1	MRC1B	MARDI	11	IR68888B	IRRI
2	MRC2B	MARDI	12	IR75596B	IRRI
3	MRC7B	MARDI	13	IR78369B	IRRI
4	MRC8B	MARDI	14	IR79125B	IRRI
5	MRC9B	MARDI	15	IR79126B	IRRI
6	MRC10B	MARDI	16	IR93559B	IRRI
7	MRC11B	MARDI	17	IR93560B	IRRI
8	0025B	MARDI	18	IR94653-3-1	IRRI
9	0047B	MARDI	19	IR94654-16-1	IRRI
10	IR58025B	IRRI			

Table 2. List of 11 agronomic traits data collectedalong with six genetic parameters estimated for the study

No.	Trait	Unit	Abbreviation
1	Days to 50% flowering (days after sowing)	Days	DFF
2	Plant height	cm	PHT
3	Culm height	cm	CHT
4	Panicle length	cm	PLT
5	Total panicle per plant	Number	TPP
6	Total spikelet per panicle	Number	TSP
7	Spikelet fertility	%	SFT
8	Thousand grain weight	g	TGW
9	Grain length	mm	GLT
10	Grain width	mm	GWD

11	Grain yield per plant	g	YPP
12	Phenotypic variance	Number	V_p
13	Genotypic variance	Number	V_g
14	Phenotypic coefficient of variation	%	PCV
15	Genotypic coefficient of variation	%	GCV
16	Broad sense-heritability	%	H^2
17	Genetic advance as percent of mean	%	GAPM

3. RESULTS AND DISCUSSION

The ANOVA revealed highly significant differences in genotype factor for all studied traits at $p<0.01$ (Table 3). This suggests the existence of genetic variability in 19 maintainer genotypes and indicates genetic improvement of studied traits is possible. This result is following previous studies [20;21;22;23;24].Estimatinggenetic parameters is essential to understand the genetic basis of plant characteristics. Moreover, the effectiveness of breeding is heavily relied on in the presence of genetic diversity.Mean, value range and genetic parameters of studied traits are presented in Table 4.

Table 3. Analysis of variance on 11 agronomic traits of 19 maintainer rice genotypes

Trait	CV (%)	Mean square		
		Replication(df = 2)	**Genotype(df = 18)**	**Error(df = 36)**
DFF	2.39	0.3684	343.2593**	2.7943
PHT	4.57	27.9123	155.3782**	17.4864
CHT	6.02	42.3860	104.6433**	15.7193
PLT	6.76	1.5965	22.5283**	3.0224
TPP	11.71	5.5439	26.1949**	3.2476
TSP	7.61	8.8947	1677.4776**	145.6355
SFT	6.38	1.6260	120.2253**	25.0326
TGW	7.46	2.1528	22.0749**	2.9398
GLT	2.28	0.0058	0.3120**	0.0244
GWD	2.77	0.0026	0.0369**	0.0028
YPP	8.16	5.1891	16.8890**	2.7398

***- $P<0.01$, CV - coefficient of variation, df – degree of freedom, DFF - days to 50% flowering (days after sowing), PHT - plant height (cm), CHT - culm height (cm), PLT - panicle length (cm), TPP - total panicle per plant, TSP - total spikelet per panicle, SFT - spikelet fertility (%), TGW – thousand grain weight (g), GLT - grain length (mm), GWD - grain width (mm), YPP - grain yield per plant (g)*

V_p values for all traits ranged from 0.014 (GWD) to 656.25 (TSP), while V_g values ranged from 0.012 (GWD) to 510.61 (TSP). This result showed that TSP and GWD characters accounted for the highest and the lowest variance value respectively. This suggests that improvingTSP trait through phenotypic selection is likely the most favorable compared to other studied traits. This result is following previous studies wherein TSP trait was among the highest recorded V_p and V_g[25;26;27;28;29]. PCV values for all traits were categorized from low to high. Result showed that TPP was the only trait with high PCV value (21.45%) while some traits were categorized as moderate PCV which includes TSP (16.15%), DFF (15.40%), YPP (13.46%), TGW (13.28%), PLT (12.00%), and CHT (10.23%). In addition, low PCV was recorded in SFT (9.61%), PH (8.70%), GWD (6.24%), and GLT (5.06%). For GCV, all traits were categorized from low to moderate. Traits recorded moderate GCV were TPP (17.98%), DFF (15.22%), TSP (14.24%), TGW (10.99%), and YPP (10.71%). Low GCV on the other hand, was recorded by PLT (9.91%), CHT (8.27%), PH (7.41%), SFT (7.19%), GWD (5.59%), and GLT (4.52%). It was found that GCV for all traits was slightly lower than their respective PCV, indicating less environmental influence on the expression of the traits. This suggests the improvement of these traits through phenotypic selection under similar environment and population structure will be likely effective. Several authors reported similar results wherein most agronomic traits recorded GCV values slightly lower than PCV values[30;31;32;33;34;35].

Table 4. Mean, value range and genetic parameters of 11 agronomic traits of rice genotypes

Trait	**Mean**	**Range**		**V_p**	**V_g**	**PCV (%)**	**GCV (%)**	**H^2 (%)**	**GAPM (%)**
		Min	**Max**						
DFF	70	47	81	116.28	113.49	15.40	15.22	97.60	30.97
PH	91.5	68.0	108.0	63.45	45.96	8.70	7.41	72.44	12.98
CHT	65.8	51.0	81.0	45.36	29.64	10.23	8.27	65.35	13.77
PLT	25.7	17.0	31.0	9.52	6.50	12.00	9.91	68.27	16.87
TPP	15	8	23	10.90	7.65	21.45	17.98	70.20	31.02
TSP	159	111	221	656.25	510.61	16.15	14.24	77.81	25.88
SFT	78.4	65.3	92.8	56.81	31.80	9.61	7.19	55.97	11.08
TGW	23.0	15.3	27.8	9.32	6.38	13.28	10.99	68.45	18.73
GLT	6.86	6.15	7.50	0.12	0.10	5.06	4.52	79.78	8.31
GWD	1.92	1.57	2.17	0.014	0.012	6.24	5.59	80.42	10.33
YPP	20.29	13.82	24.69	7.46	4.72	13.46	10.71	63.30	17.55

V_p - phenotypic variance, V_g genotypic variance, PCV - phenotypic coefficient of variation, GCV - genotypic coefficient of variation, H^2 - broad-sense heritability, GAPM - genetic

advance as percent of mean, DFF - days to 50% flowering (days after sowing), PHT - plant height (cm), CHT - culm height (cm), PLT - panicle length (cm), TPP - total panicle per plant, TSP - total spikelet per panicle, SFT - spikelet fertility (%), TGW – thousand grain weight (g), GLT - grain length (mm), GWD - grain width (mm), YPP - grain yield per plant (g)

All traits were classified as high H^2 except for SFT (55.97%). The highest heritability was observed in the DFF trait (97.60%), followed by GWD (80.42%), and GLT (79.78%). Similar results on high H^2 in DFF trait were reported [20;36;37;38;39;40;41] and high H^2 in GLT and GWD traits were reported by several authors [42;43;44;45;46;47].High heritability combined with high genetic advance may indicate the role of additive gene action governing a trait, whereas if a trait is controlled by non-additive gene action, it may give high heritability but low genetic advance as suggested by Panse [48].The trait with high heritability and high genetic advance indicates that such trait could be improved through direct selection. High H^2 combined with high GAPM were observed in some traits viz. DFF (H^2 = 97.60%, GAPM = 30.97%), TPP (H^2 = 70.20%, GAPM = 31.02%), and TSP (H^2 = 77.81%, GAPM = 25.88%). This suggests that these traits could be improved through hybridization followed by selection. In addition, this approach could be deployed to improve hybrid parental lines such as maintainer and restorer lines.

Table 5. Estimates of phenotypic correlations among 11 agronomic traits in rice genotypes

Trait	DFF	PHT	CHT	PLT	TPP	TSP	SFT	TGW	GLT	GWD	YPP
DFF	1.0000**	0.4477**	0.2482	0.6141**	-0.4722**	0.4100**	-0.2580	0.2600	0.1540	0.2699*	-0.4708**
PHT		1.0000**	0.9253**	0.5616**	-0.0637	0.1358	-0.2683*	-0.1156	0.0242	-0.0665	-0.3876**
CHT			1.0000**	0.2060	0.0446	0.0348	-0.2344	-0.2322	-0.1358	-0.0764	-0.3785**
PLT				1.0000**	-0.2618*	0.2745*	-0.1809	0.2083	0.3588**	-0.0049	-0.1746
TPP					1.0000**	-0.4105**	0.2393	-0.1888	-0.0508	-0.1517	0.2964*
TSP						1.0000**	-0.4603**	-0.1067	-0.2458	-0.1403	-0.2912*
SFT							1.0000**	-0.0420	0.0063	0.1564	0.4459**
TGW								1.0000**	0.7133**	0.7173**	0.0343
GLT									1.0000**	0.2959*	0.1578
GWD										1.0000**	0.0384
YPP											1.0000**

** - indicates significant at P<0.05, ** - indicates significant at P<0.01, DFF - days to 50% flowering (days after sowing), PHT - plant height (cm), CHT - culm height (cm), PLT - panicle length (cm), TPP - total panicle per plant, TSP - total spikelet per panicle, SFT - spikelet fertility (%), TGW – thousand grain weight (g), GLT - grain length (mm), GWD - grain width (mm), YPP - grain yield per plant (g)*

Table 6. Estimates of phenotypic path coefficient of direct and indirect effects of 10 agronomic traits on grain yield per plant

Trait	DFF	PHT	CHT	PLT	TPP	TSP	SFT	TGW	GLT	GWD
DFF	**-0.4872**	-0.9760	0.3955	0.6254	-0.0507	0.0480	-0.0678	-0.0807	0.0479	0.0750
PHT	-0.2181	**-2.1801**	1.4750	0.5720	-0.0068	0.0159	-0.0705	0.0359	0.0076	-0.0184
CHT	-0.1209	-2.0174	**1.5939**	0.2098	0.0048	0.0041	-0.0616	0.0721	-0.0422	-0.0210
PLT	-0.2992	-1.2245	0.3284	**1.0183**	-0.0281	0.0321	-0.0476	-0.0647	0.1115	-0.0008
TPP	0.2301	0.1389	0.0711	-0.2666	**0.1074**	-0.0480	0.0629	0.0586	-0.0158	-0.0423
TSP	-0.1998	-0.2961	0.0555	0.2795	-0.0441	**0.1170**	-0.1210	0.0331	-0.0764	-0.0390
SFT	0.1257	0.5849	-0.3736	-0.1842	0.0257	-0.0538	**0.2628**	0.0130	0.0019	0.0435
TGW	-0.1267	0.2520	-0.3701	0.2122	-0.0203	-0.0125	-0.0110	**-0.3105**	0.2216	0.1995
GLT	-0.0751	-0.0530	-0.2165	0.3655	-0.0054	-0.0288	0.0016	-0.2215	**0.3101**	0.0805
GWD	-0.1315	0.1441	-0.1207	-0.0028	-0.0163	-0.0164	0.0411	-0.2228	0.0899	**0.2722**
Residual effect = 0.5433										

Bold and diagonal values are direct effects, off diagonal values are indirect effects, DFF - days to 50% flowering (days after sowing), PHT - plant height (cm), CHT - culm height (cm), PLT - panicle length (cm), TPP - total panicle per plant, TSP - total spikelet per panicle, SFT - spikelet fertility (%), TGW – thousand grain weight (g), GLT - grain length (mm), GWD - grain width (mm), YPP - grain yield per plant (g)

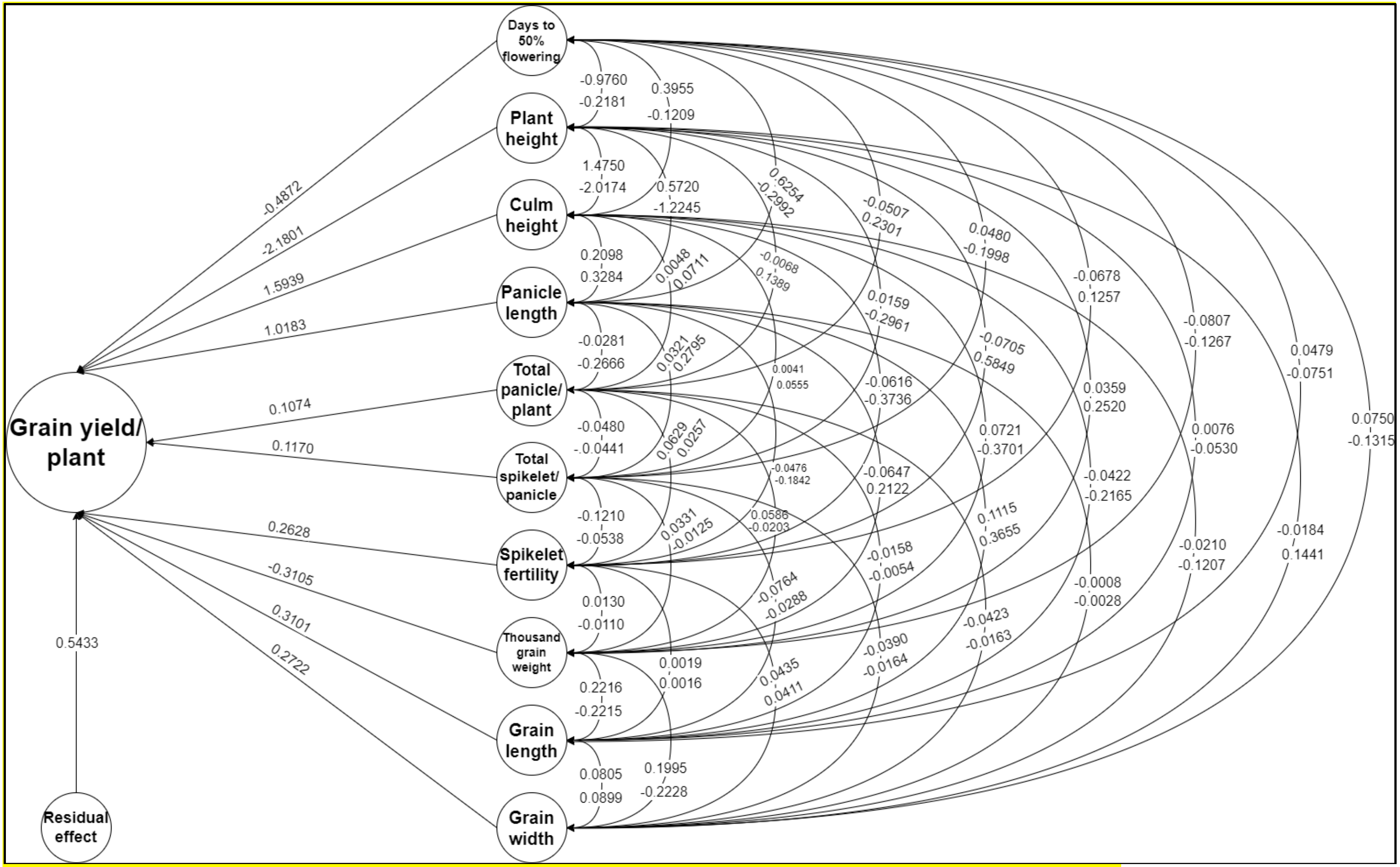

Figure 1. Phenotypic path diagram indicating direct and indirect effect 10 agronomic traits on grain yield per plant

This result conforms with previous studies for DFF [49;50],TPP [51;52;53;54], and TSP [36;53;55].This study showed that high H^2 coupled with low GAPM were observed in GLT (H^2 = 79.78%, GAPM = 8.31%). This suggests that the trait may be controlled by non-additive gene action, and improving the GLT trait through heterosis breeding could be rewarding.This result is in accordance with previous studies [56;57;58] while other studies reported GLT trait had high H^2 and high to moderate GAPM [47;59;60;61].

The phenotypic correlation coefficients among 11 agronomic traits are presented in Table 5. Significant correlations with positive magnitude were observed between YPP and two traits; TPP (r_p = 0.2964) and SFT (r_p = 0.4459). In addition, significant correlations with negative magnitude were observed between YPP and four traits viz. DFF (r_p = -0.4708), PHT (r_p = -0.3876), CHT (r_p = -0.3785), and TSP (r_p = -0.2912). This suggests that the improvement of TPP and SFT traits through selection will result in the grain yield per plant.This result is in accordance with previous studies which reported on the significant positive correlation of TPP [62;63;64] and SFT [64;65;66] with yield.

The estimates of phenotypic path coefficient of direct and indirect effect of 10 agronomic traits on YPP are presented in Table 6 and Figure 1. The estimated residual effect was 0.5433 indicated that45.7%of the variability in grain yield per plant was contributed by 10 agronomic traits under study while 54.3% due to environment factors.This result is in accordance with previous studieswherein 40-50% the variability in grain yieldconferred by yield contributing traits[67;68;69;70;71].Moreover, path analysis revealed that a very high direct effect of agronomic traits on YPP which were represented by PHT (-2.1801), CHT (1.5939), and PLT (1.0183). In addition, a high direct effect of agronomic traits on YPP were observed in DFF (-0.4872), TGW (-0.3105), and GLT (0.3101). This suggests that CHT and PLT traits could be improved through selection to improve grain yield per plant.The indirect effects of DFF (0.3955), PHT (1.4750) and PLT (0.3284) on YPP through CHT showed high to very high values with positive magnitude. In addition, SFT (-0.3736) and TGW (-0.3701) exhibited high indirect effects on YPP through CHT with negative magnitude. This suggests the possibility of indirect improvement of grain yield per plant via the path of CHT improvement through selection of DFF, PHT, and PLT traits.Previous studies reported very high positive direct effect on yield observed in SFT and TSP [53] and very high negative direct effectobserved in DFF and GLT [53;72]. In addition, high positive direct effecton yield observed in GWD, TGW, SFT, DFF, and PHT [36;20;54;72]. PHT, PLT, and TGWcontributed very high positive indirect effect on yield via TSP anda very high negative indirect effect on yield via TSP observed in TPP [53].

4. CONCLUSION

In conclusion, assessment of 19 maintainer rice genotypes has provided valuable insights into genetic parameters and trait associations. This study identified a few significant traits which are likely useful for improvement through selection such as total spikelet per panicle and total panicle per plant. It also emphasizes the importance of total panicle per plant and spikelet fertility traits for improvement of grain yield per plant. Direct selection on culm height and panicle length will likely improve grain yield per plant. Moreover, improvement of culm height by selecting days to 50% flowering, plant height, and panicle length could indirectly improve grain yield per plant. This study contributes essential knowledge for the strategic design of effective breeding programs to enhance rice productivity.Furthermore, the highlighted traits above will be consideredas selection criteriafor futuredevelopment and improvementofmaintainer lines in hybrid rice breeding.

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