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Genetic Variability, Correlation and Path Analysis of Different Hill-Rice (*Oryza Sativa*) Genotypes

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Abstract- Rice (Oryza sativa), a staple food crop is central to the lives of people around the world. Present production of rice will not suffice rapidly increasing population as the area for production is decreasing. This necessitate to increase the productivity of rice through crop improvement. In order to identify suitable traits that contribute for crop improvement through the estimation of genetic variability, correlation and path coefficient analysis an experiment on eleven rice genotypes was conducted in randomized complete block design (RCBD) with three replications under irrigated condition at Institute of Agriculture and Animal science, Lamjung. Analysis of Variance revealed that genotypes under study differed significantly for all the traits under study which implies that genotypes constitute a pool of germplasm with adequate variability. The phenotypic coefficient of variation (PCV) values were higher than genotypic coefficient of variation (GCV), revealing lower influence of environment in character expression. High heritability coupled with high genetic advance and moderate GCV were observed for leaf area, number of effective tillers per m^2 and days to 50% flowering.

Keywords: correlation, GCV, genetic advance, heritability, path analysis.

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GENETICVARIABILITY,CORRELATIONANDPATHANALYSISOFDIFFERENTHILL-RICEORYZASATIVAGENOTYPES

Strictly as per the compliance and regulations of:

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Abstract- Rice (*Oryza sativa*), a staple food crop is central to the lives of people around the world. Present production of rice will not suffice rapidly increasing population as the area for production is decreasing. This necessitate to increase the productivity of rice through crop improvement. In order to identify suitable traits that contribute for crop improvement through the estimation of genetic variability, correlation and path coefficient analysis an experiment on eleven rice genotypes was conducted in randomized complete block design (RCBD) with three replications under irrigated condition at Institute of Agriculture and Animal science, Lamjung. Analysis of Variance revealed that genotypes under study differed significantly for all the traits under study which implies that genotypes constitute a pool of germplasm with adequate variability. The phenotypic coefficient of variation (PCV) values were higher than genotypic coefficient of variation (GCV), revealing lower influence of environment in character expression. High heritability coupled with high genetic advance and moderate GCV were observed for leaf area, number of effective tillers per m^2 and days to 50% flowering. Number of effective tillers per m^2 and panicle length had significant positive correlation with grain yield. The result of path coefficient analysis revealed that panicle length exhibited maximum positive direct effect on grain yield followed by number of effective tillers per m^2, days to 50% flowering and 1000-grain weight whereas number of un-effective tillers per m^2 exhibited maximum negative direct effect on grain yield. Therefore, result suggest these traits can be used for grain yield selection and improvement.

Keywords: correlation, GCV, genetic advance, heritability, path analysis.

I. INTRODUCTION

Rice (Oryza sativa L.) is an important annual, self-pollinated, diploid (2n=2x=24) cereal crop species. Rice is mainly grown on tropics, sub-tropics, semi-arid tropics, and temperate regions of the world. Globally, rice is grown on 163 million hectares in over hundred countries that produce more than 715 million tons of paddy rice annually (FAOSTAT, 2017). In Nepal, according to MoAD (2015/16) the rice crop was grown in 1.36 million hectares with the production of 4.29 million metric tons and productivity 3.15 tons/ha. Present production trend of rice will not be able to feed increasing population in depleting land resource availability. Therefore, there is a need for increase in production through increase in productivity which could be obtained through genetic improvement.

a) *Objectives*

- To access the extent of correlation of traits with grain yield.
- To estimate direct and indirect effect of traits under study on grain yield.
- To study the genetic divergence in rice genotypes.

b) *Hypothesis testing*

- *Null hypothesis:* Rice genotypes give similar performance.
- *Alternative hypothesis:* Rice genotypes show significant difference in performance.

II. MATERIALS AND METHODS

The experiment was conducted at the field of Institute of agriculture and Animal Science, Lamjung Campus during kharif season under irrigated condition. For the experiment, 11 genotypes were studied which were laid in Randomized Complete Block Design (RCBD) with 3 replications. Pokhareli jethobudo was used as standard check against other 10 varieties. Seedling were transplanted after 25 days of seedling establishment in the plot of size 2 m^2 and plant geometry 20×20 cm. Fertilizers were applied as per general recommended dose for irrigated condition i.e 100:30:30 Kg/ha NPK where half dose of nitrogen, full dose of phosphorus and full dose of potash were applied as basal dose and split dose of nitrogen were applied after two weeding operation (i.e. 25 and 50 DAT).

Table 1: Genotypes used in the experiment

Sr. No.	Treatment	Genotypes
1	T_1	khumal-9
2	T_2	NR11050-B-B-B-B-1
3	T_3	NR10676-B-5-3
4	T_4	NR11153-B-B-18
5	T_5	NR11100-B-B-15-2-1
6	T_6	khumal-2
7	T_7	khumal-11
8	T_8	NR11105-B-B1-16-2
9	T_9	Chainung-242
10	T_{10}	khumal-6
11	T_{11}	Jethobudho

Most of the data were recorded from five randomly selected hills in each plot whose mean values

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were used for data analysis. Following characters were studied: plant height, leaf area, chlorophyll content, number of effective tillers/m^2, number of un-effective tillers/m^2, days to 50% flowering, panicle length, filled grains per panicle, grain yield, straw yield, 1000-grain weight. All data obtained for each character were subjected to analysis of variance. Various genetic parameters such as genetic variance, phenotypic variance, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H), genetic advance (GA) and genetic advance as percentage of mean (GAM) were computed. Relationship between yield and yield components were analyzed using simple correlation analysis (Weber and Moorthy, 1952) and path analysis (Dubey and Lu, 1959). Data were entered in Microsoft-excel and analyzed via Microsoft-excel, R-packages and SPSS 16.0.

III. RESULTS AND DISCUSSION

a) *Analysis of variance*

The analysis of variance exhibited the presence of significant difference among the tested genotypes for all the characters indicting the existence of variability.

Table 2: Mean performance of hill rice genotypes.

Genotype	Plant Height	Leaf Area	Chlorophyll Content	Effective Tillers	Un-effective Tillers	Panicle Length
01.khumal-9	144.88^{ab}	41.97^{b}	34.50^{ab}	180.00^{f}	30.00^{bc}	24.89^{de}
02.NR11050-B-B-B-B-1	150.78^{ab}	52.19^{a}	34.25^{ab}	220.00^{e}	76.67^{a}	31.26^{a}
03.NR10676-B-5-3	149.11^{ab}	32.47^{cd}	33.42^{b}	310.00^{a}	31.67^{bc}	25.32^{cde}
04.NR11153-B-B-18	148.75^{ab}	32.53^{cd}	33.32^{b}	226.67^{de}	40.00^{bc}	26.15^{cd}
05.NR11100-B-B-15-2-1	147.63^{ab}	42.16^{b}	33.30^{b}	250.00^{c}	38.33^{bc}	27.96^{b}
06.khumal-2	146.29^{ab}	41.85^{b}	30.15^{c}	243.33^{cd}	40.00^{bc}	26.25^{c}
07.khumal-11	105.99^{c}	28.86^{d}	36.85^{a}	191.67^{f}	56.00^{ab}	22.22^{g}
08.NR11105-B-B1-16-2	142.74^{b}	32.75^{cd}	33.49^{b}	178.33^{f}	11.67^{c}	24.47^{ef}
09.Chainung-242	114.33^{c}	28.56^{d}	36.39^{a}	171.67^{f}	53.33^{ab}	23.36^{fg}
10.khumal-6	144.33^{b}	28.76^{d}	35.18^{ab}	280.00^{b}	51.67^{ab}	28.33^{b}
11.Jethobudho	162.55^{a}	36.60^{bc}	34.31^{ab}	215.00^{e}	63.33^{ab}	25.67^{cde}
F-test	***	***	**	***	*	***
LSD (5%)	17.29	6.78	2.52	20.05	30.93	1.22
CV%	7.17%	10.99%	4.34%	5.25%	40.55%	2.74%
Grand Mean	141.58	36.25	34.11	224.24	44.79	25.62

Significance codes: 0 ‘***’, 0.001 ‘**’, 0.01 ‘*

Table 3: Mean performance of hill rice genotypes

Genotype	Flowering	TGW	Filled Grain	Straw Yield	Grain Yield	Harvest Index
01.khumal-9	91.33^{efg}	29.23^{a}	109.33^{c}	6888.89^{ab}	5250.00^{bc}	43.68^{bc}
02.NR11050-B-B-B-B-1	103.33^{b}	22.57^{cde}	162.20^{a}	5938.89^{ab}	5651.66^{abc}	48.61^{bc}
03.NR10676-B-5-3	94.33^{cde}	21.00^{e}	132.60^{bc}	7029.17^{a}	6056.25^{ab}	46.13^{bc}
04.NR11153-B-B-18	94.00^{cde}	26.43^{abc}	142.07^{ab}	6583.33^{ab}	5683.33^{abc}	46.28^{bc}
05.NR11100-B-B-15-2-1	96.67^{cd}	25.30^{abcd}	133.20^{bc}	6429.17^{ab}	6799.17^{a}	51.30^{b}
06.khumal-2	94.00^{de}	25.47^{abc}	124.53^{bc}	6877.78^{ab}	6129.17^{ab}	47.17^{bc}
07.khumal-11	88.33^{fg}	27.53^{ab}	130.20^{bc}	3383.33^{c}	5005.55^{bc}	59.50^{a}
08.NR11105-B-B1-16-2	98.33^{c}	21.13^{de}	164.33^{a}	5894.44^{ab}	5037.92^{bc}	46.01^{bc}
09.Chainung-242	87.00^{g}	28.07^{ab}	114.40^{c}	5645.83^{b}	4258.33^{c}	43.07^{c}
10.khumal-6	92.33^{def}	24.07^{bcde}	123.20^{bc}	6877.78^{ab}	6337.78^{b}	47.73^{bc}
11.Jethobudho	134.33^{a}	20.87^{e}	115.27^{bc}	6527.78^{ab}	5065.28^{bc}	43.56^{bc}
F-test	***	**	**	***	*	**
LSD (5%)	3.99	4.02	23.91	1160.85	1316.4	6.92
CV%	2.40%	9.56%	10.64%	11.01%	13.87%	9.52%
Grand Mean	97.64	24.7	131.94	6188.763	5570.404	43.31

Significance codes: 0 ‘***’, 0.001 ‘**’, 0.01 ‘*’

b) *Genetic variabiltiy*

Estimates of phenotypic variance (σ^2p) and Genotypic variance (σ^2g), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA) and genetic advance as a percentage of mean (GAM) are shown in Table.

Table 4: Estimates of variability, heritability, genetic advance and genetic advance as a percentage of mean

Traits	$\sigma^{2}g$	$\sigma^{2}p$	GCV	PCV	h^2	GA	GAM
PH	237.83	340.93	10.89	13.04	0.70	26.48	18.71
LA	51.05	66.91	19.71	22.57	0.76	12.86	35.47
CHL	2.46	4.65	4.60	6.32	0.53	2.35	6.89
EFF	1902.67	2041.67	19.45	20.15	0.93	86.74	38.68
UNEFF	208.23	538.03	32.22	51.79	0.39	18.49	41.29
PL	6.07	6.58	9.48	9.87	0.92	4.87	18.76
DF	166.70	172.20	13.22	13.44	0.97	26.17	26.80
FG	264.40	461.40	12.32	16.28	0.57	25.36	19.22
TGW	7.13	12.71	10.81	14.44	0.56	4.12	16.69
SY	641874.33	1392033.33	13.57	19.98	0.46	1120.71	18.98
GY	335694.00	933095.00	10.40	17.34	0.36	715.89	12.85

PH=Plant Height, LA=Leaf Area, CHL= SPAD reading, EFF= Effective numbers of tillers m^2, UNEFF=Number of un-effective tillers m^2, PL= Panicle Length, DF= Days to 50% flowering, SY= Straw yield, TGW= 1000-Grain Weight, FG=Number of Filled Grains per Panicle, GY=Grain Yield

The GCV value were ranged from 4.60 for chlorophyll content to 32.22 for un-effective tillers per m^2 whereas values for PCV ranged from 6.32 for chlorophyll content to 51.79 for number of un-effective tillers per m^2. The values of PCV were higher than the values of GCV indicating the influence of environment in the expression of traits. Number of un-effective tillers per m^2 was found to have high GCV and plant height, leaf area, effective number of tillers per m^2, days to 50% flowering, number of filled grains per panicle, 1000-grain weight, straw yield and grain yield were found to have moderate GCV which signifies that the direct selection through phenotype observation is effective. Chlorophyll content and panicle length were found to have the low GCV whose direct selection may not be rewarding. Similar results were obtained by Rashid et al. (2017), Umesh et al. (2015), Dhanwani et al. (2013), Sumanth et al. (2017), Islam et al. (2017). The result for grain yield was supported by Binda et al. (2017) and for number of un-effective tiller per m^2 by Limbani et. Al (2017).

The heritability estimates vary from 0.97 to 0.36 for days to 50% flowering and grain yield respectively. According to Robinson et al. (1949) the heritability estimates were categorized as low medium and high. Among the traits studied grain, chlorophyll content, number of un-effective tiller per m^2, 1000-grain weight, number of filled grains per panicle and straw yield showed moderate heritability whereas plant height, leaf area, panicle length, days to 50% flowering density showed high heritability. Above results were in agreement with results obtained by Alam et al. (2014), Konate et al (2016) and Limbani et al. (2017).

GAM ranges from 38.68 for effective number pf tillers per m^2 to 6.89 for chlorophyll content. GAM was also categorized to low, medium and high where chlorophyll content was found to have low GAM indicating non-additive gene action and selection for this trait is not rewarded. Plant height, panicle length, filled grains per panicle, 1000-grain weight, harvest index, straw yield and grain yield, leaf area, number of un-effective tiller per m^2, number of effective tillers per m^2, days to 50% flowering were found to have moderate to high GAM suggesting additive gene action whose selection will be beneficial for crop improvement. The result was similar to the finding of Akinwale et al. (2011), Binda et al. (2017), Limbani et al. (2017) and Dhanwani et al. (2013).

c) *Correlation coefficient analysis*

The correlation coefficient among yield and yield components are presented in the table.

Table 5: Correlation between yield and yield component

	PH	LA	CHL	EFF	UNEFF	PL	DF	SY	TGW	FG	GY
PH	1										
LA	0.507	1									
CHL	-.628*	-0.45	1								
EFF	0.443	-0.003	-0.379	1							
UNEFF	-0.072	0.26	0.368	0.005	1						
PL	.626*	.685*	-0.334	0.444	0.39	1					
DF	.623*	0.262	-0.129	0.011	0.339	0.226	1				
SY	.801**	0.276	-.621*	0.504	-0.277	0.463	0.205	1			
TGW	-0.59	-0.105	0.287	-0.438	0.002	-0.353	-.617*	-0.273	1		
FG	0.153	0.273	-0.191	.00031	-0.106	0.384	-0.016	-0.161	-0.49	1	
GY	0.506	0.324	-0.553	.797**	-0.109	.623*	-0.069	0.487	-0.216	0.128	1

PH=Plant Height, LA=Leaf Area, CHL= SPAD reading, EFF= Effective numbers of tillers m^2, UNEFF=Number of un-effective tillers m^2, PL= Panicle Length, DF= Days to 50% flowering, SY= Straw yield, TGW= 1000-Grain Weight, FG=Number of Filled Grains per Panicle, GY=Grain Yield

'*' Correlation is significant at 0.05 level (2-tailed)

'**' Correlation is significant at 0.01 (2-tailed)

The result showed that effective number of tillers per m^2 (.797**) and panicle length (.623*) had a significant and positive correlation with grain yield. Other traits showed non-significant correlation with the grain yield. Plant height (0.506), leaf area (0.324), straw yield (0.487), numbers of filled per panicle (0.128), showed a positive and non-significant correlation with grain yield. Chlorophyll content (-0.553), number of un-effective/m^2(-0.109) days to 50% flowering (-0.069) and 1000-grain weight (-0.216) showed non-significant and negative correlation with grain yield. This result is in agreement with the results of Ekka et al. (2011), Babu et al. (2012), Konate et al. (2016), Abarshahr et al. (2011) and Ukaoma et al. (2013).

d) *Path coefficient analysis*

The path coefficient analysis for grain yield is presented in the table.

Table 6: Path coefficient analysis of yield attributing traits of hill rice genotypes

	PH	LA	CHL	EFF	UNEFF	PL	DF	SY	TGW	FG
PH	*-0.416*	-0.211	0.261	-0.184	0.030	-0.260	-0.259	-0.333	0.245	-0.064
LA	-0.024	*-0.048*	0.022	0.000	-0.012	-0.033	-0.013	-0.013	0.005	-0.013
CHL	0.142	0.102	*-0.226*	0.086	-0.083	0.076	0.029	0.140	-0.065	0.043
EFF	0.417	-0.003	-0.356	*0.942*	0.005	0.418	0.010	0.475	-0.413	0.000
UNEFF	0.069	-0.250	-0.353	-0.005	*-0.959*	-0.374	-0.325	0.266	-0.002	0.101
PL	0.758	0.830	-0.405	0.538	0.473	*1.211*	0.274	0.561	-0.427	0.465
DF	0.452	0.190	-0.094	0.008	0.246	0.164	*0.726*	0.149	-0.448	-0.012
SY	-0.493	-0.170	0.383	-0.311	0.171	-0.286	-0.126	*-0.616*	0.168	0.099
TGW	-0.372	-0.066	0.181	-0.276	0.001	-0.222	-0.389	-0.172	*0.630*	-0.309
FG	-0.028	-0.050	0.035	-0.000057	0.019	-0.071	0.003	0.030	0.090	*-0.184*
	0.506	0.324	-0.553	0.797	-0.109	0.623	-0.069	0.487	-0.216	0.128

PH=Plant Height, LA=Leaf Area, CHL= SPAD reading, EFF= Effective numbers of tillers m^2, UNEFF=Number of un-effective tillers m^2, PL= Panicle Length, DF= Days to 50% flowering, SY= Straw yield, TGW= 1000-Grain Weight, FG=Number of Filled Grains per Panicle, GY=Grain Yield

The result showed that panicle length had highest, positive and direct effect on grain yield followed by number of effective tillers per m^2, days to 50% flowering and thousand grain weight. Plant height, leaf area, chlorophyll content, straw yield, filled grains per panicle showed negative direct effect on grain yield. As number of effective tillers per m^2 and panicle length had significant positive correlation with grain yield along with high positive and direct effect indicating that the selection for these traits was likely to bring about an overall improvement in grain yield directly. Although 1000-grain weight, days to 50% flowering had negative correlation with grain yield but they exhibited positive effect directly to the grain yield. Highest indirect effect of leaf area was observed via panicle length followed by effective tiller via panicle length. The results were in confirmation with Ekka et al. (2011), Archana et al. (2018), Ashok et al. (2016), Gayathri and Padmalatha (2018), Basavaraja et al. (2013) and Rahman et al. (2014).

IV. CONCLUSION

Grain yield has lower heritability than other yield attributing traits. So, direct selection for grain yield will not be effective. As, correlation of grain yield with effective numbers of tillers/m^2 and panicle length was observed significantly positive and exerted high positive direct effect on grain yield they could be used as selection criteria for improvement of grain yield. NR10676-B-5-3 was found to be best for grain yield and yield attributing traits. Therefore, this genotype can be subjected to further trial.

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