



GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS OF DIFFERENT HILL-RICE (*ORYZA SATIVA*) GENOTYPES

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INTRODUCTION

Rice (*Oryza sativa* L.) is an annual, self-pollinated, diploid ($2n=2x=24$) cereal crop species. Rice inhabits mainly on tropics, sub-tropics, semi-arid tropics, and temperate regions of the world. Globally, rice covers million hectares in over a 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. The present production trend of rice will not be able to feed an increasing population in depleting land resource availability. Therefore, there is a need for an increase in production through increase in productivity which could be obtained through genetic improvement.

Objectives

- To access the extent of correlation of traits with grain yield.
- To estimate the direct and indirect effect of traits that we are going to study.
- To study the genetic divergence in rice genotypes.

Hypothesis testing

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

MATERIALS AND METHODS

We conducted an experiment in the field of the Institute of Agriculture and Animal Science, Lamjung Campus during Kharif season under irrigated condition. For the research, 11 genotypes were studied, which were laid in Randomized Complete Block Design (RCBD) with three replications. We used Pokhareli jethobudo as a standard check against other ten varieties. Seedlings were transplanted after 25 days of seedling establishment in the plot of size 2 m² and plant geometry 20×20 cm. We applied fertilizers as per generally recommended dose for irrigated condition i.e. 100:30:30 Kg/ha NPK where a half dose of nitrogen, a full dose of phosphorus and a complete dose of potash was applied as basal dose and a split dose of nitrogen were applied after two weeding operation (i.e. 25 and 50 DAT).

Table 1: Genotypes used in the experiment

S.N	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 were used for data analysis. We studied the following characters: plant height, leaf area, chlorophyll content, number of effective tillers/m², number of un-effective tillers/m², days to 50% flowering, panicle length, filled grains per panicle, grain yield, straw yield, 1000-grain weight. We conducted analysis of variance for all the available data set. We computed 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 a percentage of the mean (GAM). We analyzed the relationship between yield and yield components using simple correlation analysis (Weber and Moorthy, 1952) and path analysis (Dubey and Lu, 1959). We entered data in Microsoft-excel and analyzed via Microsoft-excel, R-packages and SPSS 16.0.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance exhibited the presence of a significant difference among the tested genotypes for all the characters, indicating 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 '*'

Table3: 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 '*'

Genetic variability

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

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

Traits	σ^2_g	σ^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
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PH=Plant Height, LA=Leaf Area, CHL= SPAD reading, EFF= Effective numbers of tillers m², UNEFF=Number of un-effective tillers m², 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 values ranged from 4.60 for chlorophyll content to 32.22 for un-effective tillers per m², whereas values for PCV ranged from 6.32 for chlorophyll content to 51.79 for a number of un-effective tillers per m². The values of PCV were higher than the values of GCV, indicating the influence of the environment in the expression of traits. Number of un-effective tillers per m² was found to have high GCV and plant height, leaf area, effective number of tillers per m², 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. Rashid et al. (2017), Umesh et al. (2015), Dhanwani et al. (2013), Sumanth et al. (2017), Islam et al. (2017) obtained similar results. Binda et al. (2017) supported result for grain yield and Limbani et al. (2017) for number of un-effective tiller per m².

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 m², 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. The 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 m² 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 m², number of effective tillers per m², 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).

Correlation coefficient analysis

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

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 m², UNEFF=Number of un-effective tillers m², 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 an effective number of tillers per m² (.797**) and panicle length (.623*) had a significant and positive correlation with grain yield. Other traits showed a 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/m²(-0.109) days to 50% flowering (-0.069) and 1000-grain weight (-0.216) showed a non-significant and negative correlation with grain yield. This result is in concert 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).

Path coefficient analysis

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

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 m², UNEFF=Number of un-effective tillers m², 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 a highest, positive, and direct effect on grain yield followed by a number of effective tillers per m², days to 50% flowering, and thousand-grain weight. Plant height, leaf area, chlorophyll content, straw yield, filled grains per panicle showed a negative direct effect on grain yield. As a number of effective tillers per m² and panicle length had a 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 a negative correlation with grain yield, but they exhibited positive effects directly to the grain yield. The 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).

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/m² and panicle length was observed significantly positive and exerted a 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 trials.

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