Genetic Variability, Heritability And Correlation Analysis In Quantitative Traits Of Irrigated Rice (*Oryza Sativa* L.)

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A study was carried out to assess the genetic variability among the genotypes, correlation among traits and heritability of the traits to next generation. Eight rice genotypes were evaluated in Randomized Complete Block Design (RCBD) with three replications during Kharif (June-October) 2017 in experimental field of Lamjung Campus, Sundarbazaar, Lamjung, Western Nepal. The analysis of variance revealed statistically significant differences for all the traits under studied, which showed the presence of genetic variability among the genotypes except ineffective tiller per m². The higher value of GCV and PCV was recorded for grain per panicle, filled grain per panicle, harvest index and grain yield. The PCV value was observed higher than the GCV value which indicated the influence of environment on the expression of the traits. High heritability along with high genetic advance as percent of mean was observed for grain per panicle, panicle length, harvest index and grain yield. However, high heritability along with moderate genetic advance as percent of mean was observed for days to 50% flowering, 1000 grain weight and plant height. The effective tiller per m², harvest index,grain per panicle and filled grain per panicle exhibited significant and positive correlation with grain yield. Plant height and ineffective tiller perm² exhibited negative correlation with grain yield. Grain per panicle, harvest index and grain yield could be suitable traits for selection of the rice genotypes.

Keywords: Correlation,Genetic advance, Genetic variability, Heritability, *Oryza Sativa.*

Rice (*Oryza sativa* L.) is a cultivated crop belonging to the family Graminae, sub-family Bamboosoideae and tribe Oryzeae (Sarla and Swamy, 2005). It is diploid with 12 chromosomes (2n=24) (Garris*et al*., 2005). Rice is cultivated as low as 3m below sea level in Kerala, India and upto 3000 m above sea level in Bhutan and Nepal (Khush and Virk,2000). It is one of the major food crops all over the world and is the most widely consumed staple food for large part of the world's human population, especially in Asian region. It is the agricultural commodity which in production ranks third (741.5 million tons in 2014) worldwide after sugarcane and maize. However, in aspect of calorie intake and nutrition, it is the most important grain which provides more than

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one fifth of the calories to human, worldwide (Smith, BruceD,1998). Rice contains starch (75-80%),water (12%) and protein (7%) (Hossain *et al.*, 2015). Also, in many countries of the world, rice is the source of animal feed (Muhammad *et al.*, 2015).

The total area production and productivity of rice is about 741.4 million tons and 4.55 t/ha respectively (FAOSTAT,2017). Asia is the major rice producing region which produce about 90% of the world total production. According to recent data, China was the leading rice producer followed by India with production of over 210 million metric tons in 2017. According to MoAD (2015/16), rice cultivable land in Nepal was 1,362,90 hawith productivity 3.154 t/ha and total production of 4,299,079 metric tons.

The population is also increasing day by day at certain rate throughout the world and in Nepal too. The consumption rate is also increasing. According to Manomani and Khan (2003), 785 million tons of paddy is necessary in order to meet the future growing population by 2025. In contrast, the total productive land is decreasing and hence the productivity should be increased. In order to attain the self-sufficiency in rice and meet the growing demand that results from the decrease in productive land and population growth, we need to develop high yielding rice genotypes with suitable morphological traits for different ecosystem in hills (Mulugeta*et al.*, 2012). So, plant breeders are focusing on increasing yield through the study of yield attributing characters. For this, genetic variability is the key component which results due to the differences in genetic constitution or environment on which they are grown.Knowledge about heritability and genetic advance indicates the improvement through selection. Also, grain yield is the complex character and the association of yield with yield components is important in breeding programme which shows the direction of yield components.

MATERIALS AND METHODS

A field experiment was conducted in experimental field of Lamjung Campus with eight rice genotypes at Sundarbazaar, Lamjung which is located at an altitude of 725 meter above mean sea level, with Latitude of 28º7´ to 28º10´

N and longitude of 84º24´ to 84º 28´ E during Kharif (June- October) 2017. Seeds of 8 genotypes were sown in raised nursery bed and 26 days old seedlings of each genotype were transplanted with spacing 20cm x 20 cm in Randomized Complete Block Design(RCBD) with 3 replications. The genotypes were NR 11050-B-B-B-B-22, NR 11115-B-B-31-3, NR 11105-B-B-16-2, NR 11105-B-B-49-3, NR 11100-B-B-15-2-1, NR 11216-B-25-1, NR 11139-B-B-B-13-3 and BG.Each genotype was grown in 15 rows and 10 columns with plot size $6m^2(3m*2m)$. Recommended dose of chemical fertilizers @ 60 kg N, 60kg P and 40 kg K per hectare were applied in the form of DAP, Urea, and Potash. Only half dose of Nitrogen and full dose of phosphorus and potassium were applied as basal dose. Remaining dose of nitrogen were applied in the two split dose at 30 days after transplanting (DAT) and 60 DAT. No micronutrients were applied. Agronomic practices such as gap filling, weeding, irrigation and drainage, top dressing and plant protection measures were followed. Observations like days to 50% flowering, plant height, grains per panicle, filled grain per panicle, no. of effective tiller, no. of ineffective tiller, panicle length, 1000 grain weight, harvest index and grain yield were recorded.$1m^2$ plants population were selected randomly from each genotype in each replicationfor post harvest observations. The data were recorded in Ms.excel 2016. The data recorded for all the characters were subjected to analysis using R 3.1.1 for analysis of variance. The GCV, PCV, heritability and genetic advance was calculated in Ms.excel.The coefficient of correlation was analyzed by using SPSS 16.0. Genotypic variance was calculated using following formula given by Lush (1949).,

Vg=(Trmss-Emss)/r

Where,Vg= Genotypic variance, Trmss= Treatment mean sum of square, Emss= Error mean sum of square and r = number of replication

Similarly, phenotypic variance was calculated by using following formula;

Vp= Vg+Ve

Where, Vp= Phenotypic variance, Vg= Genotypic variance andVe= Error variance

GCV and PCV were calculated by using formula suggested by Burton, (1952)

$$GCV= \frac{\sqrt{Vg}}{x}$$

Where, x = Mean,Vg= Genotypic variance

andGCV= Genotypic coefficient of Variation

PCV= $\dfrac{\sqrt{Vp}}{\chi}$

Where, χ = Mean, Vp= Phenotypic variance and PCV= Phenotypic coefficient of Variation
As suggested by Lush (1940), heritability in broad sense is calculated by using following formula;

$h^2b = \dfrac{Vg}{Vp}*100$

where, h^2b = heritability in broad sense, Vg=Genotypic variance and Vp=Phenotypic variance
Genetic as percent of mean is the percent expected genetic advance over the population mean. It was computed by using formula (Johnson *et al.* 1955) given by Comstock and Robinson (1952).

$GAM = \dfrac{GA}{\chi} * 100$

Where, χ = Grand mean, GAM= genetic as percent of mean and

GA(Genetic advance) = $\sqrt{k} * Vp * h^2$ band k(selection differential) = 2.06 at 5% selection pressure

RESULTS AND DISCUSSION

The result for analysis of variances is presented in the table 1. The mean sum of squares due to genotypes were found significant for days to 50% flowering, plant height, grain per panicle, panicle length, 1000 grain weight, harvest index and grain yield at 1% level of significance and for filled grain per panicle and effective tiller per m²

at 5% level of significance but non significance for ineffective tiller per m². This results revealed that the variability exists in the genotypes under study. Hence from this, we can understand that the genotypes which were used for study can be used for further breeding programme. Similar findings were also obtained by Rai et.al. (2014) and Senapati and Kumar (2015).

The estimation of GCV, PCV, heritability, genetic advance and genetic advance as percent of mean were presented in the table 2. Generally, the estimates of PCV were higher than their corresponding GCV (Dutta *et al.*, 2013). This is due to environmental influences during expression of the traits. The environmental influence would be added on PCV that made the value higher.The PCV value was ranged from 7.485 (1000 grain weight) to 52.324(grain yield) while GCV varies from 7.085 (1000 grain weight) to 45.01 (grain yield). According to Deshmukh and coworkers (1986), the GCV and PCV values of more than 20% are considered high, 10-20% are considered moderate and less than 10% are considered low. Higher magnitude of PCV was recorded for grain yield (52.324), harvest index (46.445), filled grain per panicle (35.923), grain per panicle (26.387) and effective tiller per m² (23.501) while moderate estimates of PCV was recorded for plant height (12.181) and panicle length (12.523). Also, less estimates of PCV was recorded for 1000 grain weight (7.485) and days to 50% flowering (8.380). Similarly, higher magnitude of GCV was recorded

Table 1. Estimation of Analysis of variance
for different traits in Rice

S.N	Characters	Genotypes (df=7)	Replication (df=2)	Errors (df=14)
			Mean sum of squares	
1	FD	185.98**	8.17	1.26
2	PH	792.1**	12.8	96.1
3	GPS	5322**	229	465
4	FGPS	3519*	1665	951
5	EFFT	1473.3*	1038.3	468.3
6	IEFFT	752.4[ns]	596.5	289.4
7	PL	30.003**	2.658	2.009
8	TW	7.655**	0.962	0.285
9	HI	0.045**	0.023	0.0041
10	GY	0.068**	0.032	0.007

Table 2. Estimates of variability, heritability and genetic advance in different traits of rice

Traits	Vg	Vp	GCV	PCV	h²b	GA	GAM
FD	61.573	62.833	8.296	8.380	0.979	16.001	16.918
PLH	232	328.1	10.243	12.181	0.707	26.384	17.743
GPS	1619	2084	23.258	26.387	0.776	73.057	42.22
FGPS	856	1807	24.725	35.923	0.473	41.482	35.056
EFFT	335	803.3	15.176	23.501	0.417	24.348	13.865
PL	9.331	11.34	11.36	12.523	0.822	5.708	21.227
TW	2.457	2.741	7.085	7.485	0.896	3.056	13.817
HI	0.013	0.017	40.684	46.445	0.767	0.211	73.413
GY	0.020	0.027	45.01	52.324	0.739	0.252	79.761

Table 3. Estimates of correlation coefficient between different traits in rice

	FD	PLH	GPS	FGPS	EFFT	IEFFT	PL	TW	HI	GY
FD	1	-0.523	0.397	0.436	0.613	-0.282	0.25	0.671	0.626	.793*
PLH		1	0.16	0.048	-0.557	0.328	0.536	-0.26	-0.392	-0.506
GPS			1	.877**	0.601	-0.629	0.647	0.352	.813*	.714*
FGPS				1	0.498	-0.656	0.367	0.499	.817*	.766*
EFFT					1	-0.691	0.25	0.357	.846**	.871**
IEFFT						1	-0.195	-0.309	-0.673	-0.657
PL							1	0.14	0.208	0.214
TW								1	0.483	0.545
HI									1	.955**
GY										1

for grain yield (45.01), harvest index (40.684), filled grain per panicle (24.725) and grain per panicle (23.258) and while moderate magnitude of GCV was recorded for plant height (10.243), effective tiller per m² (15.176) and panicle length (11.36). Lower estimates of GCV was recorded for days to 50% flowering (8.296) and 1000 grain weight (7.085). Higher estimates of GCV and PCV showed that the traits were under genetic control. This means that the traits like grain yield, harvest index, filled grain per panicle, grain per panicle and effective tiller per m²are under genetic control. This is also an important technique in identifying the suitable traits during selection. Ubarhande *et al*. (2009) and Patil and Sarawgi (2005) also reported higher magnitude of GCV and PCV for filled grain per panicle. High estimates of PCV was also reported by Sharma *et al*.(2006) and Arun Kumar (2013) for grain yield per panicle.

The difference between the magnitude of GCV and PCV is found lower for days to 50% flowering, plant height, grain per panicle, panicle length, 1000 grain weight which represents the lower influence of environment on the expression of those traits while higher for rest of the traits that indicates higher environmental influence on expression of those traits. We should maintain the good environment as the requirement of crop for the improvement of particular traits which shows higher environmental influence. Less difference between GCV and PCV was also obtained by Vange(2008) for days to 50% flowering and panicle length. Chandra *et al*. (2009) also reported higher difference between GCV and PCV for grains per panicle.

Broad sense heritability for different quantitative characters was found ranging from 0.417 (effective tiller per m²) to 0.979 (days to 50% flowering). According to Babu *et al*., (2012) and Ashok *et al*., (2013), the magnitude of heritability is classified as low (<50%), medium (50-60%) and high (>60%). Higher value of broad sense heritability was obtained for days to 50 % flowering (0.979), 1000 grain weight (0.896), panicle length (0.822), grain per panicle (0.776), grain yield (0.739), plant height (0.707) and

lower value for filled grain per panicle (0.473) and effective tiller per m^2 (0.417). High broad sense heritability for plant height was reported by Ketan and Sarkar (2014) and Tuhina*et al.* (2015). Higher broad sense heritability for panicle length and grain yield was reported by Ammar *et al.* (2014). Akinwaler *et al.* (2011) and Seyoum*et al.* (2012) also revealed higher heritability for days toflowering, plant height, grain yield and panicle length. As we know the heritability of most of the traits was high that means the phenotype and genotype of the traits are highly correlated and the environmental contribution is lower and vice versa for low heritable traits. Also the expression of the trait like days to 50 % flowering, 1000 grain weight, panicle length, grain per panicle, grain yield and plant height were governed by additive gene action.

Genetic advance is the improvement of particular traits of new population compared with the base population in the genotypic value under selection at given selection intensity (Wolie*et al.*,2013). In this experiment, the genetic advance was calculated that ranged from 0.211 (harvest index) to 73.057 (grain per panicle) as shown in the table 2. High genetic advance was calculated for grain per panicle (73.057), filled grain per panicle (41.482), effective tillers per m^2 (24.348), plant height (26.384) and moderate genetic advance was calculated for days to 50% flowering (16.001). Also, lower genetic advance was calculated for panicle length (5.708), test weight (3.056), grain yield (0.252) and harvest index (0.211). High genetic advance for grains per panicle was reported by Chandra *et al.* (2009) and Pankaj *et al.* (2011), for effective tillers per m^2 and grain per panicle by Nandan*et al.* (2010) and for plant height by Bharadwaj *et al.* (2007). Similarly, lower magnitude of genetic advance for panicle length was reported by Padmaja*et al.* (2008).

GAMwas ranged from 13.817 (1000 grain weight) to 79.761 (grain yield). The GAM was categorized into low (0-10%), moderate (10.1-20%) and high (>20.1%) (Johnson *et al.*, 1955). The higher values of GAM were recorded for grain per panicle, filled grain per panicle, panicle length, harvest index and grain yield while lower values for effective tiller per m^2, days to 50% flowering, plant height and 1000 grain weight.

The heritability estimates only are not of practical importance unless it is studied with genetic advance. In the present study, high heritability along with high genetic advance as percent of mean were exhibited by grain per panicle, panicle length, harvest index and grain yield. This results revealed that the selection would be effective and simple and the transmissivity is due to additive gene action. These traits could be improved by mass selection.High heritability along with high genetic advance was also reported by Padmaja*et al.* (2008) and Rai *et al.* (2014) for grain yield and yield attributing traits. Also, high heritability along with moderate genetic advance was obtained for days to 50% flowering. And high heritability along with low genetic advance was obtained for panicle length, 1000 grain weight, harvest index and grain yield. Similar findings were also reported by Subudhi and Dikshit (2009) for 1000 grain weight. Again low heritability along with high genetic advance was obtained for filled grain per panicle and effective tiller per m^2.

In plant breeding, the association between two different traits could be used as a tool for indirect selection. It helps the breeder in selection by providing the knowledge of the yield components. The result of correlation analysis is shown in Table 3. Positive and highly significant correlation of effective tiller per m^2 and harvest indexwas obtained with grain yield.And there was positive and significant correlation of grain yield with days to 50% flowering, grain per panicle (Hari *et al.*, 2006), filled grain per panicle. These traits selection may be the suitable way of obtaining optimum yield in the studied genotypes. Similarly, there was positive correlation of grain yield with panicle length and 1000 grain weight. Also there was negative correlation of grain yield with plant height (Bughio *et al.*,2009) and non-effective tiller per m^2. Significant and positive correlation of grain yield with number of grains per panicle, days to 50% flowering, number of effective tillers per m^2 was also recorded by Mohana Krishna *et al.* (2009). During the selection procedure these traits may help us in selecting the suitable genotypes.

CONCLUSION

There is existence of variability among the genotypes in the present study. The phenotypic and genotypic variances revealed the scope of genotypes in the breeding programme. The higher

value of PCV was obtained in comparison with GCV which indicated the influence of environment and higher magnitude indicated the scope for selection of traits. High heritability along with high genetic advance as percent of mean was obtained for grain per panicle, filled grain per panicle, harvest index and grain yield which signifies the selection of these traits for further crop improvement. Effective tiller per m^2, days to 50% flowering, grain per panicle and harvest index aid in yield increment. Thus, we recommend for the selection of the traits like grain per panicle, harvest index and grain yield for further improvement.

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