

Research Article

GENETIC VARIABILITY AND CORRELATION COEFFICIENTS OF MAJOR TRAITS IN EARLY MATURING RAINFED RICE GENOTYPES AT PARWANIPUR, BARA, NEPAL

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ABSTRACT

Genetic variability is the fundamental requirement to develop superior cultivar variety in any breeding program. The objective of this study was to estimate the genetic variability and find out the correlation among the different quantitative traits of early rain fed rice genotypes at Regional Agricultural Research Station, Parwanipur, Bara during 2019. Twenty- two genotypes including Hardinath-3 and Anmol Mansuli as check varieties were evaluated in the randomized complete block design (RCBD) with three replications. Various Quantitative traits were evaluated and character association was estimated. Analysis of variance showed highly significant difference at 1% level of significance among the genotypes for all the traits studied except for panicle length which indicates the existence of genetic variability and potential for selection and further improvement. Phenotypic coefficient of variation was higher than genotypic coefficient of variation which indicates the influence of environment for all the traits studied. The presence of high heritability coupled with high genetic advance as percentage of mean (GAM) for most of the traits which indicates presence of additive gene action. Positive and highly significant correlations were found in number of filled grains per panicle ($r=0.259^{**}$) and dry matter ($r=0.276^{**}$) which indicates that these traits have positive effects on grain yield and it helps in selection and improvement of rice genotypes. However, negative and highly significant correlation exhibits between days to flowering ($r=-0.288^{**}$), days to maturity ($r=-0.318^{**}$), and number of tillers per m² ($r=-0.290^{**}$). Thus, overall results indicate the presence of variability and remarkable genetic advance could be considered as the most appropriate traits for improvement and selection of trait for high yielding rice genotypes.

Keywords: Correlation, genetic variability, heritability, rice genotypes.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the important staple crop in Nepal and ranks first in terms of production and productivity (Tiwari et al., 2018). It is the first most important staple food crop in Nepal and is grown in 149,1744 ha with production of 5610011 mt and productivity 3.76t/ha (MoAID, 2019). In Nepal, 73%, 24% and 3% of total rice cultivated areas in terai, mid-hills and mountains, respectively (MOAD, 2017). As the most important staple food of Nepalese people, rice supplies about 40% of the food calorie intake and contributes about 20% to the agricultural gross domestic product (AGDP) (MoAD, 2018). Although country has a high potential for rice production in irrigated areas, yield is very low in rain fed rice as compared to irrigated areas. Lack of adaptable varieties is one of the problem in rain fed conditions. Early or late maturing rice genotypes could be potential alternative to overcome drought effects under rain fed rice growing conditions. Development of high yielding varieties needs the knowledge of existing genetic variability. The available variability can be measured using genotypic and phenotypic coefficient of variation which is used to partition genetic and environmental variance (Singh et al., 2017). Grain yield is a complex polygenic quantitative trait which is greatly affected by environment and determined by the magnitude and nature of their genetic variability (Singh et al., 2000). Consequently, selection for yield may not be satisfying without taking into consideration yield component traits. Thus, positives correlated between yield and yield components are requires for effective yield component breeding increasing grain yield in rice (Ogunbayo et al., 2014). The variability, heritability and genetic advance on different traits of rice are necessary for developing appropriate breeding and

selection strategies to increase yield. The aim of this research is to evaluate rice genotypes in order to identify their genetic variability, character association in rain fed condition.

MATERIALS AND METHODS

The field experiment was conducted at the research field of Regional Agricultural Research Station, Parwanipur, Bara, Nepal during 2019 from first week of June to second week of November. It is located at 27.07° N latitude and 84.91°E' longitude with an elevation of 115 masl. The soil is silty loam. Twenty-two genotypes with two check (Anmol mansuli and Hardinath 3) was evaluated at research field of Regional Agricultural Research Station, Parwanipur, Bara in Randomized Complete Block Design (RCBD) with 3 replications. The size of plot was 5m*3m and spacing between row to row and plant to plant was 20cm *20 cm. The distance between two plots is 50 cm and distance between two replications is 1m. Seed was shown on flat bed on 4th June and 21 days' healthy seedlings were transplanted in the main field. Farm yard manure was applied 10t/ha and NPK used was 80:40:30 kg/ha. Five plants were randomly selected from each plot in each replication and their means were used for the statistical analysis. Observations were recorded on different traits like plant height, panicle length, days to flowering, days to maturity, number of tillers per m², number of filled grains per panicle, number of unfilled grains per panicle, sterility, 1000 grain weight, dry matter, harvest index, biological yield and grain yield (kg/ha).

Table 1: Genotypes details

E.N.	Genotypes	E.N.	Genotypes
1	1R 93810-2-1-1-1	12	IR 14L 145
2	Anmol Mansuli*	13	IR 14L 158

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3	GSR 310	14	IR 14L 160
4	Hardinath-3 *	15	IR 14L 363
5	HHZ25-DT9-Y1-Y1	16	IR 14L 572
6	HHZ6-DT1-L11-L11	17	IR 14L 576
7	IR 103575-76-1-1-B	18	IR 15L 1717
8	IR 103575-76-1-2-B	19	IR 96279-33-3-1-2
9	IR 103587-22-2-3-B	20	IR 98846-2-1-4-3
10	IR 106529-20-40-3-2-B	21	IR08L181
11	IR 14D 198	22	IR102774-31-21-2-4-7

Phenotypic and Genotypic coefficients of variation were calculated by using method suggested by Lush (1940) and Chaudhary and Prasad (1968).

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} * 100$$

$$\text{Genotypic Coefficient of variation (GCV)} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} * 100$$

According to SivaSubramanian and Menon, 1973 PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are regarded as low and between 10% and 20% are to be moderate. Heritability was calculated by the formula given by Falconer (1996) which is as below:

$$H = Vg / Vp * 100$$

Where, H= Heritability in broad sense; Vg= genotypic variance; Vp = Phenotypic variance

Heritability percentage is categorized as low, medium and high as followed by (Robinson et al., 1949) as follows; 0-30% Low; 30-60% moderate and > 60% High. Under Selection expected Genetic advance for each character at 5% selection intensity was computed by the formula described by (Johnson et. al., 1955).

$$\text{Genetic Advance (GA)} = k \sigma_p H$$

Where: k = constant (selection differential where k = 2.056 at 5% selection intensity); σ_p = phenotypic standard deviation; H = broad sense heritability.

Genetic advances as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula

$$\text{GAM} = \text{GAX} \times 100 \text{ (Falconer, 1996),}$$

where GAM=genetic advances as percent of mean, GA = Genetic advances under selection, X = Mean of population in which selection will be employed.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

The analysis of variance showed that there was a highly significant difference at 1% level of significance among the genotypes tested for all the traits except for panicle length. Similar results were obtained by Baekal et al., (2016), and Sumanth et al., (2017). This indicates the genotypes are highly variable especially those traits which showed significant difference. Thus, the possibility genetic improvement through selection is highly promising. The study by North (2013) also reported significant difference in genotypes. Analysis of variance for important traits in rain fed rice genotypes presented in table.

Table 2: Analysis of variance for important traits in rain fed rice genotypes

Characters	MSS Replication	MSS Treatment	Error	CV(%)
Days to 50% flowering	11.69	451.120**	6.090	2.6
Days to maturity	0.212	456.911**	2.894	0.1
Plant Height (cm)	50.57	427.52**	10.82	2.9
Panicle length (cm)	11.73	13.56*	6.54	9.5
Number of tillers per m ²	325.7	4593.8**	482.0	8.3
Number of filled grains per panicle	9316.0	10910**	2282.0	7.2
Number of unfilled grains per panicle	3.24	2.91**	183.6	10.8
Sterility	3.010	7.382**	2.654	10.3
Dry matter	4.39	5.00**	0.95	2.9
Harvest Index	9.46	253.46**	23.60	9.9
1000 seed weight	3.912	25.692**	2.376	7.2
Biological Yield (kg/ha)	27.471	31.282**	5.997	9.1
Grain yield (t/ha)	0.3676	1.6323**	0.2664	9.3

Significant codes: *** 0.01, ** 0.05

Estimation of Genetic Parameters

The highest phenotypic and genotypic coefficient of variation was exhibited in harvest index followed by number of tillers per m², 1000 seed weight, grain yield, days to 50% flowering, biological yield and dry matter. This indicates that there is possibility of traits improved through selection and hybridization. High heritability in Grain yield was also reported by Sumanth *et al.*, (2017). Moderate GCV and PCV was found in days to maturity, plant height, panicle length, filled grains per panicle, unfilled grains per panicle, and sterility. The genetic variation result showed that phenotypic coefficient of variation (PCV) was relatively higher than genotypic coefficient of variation (GCV).

CONCLUSION

The overall result showed the presence of variability in the genotypes studied. Characters having high GCV and PCV recorded for grain yield, days to 50% flowering, 1000 seed weight, number of tillers per m² suggesting existence of variability and can be utilize in efficient selection for genetic improvement program. High heritability coupled with GAM was observed for filled grains per panicle, 1000 seed weight, number of tillers per m² which indicate control of additive gene action and these traits can be selected for further yield improvement program. Number of filled grains per panicle and dry matter has positive and highly significant correlation with grain yield. Therefore, it should be considered for selection in breeding program.

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