
RESEARCH ARTICLE

Variability study and identification of promising rice genotypes for the different climatic conditions of Nepal

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Abstract

The present experiment was conducted at Regional Agricultural Research Station, Parwanipur, Bara, Nepal during 2019 with 44 rainfed rice genotypes including four released varieties in Randomized Complete Block Design (RCBD) with three replications. The objective of the study was to assess the genetic variability in the rice genotypes to identify the promising rice genotypes with high yield potentials under rainfed situation. Wide ranges of variation among the forty-four genotypes were recorded. Genotype HHZ6-DT1-L11-L11 has been observed high grain yielder (6.792 ton per hectare). Correlation analysis showed that number of filled grains per panicle, dry matter content and total number of grains per panicle showed positively significant correlation with grain yield whereas days to 50% flowering, days to maturity and number of tillers per m² showed negatively significant correlation with grain yield. Path analysis using grain yield as a dependent variable revealed that days to 50% flowering, test weight, number of filled grains per panicle, dry matter and number of grains per panicle had positive direct effects with grain

yield. The dendrogram resulting from UPGMA analysis of forty-four genotypes formed six clusters, where Cluster 1, Cluster 2, Cluster 3, Cluster 4, Cluster 5 and Cluster 6 represent 47.2%, 9.09%, 6.81%, 29.4%, 2.32% and 4.64% respectively. Genotypes under Cluster-II was higher yielder and genotypes under cluster-III was early flowered and early matured. Hence, genetic diversity has been observed among the tested genotypes so that direct selection criteria for higher grain yield is possible by evaluating the days to 50% flowering, days to maturity, plant height, number of tillers per m², number of filled grains per panicle, and thousand grain weight.

Key words: Variability, correlation, diversity, yield, rice

Introduction

Rice is the second major cultivated cereal crop in the world after wheat. 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). Development of high yielding varieties needs the knowledge of existing genetic variability. Genetic variability is the basis of plant breeding because any crop improvement depends on the amount and direction of genetic association of the traits in the base population (Karim *et al.*, 2007). It provides a wide range of genotypes that can be selected to develop new varieties (Pandey *et al.*, 2009). The early maturing genotypes, short duration genotypes, hybrids can be the good source of important alleles to develop new varieties. 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). 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 trait, quantitative in nature and a combined function of a number of constituent traits (Mustafa *et al.*, (2007). So, it is important for plant breeders to understand the degree of correlation between yield and its components. Selection based on the phenotypic expression is sometimes misleading as development of the character is the result of interaction of the heritable and non-heritable characters. Therefore, the objective of this study was to evaluate the promising rainfed rice genotypes based on variability study for Nepal region based on quantitative traits.

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. Forty four rice genotypes with four check varieties was evaluated at Regional Agricultural Research Station, Parwanipur, Bara. Under this research, genotypes were received from RARS, Bara.

The experiment was laid out in RCBD with three replications. The genotypes were allocated randomly to the 44 plots in each replication. There were altogether 132 plots. The plot size was 5m×3m with spacing of 50 cm with in plots and 1m with in replication. Seed was shown on flat bed on 4th June, 2019. 21 days old and healthy seedlings were transplanted in the main field. Farm yard manure was applied at 10 tons per hectare and NPK was 80:40:30 kg/ha. Spacing was used 20×20 cm between row to row and plant to plant. The data were collected on the ten randomly selected plants for each genotype and the figures were averaged. 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 percentage, biological yield, dry matter, 1000 seed weight, harvest index and grain yield. Data entry and processing was performed for all the traits using Microsoft Office Excel. Data were analyzed and Analysis of variance was performed by using Gen stat 15 Ed in order to test the significance of variation among genotypes. The data were analyzed for mean, coefficient of variation (CV%), LSD value and correlation coefficient. UPGMA clustering was done using software Minitab 14.

Table 1. List of rice genotypes used in experiment

Sr. No.	Accessions	Sr. No.	Accessions
1	1R 93810-2-1-1-1	23	IR10281-10-227-1-2-9
2	Anmol Mansuli*	24	IR103587-23-2-1-B
3	GSR 310	25	IR13F228
4	Hardinath-3 *	26	IR13F402
5	HHZ25-DT9-Y1-Y1	27	IR15D1031
6	HHZ6-DT1-L11-L11	28	IR15L1735
7	IR 103575-76-1-1-B	29	IR15L1745
8	IR 103575-76-1-2-B	30	IR16D1058
9	IR 103587-22-2-3-B	31	IR86515-19-1-2-1-1-1-1
10	IR 106529-20-40-3-2-B	32	IR95784-255-78-2-3-1-2
11	IR 14D 198	33	IR95809-25-1-1-1
12	IR 14L 145	34	IR98785-10-1-1-3
13	IR 14L 158	35	IR98853-3-6-1-3-2
14	IR 14L 160	36	IR99739:2-1-1-2-1
15	IR 14L 363	37	IR99784-255-78-2-3-1-2
16	IR 14L 572	38	NR21679-82-2-4-1-1-1-1
17	IR 14L 576	39	NR2168-44-2-1-1-1-2-1-1
18	IR 15L 1717	40	NR2169-10-1-1-6-2-1-3-1
19	IR 96279-33-3-1-2	41	NR2170-5-5-1-6-1-1-3-1
20	IR 98846-2-1-4-3	42	NR2181-139-1-3-1-1-1-1
21	IR08L181	43	Radha-13*
22	IR102774-31-21-2-4-7	44	Radha-4*

*check varieties

Results and discussions

The analysis of variance revealed highly significant difference ($p < 0.01$) for all the traits studied except for panicle length (Table2). Maximum height (168.5 cm) was recorded in Radha-13 and NR2170-5-5-1-6-1-1-3-1 was the shortest (99.7 cm). Kumar *et al.*, (2014) also reported significant variation in plant height. Maximum panicle length 36.48 cm was recorded in IR 14L 572 Ullah *et al.* (2011) reported similar results which confirm our results. Highly significant differences ($p \leq 0.001$) in days to 50% flowering was observed among rice genotypes ranging from 122.00 to 82.00 days. The genotypes NR2170-5-5-1-6-1-1-3-1 (122.00), IR15D1031 (121) and IR13F402 (120) days headed later than other genotypes and check

varieties. Highly significant variation for days to flowering and maturity was also observed by Chakraborty *et. al.*, (2011). The highest number of unfilled grains was 151.3 found in IR 14L 572, Whereas, the minimum number of unfilled grains was 106.3 which was found in NR2170-5-5-1-6-1-1-3-1. Thousand Seed weight has highly significant difference among the tested genotypes. The maximum grain weight was recorded 30.57gm in IR 15L 1735 and the minimum was recorded 17.01gm in GSR 310. Analysis of variance for harvest index showed highly significant difference due to genotype differences. The maximum harvest index was obtained by HHZ6-DT1-L11-L11 (64.07%) followed by IR 103587-22-2-3-B (62.47%) whereas the minimum value was gained by IR13F228 (28.18%).

Grain yield per ha varies highly significantly ($p \leq 0.001$) due to genotype differences. In this study grain yield of genotypes ranged from 6.792 to 3.767 ton per ha. Higher grain yield was recorded from HHZ6-DT1-L11-L11 (6.792) followed by NR2169-10-1-1-6-2-1-3-1 (6.556) and the minimum yield was recorded from IR98785-10-1-1-3 (3.76).

Correlation and path analysis

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). Correlation among traits can be used to identify important traits that are desired for rice breeding program. From the study, days to 50% flowering has positive and highly significant difference ($p < 0.001$) with days to maturity (.971**) and number of tillers per m^2 (.666**). This corroborates with the findings of Reddy *et al.*, (2008). Days to maturity has positive correlation with plant height (.197*) and number of tillers per m^2 (.668**), whereas it has negative but highly significant with number of unfilled grains per panicle (-.239**), harvest index (-.254**) and grain yield (-.318**). Number of tillers per m^2 had negative but highly significant correlation with Harvest Index (-.253**) and Grain yield (-.290**). 1000 seed weight has positively and highly significant correlation with Harvest Index (.262**) whereas it has non-significant correlation with Grain yield (0.1). Correlation results showed that number of filled grains per panicle had positively and highly significant correlation with grain yield (.259**) and negatively correlated with Sterility percentage (-.492**). Dry matter showed highly and positively correlation with Harvest index (.348**) and Grain yield (.276**) which indicates that with an increase in dry matter content,

harvest index and grain yield also increased with positive value as per table3. Direct effect of number of unfilled grains per panicle on grain yield per hectare had highest positive value (0.808) followed by days to 50% flowering (0.496), dry matter (0.306), thousand seed weight (0.162) as an important yield attributing component based on positive direct effect in path coefficient analysis but days to maturity (-0.695), plant height(-0.112), panicle length(-0.102), number of tillers per m^2 (-0.147)², number of filled grains per panicle(-0.418), sterility(-0.959), harvest index(-0.234) showed negative direct effects on grain yield per hectare. Total number of grains per panicle (0.091) had positive direct effects with grain yield. Seyoum *et al.*, (2012) also reported that similar findings. Higher value of direct effect was only due to its higher negative indirect effects via other yield components towards grain yield per hectare. Similarly, Direct effect of days to 50% flowering is positive but its correlation with grain yield is negative in this case selection of this trait can be done to reduce the undesirable indirect effect table 4. Correlation coefficients of filled grains per panicle have been found positive and significant with grain yield per hectare while their direct effect on grain yield per hectare was negative. Days to 50% flowering had positive and high indirect effect (0.482) on days to maturity. Days to 50% flowering, number of unfilled grains per panicle and dry matter exhibited highest (0.30-0.99) positive direct effect on grain yield per hectare, while total number of grains per panicle, and thousand seed weight exhibited positive and low (0.09-0.16) direct contribution on grain yield per hectare. Earlier Souleymane, *et. al.*, (2019) reported that selection indices are useful in selection of rice genotypes, also reported their correlation with seed yield which confirms our findings. Bal *et. al.*, (2017) reported association between seed and seed attributing traits in rice introgressions lines.

Table 2: Basic statistics of quantitative traits

Parameters	Number of filled grains /panicle	number of unfilled grains /panicle	Sterility (%)	Days to maturity (g)	Biological yield (g)	Harvest index (%)	1000 seed weight (g)	Grain yield (t/ha)	Number of tillers per m ²	Plant height (cm)	Panicle length (cm)	Dry matter
LSD	77.53	21.99	2.64	1.59	3.95	7.88	2.50	0.83	35.63	5.30	4.15	1.59
CV (%)	7.2	10.8	10.3	9.1	9.1	9.9	7.2	9.3	8.3	2.9	9.5	9.1
Grand mean	665.6	124.9	15.8	10.7	26.9	49.3	21.4	5.5	266.0			
F-test	**	**	**	**	**	**	**	**	**	*	**	**

LSD (0.001 & 0.005)

Table 3: Pearson correlation of yield and attributing characters of rainfed rice genotypes

	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Number of tillers / m ²	1000 seed weight	Number of filled grains per panicle	Number of unfilled grains / panicle	Sterility	Dry matter	Harvest index	Grain yield ton /hectare
Days to 50% flowering	1	0.971**	0.184*	0.069	.666**	-0.12	-0.079	-.226**	-0.13	0.025	-.268**	-.288**
Days to maturity		1	0.197*	0.075	.668**	-0.122	-0.048	-.239**	-0.162	0.024	-.254**	-.318**
Plant height			1	0.016	-0.004	0.125	-0.011	-0.004	0.015	-.194*	-.201*	-0.166
Panicle length				1	0.093	-0.114	0.021	.242**	.193*	-0.093	-0.032	-.171*
Number of tillers / m ²					1	-0.159	-0.119	-.213*	-0.085	0.095	-.253**	-.290**
1000 seed weight						1	-.259**	-0.027	0.153	0.132	0.262**	0.1
Number of filled grains / panicle							1	.206*	-.492**	0.029	0.085	.259**
Number of unfilled grains / panicle								1	.746**	-0.115	0.07	0.03
Sterility									1	-0.129	-0.004	-0.164
Dry matter										1	.348**	.276**
Harvest index											1	0.059
Grain yield ton per hectare												1

Table 5: Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of rice genotypes

	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Number of tillers / m ²	1000 seed weight	Number of filled grains /panicle	Number of unfilled grains / panicle	Sterility	Grains /panicle	Dry matter	Harvest index
Days to 50% flowering	0.496	0.482	0.091	0.034	0.33	-0.06	-0.039	-0.112	-0.064	-0.051	0.012	-0.133
Days to maturity	-0.675	-0.695	-0.137	-0.052	-0.464	0.085	0.033	0.166	0.113	0.044	-0.017	0.177
Plant height	-0.021	-0.022	-0.112	-0.002	0.000	-0.014	0.001	0.000	-0.002	0.003	0.022	0.022
Panicle length	-0.007	-0.008	-0.002	-0.102	-0.009	0.012	-0.002	-0.025	-0.02	-0.002	0.009	0.003
Number of tillers / m ²	-0.098	-0.099	0.001	-0.014	-0.147	0.023	0.018	0.031	0.013	0.034	-0.014	0.037
1000 seed weight	-0.019	-0.02	0.02	-0.019	-0.026	0.162	-0.042	-0.004	0.025	-0.049	0.021	0.043
Number of filled grains / panicle	0.033	0.02	0.005	-0.009	0.05	0.108	-0.418	-0.086	0.206	-0.371	-0.012	-0.036
Number of unfilled grains/ panicle	-0.183	-0.193	-0.003	0.195	-0.172	-0.022	0.166	0.808	0.603	0.165	-0.093	0.057
Sterility	0.125	0.155	-0.014	-0.185	0.082	-0.147	0.472	-0.716	-0.959	0.407	0.124	0.004
Grains per panicle	-0.009	-0.006	-0.003	0.002	-0.021	-0.028	0.081	0.019	-0.039	0.091	-0.002	0.012
Dry matter	0.008	0.007	-0.059	-0.028	0.029	0.04	0.009	-0.035	-0.04	-0.007	0.306	0.107
Harvest index	0.063	0.059	0.047	0.007	0.059	-0.061	-0.02	-0.016	0.001	-0.031	-0.081	-0.234

Cluster analysis

Genetic variability and diversity is important because it decides the direction of genetic association of the traits in the base population (Karim *et al.*, 2007). A dendrogram was constructed by using UPGMA clustering method based on average linkage and Euclidean distance (fig 1). The cluster analysis grouped the landraces into six clusters for fourteen traits (Table 5). The genotypes were clustered using days to flowering, days to maturity, plant height, panicle length, number of tillers per m², number of filled grains per panicle, number of unfilled grains per panicle, sterility percentage, total number of grains per panicle, dry matter, harvest index, 1000 seed weight, biological yield and grain yield. The critical examination of the dendrogram revealed six clusters with minimum of 37.1% similarity level. Clusters 1,2,3,4,5 and 6 consists of 21, 4, 3, 13,1 and 2 respectively. Cluster- I had genotypes that had high 1000 seed

weight and sterility percentage, whereas it had intermediate value for Days to flowering, panicle length, dry matter, and grain yield. Cluster-II had genotypes with high number of filled grains per panicle, high harvest index, early flowered, higher yielder and intermediate panicle length. Cluster-III had genotypes consists only three genotypes with intermediate value for number of tillers per m², 1000 seed weight, filled grains per panicle, early matured genotypes and low plant height. Cluster-IV consists of genotypes having lowest filled grains per panicle, intermediate grain yield, dry matter, harvest index, sterility percentage. Cluster- V consist of only one genotype i.e. Radha-13 which was late flowered and late matured, longest panicle length, high tillers per m², higher biological yield and dry matter. This genotype had lowest 1000 seed weight, shortest plant height and intermediate grain yield. Cluster- VI had genotypes of highest plant height, shortest panicle length and lowest grain yield.

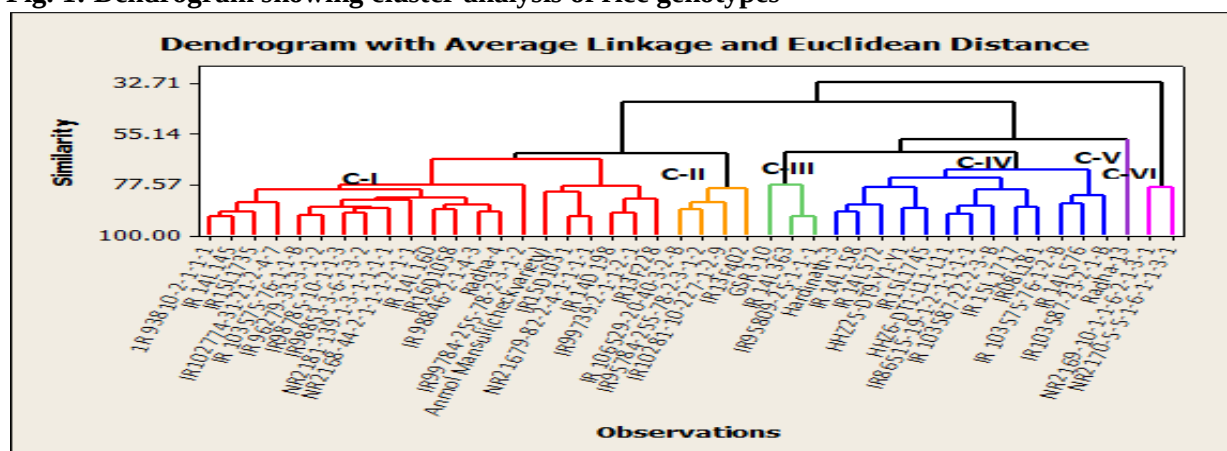
These genotypes had intermediate value for unfilled grains per panicle, 1000 seed weight, days to flowering, days to maturity, filled grains per panicle and lowest dry matter content. Average value of days to flowering, days to maturity, plant height, panicle length, tillers per m², filled grains per panicle, unfilled grains per panicle, total grains per panicle, sterility percentage, harvest index, dry matter, 1000 seed weight and grain yield is presented in table. Number of filled grains per panicle, total grains

per panicle, harvest index and grain yield was found highest in cluster- II. Thus cluster II was found to be high yield potential. Cluster-III was early flowered and early matured. So, Cluster II and III can be recommended for varietal development and crop improvement. Pandey, *et.al.*, (2009) studied the diversity among the rice genotypes and identified promising accessions based on diversity in rice which supports our findings

Table 5: Centroid of clustering 44 rice genotypes

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Grand centroid
50% flowering	94.714	89.778	86.872	113.5	115.667	105.333	94.962
Days to maturity	125.873	121.778	117.615	145.75	150.667	141.333	126.439
Plant height	115.952	113.611	111.646	114.275	102.267	168.533	114.941
Panicle length	26.615	26.94	26.945	27.65	27.767	25.8	26.863
Number of tillers per m ²	276.079	234.333	233.462	295	357.833	272.667	266
Thousand seed weight	22.588	19.959	20.863	20.518	18.755	20.13	21.481
Number of filled grains per panicle	610.857	779.556	710.769	665.583	735.833	743.667	665.553
Number of unfilled grains per panicle	121.127	136.556	132.487	123.25	108.833	111.333	124.947
Sterility	16.536	14.877	15.717	15.722	12.883	13.151	15.864
Grains per panicle	122.219	155.911	142.334	133.117	146.833	148.333	133.162
Biological yield	27.339	27.378	26.468	27.099	29.935	18.775	26.986
Dry matter	10.936	10.951	10.587	10.84	11.974	7.51	10.794
Harvest index	49.225	54.939	52.023	41.019	46.834	37.187	49.313
Grain yield	5.385	5.962	5.914	5.423	5.184	4.151	5.547

Fig. 1: Dendrogram showing cluster analysis of rice genotypes



Conclusion

The study revealed the existence of wide range of variations in phenological and yield attributing traits of forty-four rice genotypes. Genotypes differed highly significantly for the traits studied which means that there is sufficient variability for crop improvement. Genotype HHZ6-DT1-L11-L11 has the highest yield followed by NR2169-10-1-1-6-2-1-3-1. There exists strong correlation between yield and filled grains per panicle, dry matter and total number of grains per panicle which indicates improvements in any of these traits will cause an

increase in yield of rice. From the path coefficient analysis, it was revealed that days to flowering, grain per spike, dry matter and thousand seed weight exhibited positive direct effect on grain yield. Among the different characters' days to flowering, days to maturity, filled grains per panicle, 1000 seed weight and grain yield contribute mostly in classifying genotypes into different groups. Genotypes under Cluster –III was comparatively early flowered and early matured although high yielding although genotypes were under cluster-II.

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