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Varietal Evaluation and Genetic Variability in Rice (*Oryza sativa L.*) Genotypes of the Mid-Hill Region of Nepal

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Abstract

The objectives of this study were to identify promising rice genotypes and evaluate the genetic variance and effectiveness of selection of the rice varieties for several yield attributing traits. A varietal trial of fifteen rice genotypes was laid out in a randomized complete block design (RCBD) with three replications in a farmer's field in Sundarbazar, Lamjung, Nepal during the rainy season of 2018. Analysis of variance indicated that all the genotypes showed significant variation for all the traits considered. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characteristics being studied indicating the presence of environmental influence on the traits. High heritability coupled with high genetic advance as a percent of the mean was found for days to physiological maturity, number of tillers per m^2, plant height, leaf area, effective tillers per m^2, flag leaf area, test weight, grains per panicle, filled grains per panicle, harvest index, grain yield, and straw yield indicating that additive gene interaction is present in their inheritance. Direct selection can be effective for yield improvement in the populations through selection of these traits. Cluster analysis based on eighteen traits grouped the fifteen rice genotypes into four clusters. Cluster I was the largest and consisted of five genotypes. Radha 11, NR 119, and Sukhadhan-5 were the top performing genotypes having yield potentials of 5.78, 5.49, and 4.89 tons per ha, respectively.

Keywords

Cluster analysis, genetic advance, GCV, heritability, PVC

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Introduction

In Nepal, rice is the main staple crop grown in all three major ecological regions accounting for 73%, 24%, and 3% of the total rice cultivated in the Terai, Hill, and Mountain areas, respectively (MoAD, 2016). More than 70% of rice is grown under rainfed conditions, 9% under upland conditions, and 21% under partially or fully irrigated conditions (NARC, 2009). Rice fields occupy 1.36 million ha of land with an annual production of 4.23 million metric tons and productivity of 3.154 tons per ha (MoAD, 2016). The production and productivity of rice in Nepal are much less compared to other rice-growing countries. Agriculture in Nepal is a subsistence type where each farmer derives only a small part of their food requirements from fragmented plots of land cultivated under challenging conditions. Food insecurity is a major ongoing problem in Nepal, resulting in the rising problem of malnutrition in the country. The ever-increasing population is a major constraint in supplying enough food for each person's daily requirements. Climate change and natural calamities like drought, flooding, and fluctuations in rainfall patterns are also serious threats to food security.

The presence and magnitude of genetic variability for important traits in the gene pool are the basic guides for any breeding program (Akinwale *et al.*, 2011). Such variability is either naturally present or created using various techniques (Pandey *et al.*, 2009). The presence and magnitude of variability can be accessed by employing specific tools such as GCV, PCV, heritability, and genetic advance (GA), among others. Cluster analysis based on agro-morphological and yield component traits has shown considerable genetic diversity among genotypes themselves and can group them into distinct clusters (Kandel *et al*., 2019).

Previous rice researchers such as Yadav *et al*. (2019) conducted participatory evaluations of cold-tolerant rice in the mid-hill region of Nepal. Adhikari *et al.* (2018) also evaluated advanced lowland irrigated rice in Doti, Nepal. Bhandari *et al*. (2019) evaluated eleven rice genotypes in Lamjung and assessed their genetic variability. Therefore, this study was undertaken to assess the nature and magnitude of genetic variability, heritability, and genetic advance among these genotypes for further utilization in breeding programs.

Materials and Methods

Experimental site

The present study was carried out in a farmer's field in Sundarbazar, Lamjung, Nepal during the rainy season of 2018. The site is situated at 28.09°N latitude, 84.47°E longitude, and an altitude of 650 meters above mean sea level. Geographically the site is in the Gandaki province of Nepal.

Experimental design and genetic materials

The design of experiment was a RCBD with three replications and fifteen rice genotypes as the treatment as shown in **Table 1**. All the genetic materials were obtained from the Regional Agriculture Research Station (RARS), Khajura, Banke. Manabahu was used as the local check and Sukhadha-5 was used as the standard check. Twenty-five day old seedlings were transplanted in wells prepared in the puddled field. Seedlings were transplanted with a crop geometry of 20cm × 20cm and a plot area of $2m^2$, and then proper care was given with respect to water management, insect pest control, and nutrient management. Doses of 15 tons per ha of farmyard manure were applied at the time of land preparation and chemical fertilizer 60:20:20 NPK kg per ha in the forms of urea, di-ammonium phosphate (DAP), and potash, respectively. Full doses of phosphorus and potash and half doses of nitrogen were applied at basal doses while the remaining nitrogen was applied as split doses at the two stages of tillering and panicle initiation.

Data collection

Ten sample plants were observed for recording data. Observations were recorded for the phenological characteristics of days to booting, days to heading, and days to maturity; agro-morphological characteristics, namely plant height, flag leaf length, flag leaf area, panicle length, and soil plant analyzer development (SPAD) reading; yield and yield attributing characters, namely number of effective tillers per m^2, number of tillers per m^2, filled grains per panicle, grain yield, straw yield, harvest index, fertility percentage, and test weight (thousand-grain weight).

Calculation and statistical analysis

All taken data were tabulated and processed

Table 1. List of rice genotypes used in research

S.N.	Genotypes	Parents	Other details
1	Radha 11	Selection from TCA-80-4	Released variety
2	Chaite 5	PJ 17/ PJ 18	Released variety
3	NR-601-1-9	-	Genotypes
4	DRR 44	IR71700-2-47-1-1-2/IR 03L 120	Genotypes
5	NR 119	-	Genotypes
6	Radha 13	Masuri/ IR38701-49-2-6	Released variety
7	NR 1190	-	Genotypes
8	Bahuguni	IR81896-B-B-195/3*IR05F102	Released variety
9	Ghaiya 2	MTU/WKA, KAIKU	Released variety
10	Sawa Mansuli sub-1	Sambha masuri/ IR49830-7-1-2-3	Released variety
11	Sukhadhan-5*	IR 72022-46-2-3-3-2/ Swarna	Released variety
12	Chaite 4	BG 34-8/IR28/IR2095-625-1-2-32	Released variety
13	Manabahu**	-	Local landrace
14	Hardinath-1	BG951/3348/BW288-1-3	Released variety
15	Cheherang sub-1	Ciherang*2/IRRI 149	Released variety

*Note: *standard check, ** local check.*

through MS Excel version 19. The coefficient of variation (CV), mean, and analysis of variance (ANOVA) were computed using R studio version 3.6.1. Least significant difference (LSD) was computed at the 5% level of significance. Clustering of genotypes was done by Minitab version 14. PCV and GCV were computed using the formulas suggested by Chaudhary & Prasad (1968) and Deshmukh *et al*. (1986), respectively. Broad sense heritability, GA, and genetic advance as a percentage of the mean (GAM) were computed by the formulas given by Robinson *et al*. (1949), Johnson *et al*. (1955), and Falconer (1996), respectively.

Results and Discussion

Analysis of variance

The analysis of variance suggested that there were significant differences for all the agro-morphological and yield component traits of the studied rice genotypes as shown in **Table 2**. Similar results were reported by Bhandari *et al.* (2019). Adhikari *et al*. (2018) reported the existence of significant differences for days to flowering, maturity, plant height, panicle length, thousand-grain weight, and grain yield, which is accordance to our findings. Gyawali *et al.* (2018) evaluated seven rice varieties in Lamjung, Nepal and reported significant variation in the genotypes for the traits of days to booting, days to heading, days to anthesis, plant height, effective tillers per m^2, thousand-grain weight, straw yield, and harvest index.

Mean performance of the rice genotypes on the phenological and agro-morphological characteristics

The performance of the fifteen rice genotypes based on the phenological and agro-morphological traits are shown in **Table 3**. Brief explanations of each trait are given below.

Days to heading (DH)

Days to heading of the local landrace Manabahu (112 days) was found to be significantly higher and statistically on par with Sawa Mansuli sub-1, NR-601-1-9, and NR 1190. Hardinath-1 had the fewest days to heading (82 days) which was statistically on par with Chaite 4 and DRR 44. Hardinath-1 was one of the early genotypes and had a short vegetative phase and long reproductive phase.

Table 2. Mean sums of squares from ANOVA of the fifteen rice genotypes grown in Lamjung, 2018

Source of variation	Mean square		
	Replication	Genotype	Error
Characters	DF = 2	DF = 14	DF = 28
Days to booting	10.69	195**	13.81
Number of effective tillers per m^2	1153	5117**	532
Filled grains per m^2	2191	5963**	705
Flag leaf area	94.55	248**	35.47
Flag leaf length	6.24	70**	9.19
Fertility percentage	122.25	188**	28.144
Grains per panicle	1884	7883**	812
Grain yield (tons per ha)	0.957	3.22**	0.318
Days to heading	32.82	288**	13.56
Harvesting index	10.5	393**	22.2
Leaf area (cm^2)	50.22	111.4**	13.39
Days to maturity	4.2	624**	2.5
Panicle length	0.388	14.9**	0.69
Plant height (cm)	188.1	919.5**	31.7
SPAD (chlorophyll content)	4.74	12.6**	2.484
Straw yield (tons per ha)	3.001	20.71**	1.92
Test weight	0.12	66**	0.69
Number of tiller per m^2	2382	4624**	640.7

*Note: ** significant at the 1% level, DF = degree of freedom.*

Days to booting (DB)

The fewest days to booting was recorded for Hardinath-1 (75 days) which was statistically on par with Radha 11, Chaite 5, DRR 44, Bahuguni, Ghaiya 2, Chaite 4, and Cheherang sub-1. These genotypes were earlier in terms of initiation of the reproductive period. Manabahu showed the longest days to booting (102 days) and its reproductive phase started later.

Days to maturity (DM)

NR-601-1-9 showed the highest number of days to maturity (161 days) which was statistically on par with Manabahu, but Hardinath-1 (116 days) had the lowest number of days to maturity which was statistically on par with Chaite 5. This indicates that Hardinath-1 and Chaite 5 were early varieties, which can be selected for based on the variability analysis.

Plant height (PH) (cm)

The plant height of Radha 13 (147.1cm) was found to be significantly superior to all other genotypes and was followed by NR-601-1-9 (132.9cm), but Sawa Mansuli sub-1 (88.1cm) showed the shortest plant height which was statistically on par with Ghaiya 2 (90.8cm) and Chaite 5 (96.8cm).

SPAD reading for chlorophyll

Hardinath-1 showed the highest chlorophyll content at the heading stage (i.e. 60 days after transplanting) which was statistically on par with Chaite 5, NR 119, DRR 44, Cheherang sub-1, Chaite 4, and Radha 11, whereas NR 1190 had the lowest chlorophyll content.

Leaf area (LA) (cm^2)

Radha 13 showed significantly superior leaf area than all the other genotypes and was statistically on par with NR-601-1-9, whereas Sawa Mansuli sub-1 had the lowest leaf area.

Table 3. Performance of the rice genotypes on phenological and agro-morphological characteristics

S.N.	Phenological characteristics				Agro-morphological characteristics				
	Genotypes	BD	HD	MD	PH (cm)	SPAD	LA (cm^2)	FLA (cm^2)	FLL (cm)
1	Radha 11	80^{de}	90^{d}	127^{ef}	120.6^{cd}	39.37^{abcdef}	38.46^{bc}	37.29^{bc}	27.62^{cd}
2	Chaite 5	76^{e}	93^{cd}	118^{gh}	96.8^{ghi}	41.44^{ab}	29.62^{de}	26.67^{de}	25.37^{de}
3	NR-601-1-9	93^{b}	108^{ab}	161^{a}	128.3^{bc}	38.04^{cdefg}	42.84^{ab}	52.93^{a}	33.80^{ab}
4	DRR 44	79^{e}	88^{de}	126^{f}	108.2^{ef}	40.25^{abcd}	33.72^{cd}	27.38^{cde}	27.08^{cd}
5	NR 119	79^{de}	89^{d}	128^{ef}	113.8^{de}	40.30^{abc}	37.61^{bc}	32.36^{cd}	24.92^{de}
6	Radha 13	92^{bc}	104^{b}	145^{c}	147.1^{a}	35.50^{g}	45.96^{a}	50.85^{a}	31.29^{abc}
7	NR 1190	86^{cd}	108^{ab}	149^{b}	132.9^{b}	35.13^{g}	33.19^{cd}	42.95^{ab}	29.70^{bcd}
8	Bahuguni	81^{de}	97^{c}	135^{d}	104.1^{efg}	36.86^{efg}	29.22^{de}	32.87^{cd}	33.51^{ab}
9	Ghaiya 2	79^{de}	90^{d}	133^{d}	90.8^{hi}	37.31^{defg}	27.21^{de}	28.76^{cde}	29.04^{bcd}
10	Sawa Mansuli Sub-1	94^{b}	108^{ab}	149^{b}	88.1^{i}	38.84^{bcdef}	25.38^{e}	29.52^{cde}	33.75^{ab}
11	Hardinath-1	75^{e}	82^{e}	116^{h}	98.6^{fgh}	41.87^{a}	28.61^{de}	28.49^{cde}	19.58^{e}
12	Sukhadhan-5	79^{de}	91^{cd}	129^{e}	99.0^{fgh}	39.00^{bcdef}	27.76^{de}	28.20^{cde}	29.92^{bcd}
13	Chaite 4	76^{e}	83^{e}	121^{g}	102.8^{fg}	39.79^{abcde}	28.67^{de}	28.40^{cde}	20.32^{e}
14	Cheherang sub-1	80^{de}	93^{cd}	129^{ef}	102.0^{fg}	39.96^{abcd}	28.35^{de}	20.56^{e}	32.3^{abc}
15	Manabahu	102^{a}	112^{a}	161^{a}	132.8^{b}	36.65^{fg}	33.93^{cd}	31.80^{cd}	35.60^{a}
	F test	**	**	**	**	**	**	**	**
	CV(%)	13.810	3.83	1.158	5.066	4.07	11.18	17.89	10.47
	LSD(0.05)	6.21	6.15	2.62	9.41	2.63	6.12	9.96	5.06
	Grand Mean	83.68	96.04	135.46	111.11	38.7	32.7	33.27	28.92

Note: Mean value in a column having the different letter indicate significant difference at 0.01 level; (**)BD = days to booting, HD = days to heading, MD = days to maturity, PH = plant height, LA = leaf area, FLA = flag leaf area, FLL= flag leaf length, SPAD = soil plant analyzer development.

Flag leaf area (FLA) (cm^2)

NR-601-1-9 showed the highest flag leaf area which was statistically on par with Radha 13 and NR 1190, while Cheherang sub-1 had the lowest flag leaf area.

Flag leaf length (FLL) (cm)

Manabahu (35.6cm) had a significantly higher flag leaf length which was statistically on par with NR-601-1-9, Sawa Mansuli sub-1, Bahauguni, Cheherang sub-1, Radha 13, and Sukhadhan-5. The lowest flag leaf length was recorded for Hardinath-1 (19.58) which was statistically significant with Chaite 4.

Mean performance of the rice genotypes in the yield and yield attributing traits

The performance of the fifteen rice genotypes based on the yield and yield components traits are shown in **Table 4**. Brief explanations of each trait are given below.

Number of effective tillers per m^2 (ET)

Significantly higher number of effective tillers per m^2 were found in Ghaiya 2 which was statistically on par with Radha 11, NR 119, and Bahuguni, whereas NR-601-1-9 showed the lowest number of effective tillers per m^2 among all the genotypes. Radha 11, DRR 44, NR 119, Bahuguni, Ghaiya 2, Sawa Mansuli sub-1, Chaite 4, and Cheherang sub-1 were statistically on par with Sukhadhan-5.

Test weight (TW) (g)

NR-601-1-9 had a significantly higher test weight followed by Sukhadhan-5, Cheherang sub-1, Bahuguni, and DRR 44, whereas Sawa Mansuli sub-1 had the lowest thousand-grain weight among all the genotypes in this study. Bahuguni, Ghaiya 2, Radha 11, NR 119, Chaite 4, and Cheherang sub-1 were statistically on par with Sukhadhan-5.

Grains per panicle (GPP)

Radha 13 had a significantly higher number of grains per panicle, which was statistically on par with NR 1190, Chaite 5, and Manabahu. Cheherang sub-1 had the lowest number of grains per panicle and was statistically on par with Ghaiya 2, Bahuguni, Chaite 4, Hardinath-1, and Sukhadhan-5.

Straw yield (SY) (tons per ha)

NR-601-1-9 had significantly higher straw yield, which was statistically on par with NR-601-1-9, whereas the lowest straw yield per ha was recorded from Hardinath-1, which was statistically on par with Chaite 5, Ghaiya 2, Sawa Mansuli sub-1, Cheherang sub-1, Chaite 4, DRR 44, NR 119, Radha 11, Bahuguni, and Sukhadhan-5.

Number of tillers per m^2

Ghaiya 2 had a significantly higher number tillers per m^2, which was statistically on par with NR 1190, Radha 11, Bahuguni, and Chaite 4, but the NR-601-1-9 variety had the lowest number of tillers per m^2. All the varieties except NR-601-1-9, Radha 13, Hardinath-1, and Manabahu, showed a statistically similar number of tillers per m^2 with Sukhadhan-5.

Filled grains per panicle (FGPP)

Radha 13 had significantly higher number of filled grains per panicle, which was statistically on par with Chaite 5, NR 1190, NR 119, Radha 11, and Sawa Mansuli sub-1, whereas Ghaiya 2 had the lowest number of filled grains per panicle. NR-601-1-9, DRR 44, Bahuguni, Ghaiya 2, Hardinath-1, Chaite 4, and Cheherang sub-1 showed a statistically similar number of filled grains per panicle with Sukhadhan-5.

Panicle length (PL) (cm)

Manabahu had significantly longer panicles among all the genotypes studied, followed by Radha 13 and NR-601-1-9, whereas Sawa Mansuli sub-1 had the lowest panicle length.

Harvesting index (HI) (%)

Hardinath-1 had a significantly higher harvesting index, which was statistically on par with Chaite 5, Sukhadhan-5, Radha 11, and Chaite 4, but the lowest HI values were in Manabahu and NR-601-1-9.

Grain yield (GY) (tons per ha)

The grain yield of Radha 11 (5.78 tons per ha) was found to be significantly superior and statistically on par with Sukhadhan-5, NR 119, Radha 13, DRR 44, and Bahauguni, whereas Manabahu had lowest grain yield (2.33 tons per ha), which was statistically on par with NR-601-1-9, Sawa Mansuli sub-1, and NR 1190.

Fertility percentage (F) (%)

Cheherang sub-1 showed a significantly higher fertility percentage, which was not statistically significant with Sawa Mansuli sub-1, NR 119, Chaite 5, Radha 11, Bahuguni, Ghaiya 2, Radha 13, and Sukhadhan-5, whereas NR-601-1-9 had lowest fertility percentage.

Genetic variability

Estimation of the genetic variability was performed to determine the heritable and non-heritable portion of concerned traits, which is crucial in adopting breeding methods. The heritable portion of the overall observed variation can be determined by studying the components of variation such as the coefficients of genotypic and phenotypic variability, heritability, genetic advance, and genetic advance

Table 4. Performance of the rice genotypes on the yield and yield attributing characteristics

S.N.	Genotypes	Yield and yield attributing characteristics									
		ET	TW (g)	GPP	SY (tons per ha)	Tillers m^{-2}	FGPP	PL (cm)	HI	GY (tons per ha)	F (%)
1	Radha 11	248^{a}	16.6^{fg}	202^{cd}	6.45^{cde}	281^{abc}	179^{abc}	24.51^{def}	47.15^{abc}	5.78^{a}	88.26^{ab}
2	Chaite 5	171^{de}	$17.^{fg}$	228^{abc}	4.51^{de}	218^{def}	203^{ab}	22.26^{gh}	49.70^{ab}	4.47^{bc}	88.67^{ab}
3	NR-601-1-9	126^{f}	30.0^{a}	185^{cde}	12.69^{a}	179^{f}	114^{d}	26.19^{bc}	17.33^{ef}	2.67^{e}	60.71^{e}
4	DRR 44	194^{cde}	24.1^{c}	171^{def}	5.78^{de}	221^{def}	132^{cd}	23.98^{def}	45.20^{bcd}	4.78^{abc}	78.23^{cd}
5	NR 119	246^{a}	16.1^{g}	209^{bcd}	6.17^{cde}	289^{ab}	190^{ab}	24.94^{cd}	44.39^{bcd}	4.95^{abc}	90.55^{a}
6	Radha 13	156^{ef}	21.4^{de}	267^{a}	8.43^{bc}	201^{ef}	222^{a}	26.72^{b}	38.93^{cd}	4.89^{abc}	83.45^{abcd}
7	NR 1190	168^{ef}	20.6^{e}	254^{ab}	8.92^{b}	218^{def}	200^{ab}	24.61^{de}	25.96^{e}	3.08^{de}	79.26^{bcd}
8	Bahuguni	238^{ab}	26.01^{b}	123^{fg}	6.59^{cd}	274^{abc}	105^{d}	26.14^{bc}	41.83^{bcd}	4.73^{abc}	85.43^{abc}
9	Ghaiya 2	251^{a}	24.04^{c}	117^{fg}	4.74^{de}	303^{a}	97^{d}	23.04^{fg}	45.35^{bc}	3.91^{cd}	83.55^{abcd}
10	Sawa Mansuli sub1	202^{bcd}	13.69^{h}	192^{cd}	5.38^{de}	240^{cde}	176^{abc}	21.09^{h}	36.29^{d}	2.92^{e}	90.61^{a}
11	Hardinath-1	152^{ef}	21.14^{e}	137^{efg}	3.95^{e}	182^{f}	109^{d}	22.30^{gh}	53.793^{a}	4.57^{bc}	79.57^{bcd}
12	Sukhadhan-5	225^{abc}	26.98^{b}	137^{efg}	5.88^{cde}	263^{abcd}	113^{d}	23.28^{efg}	48.20^{ab}	5.49^{ab}	82.29^{abcd}
13	Chaite 4	225^{abc}	22.87 cd	130^{efg}	5.59^{de}	271^{abc}	104^{d}	24.56^{def}	46.03^{abc}	4.58^{bc}	80.06^{bcd}
14	Cheherang sub-1	208^{abcd}	26.35^{b}	111^{g}	5.53^{de}	246^{bcde}	102^{d}	23.64^{defg}	44.28^{bcd}	4.41^{c}	91.60^{a}
15	Manabahu	149^{ef}	17.79^{f}	221^{abcd}	12.25^{a}	208^{ef}	170^{bc}	30.24^{a}	16.07^{f}	2.33^{e}	74.48^{d}
F-test		**	**	**	**	**	**	**	**	**	**
CV(%)		11.66	3.82	15.87	20.191	10.54	17.92	3.40	11.76	13.29	6.434
LSD(0.05)		38.56	1.38	47.66	2.31	42.33	44.39	1.39	0.07	0.94	8.87
Grand mean		197.64	21.67	179.5	6.86	239.95	148.07	24.5	40	4.24	82.44

Note: Mean value in a column having the different letter indicate significant difference at 0.01 level (**); ET = number of effective tillers per m^{2}, TW = test weight, GPP = grains per panicle, SY = straw yield, FGPP = number of filled grains per panicle, PL = panicle length, HI = harvesting index, GY = grain yield, F(%) = fertility percentage; Values in the same column with different superscripts are significantly different.

as a percentage of the mean, which is a prerequisite for the improvement of crop.

GCV and PCV

Estimated values of the GCV and PCV for all the traits evaluated in this study are shown in **Table 5**. The coefficients of variation of the studied traits showed that the values of the PCV were slightly more than the GCV for all the traits. This indicates the presence of environmental influence in the expression of these traits (Rasel *et al*., 2018). Earlier researcher on rice, such as Kumar *et al.* (2018) and Srivastava *et al.* (2017), reported similar results. A wide range of PCVs were observed for traits ranging from 6.26 for chlorophyll content to 41.70 for straw yield. Similarly, the GCV varied from 4.75 for chlorophyll content to 36.48 for straw yield.

High GCVs and PCVs were recorded for straw yield, filled grains per panicle (28.27 and 33.48), harvesting index (27.77 and 30.16), grains per panicle (27.04 and 31.36), flag leaf area (25.27 and 30.97), grain yield (23.19 and 26.73), and test weight (21.53 and 21.87). Kumar *et al.* (2018) identified high GCVs and PCVs for effective tillers per m^2, filled grains per panicle, thousand-grain yield, harvesting index, and grain yield, which is accordance with our findings.

Table 5. Estimations of variability, heritability, and genetic advances in rice

Traits	GCV	PCV	H(%)	GA	GAM
BD	9.29	10.30	81.41	14.46	17.27
ET	19.78	22.97	74.18	69.36	35.09
FGPP	28.27	33.48	71.31	72.83	49.18
FLA (cm^2)	25.27	30.97	66.59	14.14	42.48
FLL (cm)	16.68	16.74	99.19	9.90	34.21
F (%)	8.85	10.95	65.45	12.17	14.76
GPP	27.05	31.36	74.38	86.25	48.05
GY (tons per ha)	23.19	26.73	75.27	1.76	41.45
HD	9.96	10.67	87.09	18.39	19.15
HI (%)	27.77	30.16	84.77	21.09	52.67
LA (cm^2)	17.49	20.76	70.95	9.92	30.34
MD	10.63	10.69	98.81	29.49	21.77
PL (cm)	8.89	9.52	87.23	4.19	17.11
PH (cm)	15.48	16.29	90.32	33.68	30.31
SPAD	4.75	6.26	57.60	2.87	7.42
SY (tons per ha)	36.48	41.70	76.54	4.51	65.75
TW (g)	21.53	21.87	96.93	9.46	43.66
TP	15.18	18.49	67.44	61.64	25.69

Note: H = heritability, GA = genetic advance, GAM = genetic advance of mean, BD = days to booting, ET = number of effective tillers per m^2*, FGPP = number of filled grains per panicle, FLA = flag leaf area, FLL = flag leaf length, F(%) = fertility percentage, GPP = grains per panicle, GY = grain yield, HD = days to heading, MD = days to maturity, PL = panicle length, PH = plant height, SY = straw yield, TW = test weight, TP = tillers per* m^2

Similarly, high GCVs and PCVs were recorded by Prasad *et al*. (2017) for grain yield, filled grains per panicle, thousand-grain weight, and effective tillers per m^2, and by Srivastava *et al.* (2017) for filled grains per panicle. High GCVs and PCVs indicate the presence of high variance in the traits and less influence of the environment in the expression of these traits, hence, direct selection may be effective for improvement of these traits (Srivastava *et al*., 2017). Bhandari *et al*. (2019) reported high GCVs and PCVs for thousand-grain weight, straw yield, leaf area, grain yield, and effective tillers per m^2.

Moderate values of the GCV and PCV were recorded for leaf area, effective tillers per m^2 (19.78 and 22.97), plant height (15.48 and 16.29), numbers of tillers per m^2 (15.18 and 18.49), and days to maturity (10.63 and 10.69). Similar results were also observed by Kumar *et al*. (2018) for days to maturity and plant height, as well as by Akhtar *et al.* (2011) and Babar *et al*. (2009). These values indicate the higher effect of the environment in the expression of these traits.

Low values of the GCV and PCV were recorded for days to booting (9.29 and 10.30), panicle length (8.89 and 9.52), fertility percentage (8.85 and 10.95), days to heading (9.96 and 10.67), and SPAD (4.75 and 6.26). Moderate GCVs but high of PCVs were recorded for leaf area (17.49 and 20.76) and effective tillers (19.78 and 22.97) indicating the high influence of the environment on the expression of these traits.

Low estimates of the GCV and PCV were exhibited by fertility percentage (8.85 and 10.95), panicle length (8.89 and 9.52), and chlorophyll content (4.75 and 6.26). Similarly, Prasad *et al.* (2017) and Srivastava *et al*. (2017) recorded low GCVs and PCVs for panicle length. These characteristics may be expressed by non-additive genes and the possibility of improvement of yield through selection by employing recombination breeding (Srivastava *et al*., 2017). Panicle length is a valuable and important trait for yield improvement (Rasel *et al*., 2018).

Heritability (broad sense heritability)

Estimation of the genetic variability, which is crucial in determining breeding methods, was performed to determine the heritable and non-heritable portions of the concerned traits. Calculating the heritable portion of the overall observed variation is a prerequisite for the improvement of crop and can be determined by studying the components of variation such as the coefficients of genotypic and phenotypic variability, heritability, genetic advance, and genetic advance as a percentage of the mean. Broad sense heritability was calculated for all the traits evaluated in this study. Calculated values of heritability for these traits are presented in **Table 6**. The traits investigated in the present study expressed low to high broad sense heritability estimates ranging from 19.4% to 99.1%.

Estimates of broad sense heritability were high for flag leaf length (99.19%), days to maturity (98.80%), thousand-grain weight (96.92%), plant height (90.32%), leaf length (89.87%), panicle length (87.23%), days to heading (87.09%), harvesting index (84.77%), days to booting (81.41%), straw yield (76.54%), grain yield (75.26%), grains per panicle (74.37%), effective tillers (74.17%), filled grains per panicle (71.31%), leaf area (70.94%), tillers per m^2 (67.43%), flag leaf area (66.59%), and fertility percentage (65.44%). Medium broad sense heritability was recorded for SPAD (57.60%). Similarly, Abebe *et al*. (2017) recorded high values of broad sense heritability for plant height, biomass yield, and panicle length. Srivastava *et al.* (2017) recorded high values of broad sense heritability for grains per panicle, filled grains per panicle, plant height, flag leaf length, and grain yield. Panwar *et al.* (2007) and Akinwale *et al.* (2011) recorded high values of broad sense heritability for all the traits in their studies. High values of broad sense heritability were recorded for days to maturity, days to flowering grain yield, straw yield, and plant height by Roy *et al.* (2015).

High values of broad sense heritability indicate that the traits being studied have the scope to improve through selection. These traits are less influenced by the environment and could be successfully transferred to the next generations if utilized in a hybridization program so that superior genotypic selection can be made through simple selection. Low heritability of traits indicates more influence of the environment in the phenotypic expression of that trait and hence, selection based on progeny or family testing should be done.

Genetic advance

Genetic advance as a percentage of the mean was found to be highest for straw yield (65.75%) followed by harvesting index (52.67%), filled grains per panicle (49.18%), grains per panicle (48.04%), thousand-grain weight (43.66%), flag leaf area (42.48%), grain yield (41.45%), effective tillers per m^2 (35.09%), flag leaf length (42.48%), leaf area (30.34%), plant height (30.31%), tillers per m^2 (25.69%), and days to maturity (21.76%). Similar high values of genetic advance as a percentage of the mean were previously recorded by Srivastava *et al.* (2017) for plant height, flag leaf length, number of grains per panicle, filled grains per panicle, test weight, and grain yield per plant. Medium genetic advance as a percentage of the mean values were found for days to booting (17.23%), panicle length (17.11%), days to heading (19.15%), and fertility percentage (14.75%). Low genetic advance as a percentage of the mean was found for SPAD reading (7.42%). High heritability coupled with high genetic advance as a percentage of the mean were recorded for days to maturity, number of tillers per m^2, plant height, leaf area, flag leaf length, effective tillers per m^2, grain yield, flag leaf area, test weight, panicle density, grains per panicle, filled grains per panicle, harvesting index, and straw yield.

High GCVs and PCVs, heritability, and genetic advance as a percentage of the mean were recorded for straw yield, harvesting index, filled grains per panicle, grains per panicle, thousand-grain weight, flag leaf area, grain yield, effective tillers per m^2, and leaf area. These characteristics with high values of the GCV, PCV, and heritability

Table 6. Phenological, agro-morphological, and yield attributing traits of the rice genotypes within and among four clusters

Variable	Cluster I	Cluster II	Cluster III	Cluster IV	Grand centroid
BD	79.33	83.25	89.16	84.50	83.68
HD	91.26	94.08	104.50	95.00	96.04
MD	129.60	132.83	143.75	138.83	135.46
PH (cm)	99.77	107.70	127.45	113.54	111.10
SPAD	38.58	39.69	37.18	39.96	38.69
LA (cm^2)	28.24	33.79	35.68	35.72	32.70
FLL (cm)	29.02	28.34	30.49	26.69	28.92
FLA (cm^2)	27.76	31.64	38.07	40.71	33.27
PL (cm)	24.13	23.63	25.95	24.24	24.50
ET	229.66	223.00	161.50	139.16	197.64
Tillers m^2	271.66	258.16	211.66	180.83	239.95
FGPP	104.66	169.42	199.18	111.68	148.07
GPP	124.25	194.10	243.12	161.20	179.50
TW (g)	25.24	17.64	19.28	25.58	21.67
SY (tons ha^{-1})	5.67	5.94	8.53	8.32	6.86
GY (tons ha^{-1})	4.62	4.61	3.69	3.62	4.24
HI (%)	45.14	43.25	32.66	35.56	40.03
F (%)	84.58	86.91	81.46	70.14	82.44

Note: BD = days to booting, ET = number of effective tillers per m^2, FGPP = number of filled grains per panicle, FLA = flag leaf area, FLL = flag leaf length, F(%) = fertility percentage, GPP = grains per panicle, GY = grain yield, HD = days to heading, MD = days to maturity, PL = panicle length, PH = plant height, SY = straw yield, TW = test weight, TP = tillers per m^2

accompanied by high genetic advance as a percentage of the mean might be transmitted to their progenies and therefore, phenotypic selection based on these characteristics would be effective. Panse (1957) stated that high values of heritability with low genetic advance indicated that the heritability was probably due to the effects of non-additive gene action. In general, the characteristics that show high heritability with high genetic advance are controlled by additive gene action (Patil & Lokesha, 2003) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance (Johnson *et al*., 1955). The characteristics showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of a segregating population developed from combination breeding.

Cluster analysis

Cluster analysis of the fifteen rice genotypes in this study showed that the genotypes exhibited considerable genetic variability among themselves by occupying four clusters as shown in **Table 6**. These rice genotypes were grouped based on phenological, agro-morphological, and yield related traits, namely days to booting, number of effective tillers per m^2, filled grains per panicle, flag leaf area, flag leaf length, fertility percentage, grains per panicle, grain yield, days to heading, harvesting index, leaf area, days to maturity, panicle length, plant height, SPAD reading, straw yield, test weight, and number of tillers per m^2.

Cluster analysis showed that cluster I was comprised of five genotypes, cluster II consisted of four genotypes, cluster III was comprised of four genotypes, and cluster IV consisted of two genotypes (**Figure 1**). Cluster II genotypes were characterized as having the highest fertility, smallest palnicle lengths, and lowest thousand-grain weights. Cluster III genotypes had the lowest SPAD readings at the time of flowering, and the longest number of days for booting, anthesis, and harvesting. It was also characterized by having the longest panicle lengths, largest numbers of grains per panicle, largest numbers of filled grains per panicle, and highest straw yields but lowest harvesting indicies.

Cluster IV contained the genotypes with the highest SPAD readings at the time of flowering, largest leaf areas, flag leaf areas, and thousand-grain weights, in addition to the lowest flag leaf lengths, and lowest numbers of total and effective tillers per m^2. Cluster I had the genotypes that were earliest in terms of booting, heading, and days to maturity, lowest leaf areas, lowest flag leaf areas, and lowest numbers of filled grains per panicle and grains per panicle. It was comprised of genotypes with the highest grain yields, harvesting indicies, and numbers of effective tillers per panicle.

Conclusions

The analysis of variance study showed the presence of adequate phenotypic variability among the tested genotypes for all the traits in this study. From the mean performance analysis, it was found that Radha 11 can be selected for higher grain yield. Radha 13 can be selected for grains per panicle, tallest plant height, and leaf area. Ghaiya 2 can be selected for the largest number of panicles per m^2 and effective tillers per m^2. Hardinath-1 can be selected for maximum flag leaf area, chlorophyll content, and earlier heading and maturity, while the local landrace (Manabahu) also had a high values for panicle length, straw yield, flag leaf length, and maximum days to heading, booting, and maturity, and can be selected for these traits. The PCV was greater than the GCV for all the traits being studied, meaning that some degree of environmental influence was present in the expression of these traits. A small difference between the CGV and PCV suggests less influence of the environment on the expression of the traits. High GCVs and PCVs, higher broad sense heritability, and higher GAM of the traits

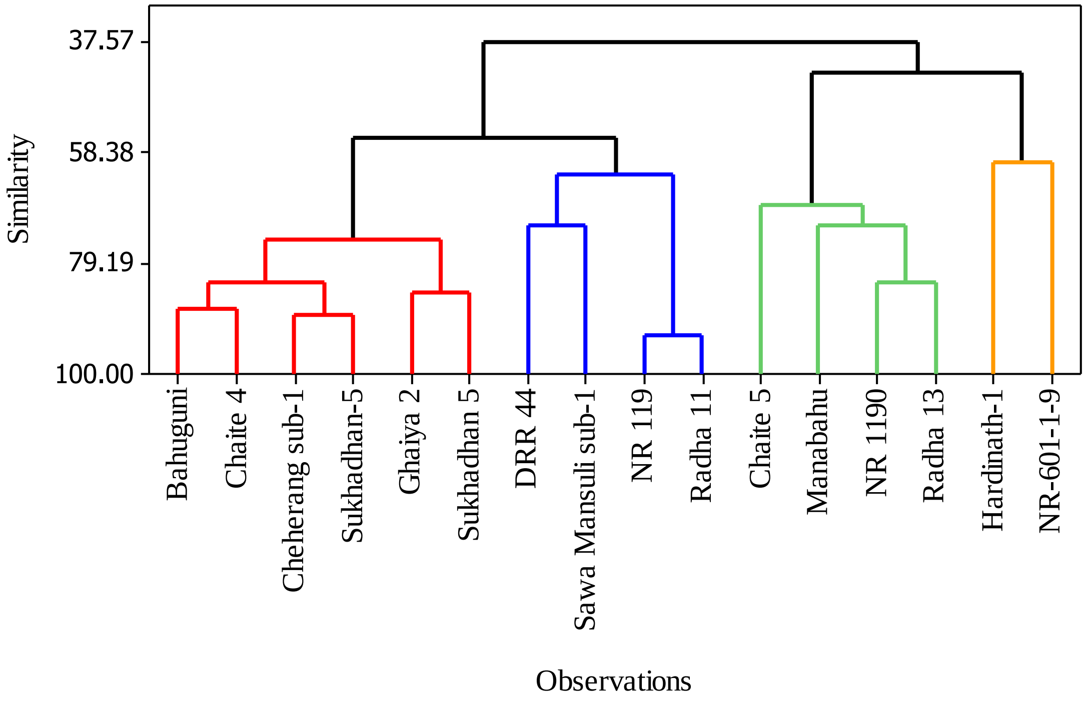

Figure 1. Cluster analysis showing the presence of variability among the tested genotypes and groupings of four distinct genotype clusters based on the phenological, agromorphological, and yield attributing characteristics

straw yield, filled grains per panicle, harvesting index, grains per panicle, flag leaf area, grain yield, thousand-grain weight, effective tillers per m^2, and leaf area indicates that there is less influence of the environment in the expression of these traits. A higher proportion of variability is heritable and improvement can be made for these traits in the next generation through direct selection. High broad sense heritability and genetic advance for these traits indicate the presence of additive gene interaction in the expression of quantitative traits and showed more opportunity for selection of these traits for improvements in yield. Cluster analysis showed the presence of considerable genetic variability among the genotypes for further improvement of the genotypes.

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