



Evaluation of Advanced Rice Genotypes of National Irrigated Rice Observation Nursery (NIRON)

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Abstract: Rice is major cereal crop for food and nutritional security of Nepalese people. The study aimed screening of superior genotypes based on quantitative traits for irrigated condition. The research was carried out at National Rice Research Program (NRRP), Hardinath in 2019. The augmented randomized complete block design was adopted with six blocks. The study tested ninety advanced breeding materials developed through conventional breeding method as testing materials and six released varieties as replicated checks. The yield attributing traits such as days to heading, days to maturity, plant height, panicle length, filled grain percentage per panicle and grain yield ton per ha were recorded. ANOVA, descriptive statistics, genetic variability and cluster performance were determined to the studied traits and genotypes. All traits showed significant differences among genotypes at 1% and 5% level of significance due to different genetic loadings of parents used in crosses. The highest GAM, PCV and GCV recorded for grains yield per ha. Broad-sense heritability recorded highest to phenological traits followed by filled grain percentage, plant height and panicle length. The grain yield had positive and highly significant ($p < 0.01$) relation with filled grain percentage. The phenological traits showed positive and highly significant correlation with each other. A circular dendrogram based on five traits (MD, PH, PL, FGP, AGY) grouped into seven clusters. Cluster 1, 2, 3 and 5 grouped early maturity type, good filled grain percentage, short plant height, and high yielding with good filled grain percentage genotypes, respectively. The high heritability coupled with genetic gain helps in precise selection of traits for further improvement. High heritability coupled with genetic advance and GCV values found for days to heading, days to maturity, filled grain percentage and plant height. This allows the selection of these traits directly for improvement because of presence of additive gene action.

Keywords: Rice, Variability, Heritability, Correlation, Dendrogram.

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Introduction

Rice is prominent and staple cereal food for millions of Nepalese people. The increasing rate of population in Nepal reflects the demand of rice inflating every year but the production is still not satisfactory. Food security of Nepal merely depends upon the production of rice which has been grown in 1.47 million hectare area and produced 5.1 million ton (MoAD 2022). About 56% area under irrigated condition and 39% area under rainfed lowland of total rice cultivated area in Nepal (Tripathi et al., 2019). To address the food security, development of high yielding rice varieties is emphasized by all stakeholders engaged in rice production. Rice research for irrigated regions in Nepal, National Rice Research Program (NRRP) of Nepal Agricultural Research Council (NARC)

has been conducting research activities and tested on multi stations across varied climatic zones for Terai regions. Breeding program National Irrigated Rice Observation Nursery (NIRON) conducted by NRRP has preliminary evaluation for normal season irrigated condition from intensive selection of thousands of segregating lines progressed throughout up to 7th Generation. The resultant high yielding, disease and insect pest resistant genotypes further validated through evaluation in advanced yield trials across different locations. However, more than 92 rice varieties have been released till date where half of the total varieties are being cultivated in Terai region throughout the country (MoAD 2022) but the production is not satisfactory to address the demand.

The efficient breeding program requires the knowledge of presence of genetic variability within and among genotypes. The variability

might be heritable and non heritable due to the presence of additive and non additive gene action. The magnitude of heritable variation helps to select the genotypes based on traits and can be incorporate in crop improvement program (Dutta et al., 2013). The understanding of genetic variability and relationship of yield and yield attributing traits have aided the guidance for crop improvement. The selection of genotype based on broadsense heritability alone misguided due to influence of environmental effects and heritable portion of variation are not always due to additive gene action (Dutta et al., 2013). Therefore, broadsense heritability in coupled with genetic advances as percentage of mean helps to predict the genetic gain under selection (Ogunbayo et al., 2014).

The cluster analysis using euclidean distance helps to measure genetic diversity existed in genotypes and grouped them based on the resembling characters. Ward's method applied in hierarchical cluster analysis which minimizes the total within cluster variance. The clustering provides an opportunity for gene constellation of diverse nature of genotypes based on traits which are responsible for genetic diversity for good hybridization program (Singh and Chaudhary, 1977) and Chanbeni *et al.* (2012).

The present study aimed to identify the superior genotypes for irrigated condition based on genetic variation existing in advance breeding rice lines/ genotypes by estimation of genetic parameter, trait association and clustering of genotypes.

Material and Methods

Experimental location

The research was conducted at National Rice Research Program (NRRP), Hardinath in 2019. The site, typical rice growing lowland was located in latitude of 26°49'N, longitude of 85°58' E with mean elevation of 93 meter above sea level with soil pH 6.3. The experimental area's precipitation occurs between June and September where maximum rainfall happens in July month.

Source of materials

The testing genotypes were developed by hybridization between local and modern inbred lines or released cultivars. Advanced breeding materials (homozygous lines bulked from F7 generation) derived from pedigree breeding method in the irrigated ecosystem crossed at NRRP, Hardinath and commercial varieties as checks were evaluated under National Irrigated Rice Observation Nursery (NIRON) presented in Table 1 and 2.

Experiment layout and traits recorded

Augmented Randomized Complete Block design with six blocks was laid out for evaluation of Ninety homozygous advanced breeding lines used as non replicated entries and six checks, Hardinath-1, Ramdhan, Radha-4, Samba Masuli sub-1, Lalka basmati and Sabitri as replicated entries. Each block consisted of 21 genotypes including checks. Each genotype was tested in 8m² plot size. The twenty five to thirty days old seedlings were transplanted manually at a hill spacing 20X20cm. The recommended fertilizer dose of 100:30:30 N:P₂O₅:K₂O kg/ha was used for nutrient management. Half of all nitrogen and full dose of

potash and phosphorous was used as basal in transplanting time. Remaining half nitrogen was split into two dosages as topdress at tillering stage and heading stage. Plant protection measurement and management was adopted as per standard protocol of IRRI.

The yield attributing traits such as days to heading, days to maturity, plant height, panicle length, filled grain percentage per panicle and grain yield ton per ha were recorded. The heading and maturity data were recorded from 80% fully exerted panicle and ripen stage (late dough) respectively. Plant height, panicle length and filled grain percentage were recorded from 5 randomly selected plants. The filled grain percentage was calculated by ratio of filled grain number and total grain number of panicle. Disease and insect pest damage were not recorded; however some of entries were infested.

Statistical analysis

ANOVA, descriptive statistics, genetic variability and cluster performance were determined to the studied traits and genotypes. The cluster analysis was performed using Euclidean distance and Ward's method to group the genotypes based on similarity of trait value. Genetic parameters such as variance (genotypic, phenotypic, environment), coefficient of variance (genotypic, phenotypic, environment), broad-sense heritability, genetic advance, and genetic advance as percentage of mean were recorded. R software with packages of augmented RCB, variability, Circular dendrogram, ggplot2, ggtree, Stats were used for analysis.

PCV and GCV were calculated according to Burton (1951, 1952) as follows:

$$PCV = \frac{\sigma_p^2}{\sqrt{\bar{x}}} \times 100$$

$$GCV = \frac{\sigma_g^2}{\sqrt{\bar{x}}} \times 100$$

And categorized according to Sivasubramanian and Madhavamenon (1973) as CV% =10 (low), 10≤ X<20 (medium) and ≥20(high).

Similarly, Broad sense heritability (H²) calculated by Lush(1940) and categorized by Robinson(1966) as follows:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

H²= <30(low), 30≤ X<60 (medium), and ≥60(high).

Genetic advance (GA) and Genetic advance as percentage of mean (GAM) were calculated and categorized according to Johnson et al (1955).

$$GA = kX\sigma_gX \frac{H^2}{100}$$

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Categorized as follows, GAM= <10(low), 10≤ X<20 (medium) and ≥20 (high).

Table1. Nepal Rice code, homozygous lines number (number of families) and their crossing parents used in NIRON 2019

SN	Nepal Rice (NR) code	No. of lines within family studied	Crossing parents
1	NR 2286	2	Ramdhan/IR83388-B-B-108-3 (Sukkha Dhan 5)
2	NR 2184-190-2-1-1-1-1	1	Kanchi Masuli/Ramdhan
3	NR 2187	17	Swarna Sub-1/Sabitri
4	NR 2188	7	IR 80310-12-B-B/Hardinath-1
5	NR 2189	2	Sabitri/IR 90250-B-475-1-B
6	NR 2190	2	Sabitri/IR 87754-43-2-2-1
7	NR 2191	24	Mithila/IR 87707-446-B-B-B (Sukkha dhan 4)
8	NR 2192-66-3-1-3-1	1	Rato Basmati/Sabitri
9	NR 2193	2	Sabitri/IR 81896-B-B-68-B
10	NR 2194	4	Radha 4/ IR 87705-83-12-B (Yaenelo 7, Myanmar variety)
11	NR 2195-22-1-1-2-1	1	Sabitri/IR 87705-83-12-B (Yaenelo 7, Myanmar variety)
12	NR 2199	17	Radha 4/Kalanamak
13	NR 2207-33-1-2-3-1	1	Sabitri/IR 74371-70-1-1 (Sukkhadhan-3)
14	NR 2212-9-1-1-1-1	1	Radha 12/Samba Masuli Sub-1
15	NR 2210-15-1-1-3-1	1	IASAAR 32/Sabitri
16	NR 2264	6	Radha 4/ ZHONG H 471
17	NR 2265-10-3-2-1	1	Katarni/Samba Masuli sub-1
	Total	90	

Table 2. Treatment list with checks used in NIRON 2019

TRT	Genotype	TRT	Genotype	TRT	Genotype
Check1	Hardinath-1	GEN27	NR 2191-6-2-4-5-1	GEN59	NR 2199-38-3-1-3-1
Check 2	Ramdhan	GEN28	NR 2191-22-1-4-1-1	GEN60	NR 2199-50-1-1-4-1
Check 3	Radha-4	GEN29	NR 2191-39-1-1-2-1	GEN61	NR 2199-54-2-1-4-1
Check 4	Samba Masuli sub-1	GEN30	NR 2191-39-2-1-4-1	GEN62	NR 2199-54-2-1-6-1
Check 5	Lalka Basmati	GEN31	NR 2191-39-2-2-2-1	GEN63	NR 2199-63-1-1-1-1
Check 6	Sabitri	GEN32	NR 2191-40-1-4-3-1	GEN64	NR 2212-9-1-1-1-1
GEN1	NR 2286-18-2-1-1-1	GEN33	NR 2191-41-1-1-3-1	GEN65	NR 2191-38-2-2-1-1
GEN2	NR 2187-2-1-1-2-1	GEN34	NR 2191-49-2-5-2-1	GEN66	NR 2187-33-2-3-4-1
GEN3	NR 2187-2-1-1-2-2	GEN35	NR 2191-50-1-1-2-1	GEN67	NR 2210-15-1-1-3-1
GEN4	NR 2187-2-1-2-1-1	GEN36	NR 2191-50-3-1-1-1	GEN68	NR 2199-19-1-1-2-1
GEN5	NR 2187-2-1-4-2-1	GEN37	NR 2191-50-3-3-2-1	GEN69	NR 2191-21-1-1-1-1
GEN6	NR 2187-4-1-1-1-1	GEN38	NR 2191-71-1-1-1-1	GEN70	NR 2191-80-1-2-1-1
GEN7	NR 2187-6-2-2-1-1	GEN39	NR 2191-122-2-1-1-1	GEN71	NR 2187-2-1-4-1-1
GEN8	NR 2187-6-4-3-3-4	GEN40	NR 2191-156-1-2-1-1	GEN72	NR 2187-25-2-7-4-1
GEN9	NR 2187-6-5-2-1-2	GEN41	NR 2191-172-2-1-1-1	GEN73	NR 2286-9-1-3-1-1
GEN10	NR 2187-21-2-2-3-2	GEN42	NR 2191-188-2-1-1-1	GEN74	NR 2264-4-1-6-3
GEN11	NR 2187-25-1-3-3-1	GEN43	NR 2191-205-2-1-1-1	GEN75	NR 2264-4-1-6-4

GEN12	NR 2187-25-2-2-2-1	GEN44	NR 2191-205-2-1-1-3	GEN76	NR 2264-4-1-6-5
GEN13	NR 2187-25-4-5-4-2	GEN45	NR 2191-236-3-1-3-1	GEN77	NR 2264-4-3-2-1
GEN14	NR 2187-32-4-1-1-5	GEN46	NR 2191-240-1-1-3-1	GEN78	NR 2264-4-3-2-2
GEN15	NR 2188-6-1-2-3-1	GEN47	NR 2192-66-3-1-3-1	GEN79	NR 2264-4-3-2-3
GEN16	NR 2188-13-2-3-1-1	GEN48	NR 2193-6-1-2-1-1	GEN80	NR 2265-10-3-2-1
GEN17	NR 2188-38-2-5-1-1	GEN49	NR 2193-6-6-1-1-4	GEN81	NR 2184-190-2-1-1-1-1
GEN18	NR 2188-43-1-2-1-2	GEN50	NR 2194-10-1-2-3-1	GEN82	NR 2187-25-2-3-2-1
GEN19	NR 2188-43-1-2-1-4	GEN51	NR 2194-10-1-2-3-2	GEN83	NR 2199-14-1-2-1-1
GEN20	NR 2188-43-1-2-2-1	GEN52	NR 2194-10-1-2-3-5	GEN84	NR 2199-14-1-2-2-2
GEN21	NR 2188-43-1-2-2-5	GEN53	NR 2194-32-1-1-3-1	GEN85	NR 2199-14-1-2-1-2
GEN22	NR 2189-1-1-1-2-1	GEN54	NR 2195-22-1-1-2-1	GEN86	NR 2199-38-3-1-1-1
GEN23	NR 2189-11-4-1-2-1	GEN55	NR 2199-14-1-2-2-1	GEN87	NR 2199-38-3-1-4-1
GEN24	NR 2190-4-2-1-3-4	GEN56	NR 2199-19-1-1-1-1	GEN88	NR 2199-50-1-2-1-1
GEN25	NR 2190-59-1-2-1-1	GEN57	NR 2199-22-1-2-3-1	GEN89	NR 2199-63-1-1-1-2
GEN26	NR 2191-1-2-2-1-3	GEN58	NR 2199-38-3-1-2-1	GEN90	NR 2207-33-1-2-3-1

Result

Significance test of yield attributing traits

The block adjusted analysis of variance showed statistical significant differences ($p < 0.01$, $p < 0.05$) among tested genotypes, commercial checks and genotype opposed to check were recorded to all studied traits (Table 3). Adjusted grain yield showed

significant differences ($p < 0.05$) for tested genotypes whereas all traits showed highly significant differences among genotypes ($p < 0.01$). Except for plant height, blocks showed non significant differences for all traits. Residual effects of the tested genotypes were observed less effect in adjusted grain yield followed by panicle length, phonological traits.

Table 3. Analysis of variance by adjusting block (Anova Block Adjusted) of NIRON, 2019

Source	Df	HD	MD	PH	PL	FGP	AGY
Treatment (ignoring Blocks)	95	325.56 **	317.01 **	209.48 **	6.92 **	87.02 **	1.64 **
Treatment: Check	5	1568.38 **	1477.31 **	834.83 **	40.02 **	74.53 **	7.89 **
Treatment: Test vs. Check	1	597.96 **	620.2 **	41.62 ns	8.45 *	362.38 **	8.24 **
Treatment: Test	89	252.68 **	248.41 **	176.23 **	5.04 **	84.63**	1.22 *
Block (eliminating Treatments)	5	2.91 ns	3.24 ns	186.49 **	1.74 ns	3.36 ns	0.31 ns
Residuals	25	3.96	2.9	36.97	1.49	8.99	0.63
ns denotes $p > 0.05$; *denotes $p \leq 0.05$; **denotes $p \leq 0.01$							
HD heading days, MD maturing days, PH plant height, PL panicle length, FGP filled grain percentage, AGY adjusted grain yield							

Descriptive statistics of checks and advanced lines Generated from F7 filial Generation

The descriptive statistics (mean, coefficient of variation, minimum and maximum value) of traits of all genotypes and checks used in NIRON 2019 has been presented in Table 5.

Regarding the checks used in the experiment, the highest days to heading and maturity was recorded for Lalka Basmati whereas shortest was recorded for Hardinath 1. Similarly, short plant height was recorded in Samba Masuli sub-1 while contrasting data obtained in Lalka Basmati. The high filled grain percentage was observed in Samba Masuli sub-1 where oppose result obtained for Lalka Basmati. Hardinath-1 showed high unfilled grain followed by Radha-4. Panicle length was shortest for Samba Masuli sub 1 and highest for Hardinth 1. The grain yield was found highest for

Ramdhan followed by Sabitri, Radha-4, Samba Masuli sub-1 but Lalka Basmati found inferior in grain yield (Table 4).

High yielding genotypes were GEN22(5.52t/ha) followed by GEN23 (4.75t/ha), GEN30 (4.5t/ha), GEN2 (4.46t/ha), Ramdhan (4.45t/ha), GEN27(4.4t/ha), GEN26 (4.43t/ha), GEN7 (4.34t/ha), GEN28 (4.17t/ha), GEN51 (4.17t/ha), GEN73 (4.12t/ha) and GEN25 (4.11t/ha). The highest filled grain percentage was recorded for genotypes GEN70 (95.25%) and GEN76 (96.75%). Longest panicle length was found in genotypes GEN35 (27.79cm) and GEN89 (28.02cm). The shorter plant stature (less than 80cm) was recorded for the genotypes GEN26 (77.03cm), GEN80 (79.86cm), GEN82 (76.86cm), GEN85 (76.86cm) and GEN86 (73.86cm). Eighteen genotypes matured early (less than 120 days) such as Hardinath-1, GEN32, GEN36, GEN37, GEN53, GEN61, GEN75, GEN76, GEN85, GEN86, GEN87, GEN88, GEN49, GEN50, GEN51, GEN53, GEN54 and GEN90 (Table 4).

Table 4. Yield and yield ancillary traits of tested Genotypes in NIRON 2019

Trt	Genotype	HD	MD	PH	PL	FGP	AGY	Trt	Genotype	HD	MD	PH	PL	FGP	AGY
1	Check1	81	115	102.83	25.03	82.81	2.61	49	GEN43	127	158	94.03	18.59	88.45	3.62
2	Check2	111	140	109.33	22.87	89.9	4.45	50	GEN44	97	130	90.03	22.59	86.24	2.85
3	Check3	94	126	99.33	23.4	85.8	3.67	51	GEN45	120	152	114.03	22.39	93.11	4.17
4	Check4	118	150	88	17.37	92.33	3.44	52	GEN46	121	152	110.53	18.79	83.92	3.49
5	Check5	124	157	123	22.2	87.91	1.21	53	GEN47	82	114	88.53	20.59	91.66	3.28
6	Check6	114	146	98.67	21.87	90.91	3.87	54	GEN48	123	154	101.53	24.99	89.4	3.67
7	GEN1	114	145	110.69	22.76	88.76	3.37	55	GEN49	128	159	104.53	22.19	82.81	1.87
8	GEN2	119	149	102.69	18.76	92.11	4.46	56	GEN50	127	159	114.53	23.19	76.33	2.78
9	GEN3	118	148	98.69	20.76	94.06	3.69	57	GEN51	121	153	128.53	23.59	80.02	3.21
10	GEN4	124	154	89.69	19.36	84.85	2.64	58	GEN52	119	150	98.53	21.99	88.64	3.22
11	GEN5	114	145	86.69	18.76	92.82	2.93	59	GEN53	120	152	132.53	24.39	79.49	3.46
12	GEN6	105	135	113.69	24.56	89.76	3.95	60	GEN54	123	154	93.53	20.79	89.77	3
13	GEN7	112	143	108.69	20.56	94.6	4.34	61	GEN55	84	115	91.53	19.19	72.97	1.46
14	GEN8	113	144	98.69	20.36	88.58	3.17	62	GEN56	119	152	99.53	20.99	76.92	1.17
15	GEN9	124	154	105.69	21.16	85.87	2.01	63	GEN57	125	157	134.53	24.79	46.92	0.72
16	GEN10	126	157	103.69	21.36	88.36	0.58	64	GEN58	121	154	106.53	19.59	79.03	0.92
17	GEN11	122	157	112.69	22.96	88.92	2.44	65	GEN59	123	154	107.53	20.19	80.86	1.87
18	GEN12	120	151	105.69	21.76	81.57	0.49	66	GEN60	105	139	101.53	22.59	62.38	0.68
19	GEN13	123	154	91.69	20.36	88.78	0.3	67	GEN61	130	160	115.86	19.16	73.68	2.21
20	GEN14	119	150	103.69	22.56	88.68	0.37	68	GEN62	129	160	115.86	19.96	81.96	1.01
21	GEN15	119	151	100.69	18.16	94.63	1.47	69	GEN63	131	161	129.86	24.76	90.88	1.71
22	GEN16	121	154	102.03	21.89	87.04	3.72	70	GEN64	128	159	121.86	20.56	95.25	3.34
23	GEN17	121	153	102.03	20.89	93.11	2.88	71	GEN65	106	138	117.86	23.16	92.72	2.24
24	GEN18	111	143	111.03	21.69	87.17	3.01	72	GEN66	120	153	89.86	23.96	88.55	3.02
25	GEN19	109	144	112.03	21.29	93.53	3.31	73	GEN67	121	151	88.86	21.16	83.37	4.12
26	GEN20	115	147	103.03	19.89	76.45	2.18	74	GEN68	131	162	100.86	20.96	80.9	2.79
27	GEN21	121	154	107.03	22.89	90.4	2.51	75	GEN69	83	114	89.86	20.56	87.01	3.07
28	GEN22	120	153	114.03	22.29	86.23	4.75	76	GEN70	83	115	104.86	21.16	96.75	2.98
29	GEN23	127	159	114.03	22.29	93.91	5.52	77	GEN71	127	158	83.86	18.56	87.96	3.48
30	GEN24	105	138	127.03	24.89	92.13	3.43	78	GEN72	119	150	103.86	19.56	86.79	3.98
31	GEN25	107	139	120.03	25.49	89.19	4.11	79	GEN73	122	153	100.86	20.36	89.88	3.54
32	GEN26	123	156	77.03	18.29	82.93	4.43	80	GEN74	119	150	79.86	19.76	84.94	2.19
33	GEN27	116	149	104.03	19.89	82.6	4.4	81	GEN75	110	143	83.86	18.56	94.37	2.35
34	GEN28	120	152	111.03	25.89	76.1	4.17	82	GEN76	120	151	76.86	15.02	82.29	3.23
35	GEN29	129	161	103.03	21.09	85.22	2.57	83	GEN77	113	146	102.86	21.62	75.18	3.24
36	GEN30	123	156	123.03	22.09	88.16	4.5	84	GEN78	115	146	98.86	20.62	83.87	2.5
37	GEN31	122	155	124.03	22.39	85.03	3.9	85	GEN79	84	116	76.86	20.82	93.39	1.09
38	GEN32	83	115	106.03	16.99	86.58	1.85	86	GEN80	84	115	73.86	18.42	90.65	1.85
39	GEN33	132	164	88.03	20.39	60.22	2.56	87	GEN81	84	115	88.86	21.22	91.39	1.8

40	GEN34	104	135	112.03	24.59	85.56	2.41	88	GEN82	85	116	94.86	22.42	83.39	0.87
41	GEN35	96	129	110.03	27.79	69.06	2.44	89	GEN83	87	119	90.86	20.22	49.89	1.26
42	GEN36	84	117	105.03	19.59	75.55	3.47	90	GEN84	86	117	92.86	22.42	83.83	0.78
43	GEN37	83	116	110.03	21.79	88.8	1.83	91	GEN85	84	119	98.86	20.22	85.49	1.46
44	GEN38	120	151	108.03	20.59	93.3	2.54	92	GEN86	113	146	99.86	21.22	66.65	1.57
45	GEN39	130	161	129.03	24.19	90.66	2.64	93	GEN87	85	117	116.86	24.42	70.91	2.32
46	GEN40	94	126	136.03	25.19	83.55	3.11	94	GEN88	80	112	101.86	19.82	87.48	2.44
47	GEN41	96	127	127.03	23.19	68.07	0.95	95	GEN89	130	161	163.86	28.02	85.31	2.35
48	GEN42	103	135	117.03	24.19	91.52	1.97	96	GEN90	88	120	113.86	23.62	89.07	2.24

Genetic parameters for estimation of variability among the traits

The coefficient of variation due to phenotype and genotype were ranged from 10.4-41.16 and 8.74-28.48, respectively. The PCV and GCV were recorded highest for grains yield per ha and lowest for panicle length. The contribution of genotypic effect on phenotypic coefficient of variation was highest for maturity (99.22%) and heading days (99.2%), filled grain percentage (94.56%), plant height (88.88%), panicle length(84.03%), and grain yield per ha (69.19%) (Table 5).

Broadsense heritability was found highest for phonological traits (98.83 and 98.43) followed by filled grain percentage (89.37), plant height (79.02) and panicle length(70.54). The moderate broad sense heritability was recorded for grain yield (47.89). Genetic advance was found higher for phonological traits followed by plant height. The moderate genetic advance was recorded for filled grain percentage and lowest for grain yield. Similarly, genetic gain as percentage of mean (GAM) was recorded highest for all traits except for panicle length. The highest value for GAM was recorded for grain yield (Table 5).

Table 5. Descriptive statistics and Genetic variability analysis of yield and ancillary characters of 96 genotypes of NIRON (2019)

Trait	Mean	Range	CV	GCV		PCV		H ²		GA		GAM	
Heading Days	111.41	79-132	1.8	14.16	M	14.27	M	98.43	H	32.28	H	28.97	H
Maturity Days	143.33	111-164	1.2	10.93	M	11	M	98.83	H	32.14	H	22.42	H
Plant Height	104.72	73.86-136	5.82	11.27	M	12.68	M	79.02	H	21.64	H	20.67	H
Panicle Length	21.58	15.02-28.02	5.61	8.74	L	10.4	M	70.54	H	3.27	L	15.14	L
Filled Grain(%)	84.76	46.92-96.75	3.5	10.26	M	10.85	M	89.37	H	16.96	M	20.01	H
Grain Yield (Ton/ha)	2.68	0.3-5.52	28.37	28.48	H	41.16	H	47.89	M	1.09	L	40.66	H

Note: H= High, M= Moderate, L= Low, GCV= Genotypic coefficient of variance, PCV=phenotypic coefficient of variance, H²= heritability in broad sense, GA= Genetic advance, GAM= Genetic advance as percent mean

Correlation between the studied traits of 96 genotypes in NIRON 2019

The grain yield had positive and highly significant ($p < 0.01$) relation with filled grain percentage. The grain yield showed positive and non significant relation with phonological traits where negative relation with plant height and panicle length. Similarly,

filled grain percentage showed negative and non significant relation with plant height and panicle length. The phonological traits showed positive and highly significant correlation with each other. Similarly, phonological traits showed negative and significant ($p < 0.05$) relation with plant height and panicle length. The plant height and panicle length had positive and high significant ($p < 0.001$) relation with each other's (Table 6).

Table 6. Phenotypic correlation between the studied traits of 96 genotypes in NIRON 2019

	HD	MD	PH	PL	FGP	AGY
HD	1	0.9968***	0.0342ns	-0.2255*	0.0807ns	0.1086ns
MD		1	0.0294ns	-0.2227*	0.0768ns	0.0939ns
PH			1	0.4090***	-0.1136ns	-0.1414ns
PL				1	-0.1612ns	-0.0336ns
FGP					1	0.3366**
AGY						1

HD=heading days, MD=maturity days, PH= plant height, PL=Panicle length, FGP= filled grain percentage, AGY= adjusted grain yield

Note: ns means $p \geq 0.05$, * means $p < 0.05$, ** means $p < 0.01$, and *** means $p < 0.001$

Cluster dendrogram using five traits of ninety-six genotypes in NIRON 2019.

A circular dendrogram based on five traits (MD, PH, PL, FGP, AGY) comprised of seven clusters was constructed by using Euclidean distance and Ward D2 method (Figure1). The first cluster consists of seventeen genotypes including two checks (Hardinath-1 and Radha-4). Similarly, second cluster consisted ten genotypes including check Ramdhan. Likewise, third cluster had nine genotypes including check Samba Masuli sub-1. Fourth cluster had fifteen genotypes including check Lalka Basmati. The fifth cluster had twenty nine genotype including check Sabitri. Clusters sixth and seventh had eight genotypes on each cluster, respectively (Table 7).

Genotypes fall under cluster 1 were grouped on basis of early maturity type, average high filled grain percentage, low yield and low plant height. The check varieties of cluster 1 namely Hardinath-1 and Radha-4 had highest yielder than rest of genotypes. Similarly, cluster 2 comprised genotypes had good panicle length, medium maturity, good filled grain percentage and average grain

yield. High yielding genotypes under this cluster were GEN6, GEN1, GEN 25 and check variety Ramdhan. The cluster 3 comprised genotypes grouped on basis of long maturity duration, less plant height (<100cm), low panicle length. The high yielding genotypes under this group were GEN26, GEN43 and Check variety Samba Masuli sub-1. The cluster 4 had very low yielding genotypes, long maturity period and less filled grain percentage. Similarly, cluster 5 comprised genotypes had high yielding genotypes, long maturity duration, and good filled grain percentage. The high yielding genotypes (>4 ton/ha) were GEN2, GEN7, GEN22, GEN23, GEN27, GEN 30, GEN 45, GEN 48, GEN67 and check variety Sabitri. Genotypes GEN72, GEN46, GEN31, GEN3 were also yielded more than 3.5 ton/ha. The cluster 6 had genotypes attributed to good panicle length, long maturity duration, high plant height, low filled grain percentage and good yield potential. The promising genotypes under this cluster were GEN28, GEN51 and GEN53. The cluster 7 comprised genotypes had low filled grain percentage, good panicle length, low yield and medium maturity.

Table 7. Clusters, genotypes number, genotypes and average yield attributing characters in cluster dendrogram

Cluster	Genotype no.	Genotypes	MD	PH	PL	FGP	AGY
1	17	Check1, Check3, GEN32, GEN36, GEN37, GEN44, GEN47, GEN55, GEN69, GEN70, GEN79, GEN80, GEN81, GEN82, GEN84, GEN85, GEN88	117	98	21	86.24	2.18
2	10	Check 2, GEN1, GEN6, GEN24, GEN25, GEN34, GEN40, GEN42, GEN65, GEN90	134	117	24	89.23	3.01
3	9	Check 4, GEN4, GEN5, GEN26, GEN43, GEN71, GEN74, GEN75, GEN76	152	85	18	87.56	3.11
4	15	Check 5, GEN9, GEN10, GEN12, GEN13, GEN14, GEN20, GEN29, GEN49, GEN56, GEN58, GEN59, GEN61, GEN62, GEN68	156	105	21	82.71	1.53
5	29	Check6, GEN2, GEN3, GEN7, GEN8, GEN11, GEN15, GEN16, GEN17, GEN18, GEN19, GEN21, GEN22, GEN23, GEN27, GEN30, GEN31, GEN38, GEN45, GEN46, GEN48, GEN52, GEN54, GEN 64, GEN66, GEN67, GEN72, GEN73, GEN78	151	104	21	89.68	3.51
6	8	GEN28, GEN39, GEN50, GEN51, GEN53, GEN63, GEN77, GEN89	156	123	24	81.85	3.00
7	8	GEN 33, GEN 35, GEN41, GEN57, GEN60, GEN83, GEN86, GEN87	137	110	23	61.78	1.59

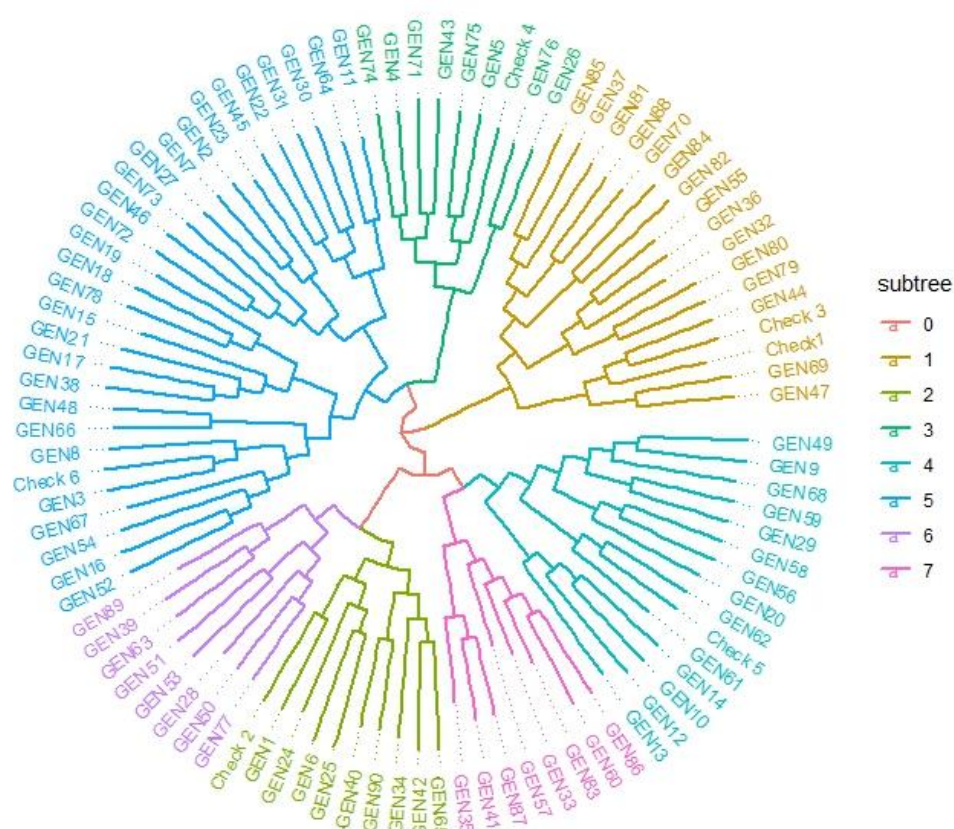


Figure 1: Circular dendrogram showing seven clusters of different colors using ward D2 method

Discussion

Genotype selection at nursery field condition i.e. initial stage of evaluation of lines before testing in multi environment for yield and yield attributing traits is very crucial step in varietal improvement and development procedure. In addition, it became difficult to select the genotype where parents used in cross have different genetic background. Considering only yield is main component in selection misguidewhole varietal improvement program. Therefore, the breeder must know the genetic and non-genetic component interactions of indispensable trait i.e. yield and contributing traits directly or indirectly affects the yield. To understand the Genotypes' potential in terms of yield and yield affecting traits, the estimation of variability presence, heritable nature of traits, genotypes performance on selection and clustering the genotypes based on performance of traits is inevitable activities for a good plant breeder. The genetic diversity and transmission of desired characteristics are the main sources for genotype selection based on phenotypic data. The genetic diversity has estimated by analyzing the genotypic and phenotypic variation, coefficient of variation, broad sense heritability, genetic advance (Baraki et al., 2020 and Shilpashree et al., 2021).

This study revealed the presence of genotypic variation and trait variability among genotypes might be due to different genetic loadings of parents used in crosses. It suggested the genotypes had variability for the effective selection. Similar finding were reported by Ata-Ul-Karim et al (2022), Dutta et al.(2013), Iqbal et al.(2018), Adhikari et al. (2018) and Tiwari et al.(2019).

The information on less value of GCV and PCV of phonological traits, filled grain percentage, plant height and panicle length

suggested the less environmental effects. These traits exhibit fitness on selection based on phenotypic value alone. But, the contrasting figure was observed for grain yield per ha. The previous finding from Ajmera et al. (2017) Abebe et al.(2017) and Adhikari et al. (2018) reported similar result. The medium heritability on grain yield might be due to the polygenic inheritance affected by environments. Gyawali et al. (2018), Bandi et al.(2018), Abebe et al.(2017) findings supported the current result. Regarding the panicle length, low GCV and PCV value, high heritability and moderate GAM supported by earlier findings of Saha et al., 2019 and Iqbal et al., 2018.. High GCV and PCV and GAM were recorded for grain yield and high heritability for phonological traits in rainfed environment (Tiwari et al., 2019). Ghosal et al. (2010) found low GCV, PCV, high heritability and moderate GAM for panicle length as per result obtained in this study. Similarly, high GAM was recorded for grain yield per ha. Dutta et al.(2013) found low GCV, PCV and high heritability with moderate GAM for the filled grain percentage which is at par with the present result. The heritability estimation gives information of trait inheritance from parents to progeny. Similarly, GAM (genetic advance) gives information of actual genetic gain expected under selection. Phenotypic performance shows in high heritability whereas lacks the genetic information. The high heritability coupled with genetic gain helps in precise selection of traits for further improvement.

In the present study, high heritability coupled with genetic advance and GCV values showed traits were days to heading, days to maturity, filled grain percentage and plant height. This allows the selection of these traits directly for improvement because of presence of additive gene action. Johnson et al. 1955 suggested the

accuracy of selection of genotypes based on GCV, heritability and GAM has more effective.

Regarding broad sense heritability, highest was found for phenological traits followed by filled grain percentage whereas lowest heritability was recorded for grain yield per ha (less than 50%). The highest broad sense heritability of traits showed there has no need of selection on that tested environment because of less influence of environment. In addition, it aids the genetic gain of that trait on each year. Other yield attributing traits could be tested for stable yield performance ability of genotype. Genetic advance as per mean was recorded highest (>20%) for grain yield per ha followed by heading days, maturity days, plant height and filled grain percentage. The lowest genetic advance as per mean was recorded for panicle length.

The yield has interconnected with different traits. The interrelationship between the grain yield and filled grain percentage had positive and significant. This showed increased in filled grain number per panicle increases grain yield. Similar result was reported by Zhao et al. (2020). Similarly, Ghosal et al. (2010) reported positive and significant relation of plant height and panicle length at phenotypic and genotypic level.

The Euclidian distance showed that the clusters were mostly formed based on the origin or geographical area of the genotypes. The genotypes from the same geographical origin mostly grouped together; however, the less frequent genotypes from different origins also grouped within the same cluster. Fifty-eight rice varieties grouped into four clusters based on 18 morphological characters in a study by Ahmadikhah et al. 2008. Rahman et al. 2011 also divided 21 rice varieties into five clusters based on 14 physiological traits. Iqbal et al. 2018 also divided 14 rice elite genotypes into four clusters based on 9 traits. Tejaswini et al. 2016 reported twelve clusters based on six crosses having 114 families considering 10 characters.

Mean performance of a cluster is the mean values of individual characters of the genotypes included in it. Analysis of cluster means indicates the existence of considerable differences for mean values in different traits. High cluster mean indicates that the genotypes of the cluster can be used for development of that particular character.

Conclusion

There has diversity among genotypes based on studied traits. These genotypes could be useful for breeding program for specific trait introgression. Similarly, high heritability combines with genetic advances as percentage of mean for traits such as phenology, filled grain percentage and plant height suggested these could be select directly. The potential high grain yield genotypes such as GEN23, GEN22, GEN30, GEN2, GEN7, GEN26 and GEN27 could be useful for varietal testing in multi environments for its stability and adaptability. Genotypes falls under cluster 5 could be useful for breeding program for high yielding and can be shorten its maturity duration with cross of early varieties or genotypes of cluster 1.

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References

1. Abebe, T., Alamerew, S., & Tulu, L. (2017). Genetic variability, heritability and Genetic advance for yield and its related traits in rainfed lowland rice (*Oryzasativa* L.) Genotypes at Fogera and Pawe, Ethiopia. *Advances in crop Science and Technology*, 5(2), 272.
2. Adhikari, B. N., Joshi, B. P., Shrestha, J., & Bhatta, N. R. (2018). Genetic variability, heritability, Genetic advance and correlation among yield and yield components of rice (*Oryzasativa* L.). *Journal of Agriculture and Natural Resources*, 1(1), 149-160.
3. Ahmadikhah, A., S. Nasrollanejad, and O. Alishah (2008). "Quantitative studies for investigating variation and its effect on heterosis of rice," *International Journal of Plant Production*, vol. 2, pp. 297– 308, 2008.
4. Ata-Ul-Karim, S. T., Begum, H., Lopena, V., Borromeo, T., Virk, P., Hernandez, J. E., Gregario, G.B., Collard, BCY, & Kato, Y. (2022). Genotypic variation of yield-related traits in an irrigated rice breeding program for tropical Asia. *Crop and Environment*, 1(3), 173-181.
5. Bandi H. R. K., Satyanarayana, P. V., Babu, D. R., Chamundeswari, N., Rao, V. S., and Raju, S. K. (2018). Genetic variability estimates for yield and yield components traits and quality traits in rice (*Oryzasativa* L.). *Int.J.Curr.Microbiol.App.Sci*.2018.7(5): 551-559
6. Baraki F., Gebregergis, Z., Belay, Y., Berhe, M., Teame, G., Hassen, M., Gebremedhin, Z., Abadi, A., Negash, W. and Atsbeha, A.J.H. (2020). Multivariate analysis for yield and yield-related traits of sesame (*Sesamumindicum* L.) genotypes. *Heliyon* 2020, 6, e05295.
7. Bhattarai A.N. 1969. A review of rice improvement in Kathmandu Valley. *Nepalese Journal of Agriculture* 4: 47-57.
8. Burton GW. 1951. "Quantitative inheritance in pearl millet (*Pennisetumglaucum*). *Agronomy Journal* 43(9). 409-417.
9. Burton GW. 1952. "Quantitative inheritance in grasses. Vol. 1." In *Proceedings of the 6th International Grassland Congress*, Pennsylvania State College, 17-23.
10. Chanbeni Y, Ovung Lal GM, Prashant Kumar R (2012). Studies on genetic diversity in Rice (*Oryza sativa* L.). *J. Agric. Technol.* 8(3):1059-1065.
11. Dutta P, Dutta P.N. and Borua P. K (2013). Morphological Traits as Selection Indices in Rice: A Statistical View. *Univ. J. Agric. Res.* 1(3):85-96.
12. Ghosal S., Biswas, P. L., Khatun, M., & Khatun, S. (2010). Genetic variability and character associations in irrigated rice (*Oryzasativa* L.). *Bangladesh Journal of Plant Breeding and genetics*, 23(2), 23-28.
13. Gyawali S., Poudel, A., and Poudel, S. (2018). Genetic variability and association analysis in different rice genotypes in mid hill of western Nepal. *Acta Scientific Agriculture*, 2(9), 69-76.

14. Iqbal T., Iqbal, H., Nazir, A., Muhammad, N. and Fawad, A. (2018). Genetic variability, correlation and cluster analysis in elite lines of rice (*Oryzasativa* L.). *Archives*, 2(6), 234-240.
15. Johnson HW, Robinson HF and Comstock, R.E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J.* 47: 477-482.
16. Lush, JL(1940). "Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics." *Proceedings of the American Society of Animal Nutrition*, 1940(1), 293-301.
17. MoAD 2022. Agriculture and Livestock diary 2080. Ministry of Agriculture and Livestock, Nepal
18. Ogunbayo SA, Sié M, Ojo DK, Sanni KA, Akinwale MG, Toulou B, Shittu A, Idehen EO, Popoola AR, Daniel IO and Gregoria GB (2014). Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). *J. Plant Breed. Crop Sci.* 6(11):153-159.
19. Rahman, M. M., M. G. Rasul, M. K. Bashar, M. A. Syed, and M. R. Islam (2011). "Parent selection for transplanted aman rice breeding by morphological, physiological and molecular diversity analysis," *Libyan Agriculture Research Center Journal International*, vol. 2, pp. 26–28.
20. Robinson, HF, Comstock RE and PH Harvey (1955). "Genetic variances in open pollinated varieties of corn." *Genetics*, 40(1), 45-60.
21. Saha, S. R., Lutful, H., Haque, M. A., Islam, M. M., & Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryzasativa* L.) landraces. *Journal of the Bangladesh Agricultural University*, 17(1), 26-32.
22. Shilpashree, N.; Devi, S.N.; Manjunathagowda, D.C.; Muddappa, A.; Abdelmohsen, S.A.; Tamam, N.; Elansary, H.O.; El-Abedin, T.K.Z.; Abdelbacki, A.M.; and V. Janhavi (2021). Morphological characterization, variability and diversity among vegetable soybean (*Glycinemax* L.) genotypes. *Plants* 2021, 10, 671.
23. Singh RK, Chaudhary BD (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi pp. 215-218.
24. Sivasubramaniam S, Madhacamenon P. 1973. "Genotypic and phenotypic variability in rice." *The Madras Agricultural Journal*, 60(9-13), 1093-1096.
25. Tejaswini K.L.Y., S Manukonda, P. V. Ramana Rao, B.N.V.S.R. Ravi Kumar, L A Mohammad and S. K Raju. 2016. Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *Journal of Agricultural and Crop Research* Vol. 4(9), pp. 129-139, December 2016 ISSN: 2384-731X.
26. Tiwari, D. N., Tripathi, S. R., Tripathi, M. P., Khatri, N., & Bastola, B. R. (2019). Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, 2019.
27. Tripathi BP, HN Bhandari and JK Ladha. 2019. Rice strategy for Nepal. *Acta Scientific Agriculture* 3(2) (2019). ISSN: 2581-365X.
28. Zhao, H., Mo, Z., Lin, Q., Pan, S., Duan, M., Tian, H. Wang S. & Tang, X. (2020). Relationships between grain yield and agronomic traits of rice in southern China. *Chilean journal of agricultural research*, 80(1), 72-79.