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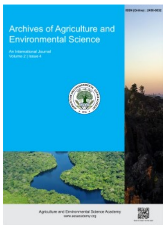

ORIGINAL RESEARCH ARTICLE

Genetic variation and trait association of fine rice genotypes

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ABSTRACT

To explore high yielding genotype and significant yield contributing trait, field experiment was conducted using alpha lattice design replicated three times at the National Wheat Research Program (NWRP), Bhairahawa, Nepal in 2022. Eighteen fine rice genotypes were evaluated based on nine quantitative traits (Heading days, maturity days, plant height, panicle length, effective tillers, filled grains per panicle, unfilled grains per panicle, thousand grain weight and grain yield per hectare). Variance analysis, correlation and estimation of genetic parameters were conducted to comprehend genetic variations and interrelationships among traits within genotypes. The results showed most of traits except unfilled grains had statistical significance differences. Tarahara-107 (3940 kg/ha) had the highest grain yield followed by Tarahara-2 (3700 kg/ha) and NR 2381-RGA1-RGA2 (3665 kg/ha). Similarly, grain yield showed positive and significant association with filled grains at both phenotypic and genotypic level (r_p = 0.7074 ** and r_g= 0.9482 **). Elevated values of PCV and GCV were recorded for filled grains (22.05 and 17.57). The high value GAM coupled with high heritability was recorded for filled grains (28.83%), plant height (23.10%), number of effective tillers (21.57%) and thousand grain weight (19.37%). Thus, identified genotypes NR 2380-RGA1-RGA2 and NR 2381-RGA1-RGA2 exhibited early and potential high yielding genotypes while Tarhara-107 and Tarhara-2 identified as high yield, medium maturity and good filled grain number per panicle. In addition, filled grains trait displayed tightly linked with grain yield and possess high GCV, PCV, GAM with moderate heritability indicated direct selection could be employed for trait enhancement in breeding program.

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INTRODUCTION

Rice holds the primary position as the most significant staple cereal grain crop in Nepal. Rice emerges as the most crucial strategic crop for ensuring global food and nutrition security (Gadal *et al.*, 2019). Rice contributes 13 percent and 4 percent to the Agricultural Gross Domestic Product (AGDP) and in the national gross domestic product (GDP), respectively (MoALD, 2022). The rice covered 1.447 million hectares of land and total rice production has 5.486 million tons. However, demand of milled rice is 4 million ton causing deficit of around 0.48 million ton while considering milling rate of 64 percentage (MoALD, 2022). The demand for rice continues to rise each year, and the country's reliance on rice imports has grown due to insufficient domestic production, with a preference for fine rice (Joshi *et al.*, 2020). Furthermore, there are total 82 cultivated rice released varieties in Nepal among them very few are fine rice varieties (MoALD, 2022). To address the demand and production issues, development of high yielding fine rice varieties with promising traits through effective breeding strategies must be needed. Over time, the consumption patterns of rice in Nepal have gradually shifted away from coarse rice towards fine and aromatic varieties. Fine rice varieties are preferred for their superior taste and command a premium price in the market, with a demand that is notably high in Nepal (Sah *et al.*, 2002). To address the increasing demand for fine and aromatic rice, "Fine and Aromatic Rice" mission program was launched in 2015 AD, covering 20 rice producing districts to enhance the cultivation of fine and aromatic rice in Nepal (CDD, 2015). Government aims to encompass 35 % of total rice area with fine rice varieties in 2022/23 which is twice times increase of area from 2015. This, in turn, holds the promise of improving the economic well-being of rice farmers as well as nation by reducing the reliance on fine rice imports.

The genetic enhancement of a breeding population hinges on the extent of genetic diversity it possesses. Genetic traits are often controlled by multiple genes and are strongly affected by the environment. The variation coefficients alone do not provide a comprehensive view of heritable variation. It can be determined more accurately when considered alongside heritability and genetic advance studies. Consequently, heritability and genetic advance were assessed to understand the potential for enhancing various traits through selection (Singh *et al.*, 2011). Heritability is crucial for assessing how traits respond to selection. Tiwari *et al.* (2019) also reported high genetic advance and heritability are ideal for selecting specific traits. To improve yield-related attributes, it's essential to understand their genetic variability such as Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), relationships, and their impact on yield, which is vital for effective breeding programs. Based on the estimation of the genetic variability, heritability and correlation, aim of this study was to identify high yielding fine rice genotype and inheritance pattern of traits which would facilitate more effective selection for successful breeding programs.

MATERIALS AND METHODS

The research was conducted at the National Wheat Research Program (NWRP), Bhairahawa, Nepal in rainy season of 2022. This location is situated at approximately 27°32'N latitude and 83°25'E longitude, with an elevation of 104 meters above sea level. It experiences a sub-tropical climate. The soil at the research site had a clay-like texture (NWRP, 2022). Eighteen fine rice genotypes including standard check varieties Samba Masuli sub-1 and Lalka Basmati, received as coordinated varietal trial-fine and aromatic (CVT-FAR) of National Rice Research Program (NRRP), Hardinath were used as experimental materials (Table 1). The field experiment was conducted following Alpha lattice design with 3 blocks and 6 plots per block replicated three times. 30 days-old seedlings of each genotype were transplanted using 2 to 3 seedling per hill in 4 × 2 m^2 plot area with 20 cm and 20 cm space between rows and hills, respectively. Fertilizers were applied at the rate of 100:30:30kg N: P_2O_5: K_2O per hectare. Half dose of nitrogen and full dose of phosphorous and potash were applied as basal dose during final land preparation. The remaining half dose of nitrogen was equally split into two and applied as topdressing at tillering stage and before heading stage. Plant protection measures, irrigation and weeding were carried out as required, following the guidelines outlined in the IRRI Protocol. Days to heading, days to maturity, plant height (cm), effective tiller number per meter square, panicle length (cm), number of filled grains per panicle, number of unfilled grains per panicle, 1000-grain weight (g), grain yield (Kg/hectare) were phenotyped. Analysis of variance (ANOVA), genetic variability parameters, association analysis were conducted using agricolae, variability packages of R studio software version 1.3.1093. Genetic parameters were also estimated to understand genetic variations among the test genotypes and to determine genetic and environmental effects on different characters. These parameters included as following: Phenotypic (Vp) and Genotypic variance (Vg), Phenotypic coefficient of variance (PCV), Genotypic coefficient of variance (GCV), Broad sense heritability, Genetic advance (GA) and Genetic advance as percent of mean (GAM).

PCV and GCV were calculated according to Burton (1951, 1952) and characterized according to (Sivasubramanian and Madhavamenon, 1973) as CV% =10 (low), 10≤ X<20 (medium) and ≥20 (high).

Table 1. List of Eighteen fine rice genotype received from NRRP, Hardinath in 2022.

TRT	Genotype	TRT	Genotype
1	NR 2191-240-1-1-3-1	10	NR 2188-43-1-2-2-5-1
2	NR 2264-4-1-6-4	11	NR 2210-15-1-1-3-1
3	NR 2264-4-1-6-5	12	NR 2181-465-1-1-1-1
4	NR 2380-RGA1-RGA2	13	NR 2191-22-1-4-1-1
5	NR 2381-RGA1-RGA2	14	NR 2215-6-4-2-2-2
6	NR 2191-236-3-1-3-1	15	NR 2229-4-2-1-1-1
7	Tarahara-107	16	NR 2264-9-2-4-2-2
8	Tarahara-109	17	Samba Masuli sub-1 (Check)
9	Tarahara-2	18	Lalka Basmati (Check)

$$PCV = \frac{\sigma_p^2}{\sqrt{\bar{x}}} X100$$

$$GCV = \frac{\sigma_g^2}{\sqrt{\bar{x}}} X100$$

Broad sense heritability (H2) calculated according to (Lush, 1940) and categorized by Robinson (1966) as H^2= <50(low), 50≤ X<75 (medium), and ≥75(high).

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

Genetic advance (GA) and Genetic advance as percentage of mean (GAM) were calculated and categorized stated by (Johnson *et al.*, 1955).

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

$$GAM = \frac{GA}{\bar{X}} X100$$

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

RESULTS AND DISCUSSION

Significance differences among the genotypes

All of the assessed traits, except for unfilled grain per panicle exhibited statistical significance differences among the tested genotypes (Table 2). Shrestha *et al.* (2021) also reported significant differences among the evaluated genotypes for plant height, panicle length, effective tiller number per meter square, thousand grain weight and grain yield. Dhungana *et al.* (2020), also reported significant difference in thousand grain weight. Also, KC *et al.* (2020), found significance differences in plant height among studied genotypes. The result revealed enormous variability and diversity among genotypes for the traits studies. These traits could be selected for genetic improvement and trait introgression through conventional breeding. Earliness is always desirable characters for fine and semi fine grain type which affects directly on final production. The genotypes NR 2380-RGA1-RGA2 and NR 2381-RGA1-RGA2 were matured earlier (132days and 135 days for maturity) among tested, respectively. Lalka Basmati had the tallest in plant height (130cm), while NR 2264-4-1-6-5 had short plant height (80 cm). The long stature of genotype may lodge and directly affected on the grain quality and yield. The short stature genotype assumed to be fertilizer responsive and may direct effect on grain production. The genotype NR 2380-RGA1-RGA2 had the longest panicle (27cm) while NR 2191-240-1-1-3-1 had short panicle length (17cm). Genotype NR 2264-9-2-4-2-2 had the highest tillers per square meter (377) and Tarahara-2 had the lowest (242). Usually, thousand grain weight determined fine or coarse type grain. The increment in thousand grain weight is supposed to be bold and vice versa. Genotype NR 2191-240-1-1-3-1 and Tarahara-2 had fine grain (15g), while Lalka Basmati had bold grains (23g). Regarding grain yield per hectare, genotype Tarahara-107 (3940 kg/ha) had the highest grain yield followed by Tarahara-2 (3700 kg/ha), NR 2381-RGA1-RGA2 (3665 kg/ha), NR 2229-4-2-1-1-1 (3575 kg/ha). Tarahara-2 also showed highest grain yield with filled grains number (154 per panicle) which might be due to their significant positive association which coincides with result from Basanti *et al.* (2018). Genotypes NR 2380-RGA1-RGA2 and NR 2381-RGA1-RGA2 were earlier matured genotypes with good filled grains and yield might be due to high solar radiation with optimum temperature interaction (Mehraj *et al.*, 2019).

Table 2. Performance of yield and yield attributing traits of eighteen fine rice genotypes.

TRT	Genotype	DH	DM	PH	PL	TL	TGW	FG	UFG	GY
1	NR 2191-240-1-1-3-1	109	143	82	17	338	15	80	25	2593
2	NR 2264-4-1-6-4	108	141	89	21	269	18	121	28	2813
3	NR 2264-4-1-6-5	123	150	80	21	292	16	95	34	2975
4	NR 2380-RGA1-RGA2	103	132	91	27	257	17	128	49	3027
5	NR 2381-RGA1-RGA2	104	135	97	21	271	19	129	34	3665
6	NR 2191-236-3-1-3-1	124	152	93	22	311	18	104	42	3424
7	Tarahara-107	107	141	91	21	325	18	143	37	3940
8	Tarahara-109	108	143	91	23	265	17	134	22	3270
9	Tarahara-2	107	141	91	23	242	15	154	25	3700
10	NR 2188-43-1-2-2-5-1	115	143	94	23	298	21	128	35	3183
11	NR 2210-15-1-1-3-1	126	157	83	21	347	20	87	38	2586
12	NR 2181-465-1-1-1-1	126	153	95	25	281	21	100	21	3330
13	NR 2191-22-1-4-1-1	128	154	102	23	326	19	120	35	3497
14	NR 2215-6-4-2-2-2	114	144	91	21	297	20	93	24	2767
15	NR 2229-4-2-1-1-1	125	154	101	22	282	17	132	20	3575
16	NR 2264-9-2-4-2-2	104	135	103	23	377	16	95	21	2569
17	Samba Mansuli sub-1	124	144	82	20	332	17	108	25	2776
18	Lalka Basmati	129	155	130	25	252	23	85	22	2489
Mean		116	145	93.61	22.24	298	18.23	113	30	3121.11
CV		2.4	3.4	4.3	4.7	5.6	6.6	13	42.3	14.1
F value		31.39	6.87	21.9	11.72	12.09	9.17	6.48	1.29	2.95
Significance at 5% level		***	***	***	***	***	***	***	ns	*

Note: *** significance at 0.1%, ** significant at 1%, * significant at 5%, ns non-significant.

DH= Days to heading, DM=Days to maturity, PH=Plant height, PL=Panicle length, TL=Effective tillers per square meter, TGW= Thousand grain weight, FG= Filled grain number, UFG= Unfilled grain number, GY= grain yield in kg per hectare.

Table 3. Phenotypic and genotypic correlation among the quantitative traits of eighteen genotypes.

		DM	PH	PL	TL	TGW	FG	UFG	GY
DH	p	0.852 **	0.1933 NS	0.0578 NS	0.0862 NS	0.3513 **	-0.368 **	-0.0265 NS	-0.163 NS
	g	0.9847 **	0.2308 NS	0.0661 NS	0.1022 NS	0.4885 *	-0.4721 *	-0.2676 NS	-0.125 NS
DM	p	1 **	0.1467 NS	-0.0077 NS	0.0348 NS	0.2406 NS	-0.3129 *	-0.1099 NS	-0.1906 NS
	g	1 **	0.2513 NS	-0.0227 NS	0.0838 NS	0.486 *	-0.436 NS	-0.3364 NS	0.0698 NS
PH	p		1 **	0.5397 **	-0.3056 *	0.4922 **	-0.0207 NS	-0.1912 NS	0.0236 NS
	g		1 **	0.6395 **	-0.3146 NS	0.6168 **	-0.0868 NS	-0.5976 **	-0.0992 NS
PL	p			1 **	-0.4128 **	0.3536 **	0.2377 NS	0.0699 NS	0.1447 NS
	g			1 **	-0.5212 *	0.3707 NS	0.2159 NS	0.313 NS	0.1086 NS
TL	p				1 **	-0.1281 NS	-0.3464 *	0.0252 NS	-0.2415 NS
	g				1 **	-0.2493 NS	-0.4828 *	0.2169 NS	-0.3388 NS
TGW	p					1 **	-0.1225 NS	0.0234 NS	-0.0187 NS
	g					1 **	-0.371 NS	-0.0306 NS	-0.2969 NS
FG	p						1 **	0.0831 NS	0.7074 **
	g						1 **	0.404 NS	0.9482 **
UFG	P							1 **	0.1182 NS
	g							1 **	0.5604 *

**significance at 1% level, * significance at 5% level, NS non-significant, p= phenotypic correlation and g= genotypic correlation; DH= days to heading, DM= days to maturity, PH=plant height, PL=panicle length, TL=effective tillers number, TGW= thousand grain weight, FG=filled grain number per panicle, UFG= unfilled grain number per panicle, GY=grain yield in kg/ha.

Phenotypic and genotypic correlation between yield and yield attributing traits

The correlation serves as tool to determine the association and interrelations between two variables. Correlation analysis aids plant breeder to understand effect of one trait to others which helps to indirect selection of such traits. The genotypic correlation values were higher than the phenotypic correlation values indicating the masking effects of environment on these traits (Table 3). Oladosu *et al.* (2018) also reported the relationship among traits in both genotypic and phenotypic levels. Grain yield displayed highly significant and positive correlation with filled grains per panicle at both levels (r_p = 0.7074 ** and r_g= 0.9482 **). Similar result reported by Oladosu *et al.* (2018) and Khalequzzaman *et al.* (2023). Regarding the relationship of grain yield with unfilled grains per panicle, positive and significant correlation at phenotypic level (r_g= 0.5604 *) but non-significant at genotypic level (r_g= 0.1182 NS) was recorded. However, Oladosu *et al.* (2018) reported negative and non-significant relationship of grain yield with unfilled grains at phenotypic level whereas positive and significant relation at genotypic level, which was in contrast to our findings. Likewise, grain yield showed non-significant and positive relation with panicle length but negative association with remaining other traits at both phenotypic and genotypic levels. The genetic and phenotypic correlation between the grain yield and filled grain per panicle permits the selection of high yielding genotype indirectly. However, the correlation of grain yield with unfilled grains per panicle was phenotypically non-significant but genotypically significant suggests that breeders need to prioritize enhancing traits related to filled grains per panicle to improve rice varieties for higher yields.

Phenological traits (days to heading and maturity) exhibited a strong and significantly positive correlation with each other at both levels (r_p = 0.852**, r_g = 0.9847**). Similar result was reported by Tiwari *et al.* (2019) and Ghimire and Mahat (2019). Days to heading showed positive association with thousand grain weight which was also reported by Ghimire & Mahat, (2019); Gyawali *et al.* (2018) and Shrestha *et al.* (2018). There was negative and significant association between days to maturity and filled grain whereas contrasting result was reported by Kumar *et al.* (2022) and Singh *et al.* (2023). Plant height showed positive and highly significant association with panicle length (r_p= 0.5397 ** and r_g= 0.6395**). Concurrent report was provided by Adhikari *et al.* (2018); Faysal *et al.* (2022) and Gyawali *et al.* (2018) whereas contrasting result was shown by Mandal *et al.* (2023). Similarly, plant height had positive and significant relation with thousand grain weight (r_p= 0.4922** and r_g= 0.6168**) which was also reported by Faysal *et al.* (2022) and Shrestha *et al.* (2021) but contrasting result was reported by Ahamed *et al.* (2021) and Tiwari *et al.* (2019). However, it showed negative and significant relation with tillers per square meter at phenotypic level (r_p= -0.3056*) but non-significant at genotypic level (r_g = -0.3146 NS). Mandal *et al.* (2023) reported negative and significant relation at both levels. Contrasting result was reported by Tiwari *et al.* (2019). Similarly, plant height showed negative and non-significant relation with unfilled grains at phenotypic level (r_p= -0.1912 NS) but highly significant at genotypic level (r_g = -0.5976*). Plant height was positive and significant association with panicle length and 1000 grain weight. Similar association between them was found by Ghimire and Mahat (2019) and Shrestha *et al.* (2021). However, contrasting result was reported by Mandal *et al.* (2023) for panicle length.

Panicle length showed negative and significant association with effective tiller number per meter square at both levels (r_p = -0.4128**, r_g = -0.5212*). In contrast to this, weak positive correlation between them was found by Adhikari *et al.* (2018) and Gyawali *et al.* (2018). Similarly, it showed positive and significant relation with thousand grain weight at phenotypic level (r_p = 0.3536**) but non-significant at genotypic level (r_g = 0.3707 NS). The relation of panicle length with thousand grain weight at phenotypic level was also reported by Faysal *et al.* (2022) and

Table 4. Genetic parameters of yield and yield attributing traits of eighteen genotypes.

Genetic parameters	Ve	Vg	Vp	ECV	GCV	PCV	H^2	GA	GAM
DH	10.09	87.93	98.03	2.74	8.09	8.54	0.90	18.30	15.79
DM	25.30	48.04	73.34	3.46	4.77	5.89	0.66	11.56	7.95
PH	18.89	126.66	145.55	4.64	12.02	12.89	0.87	21.63	23.10
PL	1.14	4.00	5.14	4.80	8.99	10.19	0.78	3.64	16.34
TL	408.53	1291.88	1700.41	6.79	12.07	13.85	0.76	64.54	21.67
TGW	1.67	4.13	5.79	7.08	11.14	13.20	0.71	3.53	19.37
FG	227.07	394.46	621.52	13.33	17.57	22.05	0.63	32.59	28.83
UFG	169.00	12.71	181.71	43.52	11.94	45.13	0.07	1.94	6.50
GY	220786.30	122057.30	342843.60	15.05	11.19	18.76	0.36	429.42	13.76

Note: Ve = Environmental variance, Vg = Genotypic variance, Vp = Phenotypic variance, ECV= Coefficient of environmental variance, GCV= Coefficient of genotypic variance, PCV= Coefficient of phenotypic variance, H^2= Broad sense heritability, GA= Genetic advance, GAM= Genetic advance as percentage of mean.

Shrestha *et al.* (2021) but contrary result was reported by Adhikari *et al.* (2018) and Ahamed *et al.* (2021). Number of tillers per square meter had negative and significant relation with filled grain at both levels (r_p = -0.3464**, r_g = -0.4828*). Similarly, it showed positive and non-significant relation with phenological traits and unfilled grains. Thousand grain weight showed negative and non-significant relation but small magnitude with filled grains and grain yield. Fentie *et al.* (2021) also reported negative association of grain yield with thousand grain weight. Filled grains showed negative and non-significant relation with most of traits except for panicle length and unfilled grains with small magnitude at phenotypic level. Similarly, the negative association between filled grains and thousand grain weight was reported by Kumar *et al.* (2022).

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV)

Phenotypic coefficient of variation was consistently higher than the genotypic coefficient of variation for all the traits under investigation (Table 4). Similar results were reported Similar results were reported by Ghimire and Mahat, (2019); Kumar *et al.* (2022) and Williams *et al.* (2021). This disparity suggests that environmental factors significantly influence the expression of these traits (Adhikari *et al.*, 2018; Gyawali *et al.*, 2018). The highest PCV and moderate GCV values (>20%) were recorded for unfilled grain numbers (45.03 and 11.94), followed by filled grain numbers (22.05 and 17.57) and grain yield per hectare (18.76 and 11.19). Among them, high value of PCV coupled with GCV for filled grain numbers would be effective for selection. Similar result was also reported by Hossain *et al.*, 2018. The PCV and GCV values were lowest (<10%) for days to maturity (5.89 and 4.77), days to heading (8.54 and 8.09) and panicle length (10.19 and 8.99) which might be due to presence of positive and negative alleles in the population (Hossain *et al.*, 2018). Remaining all traits showed moderated GCV value (10-20%). In addition, ECV was highest for unfilled grains per panicle (43.53%), moderate for grain yield (15.05%) and filled grains (13.33%) and low for remaining other traits. High PCV and ECV and moderate GCV for unfilled grains per panicle indicates that there is a significant amount of variability among the observed individuals or samples within a population and this variability could be due to a combination of genetic and environmental factors such as soil quality, climate, management practices etc. The low difference between GCV and PCV values for days to heading, days to maturity, plant height, panicle length, effective tiller number per meter square and thousand grain weight suggested presence of sufficient genetic variability for the traits which might help for further selection. Low difference between GCV and PCV value for panicle length was also reported by Kumar *et al.* (2022) and Williams *et al.* (2021). Williams *et al.* (2021) also reported low difference between GCV and PCV value for days to maturity and plant height.

Heritability

Broad sense heritability is a means of determining the proportionate impacts of genetic and non-genetic factors on the overall phenotypic variability within a population. This concept holds significant importance in the field of quantitative genetics, especially when it comes to making informed decisions in selective breeding programs. Among the studied traits broad sense heritability ranged from 0.90 (days to heading) to 0.07(unfilled grains per panicle) (Table 4). Days to heading (0.90), plant height (0.87), panicle length (0.78) and effective tiller number per meter square (0.76) were highly heritable (>75%) traits. It suggests that they are highly responsive to selective breeding efforts aimed at enhancing those specific characteristics. Similar result was reported by Bhandari *et al.* (2019) except for days to heading. Thousand gain weight (0.71), days to maturity (0.66) and filled grains per panicle (0.63) showed moderate heritability (50 -75%). Whereas grain yield (0.36) and unfilled grains per panicle (0.07) showed low heritability (<50%) which suggests direct selection of these traits will be ineffective. Similar result was reported by Bhandari *et al.* (2019) except for unfilled grains for panicle. A very low heritability of unfilled grains per panicle means that the observed variation in this trait within a population is primarily due to environmental factors rather than genetic factors and most of the differences are driven by the specific environmental conditions or management practices which is not strongly inherited from one generation to the next, and it is highly responsive to changes in environmental conditions. In our research, as well as in studies conducted by Adhikari *et al.* (2018); Bandhi *et al.* (2018) and Gyawali *et al.* (2018), it was consistently observed that grain yield exhibited heritability levels ranging from low to moderate.

Genetic advance (GA) and genetic advance in percentage (GAM)

Estimated heritability itself alone is not very much useful because it includes the effect of both additive and non-additive gene. The genetic advance is therefore a useful indicator to achieve expected result on the trait of interest of a population after selection (Adhikari *et al.*, 2018). Genetic advance in percentage of mean (GAM) gives more precise result in comparison to only genetic advance (GA) (Adhikari *et al.*, 2018). The GA ranged from 1.94 (unfilled grains per panicle) to 429.42 (grain yield). Similarly, GAM ranged from 6.50% (unfilled grains per panicle) to 28.83% (filled grains per panicle) (Table 4). Among the traits, high values of GAM (>20%) were recorded for filled grains per panicle (28.83%), plant height (23.10%) and effective tiller number per meter square (21.67%). Similar result was reported by Hossain *et al.* (2018) for filled grains per panicle and plant height. Moderate GAM (10-20%) was recorded for thousand grain weight, panicle length, days to heading and grain yield. Similarly, low GAM (< 10%) resulted for unfilled grains per panicle and days to maturity. Abebe *et al.* (2018) and Adhikari *et al.* (2018) also reported low GAM for days to maturity. Contrary to this result, Hossain *et al.* (2018) reported high GAM for unfilled grain per panicle. A high genetic advance as a percentage of mean for plant height, effective tiller number per meter square indicates that genetics play a dominant role in determining expression of these traits, and it has a strong potential for genetic improvement through selective breeding or genetic manipulation. The high to medium heritability and genetic advance for traits such as days to heading, plant height, panicle length, effective tillers per square meter, thousand grain weight and filled grains per panicle are primarily control by genetic factor and could be selected based on their phenotypic performance. The low heritability with low GA for traits unfilled grain and grain yield indicated there has presence of non-additive genes and are influenced by genotype x environment interaction for expression of their trait.

Conclusion

Genotypes NR 2380-RGA1-RGA2 and NR 2381- RGA1-RGA2 exhibited early and potential high yielding genotypes while Tarhara-107 and Tarhara-2 identified as high yield, medium maturity and good filled grain number per panicle. Similarly, filled grains trait displayed tightly linked with grain yield and possess high GCV, PCV, GAM with moderate heritability indicated direct selection could be employed for trait enhancement in breeding program.

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Conflict of interest

The authors declare that there is no conflict of interests regarding the publication of this research article.

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