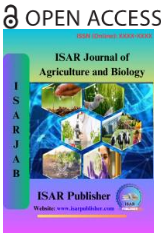

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Genetic estimation and Traits relationship of Spring Rice genotypes

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Abstract: Estimation of genetic parameters and interrelationships between traits assessed through the genetic and phenotypic variation among the genotypes provides a way for crop/trait improvement. Twenty genotypes including checks (Hardinath-1 and Chaite-5) were evaluated for eight traits in an alpha lattice design with three replications at the National Rice Research Program, Hardinath in the spring season of 2024. The analyzed result revealed variation among the genotypes from studied traits was due to inherent nature and genetic background. The studied genotypes matured in less than 125 days. The early maturity is a crucial trait in spring season rice which facilitates following main season rice cultivation in Nepal. The high-yielding genotypes IR 17A 3012, IR 17L 1368 and Hardinath 1-10 could get notified directly as a variety or applied in breeding programs. The high GCV, PCV and ECV values were recorded in filled grains per panicle, grain yield per ha, tillers per hill, and thousand-grain weight suggesting the genotypes have diverse genetic backgrounds and could be selected for further trait enhancement in the breeding program. The highest broad sense heritability was recorded for maturity days (0.89), heading days (0.88), plant height (0.74), and thousand-grain weight (0.66) indicating a high response to selection of particular traits merely governed by genotype and less influenced by environment. High heritability coupled with high GAM was recorded for thousand-grain weight (0.66, 24.31) indicating the trait was under the control of additive gene action and that direct selection of these traits would be effective for crop improvement. Positive and strong associations between grain yield per ha with heading days and maturity days at both genotype and phenotype levels and with filled grains per panicle at the genotypic level indicate grain yield dependent on independent variables (phenological and filled grains per panicle) in spring season rice. Thus, trait selection based on variability and association helps to select potential varieties or parent lines applicable in the spring rice breeding program.

Keywords: Spring rice, Variance, Correlation, Genetic parameter.

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Introduction

Rice, the primary staple cereal crop, contributes 5% of the gross domestic product of agriculture and supplies food and calories to more than half of the people of Nepal. Rice has cultivated in 1.44 million hectares area with production of 5.48 million tons, and productivity of 3.8 t/ha in the year 2023/24 (MoALD 2024). The Main (Barkhe) season holds 92% of the rice cultivated area followed by 7% area under the Spring (Chaite) season (CDD, 2015). Spring (Chaite) season starts from sowing in February and harvest in May/June. Spring rice is cultivated where irrigation water is assured. In the spring season, rice gets a better yield advantage over other seasons due to the maximum receive of sunshine and photoperiod activity. Thus, the spring season has the potential to increase rice yield and cultivation area.

The phenotypic variation of a population is composed of genetic and non-genetic factors present in individuals. The relative influence due to differences in genetic and non-genetic factors on phenotypic variation in a population is analyzed by heritability. The traits showed high heritability indicating a high response to selection which is governed by genotype and less influenced by environment. Similarly, low heritability indicated a high influence of environment on genotype so there is phenotypic plasticity. Heritability indicates the possibility and extent to the improvement of traits through selection and is important to the breeder (Robinson et al., 1949).

Genetic advance (a product of heritability and selection differential of concern trait) as a predictor of progress made from the selection of relevant population (Islam et al., 2015). High GAM indicated the presence of additive genes that control traits that could be

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improved through direct selection. Moderate GAM indicated the intermediate action of both additive and non-additive genes on the control of traits. Low genetic advance indicated nonadditive genes-controlled characters where heterosis breeding could be applied to create variation. Regarding the correlation coefficient, genotypic coefficient values were mostly higher than phenotypic coefficient values due to the strong influence of the inherent ability of genotypes on the expression of traits.

Nowadays, due to the inflated population, accessibility of roads, purchase capacity, and fine rice consumption rice imports in Nepal mainly from India, and other countries are still increasing. Due to the open border, thousands of tons of rice seed and milled rice are carried to Nepal informally. The high-yielding varieties or double rice cropping system through the increased area in the Spring season may address the production requirement. The spring season was previously used to cultivate and produce coarse grain for beaten rice. But nowadays the scenario has changed, and farmers have been demanding spring rice varieties that encompass fine, good eating quality, good milling quality, high yielding, and short maturity.

This study is continuing part of testing and evaluation as a Coordinated Varietal Trial (CVT) to develop a high-yielding, early-maturing rice variety suitable for the spring season. The study will evaluate the inheritance and improvement of agro-morphological traits based on the genetic basis and inter-relationship of traits.

Material and Methods

The experimental site was the National Rice Research Program situated at latitude 26^0 47'46.5" N and longitude 85^0 57'49.35" E and 75masl altitude. The twenty genotypes including checks (Hardinath-1 and Chaite-5) were replicated thrice and laid out in a random complete block design (RCBD). The size of the individual plots was 15 m2 (5m x3m). The spacing between the hills was 20 cm X 20 cm, and a hill consisted of 2-3 seedlings. Twenty-five days old seedlings were used in transplantation. The fertilizer dose was applied in the ratio of 100:30:30 kg NPK/ha in which half dose of nitrogen and full dose of phosphorous and potash were used as basal dose. The remaining half dose of nitrogen was split into two doses and top-dressed at the tillering and reproductive stage. The intercultural operation was applied as recommended in spring season rice cultivation (NRRP). The quantitative traits include days to heading days, maturity days, plant height, panicle length, tillers no. per hill, filled grains number per panicle, thousand-grain weight, and grain yield per ha were recorded. The quantitative data were analyzed using statistical software, R package-Agricolae for analysis of variance, and variability package for variance and correlation estimation.

Variances at phenotype and genotype were calculated as per Johnson et al., 1955. Similarly, the coefficient of variation at genotypic (GCV)and phenotypic (PCV) were calculated according to Burton, 1952. GCV and PCV were ranked according to Sivasubramanian and Madhavamenon (1973) as; low = 0–10%, intermediate = 10–20%, and high = greater than 20%. Broad sense heritability was estimated and categorized as suggested by Johnson et al., 1955 as; low=0-30%, intermediate = 30-60% and high = above 60%. Similarly, expected genetic advance (GA) and genetic advance as a percent of mean were calculated as a procedure given by Johnson et al., 1955 and categorized as; low = less than 10%, intermediate = 10-20%, and high = more than 20%.

Table1. List of advanced spring rice genotypes used in the experiment

Treatment	Genotype	Treatment	Genotype
1.	IR 17L 1588	11.	IR17A1732
2.	IR127026-B-34-3-12	12.	IR17A1660
3.	IR16L1769	13.	IR16L1411 127
4.	IR17L1368	14.	SVMET 161
5.	IR16L1755	15.	SVIN 291
6.	P#14-30-SP#27	16.	IR17A3012
7.	IR19A4188	17.	IR17A2252
8.	IR16A2094	18.	Hardinath-1-10
9.	IR17L1446	19.	Hardinath-1 (Check)
10.	IR15A2619	20.	Chaite-5 (Check)

Results and Discussion

Mean performance of yield and yield attributing traits of Spring rice genotypes

The statistically significant differences among the genotypes for studied traits were found at 5% and 1% levels of significance (Table 2). Similar findings were reported for most of the traits of spring rice by Yadav et al. (2014), Adhikari et al. (2018), Yadaw et al. (2023), and Bhusal et al. (2023). These results indicated variation in genotypic composition which could be useful in the future breeding program.

Table 2. Mean performance of yield and yield attributing traits of Spring rice

TRT	Genotypes	HD	MD	PH	PL	TLH	FG	TGW	GY
1	IR 17L 1588	95	121	95.8	23.0	10	101	21	4.70
2	IR127026-B-34-3-12	95	121	96.1	23.9	12	124	18.67	4.40
3	IR16L1769	98	121	95.2	21.3	12	93	21	4.63
4	IR17L1368	95	120	102.7	22.1	11	95	23.33	5.03
5	IR16L1755	96	122	97.9	23.0	12	73	22	4.23
6	P#14-30-SP#27	81	107	90.4	22.5	18	83	21.33	1.53
7	IR19A4188	98	121	90.1	21.6	17	109	22.67	4.50
8	IR16A2094	97	121	90.1	25.0	11	71	21.67	4.43
9	IR17L1446	96	120	91.4	22.7	11	66	20.33	2.37
10	IR15A2619	96	119	93.9	22.4	12	83	22.67	3.23
11	IR17A1732	84	103	83.0	20.2	13	83	30.33	3.90
12	IR17A1660	86	110	83.3	20.1	13	81	25.33	3.97
13	IR16L1411	95	119	90.0	22.7	14	92	24.67	4.50
14	SVMET 161	98	122	89.5	20.9	14	75	26.67	4.80
15	SVIN 291	100	124	98.4	23.9	14	90	23	2.90
16	IR17A3012	95	119	99.0	22.8	11	138	26.67	5.33
17	IR17A2252	93	118	91.9	20.9	12	76	28.33	4.63
18	Hardinath-1-10	101	123	98.3	24.8	17	86	22.33	5.17
19	Hardinath-1	96	122	97.0	22.0	12	124	15	3.80
20	Chaite-5	95	120	103.5	23.9	12	157	18.33	4.93
Mean		94	119	93.9	22.5	13	95.12	22.78	4.15
CV		1.94	1.63	3.3	6.2	19.18	26.98	10.35	20.41
LSD		3.12	3.31	5.31	2.4	4.26	43.87	4.03	1.45
Rep		NS	*	NS	NS	NS	NS	NS	NS
Treatment		***	***	***	**	**	**	***	***
F-Value		3.14E-15	1.19E-15	2.45E-09	1.87E-03	8.70E-03	5.50E-03	2.54E-07	1.40E-04

Note: HD= days to heading, MD= days to maturity days, PH= Plant height, PL= Panicle length, TLH= tillers no. per hill, FG= filled grains per panicle, TGW= thousand grain weight, GY= grain yield in ton/ha

The heading days ranged from 81 to 101 days with a mean of 94 days. The earlier heading was observed for genotype P#14-30-SP#27 (81 days) while the late heading was observed for SVIN 291 (100 days) and Hardinath 1-10 (101 days). Similarly, maturity days ranged from 103 to 124 days with an average of 119 days. The early maturing genotypes were IR 17A 1732 (103 days) followed by P#14-30-SP#27 (107 days). Similarly, late-matured genotypes were SVIN 291 (124 days) followed by Hardinath 1-10 (123 days). A Concurrent result in spring rice was reported by Yadaw et al. (2023) and Bhusal et al. (2023). The early heading facilitates double-season rice cultivation and maintains the quality of seed or grain before monsoon onset. It would help the crop to escape genotypes from high temperatures and drought in the flowering period. Yoshida (1981) also suggested ideal heading days in the spring season rice complete in 122-125 days. The earliness trait in the spring season rice is important for food security, adjustment in cropping system, and global warming issues.

The plant height ranged from 83cm to 103.5cm with a mean of 93.9cm. The short-stature genotypes IR 17A 1732 and IR 17A 1660 had plant height of 83cm. Similarly, long-stature genotypes IR 17L 1368 and check variety Chaite-5 had 102.7 cm and 103.5 cm, respectively. A similar report was reported by Yadaw et al., 2023 and Subedi et al. 2024 on rice height differences. Chhogyl et al. 2013 suggested short short-stature is the ideal plant height in the spring season. Skazhennik et al., 2019 also reported moderate plant height preferred by farmers because of lodging resistance.

The short panicle length was observed in genotypes IR 17A 1732 and IR 17A 1660 with 20cm. The long panicle length was observed in genotypes IR 16A 2094 and Hardinath 1-10 with 25cm and 24.8cm, respectively. Panicle length determines the grain yield based on the ability to hold grain numbers. This indicates panicle length also contributes significantly to grain yield (Khan et al., 2023). The genotype IR 17L 1588 (10) had least tillers no. per hill, while highest for P#14-30-SP#27 (18) followed by both genotypes IR 19A 4188 and Hardinath 1-10 (17). Genetic composition of genotypes to produce tillers with filled grain panicles and environmental factors such as spacing, available nutrition, competition with weeds and diseases impact grain yield.

Genotype Chaite-5 (157 grains) was found with high-filled grains per panicle followed by IR 17A 3012 (138 grains), genotypes IR 127026-B-34-3-12 and Hardinath-1 with 124 grains. A similar result for Chaite-5 was also reported by Shrestha et al., 2022. The highest thousand-grain weight was recorded for genotype IR 17A 1732 (30.33 g) while the lowest was for Hardinath-1 (15g). The thousand-grain weight is a heritable trait influenced by grain size (grain length, width and thickness) (Fan et al., 2006). Islam et al., (2013) reported variation in thousand grain weight is influenced by the genetic composition of the genotypes. The amount of photosynthetic assimilates translocated to grains after the heading of genotype determines the thousand-grain weight and percentage of filled spikelet (Ishii, 1995).

The grain yield of genotypes ranged from 1.53 t/ha to 5.33 t/ha with a mean of 4.15 t/ha. The highest grain yield was obtained in genotype IR 17A 3012 (5.33 t/ha) followed by Hardinath 1-10 (5.17 t/ha) and IR 17L 1368 (5.03 t/ha). A similar result in yield variation of spring rice was reported by Yadaw et al. (2023), Chaudhary et al., 2023; Acharya et al., 2024 and Adhikari et al., 2018. Yield is complex and dependent on the cumulative effects of independent variables or traits. The variation in yield was due to the genetic, environmental, and interaction effect that caused the proportional contribution of individual traits.

Genetic parameters of the rice genotypes

In all studied traits, the phenotypic coefficient of variation was higher than the genotypic might be due to environmental factors influences. Similar results were reported by Adhikari et al., 2018; Tiwari et al., 2019 and Lamichhane et al., 2021. The highest variance due to genotype, environment, and phenotype was observed for filled grain per panicle (VG: 357.58, VE: 658.96, and VP: 1016.54). Lamichhane et al., 2021 confirm the variances in filled grain. The filled grain traits could be selected based on their phenotypic expression.

Table3. Genetic parameter of yield and yield attributing traits of Spring rice

Traits	Mean	Range	VE	VG	VP	ECV	GCV	PCV	Hb	GA	GAM
HD	94	78±104	3.34	24.38	27.72	1.94	5.23	5.58	0.88	9.54	10.10
MD	119	101±127	3.75	29.09	32.84	1.63	4.54	4.83	0.89	10.46	8.81
PH	93.9	82.2±106.6	9.66	27.89	37.55	3.31	5.63	6.53	0.74	9.38	9.99
PL	22.5	18.8±26.6	1.94	1.30	3.24	6.20	5.08	8.01	0.40	1.49	6.63
TLH	13	9±21	6.22	3.04	9.26	19.18	13.41	23.41	0.33	2.06	15.83
FG	95	42±197	658.96	357.58	1016.54	26.99	19.88	33.52	0.35	23.10	24.29
TGW	22.78	14±32	5.55	10.90	16.45	10.35	14.50	17.82	0.66	5.53	24.31
GY	4.15	0.5±6.2	0.72	0.71	1.43	20.42	20.32	28.81	0.50	1.23	29.53

Note: HD= Heading days, MD=maturity days, PH=plant height, PL=panicle length, TLH=tillers per hill, FG=filled grains per panicle, TGW=Thousand grain weight, GY=grain yield ton/ha

VE= variance due to environment, VG=variance due to genotype, VP=variance due to phenotype, ECV=coefficient of variation due to environment, GCV= coefficient of variance due to genotype, PCV= coefficient of variation due to phenotype, Hb= Heritability in broad sense, GA= Genetic Advance, GAM= Genetic advance as per mean

The filled grains per panicle showed the highest PCV and ECV values (33.52 and 26.99) and GCV values (19.88). The PCV was highest for filled grain per panicle followed by grain yield per ha, tillers no. per hill and thousand grain weight. Adhikari et. al., 2018 also found the highest PCV for traits filled grains per panicle, grain yield per ha, and effective tillers no. per square meter. Similarly, GCV value was recorded high for grain yield per ha (20.32), filled grains per panicle (19.88), thousand-grain weight (14.5) and tillers no. per hill (13.41). Similar results for the highest GCV were also reported by Adhikari et al. (2018) and Sreelakshmi and Babu (2020). The high GCV and PCV values suggested the genotypes have diverse genetic basis and trait selection could be done based on phenotype value for crop improvement. Similarly, ECV was highest for filled grain per panicle followed by grain yield per ha, tillers no. per hill and thousand-grain weight. The heading days, maturity days, plant height and panicle length showed low GCV, PCV and ECV. Low GCV and PCV for days to flowering, plant height and panicle length were reported by Hossain et al., 2015; Adhikari et al., 2018 and Sreelakshmi and Babu (2020). Bhargavi et al., 2021 reported low GCV and moderate PCV for days to maturity and panicle length. Sreelakshmi and Babu, 2020 also reported low GCV and PCV for days to maturity. Lamichhane et al., 2021 reported low GCV and PCV for days to flowering and panicle length. The scope of selection and improvement could be measured through a high coefficient of variability of respective traits. Similarly, a low coefficient of variability suggested the creation of variation through hybridization or mutation followed by selection.

The broad sense heritability was found highest for maturity days (0.89), heading days (0.88), plant height (0.74) and thousand-grain weight (0.66). Sreelakshmi and Babu (2020), Devkota et al. (2023), Hossain et al. (2015) and Adhikari et al. (2018) reported similar findings. High heritability estimated traits (heading days, plant height, maturity days and thousand-grain weight) indicated a high response to selection for particular traits due to being less affected by the environment. Intermediate heritability was recorded by grain yield per ha (0.5), panicle length (0.40), filled grain per panicle (0.35) and tillers no. per hill (0.33). Concurrent results reported by Adhikari et al., 2018 for grain yield per ha, filled grain per panicle and panicle length.

The genetic advance was recorded highest for the filled grain (23.10) followed by maturity days (10.46). The low genetic advance recorded for grain yield per ha (1.23) followed by panicle length (1.49) and tillers no. per hill (2.06). Low genetic advance indicated nonadditive genes-controlled characters where heterosis breeding could be applied.

Genetic advance as per mean was recorded highest for grain yield per ha (29.53) followed by thousand-grain weight (24.31), filled grain no. per panicle (24.29). Moderate genetic advance per mean was recorded for tillers per hill (15.83) and heading days (10.10). The lowest genetic advance per mean was recorded for panicle length (6.63) followed by maturity days (8.81) and plant height (9.99).

High heritability coupled with high GAM was recorded for TGW (0.66, 24.31) indicating that these traits were mostly under the control of additive gene action and that direct selection of these traits would be effective for crop improvement. Aravind et al. (2019), Bhargavi et al., 2021, Demeke et al. (2023) and Devkota et al. (2023) for weight of 1000 fully developed grains.

Moderate heritability coupled with high GAM was recorded for GY (0.50, 29.53), and FG (0.35, 24.29). A similar report by Demeke et al., 2023 presented high GAM with high heritability for grain yield. Bhargavi et al., 2021 reported high heritability with high GAM for grain yield. Islam et al., 2015 reported high heritability with moderate GAM for filled grains per panicle.

High heritability and coupled with moderate GAM were recorded for heading days (0.80, 10.10). A similar report by Demeke et al., 2023 for heading days. Moderate heritability coupled with moderate GAM was recorded for tillers per hill (0.33, 15.83). Moderate GAM of heading days and tillers per hill indicated intermediate additive and non-additive gene action control characteristics.

High heritability and low GAM were recorded for maturity days (0.89, 8.81), and plant height (0.74, 9.99). Moderate heritability and low GAM were recorded for panicle length (0.40, 6.63). Low GAM was also reported by Adhikari et al., 2018 for maturity days, plant height and panicle length; Mallimar et al. (2015) for maturity, and panicle length; Islam et al., 2015 for plant height.

Table 4. Genetic and phenotypic interrelationship of eight quantitative traits of spring rice genotypes

Trait	Level	MD	PH	PL	TLH	FG	TGW	GY
HD	Geno	0.9599 **	0.6014 **	0.5813 **	-0.2965 NS	0.193 NS	-0.3608 NS	0.5413 *
	Pheno	0.9452 **	0.4882 **	0.4077 **	-0.1643 NS	0.0749 NS	-0.2594 *	0.3588 **
MD	Geno	1 **	0.6811 **	0.6346 **	-0.3047 NS	0.2511 NS	-0.5074 *	0.474 *
	Pheno	1 **	0.5819 **	0.4558 **	-0.1937 NS	0.1125 NS	-0.3983 **	0.2699 *
PH	Geno		1 **	0.6895 **	-0.2779 NS	0.7446 **	-0.5631 **	0.3731 NS
	Pheno		1 **	0.4522 **	-0.2018 NS	0.3631 **	-0.4217 **	0.2454 NS
PL	Geno			1 **	-0.1266 NS	0.2671 NS	-0.6252 **	0.1234 NS
	Pheno			1 **	-0.0082 NS	0.1789 NS	-0.3946 **	-0.004 NS
TLH	Geno				1 **	-0.2069 NS	0.2375 NS	-0.4893 *
	Pheno				1 **	-0.032 NS	0.0076 NS	-0.1126 NS
FG	Geno					1 **	-0.337 NS	0.5272 *
	Pheno					1 **	-0.4648 **	0.2511 NS
TGW	Geno						1 **	0.2197 NS
	Pheno						1 **	0.141 NS

Note: Geno= Genotypic level, Pheno= Phenotypic level, HD=Heading days, MD=Maturity days, PH=Plant height, TLH=Tillers per hill, FG=Filled grains per panicle, TGW= Thousand grain weight, GY=Grain yield ton/ha

NS= Non significant differences at 5% level. *= significant at 5% level, **= Significant at 1% level

Grain yield had positive and highly significant relation with heading days, maturity days at both levels and a significant relation with filled grain per panicle at genotypic level. Oladosu et al, 2018 reported similar results for days to flowering, maturity, and filled grains per panicle at genotypic and phenotypic levels. Tiwari et al. (2019) supported grain yield with days to heading and maturity in rainfed lowland rice genotypes. Manohar and Singh (2015) also reported a significant relation between grain yield with filled grains per panicle at the genotypic level. Similarly, grain yield had a negative significant relation with tillers per hill at the genotypic level. Oladosu et al. (2018) reported a contradictory result between grain yield and tillers per hill at the genotypic level.

The heading days showed a positive and highly significant relationship with maturity days, plant height, and panicle length at both phenotypic and genotypic levels. The positive and highly significant relation reported by Tiwari et al., 2019 for days to heading and maturity. But Oladosu et al, 2018 reported positive significant relation at the phenotypic level and a negative non-significant at the genotypic level. Similarly, heading days showed a positive highly significant relation to grain yield per ha at the phenotypic level but significant at the genotype level. Non-significant and positive correlation of heading days with filled grain per panicle but negative with tillers per hill at both genotype and phenotypic levels. The heading days showed a negative significant relation to thousand-grain weight at the phenotypic level but non-significant at the genotypic level.

The maturity days showed positive and highly significant relation with plant height, panicle length and significant relation with grain yield per ha at both genetic and phenotypic levels. Negative and significant relations of maturity days to thousand-grain weight and non-significant relations with tillers per hill were observed at both levels. Tiwari et al., 2019 reported a negative relation between days to heading and maturity with thousand-grain weight. Chaubey and Singh (1994) observed a significant positive relation between panicle length and days to maturity.

Plant height showed a highly significant relation and positive correlation with panicle length and filled grain per panicle but a negative correlation with thousand-grain weight at both levels (Tiwari et al., 2019 reported a similar relationship between plant height with thousand-grain weight at both levels). The nonsignificant and negative correlation of plant height was observed to tillers per hill and positive with grain yield per ha at both levels. Plant height relation with grain yield was also reported by Tiwari et al., 2019 at both levels.

Filled grains per panicle showed nonsignificant relations with most of the traits except plant height. It also showed a negative highly significant relation with thousand grain at the phenotypic level and a positive significant relation with grain yield per ha at the genotypic level. Karim et al., 2014 and Biswas et al. 2000 reported a negative association between filled grains per panicle and thousand-grain weight in aromatic rice. Thousand grain weight had a non-significant relation with grain yield per ha, tillers per hill at both levels. Concurrent findings by Tiwari et al., 2019 for grain yield.

Conclusion

There is a low varietal choice to farmers for spring rice due to few varieties developed. The food shortage at the global level is becoming a major issue and Nepal is importing rice worth 50 billion rupees in 2021/22. The earliness trait is inevitable for the spring season along with high yielding. Genotype IR 17A 3012, Hardinath 1-10 and IR 17L 1368 produced higher yields and matured earlier as checks Hardinath-1 and Chaite-5. These genotypes could be selected for variety notification after multilocation testing or used in crop improvement programs.

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Disclosure of conflict of interest

No conflict of interest to be disclosed.

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