GENETIC VARIATION FOR GRAIN YIELD, YIELD COMPONENTS AND QUALITATIVE TRAITS IN RICE (*Oryza sativa* L.) MUTANTS

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A study was performed to select the most successful rice mutants and to estimate the heritability of grain yield and some agro-morphological and quality traits. 65 rice genotypes including four local landraces (Hashemi, Tarom, Alikazemi and Sangjo), four released cultivars (Khazar, Fajr, H.P and Sephidrod) and 57 mutant lines (M5) were studied. The experiment was carried out during the spring of 2013-14 at Rice Research Institute of Iran (RRII) in Rasht. Analysis of variance indicated significant effects of genotype on all of the traits. Higher genotypic (GCV) and phenotypic coefficient of variation (PCV) were obtained for number of unfilled grains and grain yield. In general, very narrowly differences between PCV and GCV indicated fewer influence of environment on all of the studied traits. Broad sense heritability and genetic advance over mean were high for panicle weight, panicles per plant, number of filled grains, number of unfilled grains and grain yield. The high genetic advance over mean coupled with moderate to high heritability suggested the importance of additive gene action for the above mentioned traits. Mutant TM6-B-7-1 had high grain yield, panicles per plant, plant height, spikelets per panicle, panicle weight and hundred grain weights and can be used for future breeding programs to incorporate these characters in local genotypes.

Keywords: Additive effect, heritability, selection, genetic advance.

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INTRODUCTION

Rice (*Oryza sativa* L.) as the staple food for one third of the world's people and the second most important cereal crop, prepares 75% of calories and 55% of protein in the daily diet of people (BHUIYAN *et al.,* 2002).

Grain yield is the main trait targeted for improvement of rice productivity. In rice breeding programs, the main aim is to develop genotype for the improvement of yield under adverse agro-climatic conditions. The scope of crop improvement by breeding is determined by the value of heritabilities or genetic variation to that of non heritable. The success of breeding programs depends on the genetic diversity of the crop (CARENA, 2009). The variation obtained by hybridization often is insufficient; and therefore, it is suggested that the application of mutation treatment to hybrids or local genotypes may be one means of adding the variability inherent in the cross (ISMACHIN and SOBRIZAL, 2006). The objective of mutation induction is to generate new genetic variability leading to development of new varieties. The frequency rate of spontaneous mutation is very low and the use of this source of variation is difficult in plant breeding programs. Therefore, the desirable genotypes with applicable quality traits, agronomical traits and abiotic and biotic stress tolerant may be isolated through induced mutagenesis (MOHAN JAIN, 2010). In rice the main improved traits were early maturity, disease resistance and plant height (semi-dwarfness) (CHEN *et al.,* 2006). Mutagenesis approaches using chemicals or irradiation have been greatly used to diversify grain yield and quality in rice (MO *et al.,* 2013). Gamma rays are the most popular mutagen and the mutated traits are responsible for the expression of agronomic, grain quality, pests and disease resistance and phenotypes (GUIMARAES, 2009). Food and Agriculture Organization of the United Nation (FAO) and International Atomic Eenergy Agency (IAEA) mutant varieties database indicates that there were 2541 released mutant cultivars, up to March 2007. The largest numbers are from cereals (1212), which rice presented the highest number (525) (GUIMARAES, 2009).

Yield improvement is a major breeding purpose of most crop improvement programs in rice. Choice of genotypes that produced progeny with desired character combinations, is leading to the success of a self-fertilized plant breeding program. The nature and magnitude of genetic variability influenced the genetic improvement of suitable characters in crop (LOSS and SIDDIQUE, 1997).

Many researches estimated heritability, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) in rice and indicated high values of PCV and GCV for number of unfilled grains, number of panicle per plant, panicle weight and grain yield (KHAN *et al.,* 2009; SADEGHI, 2011; ASHFAQ *et al.,* 2012; OSMAN *et al.,* 2012; YADAV *et al.,* 2008). Genetic advance gives an estimate of reliable gain at a specified intensity of selection, which is an important tool in plant breeding on scientific basis. Therefore, heritability estimates along with genetic advance are beneficial in laying emphasis in selection for yield and yield components. However, the extent of improvement of a character would depend mainly on the amount of variability in the population where selection has to be made (SHARIFI, 2015). Heritability of rice cooking quality traits has been studied also by some researchers and high heritability was indicated for amyloze content (AC) (SHARIFI *et al.,* 2010 b). High values of heritability were also reported in yield and yield components of rice by VERMA *et al.,* (2003) HOSSEINI *et al.,* (2005), SHARIFI *et al.,* (2010 a), AHMADIKHAH (2010), SUBBAIAH (2011), KARIM *et al.,* (2007) and DINESH *et al.,* (2011). OSMAN *et al.,* (2012) observed high heritability coupled with high genetic advance for tillers per plant, plant height, 1000 grain weight and high heritability with low

genetic advance for 50% flowering and days to maturity. SELVARAJ et al., (2011) also identified high heritability, genetic advance and GCV for tillers per plant, productive tillers per plant, plant height and grain yield. High heritability and low genetic advance indicated non-additive gene action; whereas, high heritability coupled with high genetic advance revealed the additive gene action and supplied good scope for further improvement (PANSE, 1957). High heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present (TIAWARI et al., 2011).

In the present study, an attempt has been made to evaluate variability created by induced mutation and studying morphological variability of the induced mutants. The other propose of present study were the estimation of heritability via variance components for grain yield, yield component and some of quality traits.

MATERIAL AND METHODS

Experimental field area

Four local landraces (Hashemi, Tarom, Alikazemi and Sangjo), four high yielding cultivars (Khazar, Fajr, H.P and Sephidrod) and 57 mutant lines (M5) were grown in a randomized complete block design with three replications, during the spring of 2013-14 at the experimental farm of Rice Research Institute of Iran (RRII) in Rasht. The farm is situated between 49˚E longitude and 37˚N latitude at an altitude of 7 m below the mean sea level in north of Iran. Seeds of each genotypes were exposed to 300Gy, {Gy=Grey (1Grey=10krad)} gamma rays treatments from Cobolt60 source at Iranian Agricultural Atomic Research Institute, Tehran at equilibrium moisture content of eight percent during 2010. Following irradiation mutagen treatment of seeds, different M1 were grown in the field. Surviving plants were self to get the seeds of respective M2 and again self to get M3, M4 and M5. Radio sensitivity was determined by measurements of germination, seedling height and root length under field on the M_1 generation.

The M5 mutant line and parental genotype seeds were sown in a nursery on the 10 May 2014 and 25 day old seedlings were transplanted to the field. The experimental plots had 25×25 cm spacing, in four-row of three m length. One-third amount of recommended nitrogen (200 kg ha^{-1}) and whole phosphorous (100 kg ha^{-1}) was applied at the time of transplanting the seedlings. The remaining two-third of nitrogen was utilized in two split doses 30 days after transplanting and at the time of panicle initiation. Hand weddings were done at 30 and 50 days after transplanting. The permanent flood water level was maintained at 10 cm. The observations were recorded on ten plants randomly selected from the two centre rows in each replication.

Estimated characters

In the analysis, the following traits were measured based on, Standard Evaluation System for Rice (SES, 2002): Grain yield (GY), plant height (PH), number of panicle per plant (NPP), panicle length (PL), spikelets per panicle (SNP), internodes length (IL), filled grains per panicle (FG), grain productivity (GP), hundred grain weight (HGW), grain length (GL), grain width (GW), amylose content (AC) and gelatinization temperature (GT).

Statistical analysis

The genotypic and phenotypic variances (σ_g^2 and σ_p^2) were calculated from the partitioning mean squares expectation as follows (ROY, 2000):

$$\sigma_g^2 = \frac{MSg - MSe}{r}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 / r$$

Where, g and r are number of genotype and replication, respectively; σ_p^2, σ_g^2 and σ_e^2 are components of variance for phenotypic, genotypes and error, respectively.

The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was computed through following formula (ROY, 2000):

$$GCV(\%) = \frac{\sigma_g}{\bar{X}} \times 100$$

$$PCV(\%) = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

$\bar{X}$ = General mean of the characters

Broad sense heritability (H^2) was estimated as: genotypic variance/phenotypic variance (ROY 2000):

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

The extent of genetic advance to be expected from selecting five percent of the superior progeny was calculated by using the following formula (ROY, 2000):

Genetic advance (GA) = ih² σp

i = Intensity of selection

h² = Heritability in broad sense

σp = Phenotypic standard deviation

The value of i was taken as 2.06 assuming 5 percent selection intensity. Genetic advance over mean was estimated using the following formula:

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

Where,

GA = Genetic advance

$\bar{X}$ = general mean of the character

Statistical analysis of variance was done by SAS 9.1. Genetic parameters were estimated by Excel software according above formula.

RESULTS AND DISCUSION

The radiosensitity test on the M_1 generation indicated a decrease in germination, seedling height and root length under field condition with the increase in radiation dose.

Analysis of Variance (ANOVA) and Mean comparison

The mutants and parental genotypes indicated highly significant variations for days to 50 percent flowering, plant height, internodes length, number of panicle per plant, panicle length, panicle weight, spikelet number per panicle, number of filled grains, number of unfilled grains,

grain productivity, hundred grain weight, grain length, grain width, amylose content and gelatinization temperature (Table 1).

Table 1. Analysis of variance for some of agronomic and quality traits

SOV	df	DFl	PH	IL	NPP	PL	PW	SNP	FG	UnG
R	1	0.5	0.34	1.72	3.33**	0.56	0.00025	0.35*	44.29	0.06
G	64	52.17**	297.09**	59.31**	11.59**	8.39**	0.306**	1.56**	423.11**	253.87**
E	64	2.02	1.68	0.5	0.23	0.26	0.0015	0.082	12.44	2.47
CV		1.69	1.08	1.62	3.73	1.90	1.69	3.44	3.74	11.95

Cont. Table 1. Analysis of variance for some of agronomic and quality traits

SOV	df	GP	HGW	GL	GW	GLW	GY	AC	GT
R	1	3.67	0.02*	0.017	0.00009	0.006	45980.3	0.48**	0.30**
G	64	149.59**	0.16**	0.65**	0.077**	0.455**	1771415.3**	2.003**	0.36**
E	64	1.42	0.0043	0.005	0.0018	0.012	15736.4	0.039	0.0069
CV		1.35	2.56	0.70	1.68	2.75	3.06	0.89	1.92

*, **– significant at the 0.05 and 0.01 probability level, respectively.

DFl: day to flowering; PH: plant height; IL: internodes length; GY: grain yield; NPP: number of panicle per plant; PL: panicle length; PW: panicle weight; SNP: spikelet number per panicle; FG: number of filled grains; UnG: number of unfilled grains; GP: grain productivity; HGW: hundred grain weight; GL: grain length; GW: grain width; AC: amylose content; GT: gelatinization temperature.

The values of mean comparison were indicated in Table 2. Mean number of days to flowering (84.1 days) revealed ~~the~~ differences among the mutants ranging from 77-98 days. The lowest and highest values of days to flowering were obtained in Hashemi and KM5-250-3-1-E, respectively. Between the mutants, wide range of plant height was observed from 84.33-145.17 cm with a mean of 119.35 cm. Mean of internodes length (43.63 cm) revealed differences among the genotypes ranging from 29.33-63.17 cm. Mutant KM5-200-43-1-E (29.33 cm) had shortest internode followed by mutant FM6-200-E6 (31.58 cm) and FM6-200-E5 (31.92 cm), highest internodes length was observed for landrace varieties Tarom (63.17 cm) followed by Hashemi (60.25 cm). Very wide range of number of panicle per plant was observed from 8.17-19.83 with mean of 12.94. Number of panicle per plant was less in mutant HM5-250-41-2-E (8.17) followed by KM5-250-3-1-E (8.50) and more in mutant TM6-230-1-1 (19.83) followed by TM6-220-10-4-1 (19.17). Mean panicle length was found to be 26.78 cm with the range of 23.01-32.25 cm. Lowest panicle length was observed in the landrace Sangjo (23.01 cm) followed by mutant KM5-200-17-1 (23.92 cm), where as highest panicle length was found in mutant HM5-300-5-3 and HM5-250-25-1-3 with 32.25 cm and 31.25 cm, respectively. Mean of panicle weight (2.34 g) revealed the differences among the genotypes ranging from 1.55-3.41 g. Lowest panicle weight observed in Mutant TM6-230-1-2 (1.55 g) followed by mutant HM5-250-26-1 (1.60 g), where as highest panicle weight indicated in mutant HM5-250-E-1-1 (3.41 g) followed by mutant HM5-250-7-4-3 (3.11). Mean number of spikelets per panicle was found to be 8.34 and ranging from 6.67 (mutant TM6-220-10-4-1) to 10.50 (SEPIDROUD). Wide range of number of filled grains among the genotypes was observed from 60.83 (mutant HM5-250-E-18-1) to 126.75

(mutant HM5-250-E-1-1) with mean of 94.22. Wide range of number of unfilled grains among the genotypes was observed from 3.50-41.50 with mean of 13.17.

Table 2. Mean comparison of some of agronomic and quality traits

Genotype	DFl	PH cm	IL (cm)	NPP	PL (cm)	PW (g)	SNP	FG	UnG
TM6-220-10-4-1	82.00	129.00	44.33	19.17	28.08	2.64	6.67	108.33	6.00
TM6-230-VE-7-5-1	79.00	122.83	40.70	15.83	24.78	2.60	8.33	92.50	6.83
TM6-230-VE-8-4-1	78.00	118.83	41.83	13.83	24.17	2.46	8.17	84.83	6.50
TM6-250-10-7-1	83.00	125.00	44.08	14.50	27.83	2.76	9.17	106.33	7.00
TM6-250-15-5-1	84.00	120.00	45.08	17.83	24.92	2.54	8.00	93.67	7.50
TM6-B-2-1-E	81.00	125.00	42.83	16.83	27.25	2.29	8.33	77.83	19.00
TM6-B-7-1	79.00	125.83	41.50	12.17	24.28	2.99	9.00	104.83	3.67
TM6-B-19-1-E	81.00	125.00	42.67	14.17	25.25	2.32	7.83	72.83	6.00
TM6-B-19-2	85.00	116.83	40.25	12.00	25.17	2.54	7.17	92.00	7.67
TM6-230-1-1	81.00	116.17	43.58	19.83	24.42	1.71	6.83	61.83	26.67
TM6-230-1-2	85.00	127.00	43.58	14.00	25.25	1.55	6.83	70.67	6.00
TM6-300-5-1	83.00	116.33	42.17	14.83	24.51	2.27	8.33	99.00	5.83
TM6-250-11-5	86.00	113.00	40.50	13.00	24.53	2.27	7.00	81.33	7.00
FM6-200-E6	81.00	94.33	31.58	13.67	27.00	2.25	9.67	115.17	26.83
FM6-200-E5	85.00	94.17	31.92	12.50	27.50	2.28	9.67	98.17	32.17
HM5-250-7-4-2	84.00	126.83	43.50	14.50	28.87	2.53	9.17	107.83	5.83
HM5-250-7-4-3	81.00	124.33	45.17	11.67	30.83	3.11	9.50	106.67	4.67
HM5-250-7-5-2	80.00	131.00	42.50	14.33	24.92	2.37	8.50	85.67	4.83
HM5-250-7-7-2	78.00	123.00	47.25	9.83	28.67	2.77	9.50	120.83	9.50
HM5-250-25-1-3	79.00	130.00	49.67	15.00	31.25	2.20	7.83	89.17	5.00
HM5-250-26-1-E-1	83.00	131.67	42.17	16.00	25.75	1.90	7.83	92.83	5.33
HM5-250-42-1-E-1	82.00	125.17	43.75	11.33	28.25	2.73	8.50	84.33	9.00
HM5-250-E-1-1	80.00	128.17	41.58	10.17	25.92	3.41	9.50	126.75	7.50
HM5-250-E-3-2	79.00	121.33	44.17	16.00	30.92	2.19	7.50	69.67	10.50
HM5-250-E-5-2	86.00	125.17	41.17	13.00	26.83	2.59	8.83	94.33	7.17
HM5-250-E-18-1	85.00	116.50	44.75	11.00	27.17	1.58	7.50	60.83	7.33
HM5-250-2-4	81.00	124.67	46.33	11.00	30.58	1.81	7.67	83.50	6.50
HM5-250-3-1	84.00	119.17	42.42	11.67	27.08	2.19	7.00	95.67	7.00
HM5-250-5-1	82.00	113.50	38.17	11.17	25.00	2.06	8.00	104.83	4.17
HM5-250-6-6	83.00	120.00	46.25	9.17	25.25	2.05	8.83	92.83	4.17
HM5-250-7-1	80.00	114.83	46.87	14.50	28.50	2.23	8.50	86.33	3.67
HM5-250-7-6	79.00	125.00	46.37	15.00	27.03	2.51	8.33	102.67	7.33
HM5-250-12-1	80.00	126.50	49.67	10.33	30.00	2.17	7.17	78.33	8.50
HM5-250-23-2	84.00	118.00	45.00	12.67	25.92	1.77	7.33	82.50	9.00
HM5-250-26-1	84.00	118.67	47.67	14.17	27.25	1.60	7.17	76.17	8.83
HM5-250-34-1	86.00	125.33	43.17	12.00	28.58	2.54	7.50	105.67	3.50
HM5-250-41-1-E	81.00	131.33	38.00	8.83	26.42	2.28	7.33	100.00	9.00
HM5-250-41-2-E	83.00	132.50	46.58	8.17	27.58	2.67	8.17	106.50	4.50
HM5-250-42-1-E	84.00	123.17	52.33	11.17	30.17	3.05	8.67	93.17	6.00

Genotype									
HM5-300-E-1	81.00	132.00	43.67	12.17	24.42	2.48	8.33	108.00	6.50
HM5-300-3-1	80.00	115.33	42.50	12.67	27.75	2.26	8.33	93.33	6.83
HM5-300-3-2	82.00	125.67	45.00	11.50	30.37	2.57	7.50	82.67	6.00
HM5-300-5-1	84.00	112.83	41.67	11.17	26.50	2.50	9.50	100.83	6.83
HM5-300-5-3	83.00	128.17	47.42	12.50	32.25	2.61	9.00	109.67	8.17
HM5-300-6-E	81.00	112.67	41.09	13.33	26.67	1.85	8.50	83.33	5.33
HM5-300-16-1	80.00	132.67	40.50	12.33	25.17	2.72	8.50	103.17	7.83
KM5-200-4-2-E	91.00	108.67	42.33	9.67	27.25	2.57	10.17	114.83	23.83
KM5-200-17-1	88.00	110.17	41.42	12.83	23.92	2.20	9.67	87.00	35.17
KM5-200-19-1	93.00	106.33	40.58	13.83	25.25	1.69	9.00	83.17	37.83
K5-200-19-2	92.00	111.33	42.00	11.67	26.00	1.96	8.17	80.50	28.83
KM5-200-21-1	95.00	92.83	35.17	11.50	24.78	2.91	8.67	95.67	33.67
KM5-200-24-1	89.00	104.67	41.25	11.17	26.00	2.35	8.33	85.17	28.33
KM5-200-43-1-E	94.00	84.33	29.33	12.67	25.50	1.96	8.50	79.33	29.67
KM5-250-2-2-E	92.00	105.33	40.08	10.33	25.17	2.35	7.83	92.33	38.67
KM5-250-3-1-E	98.00	98.83	37.83	8.50	26.00	3.02	9.67	91.33	32.50
KM5-250-5-1	94.00	105.83	46.08	11.83	27.08	1.67	7.83	75.17	24.67
HASHEMI	77.00	145.17	60.25	12.83	27.95	2.19	8.33	101.00	7.83
KHAZAR	94.00	126.00	49.33	11.17	27.33	2.28	9.17	114.83	34.83
FAJR	96.00	94.33	38.25	15.33	24.33	2.25	9.67	120.83	41.50
TAROM	81.00	145.17	63.17	14.33	25.75	2.16	8.33	107.00	8.00
H.P	82.00	132.00	48.67	15.00	28.28	2.23	7.50	111.00	10.17
SEPIDROUD	93.00	104.17	42.33	16.83	27.00	2.53	10.50	89.67	32.00
ALI KAZEMI	79.00	126.67	48.92	11.83	26.63	2.38	8.00	98.50	7.00
SANGJO	82.00	132.00	52.33	14.17	23.01	2.42	8.17	115.17	7.33
Mean	84.1	119.35	43.63	12.94	26.78	2.34	8.34	94.22	13.17
Min	77.00	84.33	29.33	8.17	23.01	1.55	6.67	60.83	3.50
Max	98.00	145.17	63.17	19.83	32.25	3.41	10.50	126.75	41.50
LSD (5%)	2.84	2.59	1.41	0.96	1.02	0.07	0.57	7.05	3.14

DFl: day to flowering; IL: internodes length; GY: grain yield; PH: plant height; NPP: number of panicle per plant; PL: panicle length; PW: panicle weight; SNP: spikelet number per panicle; FG: number of filled grains; UnG: number of unfilled grains; GP: grain productivity; HGW: hundred grain weight; GL: grain length; GW: grain width; AC: amylose content; GT: gelatinization temperature. LSD (5%): Least significant differences at 5% probability level.

Cont. Table 2. Mean comparison of some of agronomic and quality traits

Genotype	GP	HGW (g)	GL (mm)	GW (mm)	GL/W	GY (kg/ha)	AC (%)	GT (score)
TM6-220-10-4-1	94.77	2.54	9.78	2.50	3.92	5599.50	22.20	4.28
TM6-230-VE-7-5-1	93.06	3.10	9.89	2.57	3.86	5312.50	21.25	4.09
TM6-230-VE-8-4-1	92.84	2.86	9.64	2.95	3.27	4991.00	22.05	4.04
TM6-250-10-7-1	93.82	2.93	9.48	2.80	3.39	5078.50	22.65	4.18
TM6-250-15-5-1	92.59	2.67	9.73	2.52	3.87	5790.50	21.45	4.56
TM6-B-2-1-E	80.35	2.85	9.69	2.88	3.36	5341.50	21.50	4.29
TM6-B-7-1	96.62	2.95	9.86	2.92	3.38	5861.00	22.05	4.58

TM6-B-19-1-E	92.40	3.11	9.58	2.78	3.44	5243.50	22.50	4.16
TM6-B-19-2	92.31	3.05	9.53	2.82	3.39	4913.00	21.80	4.24
TM6-230-1-1	69.97	2.71	9.79	2.45	4.00	3980.00	23.20	4.05
TM6-230-1-2	92.21	2.64	9.03	2.45	3.69	4313.00	22.25	4.19
TM6-300-5-1	94.41	2.99	10.05	2.63	3.82	3560.00	21.40	4.18
TM6-250-11-5	92.16	2.83	9.65	2.70	3.58	3425.50	21.45	4.44
FM6-200-E6	81.22	2.12	11.18	2.23	5.01	5528.50	22.95	4.25
FM6-200-E5	75.40	2.05	11.26	2.20	5.12	4837.50	23.40	3.80
HM5-250-7-4-2	94.92	2.50	10.23	2.47	4.15	5173.50	21.60	4.74
HM5-250-7-4-3	95.81	2.47	10.32	2.45	4.22	2739.50	21.05	4.78
HM5-250-7-5-2	94.70	2.64	10.47	2.43	4.31	4221.50	21.55	4.53
HM5-250-7-7-2	92.77	2.64	10.27	2.50	4.11	3506.00	22.65	4.21
HM5-250-25-1-3	94.67	2.46	9.76	2.45	3.99	3533.00	21.40	4.24
HM5-250-26-1-E-1	94.70	2.31	9.82	2.30	4.27	3345.00	22.30	3.74
HM5-250-42-1-E-1	90.33	2.50	10.36	2.78	3.72	3474.50	23.25	3.90
HM5-250-E-1-1	94.42	2.86	10.36	2.70	3.84	5506.50	22.50	4.20
HM5-250-E-3-2	86.92	2.51	9.71	2.32	4.19	5487.00	21.60	4.34
HM5-250-E-5-2	92.86	2.30	10.30	2.37	4.35	4744.00	23.00	4.21
HM5-250-E-18-1	89.24	2.66	10.28	2.35	4.37	3828.00	22.55	4.18
HM5-250-2-4	92.83	2.67	10.68	2.37	4.52	3078.00	21.70	4.27
HM5-250-3-1	93.28	2.27	10.30	2.38	4.33	3422.50	21.90	4.27
HM5-250-5-1	96.17	2.42	9.96	2.45	4.07	2328.50	21.00	4.01
HM5-250-6-6	95.75	2.67	10.25	2.45	4.19	3587.50	22.65	4.12
HM5-250-7-1	95.94	2.73	10.79	2.55	4.24	3889.50	21.60	4.02
HM5-250-7-6	93.23	2.54	10.62	2.57	4.14	5621.50	23.45	4.60
HM5-250-12-1	90.28	2.57	10.23	2.38	4.29	4710.50	21.60	4.63
HM5-250-23-2	90.07	2.46	10.30	2.52	4.10	3750.50	22.40	4.03
HM5-250-26-1	89.60	2.45	10.85	2.48	4.37	3491.50	21.80	4.52
HM5-250-34-1	96.71	2.72	10.27	2.40	4.29	3885.50	20.55	3.85
HM5-250-41-1-E	91.62	2.43	10.34	2.42	4.29	3426.50	22.50	4.36
HM5-250-41-2-E	95.89	2.88	10.13	2.45	4.14	3722.00	21.60	4.34
HM5-250-42-1-E	93.89	3.21	10.89	2.82	3.87	4053.50	21.35	3.98
HM5-300-E-1	94.29	2.67	10.16	1.97	5.17	5308.50	21.80	4.14
HM5-300-3-1	93.21	2.56	10.03	2.78	3.61	5161.00	22.40	4.32
HM5-300-3-2	93.13	2.96	9.97	2.83	3.52	4179.00	21.45	4.04
HM5-300-5-1	93.70	2.64	10.27	2.63	3.90	3237.00	21.93	4.25
HM5-300-5-3	93.19	3.11	10.57	2.80	3.78	3588.50	22.30	4.18
HM5-300-6-E	93.88	2.36	10.94	2.38	4.60	2300.50	20.70	3.92
HM5-300-16-1	92.78	2.60	10.40	2.53	4.11	3660.50	22.65	4.02
KM5-200-4-2-E	83.02	2.31	10.86	2.57	4.23	3401.00	23.55	4.49
KM5-200-17-1	71.21	2.12	11.69	2.48	4.71	4187.50	22.65	4.69
KM5-200-19-1	68.68	2.28	10.72	2.65	4.05	4317.50	21.50	4.30
K5-200-19-2	73.93	1.89	10.49	2.42	4.35	3602.50	22.75	4.04
KM5-200-21-1	74.06	2.12	11.16	2.55	4.38	2269.00	23.30	5.17

KM5-200-24-1	74.99	2.24	10.23	2.48	4.12	2807.00	23.55	4.62
KM5-200-43-1-E	72.75	2.42	11.09	2.63	4.22	2857.50	24.30	4.30
KM5-250-2-2-E	70.63	2.34	10.32	2.55	4.05	3109.50	21.60	4.26
KM5-250-3-1-E	73.64	2.64	10.56	2.85	3.71	3050.50	23.35	4.63
KM5-250-5-1	75.44	2.24	10.71	2.42	4.43	4909.50	23.70	4.17
HASHEMI	92.79	2.60	10.32	2.43	4.24	3686.50	21.60	4.29
KHAZAR	76.73	2.36	10.50	2.47	4.26	4227.50	23.50	4.60
FAJR	74.48	2.37	11.38	2.18	5.21	5112.00	22.65	4.17
TAROM	93.03	2.91	10.50	2.53	4.15	3646.50	21.60	4.30
H.P	91.53	2.58	10.72	2.48	4.32	3756.00	20.45	4.17
SEPIDROUD	73.79	2.53	12.50	2.23	5.60	4540.00	25.30	6.95
ALI KAZEMI	93.32	2.86	10.55	2.42	4.37	3586.50	19.05	4.24
SANGJO	94.01	2.42	10.55	2.48	4.25	3370.00	22.55	4.27
Mean	88.33	2.58	10.36	2.52	4.14	4096.45	22.18	4.31
Min	68.68	1.89	9.03	1.97	3.27	2269.00	19.05	3.74
Max	96.71	3.21	12.50	2.95	5.60	5861.00	25.30	6.95
LSD (5%)	2.38	0.13	0.14	0.085	0.23	250.68	0.39	0.16

DFl: day to flowering; IL: internodes length; GY: grain yield; PH: plant height; NPP: number of panicle per plant; PL: panicle length; PW: panicle weight; SNP: spikelet number per panicle; FG: number of filled grains; UnG: number of unfilled grains; GP: grain productivity; HGW: hundred grain weight; GL: grain length; GW: grain width; AC: amylose content; GT: gelatinization temperature.

LSD (5%): Least significant differences at 5% probability level.

Mutant HM5-250-34-1 (3.5) had lowest number of unfilled grains followed by mutant HM5-250-7-1 and TM6-B-7-1 (3.67), while the highest number of unfilled grains was observed for FAJR (41.50). Average grain productivity was found to be 88.33 with a range of 68.68 (KM5-200-19-1) to 96.71 (HM5-250-34-1). Average of hundred grain weight was found to be 2.58 g with range of 1.89-3.21 g. Lowest hundred grain weight observed in mutant K5-200-19-2 (1.89 g), whereas highest weight recorded in mutant HM5-250-42-1-E (3.21 g) followed by TM6-B-19-1-E and HM5-300-5-3 (3.11 g). Range for grain length was observed from 9.03-12.50 mm with mean of 10.36 mm. The lowest grain length observed in the mutant TM6-230-1-2 (9.03 mm) followed by mutant TM6-230-VE-8-4-1 (9.48 mm), whereas highest grain length found in improved check variety Sepidroud (12.50 mm). Wide range among the genotypes was observed from 1.97 mm (mutant HM5-300-E-1) to 2.95 mm (mutant TM6-230-VE-8-4-1) with mean of 2.52 mm. Mean grain length to width ratio was found to be 4.14 with range of 3.27 (TM6-230-VE-8-4-1) to 5.60 (Sepidroud). Very wide range of grain yield among the genotypes was observed from 2269.00 to 5861.00 kg/ha with mean of 4096.45 kg/ha. Highest grain yield observed in the mutant TM6-B-7-1 and TM6-250-15-5-1 with 5861 and 5790.5 kg/ha and lowest in the mutant KM5-200-21-1 (2269 kg/ha) and mutant HM5-300-6-E (2300.5 kg/ha).

Mean amylose content was found to be 22.18% with range of 19.05% (Ali Kazemi) - 25.30% (Sepidroud). Mean gelatinization temperature was observed to be 4.31 with range of 3.74-6.95. The lowest gelatinization temperature found in the mutant HM5-250-26-1-E-1 and highest value observed in Sepidroud (6.95) followed by mutant KM5-200-21-1 (5.17).

Highly significant genotypic differences which were observed among genotypes for all of the studied traits revealed a wide range of genetic variability for all characters. Similar genetic

variations have been reported by MACHUNDE (2013), AKINWALE et al., (2011) and SINGH et al., (2011). Genetic variability is the most essential requirement for any successful crop improvement program. Most of the genetic variability available in plant collections is the result of spontaneous mutation, recombination and exposure to natural selection over centuries. As time passed and man's pursuit for the better genotypes progressed, the concept of hybridization and mutations were evolved as a means to generate more variability through recombination. Like in other crops, hybridization has been practiced clearly well for the last few years by the rice breeders. The combination of induced and recombinational variability is expected to result in the release of much larger spectrum of variability for productivity and other component traits than the variability released by either recombinational or mutational approach individually (SINGH et al., 2011). The results obtained from the present investigation indicated that all of the mutants under the study displayed considerable amount of differences in their mean performance concerning to all the characters studied. This had also been illustrated by highly significant mean of squares for these traits which indicated that the lines used for the study were genetically diverse.

Based on mean grain yield, mutants TM6-B-7-1 and TM6-250-15-5-1 are suitable to be selected for grain yield improvement as they had consistently maintained higher grain yield. TM6-B-7-1 consistently flowered earliest in comparison to the other mutants. It also recorded a medium plant height, number of panicle per plant, spikelet number per panicle, panicle weight and hundred grain weights. Therefore, this genotype maintained a high grain yield through compensatory effect of having medium number of panicles per plant, number of filled grains per panicle, number of spikelet per panicle, panicle weight and hundred grain weights. LAZA et al., (2004) concluded that rice cultivars with large panicles produced fewer tillers and hence fewer panicles than the cultivar with small panicles. In this regard, having "heavy panicles" or improvement of panicle weight in rice would necessarily lead to increase in grain yield. XING and ZHANG (2010) reported that rice varieties display tremendous levels of variation in yield owing to diversity of genetic constitution. Many characters interacted with each other to give grain yield. The variation revealed in individual characters contribution towards yield revealed the genetic divergence in the material. Grain yield per plant and number of panicles per plant were attributed to the major genetic variability among genotypes for grain yield.

Genetic Variability, Heritability and Genetic Advance

Phenotypic coefficient of variation (PCA), genotypic coefficient of variation (GCA), heritability (h^2), genetic advance (GA) and genetic advance over mean (GAM) for 17 studied traits are displayed in Table 3. Higher GCV and PCV were obtained for unfilled grains per panicle, grain yield, internodes length, plant height, panicles per plant, filled grains per panicle and tillers per plant. Panicle weight revealed moderate GCV and PCV, while days to flowering, panicle length, spikelets per panicle, grain productivity, hundred grain weight, grain length to width ratio, grain length, grain width, amylose content and gelatinization temperature recorded low genotypic and phenotypic coefficients of variation. Broad sense heritability was high for all of the studied traits. Genetic advance were ranged from 0.39 (grain width) to 1921.49 (grain yield). The lowest value of genetic advance over mean was observed for amylose content (9.11), while the highest value of genetic advance over mean was found in number of unfilled grains (174.52) followed by grain yield (46.91), number of panicle per plant (37.57) and panicle weight (34.23).

Table 3. Estimation of genetic parameters of some of agronomic and quality traits

Traits	Vg	Vp	h2B	GCV	PCV	GA	GAM
DFl	25.07	26.09	96.12	5.95	6.07	10.11	12.03
PH (cm)	147.71	148.55	99.43	10.18	10.21	24.96	20.92
IL (cm)	29.41	29.66	99.15	12.43	12.48	11.12	25.50
NPP	5.68	5.80	97.99	18.43	18.61	4.86	37.57
PL (cm)	4.07	4.20	96.89	7.53	7.65	4.09	15.27
PW (g)	0.15	0.15	99.49	16.66	16.70	0.80	34.23
SNP	0.74	0.78	94.71	10.31	10.59	1.72	20.67
FG	205.33	211.56	97.06	15.21	15.44	29.08	30.87
UnG	125.70	126.94	99.02	85.13	85.55	22.98	174.52
GP	74.08	74.80	99.05	9.74	9.79	17.65	19.98
HGW (g)	0.08	0.08	97.31	10.90	11.05	0.57	22.15
GL (mm)	0.33	0.33	99.20	5.52	5.54	1.17	11.32
GW (mm)	0.04	0.04	97.65	7.47	7.56	0.39	15.21
GL/W	0.22	0.23	97.17	11.41	11.58	0.95	23.17
GY (kg/ha)	877839.50	885707.70	99.11	22.87	22.97	1921.49	46.91
AC (%)	0.98	1.00	98.03	4.47	4.51	2.02	9.11
GT (score)	0.17	0.18	98.06	9.70	9.79	0.85	19.79

DFl: day to flowering; IL: internodes length;   GY: grain yield; PH: plant height; NPP: number of panicle per plant; PL: panicle length; PW: panicle weight; SNP: spikelet number per panicle; FG: number of filled grains; UnG: number of unfilled grains; GP: grain productivity; HGW: hundred grain weight; GL: grain length; GW: grain width; GL/W: grain length to width ratio; AC: amylose content; GT: gelatinization temperature.

The mutants indicated a wide range of variation and provide a broad extent sources for selection of superior and desired mutants by plant breeders. Therefore, an estimation of heritable and non-heritable components is essential in adopting appropriate breeding procedure. The heritable portion of the overall observed variation can be clarified by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance. Presence of narrow gap between PCV and GCV suggested low environmental influence on expression of all of the traits. Number of unfilled grains and grain yield recorded high values of phenotypic and genotypic coefficient of variation, suggesting that these characters are under the influence of genetic control. Hence, simple selection can be relied upon and practiced for further improvement of these characters. These results are in consonance with KHAN *et Al.,* (2009), SADEGHI, (2011), ASHFAQ *et al.,* (2012) and OSMAN *et al.,* (2012) that indicated high values of phenotypic and genotypic coefficient of variation for grain yield in rice genotypes. GCV and PCV were moderate for internodes length, plant height, panicles per plant, filled grains per panicle, tillers per plant and panicle weight. Similarly, YADAV *et al.,* (2008) reported moderate GCV for tillers per plant and spikelets per panicle. Thus, selection of panicles per plant and filled grains per panicle on the basis of the phenotypic value may still be effective. Low GCV and PCV were recorded for days to flowering, panicle length, spikelets per panicle, grain productivity, hundred grain weight, grain length to width ratio, grain length, grain width, amylose content and gelatinization temperature, which is in accordance with the findings of KARIM *et al.,* (2007) and DINESH *et al.,* (2011). Genotypic coefficient of variations value would

be more applicable for the assessment of inherent or real variability as it exhibits the heritable portion only (ROY, 2000). The estimated GCV for different traits is evident, that the influence of environment on the expression of these characters was invariably low.

Heritability estimates displays the heritable portion of variability present in different characters. The understanding of heritability allows the plant breeder to make a decision in the course of selection procedure to be followed under a given situation. However, heritability values coupled with genetic advance would be more reliable (JOHNSON et al., 1955) and useful in formulating selection procedure. Heritability values were high for all of the studied characters, suggesting the greater effectiveness of selection and improvement to be expected for these characters in future breeding programs as the genetic variance is mostly due to additive gene expression. These results are in accordance with the findings of VERMA et al., (2003), HOSSEINI et al., (2005), SHARIFI et al., (2010 a), AHMADIKHAH (2010), SUBBAIAH (2011), KARIM et al., (2007) and DINESH et al., (2011) and LIN et al., (2005). High heritability together with high GCV exhibited by grain yield, number of panicle per plant and panicle weight imply that these characters under additive gene effects and could be relied upon for further selection based on phenotypic performance (VANAJA and BABU, 2008). High heritability coupled with high genetic advance over mean was observed for panicles per plant, panicle weight, filled and unfilled grains per panicle and grain yield. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance, hence are amenable for simple selection. The high genetic advance over mean coupled with moderate to high heritability suggested the importance of additive gene action for these traits (PANSE, 1957). This result conforms to the findings of AHMADIKHAH (2010) who observed high heritability coupled with high genetic advance for all studied traits. It is worth to emphasize that a very significant improvement is possible through selection of all these characters with high broad sense heritability coupled with adequate genetic advance. The high heritability and low genetic advance for remaining characters indicating the presence of non additive gene action and role of environment in expression of these traits (PANSE, 1957). Therefore, priority should be given to those traits which recorded higher estimates of genetic advance as percent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection.

CONCLUSIONS

Phenotypic and genotypic coefficients of variations were found to be differing very narrowly indicating lesser influence of environment over all of the studied characters. Broad sense heritability and genetic advance over mean were high for panicles per plant, panicle weight, filled and unfilled grains per panicle and grain yield. High heritability coupled with low or moderate genetic advance was recorded for remaining traits. Hence, most of the characters are amenable for simple selection. Mutant TM6-B-7-1 had high grain yield, plant height, panicles per plant, spikelets per panicle, panicle weight and hundred grain weights and can be utilized for future breeding programs to incorporate these characters in local genotypes. Other mutants which are outstanding for a single trait can be used as genetic stocks for further improvement of rice are TM6-250-15-5-1, HM5-300-E-1, HM5-250-7-6, HM5-250-E-3-2, HM5-250-E-1-1, HM5-250-7-4-2, FM6-200-E6, TM6-B-19-1-E, TM6-B-2-1-E and TM6-250-10-7-1.

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GENETIČKE VARIJACIJE ZA PRINOS ZRNA, KOMPONENTE PRINOSA I KVALITATIVNA SVOJSTVA MUTANTA PIRINČA (*Oryza sativa* L.)

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Izvod

Izvršeno je istraživanje za izbor najuspešnijih mutanata pirinča i za procenu naslednosti prinosa zrna i nekih agro-morfoloških i kvalitetnih svojstava. Istraživano je 65 genotipova pirinča, uključujući četiri lokalne vrste (Hashemi, Tarom, Alikazemi i Sangjo), četiri priznate sorte (Khazar, Fajr, H.P i Sephidrod) i 57 mutantnih linija (M5). Eksperiment je izveden tokom proleća 2013-14 u Iranu institutu za pirinač (RRII) u Rashtu. Analiza varijanse pokazala je značajne efekte genotipa na sve osobine. Dobijeni su veći genotipski (GCV) i fenotipski koeficijent varijacije (PCV) za broj nenalivenih zrna i prinos zrna. Uopšte, vrlo uske razlike između PCV i GCV ukazivale su na manji uticaj okoline na sve ispitivane osobine. Heritabilnost u širem smislu i genetička dobit iznad prosečne vrednosti bili su visoki za masu klasa, broj kalsova po biljci, broj nalivenih zrna, broj nenalivenih zrna i prinos zrna. Visoka genetska dobit nad sredinom u kombinaciji sa umerenom do visokom heritabilnošću sugeriše važnost aditivnog delovanja gena za gore navedene osobine.Mutant TM6-B-7-1 imao je visok prinos zrna, broj klasova po biljci, visinu biljke, težinu klasova, i težinu sto zrna i mogu se koristiti u budućim programima oplemenjivanja kako bi se ta svojstva ugradila u lokalne genotipove.