

Induced genetic variability by gamma radiation and traits association study in mungbean (*Vigna radiata* L.)

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Abstract: The present study was carried out to estimate interrelationship and genetic diversity in M₃ generation of *Vigna radiata* in response to gamma radiation. The experimental materials comprised the four irradiated lines of mungbean AUM-18, AUM-19, AUM-31 and M-2004 that were irradiated at 250 Gy, 350 Gy and 450 Gy doses of gamma rays. The experiment was laid out in split plot design, with two replications. Each replication was divided into main plot and subplot. Dose levels were assigned to main plots and varieties in subplots. High heritability estimates were observed for all traits. Phenotypic correlation of seed yield per plant with germination percentage and seeds per pod was positive and highly significant however positive and significant phenotypic correlation of clusters per plant and 100-seed weight while pods per plant was negative and significant. Higher heritability and significance correlation indicated that germination percentage, 100-seed weight and seeds per pod may be used to select higher yielding mungbean genotypes.

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1. Introduction

Mungbean is one of the most important legume crops of South Asia and is cultivated widely in China, India and Pakistan. It belongs to the Fabaceae family. Cross breeding method is limited for enhancing production of mungbean because of low genetic variability. Mutation is the sudden change in the gene sequence it can be induced in seed as well as in the vegetative portion of the plant. For the achievement of high yielding varieties genetic variability is important. Correlation is the process through which we can measure the phenotypic and genotypic relation. It also provides us the information about relationship about dependent and independent variables. Correlation analysis informs us about the relative importance of the breeding traits. Induced mutation is one of the prime methods for the development of high genetic variability and could be an effective tool for the improvement of crop production. Production can be increased by improving the available genotypes through mutation breeding or by using other advanced breeding methods (Wright, 1935). Natural genetic source can be enhanced by the induced mutation and have been used in developing improved cultivars of cereals, fruits and other crops. Desirable mutation depends upon the selection of effective mutagens (Solanki *et al.* 1994, Mahabatra *et al.* 1983; Anwar *et al.* 2103; Ali *et al.* 2014a,b,c and Jahangir *et al.* 2013). Since last seven decades, more than 2252 mutant varieties have been developed (Maluszynski *et al.*

2000 and Qamar *et al.* 2013a,b). Shah *et al.* 2008 reported that gamma rays may cause genetic changes in organism, break the gene linkage and produce many new promising traits for the improvement of crop plants. Mutations are the source of variability in the existing varieties and early maturing lines can be developed which are helpful in the summer season. The aim of the current study is to estimate effect of gamma radiation doses on mungbean genotypes and *also to* observe the variation and correlation for various morphological characters of mungbean. This may give us a guideline for improving and selecting the characters that are economically important.

2. Material and methods

The experiment was carried out in the research area of the Department of the Plant Breeding and Genetics, University of Agriculture Faisalabad, during spring 2012. M₂ seeds of four irradiated genotypes of mungbean as AUM-18, AUM-19, AUM-31 and Mung-2004 were sown to raise M₃ generations. The experiment was laid out in split plot design, with two replications. Each replication was divided into main plot and sub-plot. Varieties were assigned to main plot and dose levels to sub-plots. Each treatment comprised three lines, four meter in length having row-to-row and plant-to-plant distances 30 and 10cm, respectively. Uniform agronomic practices were carried out for all entries throughout growing period of the crop. Ten plants from each treatment were selected randomly

and data was recorded for some important morphological traits i.e., germination percentage, plant height, clusters per plant, pods per plant, seeds per pod, pod length (cm), branches per plant, 100-seed weight (g), seed yield per plant (g) and biological yield (g).

3. Statistical Analysis

The data for each character was statistically analyzed for variance (Steel *et al.* 1997). Heritability estimates (h^2_{BS}) were calculated by performing analysis of variance and estimating genetic and phenotypic components of variance as given by Cochran and Cox (1957). Phenotypic (r_p) and genotypic (r_g) correlation coefficient was calculated as outlined by Kwon and Torrie (1964). Standard error of genotypic correlation coefficients (SE of r_g) were calculated according to Reeve (1955).

4. Results and discussions

4.1. Germination percentage

The table 4.13 showed that coefficient of variance was 1.07%, phenotypic and genotypic coefficients were recorded 3.93% and 3.58% respectively. Heritability estimate was 95% with genetic advance 3.83. The results were in agreement with Singh (2004) Neha *et al.* (2005), Sadiq (2005), Kapoor *et al.* (2005), Hakim *et al.* (2006), Idrees *et al.* (2006), Tadele *et al.* (2006) Sadiq *et al.* (2007), Gul *et al.* (2007), Khan and Goyal (2009), Jagadeesan *et al.* (2008) and Gill *et al.* (2000) who also reported high heritability. Among the genotypes AUM-31 (56.88 %) performed best followed by AUM-18 (55.99 %) (table 4.2). The results regarding AUM-19 and Mung-04 were at par. Among radiation doses D_1 (25kR) 57.06% performed best. D_3 (45kR), expressed the minimum 51.055% germination percentage. As regarded the results maximum germination percentage was obtained by the AUM-18 (57.95%) and AUM-19 (57.54%) at D_1 level the results regarding the varieties AUM-31 (58.3%) and Mung-04 (54.1%) were ranked at first and second position at D_2 dose level. At dose level D_3 among genotypes AUM-31 (56.10 %) produced maximum germination rate followed by AUM-18 (55.1%). It is cleared from results that AUM-31 may be used as good source of mutation in mutation breeding program of mungbean. Table 4.12 shows that the highly significant and positive phenotypic correlation was observed with seed yield per plant. Genotypic correlation ranged for this trait was (-0.305 to -0.815). High genotypic correlation of germination percentage was found with seed yield per plant. A negative and non significant phenotypic correlation of germination percentage with plant height, branches per plant, cluster per plant, pod length and positive and non significant phenotypic correlation with pods per

plant, seeds per pod and biological yield.

4.2. Plant height (cm)

It is cleared from table 4.13 that the value of coefficient of variance was 1.50%, phenotypic and genotypic coefficients were 16.19% and 14.45% respectively for plant height. Heritability estimates were 95.56% with genetic advance 14.50. The result were in agreement with Sinha *et al.* (1996), Islam *et al.* (1999) and Gill *et al.* (2000) who reported high heritability and genetic advance for plant height but differ from Loganathan *et al.* (2001). Maximum plant height was obtained by AUM-19 (57.58 cm) followed by the AUM-18 (53.91 cm). Minimum plant height was obtained by AUM-31 (42.31 cm) and among radiation doses D_1 (25kR), 56.70 performed best followed by the D_2 (35kR), 52.43 cm. D_3 (45kR), 47.75 cm and D_0 (Control), 48.34 cm have got the minimum plant height. As regard the interaction results AUM-19 produced maximum plant height (67.34 cm) followed by AUM-18 (56.93 cm) whereas third position was occupied by Mung-04 (53.09cm) and minimum plant height was gained by AUM-31 at D_1 (49.45 cm). For dose level D_2 , genotype AUM-19 produced maximum plant height (64.56 cm) by AUM-18 (50.84 cm), Mung-04 (50.54 cm) was ranked at third position whereas minimum (43.81 cm) was observed for AUM-31. At dose level D_3 , genotype AUM-18 produced maximum plant height (53.94 cm) followed by Mung-04 (49.86 cm). AUM-19 (49.19 cm) got the third position whereas minimum (38.03 cm) was observed for AUM-31 (table 4.3). It is concluded from results that AUM-18 genotypes may used to develop higher plant height mungbean genotypes that may be helpful to improve crop yield. AUM-18 may be used in the mutation breeding program for plant height improvement. Table 4.12 indicates that genotypic correlation ranged for this trait was (-0.468 to 0.107). High genotypic correlation of plant height was found with seed yield per plant. There exists highly significant phenotypic correlation of plant height, branches per plant and cluster per plant. However it had negative and non-significant phenotypic correlations with pods per plant, seed yield per plant and positive non-significant phenotypic correlation with seeds per pod. It had negative and highly significant phenotypic correlation with 100-seed weight.

4.3. Branches per plant

It is cleared from table 4.13 that the value of coefficient of variance was 2.88%, phenotypic and genotypic coefficient were 11.85% and 10.83% respectively for branches per plant. Heritability estimates was 83.49% with genetic advance 2.375. The results were in agreement with Singh (2004) Neha *et*

al. (2005), Sadiq (2005), Kapoor *et al.* (2005) Hussain Khan *et al.* (2005), Hakim *et al.* (2006), Idrees *et al.* (2006), Tadele *et al.* (2006) Sadiq *et al.* (2007), Gul *et al.* (2007), Khan and Goyal (2009), Jagadeesan *et al.* (2008) and Gill *et al.* (2000) who reported high heritability. The results regarding the interaction of genotypes, treatments and averages are given in the table 4.4. Table showed that the results regarding AUM-19 (13.93 branches/plant) and AUM-18 (13.62 branches/plant) are at par. Mung-04, (12.96 branches/plant) got third position and minimum number of branches was observed in AUM-31 (11.95 branches/plant). Among radiation doses D₁ (25kR), 14.65 branches/plant perform best followed by the D₂ (35kR), 13.71 branches/plant. D₃ (45kR), 12.67 branches/plant and Control (D₀) 11.45 branches/plant have got the minimum branches. As regard the interaction results, significant maximum branches/plant was obtained by the AUM-19 (16 branches/plant) and AUM-18 (14.85 branches/plant) at

D₁ level. The AUM-18 (15.25 branches/plant) was ranked at first followed Mung-04 13.60 branches/plant and AUM-19 13.05 branches/plant at D₂ dose level. At dose level D₃ among genotype AUM-19 (14.25 branches/plant) produced maximum branches. The results showed that AUM-18 and AUM-19 may be used for the improvement of branches per plant that may be helpful in the improvement of crop yield. Branches per plant had positive and highly significant phenotypic correlation with cluster per plant and pod length. However, it had negative and non significant phenotypic correlations with pods per plant, biological yield and negative significant phenotypic correlation with seed yield per plant and 100-seed weight. Genotypic correlation ranged for this trait was (0.948 to -0.2263). High genotypic correlation of plant height at 90% pod maturity was found with seed yield per plant however low correlation of plant height at 90% pod maturity was observed with plant height at 90% pod maturity (Table 4.12).

Table 4.1: Mean Squares for various traits of mungbean

SOV	GP	PH	B/P	C/P	P/P	PL	G/P	100-SW	BY	SY/P
Genotypes	21.794	183.049	4.819	10.158	53.827	1.183	11.362	0.203	4.719	4.719
Dose	44.956	56.817	7.808	37.415	133.820	0.320	4.031	0.297	5.531	5.531
G*D	15.153	54.633	1.508	1.926	8.167	0.735	1.942	0.186	0.949	0.949

Table 4.2: Interaction between genotypes and irradiation doses affecting germination percentage

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	56.17bcde	57.3abcd	53.21cd	54.7cd	55.345b
25kR (D ₁)	56.95cd	57.95abcd	57.54ab	55.83bc	57.0675a
35kR (D ₂)	58.3a	53.61e	53.57bc	54.1ab	54.895bc
45kR (D ₃)	56.10cde	55.1abc	47.01e	46.01e	51.055d
Average	56.88a	55.99b	52.8325c	52.66cd	

Table 4.3: Interaction between genotypes and irradiation doses affecting plant height (cm) at 90% pod maturity

Doses	Varieties				
	UM-31	UM-18	UM-19	lung-04	verage
Control (D ₀)	37.97d	53.94b	49.24cd	52.21ab	48.34cd
25kR (D ₁)	49.45a	56.93a	67.34a	53.09a	56.7025a
35kR (D ₂)	43.81b	50.84d	64.56b	50.54bc	52.4375b
45kR (D ₃)	38.03c	53.94bc	49.19cde	49.86bcd	47.755cd
Average	42.315d	53.9125b	57.5825a	51.425c	

Table 4.4: Interaction between genotypes and irradiation doses affecting branches per plant

DOSES	VARIETIES				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	6.2 ^a	5.3 ^{bc}	5.2 ^{bcd}	5.45 ^{ab}	5.5375abc
25kR (D ₁)	6.380 ^{bcd}	5.960 ^{cde}	6.320 ^{cde}	5.930 ^{cde}	6.1475ab
35kR (D ₂)	7.010 ^b	5.850 ^{de}	5.665 ^e	5.655 ^e	6.0475ab
45kR (D ₃)	6.600 ^{bc}	7.725 ^a	5.930 ^{cde}	6.015 ^{cde}	6.5675a
	6.5475a	6.20875ab	5.77875abc	5.765abc	

Table 4.5: Interaction between genotypes and irradiation doses affecting clusters per plant

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	4.20bcd	5bcd	4.9bcd	5bcd	4.775abc
25kR (D ₁)	5.30a	5.24a	5.3a	5.3a	5.285a
35kR (D ₂)	5.10cde	5.2ab	5.1bc	5.1bc	5.125abc
45kR (D ₃)	5.31bc	5.1abc	5.2ab	5.2ab	5.2025ab
Average	4.9775abc	5.135ab	5.125abc	5.15a	

Table 4.6: Interaction between genotypes and irradiation doses affecting pods per plant

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	4.20bcd	5bcd	4.9bcd	5bcd	4.775abc
25kR (D ₁)	5.30a	5.24a	5.3a	5.3a	5.285a
35kR (D ₂)	5.10cde	5.2ab	5.1bc	5.1bc	5.125abc
45kR (D ₃)	5.31bc	5.1abc	5.2ab	5.2ab	5.2025ab
Average	4.9775abc	5.135ab	5.125abc	5.15a	

Table 4.7: Interaction between genotypes and irradiation doses affecting pod length (cm)

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	7.5bc	6.56bcd	6.53bc	5.76bc	6.5875bc
25kR (D ₁)	12.55a	8.02a	11.55a	9.52a	10.41a
35kR (D ₂)	8.05ab	7.02ab	6.49bcd	6.01b	6.8925bc
45kR (D ₃)	7.05bcde	6.49bcde	5.07de	4.5cd	5.7775bcd
Average	8.7875a	7.0225bc	7.41b	6.4475d	

Table 4.8: Interaction between genotypes and irradiation doses affecting seeds per pod

DOSES	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	10.23d	11.45d	12.45d	11.67bc	11.45d
25kR (D ₁)	13.25a	14.85ab	16.00a	14.50a	14.65a
35kR (D ₂)	12.95ab	15.25a	13.05c	13.60b	13.7125ab
45kR (D ₃)	11.40abc	12.95abc	14.25b	12.10bc	12.675abc
Average	11.9575bc	13.625ab	13.9375a	12.9675b	

Table 4.9: Interaction between genotypes and irradiation doses affecting 100-seed weight

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	6.06cd	5.15bc	5.8ab	5.03ab	5.51bc
25kR (D ₁)	8.82a	7.65a	5.01bcd	7.55a	7.2575a
35kR (D ₂)	7.3bc	6.24ab	5.09bc	5.87cd	6.125b
45kR (D ₃)	5.59cde	4.18cd	6.41a	6.01abc	5.5475bc
Average	6.9425a	5.805abc	5.5775abc	6.115ab	

Table 4.10: Interaction between genotypes and irradiation doses affecting seed yield per plant

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	8.01bc	8.1bc	6bcde	6.42bc	7.1325ab
25kR (D ₁)	9.28a	9.6a	7.5a	8.23a	8.6525a
35kR (D ₂)	9.05ab	8.2bcd	6.3bcd	6.27bcd	7.455ab
45kR (D ₃)	7.81cd	6.7de	6.32bc	7.43ab	7.065abc
Average	8.5375a	8.15ab	6.53d	7.0875bc	

Table 4.11: Interaction between genotypes and irradiation doses affecting seed yield per plant (g)

Doses	Varieties				
	AUM-31	AUM-18	AUM-19	Mung-04	Average
Control (D ₀)	6.06bc	5.56cd	4.22cde	5.99ab	5.4575ab
25kR (D ₁)	7.28a	7.61a	5.57a	6.23a	6.6725a
35kR (D ₂)	7.05ab	6.28bc	4.33bc	4.27de	5.4825ab
45kR (D ₃)	5.18cd	4.73de	4.3bcd	5.43bcd	4.91c
Average	6.3925a	6.045ab	4.605d	5.48c	

Means sharing the common letters were non-significant at 5% probability level

4.4 Cluster per plant

It is cleared from table 4.13 that the value of coefficient of variance was 5.51%, phenotypic and genotypic coefficient were 22.29% and 21.56 respectively for cluster per plant. Heritability estimates was 92.49% with genetic advance 4.46. The results were in agreement with Arshad *et al.* (2004), Kapoor *et al.* (2005), Parimal and Chakraborti (2005); Amir *et al.* (2012) and Bibi *et al.* (2012) who reported high heritability. But not agree with Idrees *et al.* (2006) who reported high heritability with high genetic advance. From the results of table 4.5 it was observed that among the genotypes AUM-31 (8.78 clusters/plant) performs best. The results regarding AUM-19 and AUM-18 are at par. The minimum cluster per plant was observed in Mung-04, (6.44). Among radiation doses D₁ (25kR) 10.41 clusters/plant perform best. The results regarding the Control (D₀) and D₂ (35kR) are at par. D₃ (45kR), 5.77 clusters/plant have got the minimum cluster. As regard the interaction results significant maximum germination percentage was obtained by the AUM-31 (12.55 cluster/plant) and AUM-19 (11.55 clusters/plant) at D₁ level. The results regarding the varieties AUM-31 (8.05 clusters/plant) and AUM-18 (7.02 cluster/plant) was ranked at first and second position at D₂ dose level. At dose level D₃ among genotype AUM-31 (7.05 clusters/plant) produced maximum cluster followed by clusters/plant AUM-18 (6.49 clusters/plant). It is revealed from results that AUM-31 showed better results for clusters per plant at all treatment levels. The genotype AUM-31 may be used for the development of higher yielding mungbean genotypes through mutation breeding program. Table 4.12 indicated negative and significant phenotypic correlation of cluster per plant with pods per plant, biological yield and 100-seed weight. However, it had positive and highly significant phenotypic correlations with pod length. It had negative and non significant phenotypic correlations with seeds per pod and seed yield per plant. Genotypic correlation ranged for this trait was (0.991 to -0.981). High genotypic correlation of branches per plant was found with pods per plant however low correlation of branches per plant was observed with pod length. The results were disagreeing with Dhuppe *et al.* (2005).

4.5 Pods per plant

The table 4.13 expressed that the value of coefficient of variance was 2.70%, phenotypic and genotypic coefficients were 19.30% and 18.85% respectively for pods per plant. Heritability estimates was 97.85% with genetic advance 10.415. The result were in agreement with Singh (2004), Neha *et al.* (2005), Sadiq (2005), Veerasmani *et al.* (2005), Khan *et al.* (2005), Hakim *et al.* (2006), Idrees *et al.* (2006), Tadele *et al.* (2006); Gul *et al.* (2007); Ahmad *et al.* (2011); Ali *et al.* (2011a,b,c); Ali *et al.* (2012a,b); Hussain *et al.* (2012); Ahsan *et al.* (2013) and Hussain *et al.* (2013) who reported high heritability. Table 4.6 showed that the maximum pods per plant was obtained by AUM-19 (30.32 pods/plant) followed by the AUM-18 (27.28 pods/plant) minimum pods per plant was obtained by AUM-31 (22.21 pods/plant) and among radiation doses D₁ (25kR), 30.02 pods/plant perform best followed by the D₂ (35kR), 26.92 pods/plant. D₃ (45kR), 22.22 and D₀ (Control), 24.45 pods/plant have got the minimum pods per plant. As regard the interaction results, AUM-19 (34.05 pods/plant) produced maximum pods per plant followed by AUM-18 (32.0 pods/plant) whereas third position was occupied by Mung-04 (30.0 pods/plant) and minimum pods per plant was gained by the (24.06 pods/plant) by AUM-31 at D₁. For dose level D₂, genotypes AUM-19 (32.02 pods/plant) produced maximum pods per plant by AUM-18 (28.55 pods/plant), Mung-04 (25.04 pods/plant) was ranked at third position whereas minimum (22.07 pods/plant) was observed for AUM-31. At dose level D₃ the results of genotypes, AUM-19 (23.0 cm pods/plant) AUM-19 (23.0 pods/plant), Mung-04 (22.3 pods/plant) and AUM-31 (22.06 pods/plant) are at par. It is indicates from results that genotype AUM-19 may be used for the development of higher yielding mungbean genotypes through mutation breeding program. The number of pods may be increased due to mutation. Table 4.12 revealed negative and significant phenotypic correlation of pods per plant with pod length. However, it had positive and significant phenotypic correlations with seeds per pods and seed yield per plant, positive and highly significant phenotypic correlation with 100-seed

weight and biological yield. Genotypic correlation ranged for this trait was (0.979 to -0.678). High genotypic correlation of cluster per plant was found with 100-seed weight however low correlation of cluster per plant was observed with pods per plant. The results were agreed with Sadiq *et al.* (2005); Ahmad *et al.* (2012); Ali *et al.* (2011a,b,c); Ali *et al.* (2012a,b) and Ahsan *et al.* (2013).

4.6 Pod length (cm)

The table 4.13 showed that the value of coefficient of variance was 4.410%, phenotypic and genotypic coefficient were 12.49% and 12.07% respectively for pod length. Heritability estimates was 90.54% with genetic advance 7.111. The results were in agreement with Arshad *et al.* (2002), Veerasmani *et al.* (2005), Kapoor *et al.* (2005), Sadiq (2005), Khan *et al.* (2005), Hakim *et al.* (2006), Tadele *et al.* (2006); Gul *et al.* (2007); Ahmad *et al.* (2012); Ali *et al.* (2011a,b,c); Ali *et al.* (2012a,b) and Ahsan *et al.* (2013) who reported high heritability. Maximum pod length was obtained by AUM-31 (6.54 cm) followed by the AUM-18 (6.20 cm) minimum pods per plant was obtained by Mung-04 (5.765 cm) and among radiation doses D₃ (45kR), 6.5675 cm perform best followed by the D₁ (25kR), 6.1475 cm. D₀ (Control), 5.53 cm have got the minimum pod length. For dose level D₂, genotypes AUM-31 (7.01 cm) produced maximum pod length followed by AUM-18 (5.850 cm), AUM-19 (5.66 cm) and Mung-04 (5.65 cm) have got the same results. At dose level D₃ the results of genotypes, AUM-18 (7.72 cm), AUM-31 (6.60 cm), was ranked at first and second position respectively, Mung-04 (6.01 cm) was ranked at third position and minimum pod length was obtained by AUM-19 (5.93 cm). The results indicates that maximum pod length was recorded for AUM-31 and AUM-18 that cleared it that selection on the basis of pod length may be helpful to improve crop yield following mutation breeding program. The results given in table 4.12 revealed negative and non significant phenotypic correlation for pods length with seeds per pod. However, it had negative and highly significant phenotypic correlation with 100-seed weight, negative and significant phenotypic correlation with biological yield and seed yield per plant. Genotypic correlation ranged for this trait was (-0.1766 to -0.765). High genotypic correlation of pods per plant with was found pod length however low correlation of pods per plant was observed with seed yield per plant. The results were agreed with Kumar *et al.* (2004).

4.7 Seeds per pods

The value of coefficient of variance was 3.74%, phenotypic and genotypic coefficient were 31.45% and 32.57% respectively for seeds per pod Table 4.8.

Heritability estimates was 97.81% with genetic advance 5.28(Table 4.13). The result were in agreement with Singh (2004), Sadiq (2005), Veerasmani *et al.* (2005), Khan *et al.* (2005), Hakim *et al.* (2006), Idrees *et al.* (2006), Tadele *et al.* (2006); Gul *et al.* (2007); Ali *et al.* (2011a,b,c); Ali *et al.* (2012a,b); Ali *et al.* (2013a,b,c) and Waseem *et al.* (2014) who reported high heritability. Minimum number of branches was observed in AUM-18 (5.80 seeds/pod) and AUM-19 (5.57 seeds/pod). Among radiation doses D₁ (25kR), 7.25 seeds/pod perform best followed by the D₂ (35kR), 6.12 seeds/pod. D₃ (45kR), 5.54 and D₀ (Control), 5.51 seeds/pod have got the minimum seeds. As regard the interaction results, significant differences were observed for interaction of AUM-31 with all others at D₁. For dose level D₂, genotypes AUM-31 (7.3 seeds/pod) produced maximum seeds per pod followed by AUM-18 (7.65 seeds/pod) and Mung-04 (5.87 seeds/pod) whereas minimum (5.09 seeds/pod) was observed for AUM-19. There was significant interaction of AUM-31 with all others. At dose level D₃ genotype AUM-19 (6.41 seeds/pod) produced maximum seeds per pod followed by and Mung-04 (6.01 seeds/pod) whereas minimum (4.18 seeds/pod) was observed for AUM-18. The results indicated higher number of seeds per pod was recorded for AUM-19 and Mung-04, these genotypes may be used for the improvement of crop yield for following mutation breeding program. Table 4.12 indicated positive and non significant phenotypic correlation of seeds per pod with 100-seed weight, biological yield and seed yield per plant. Genotypic correlation ranged for this trait was (0.696). High genotypic correlation of pod length was found with 100-seed weight however low correlation of pod length was observed with seed yield per plant. The results were agreed with Sadiq *et al.* (2005).

4.8 100-seed weight (g)

The table 4.13 showed that the value of coefficient of variance was 7.32%, phenotypic and genotypic coefficient were 8.47% and 8.37% respectively for 100-seed weight. Heritability estimates was 97.85% with genetic advance 10.415. The result were in agreement with Arshad *et al.* (2002), Sadiq *et al.* (2005), Sadiq (2005), Jagadeesan *et al.* (2008) and Tah and Sexena (2009) and who reported high heritability and partial agree with Neha *et al.* (2005) and Veerasmani *et al.* (2005). The results regarding 100-seed weight are presented in table 4.9 which revealed that genotypes AUM-18 (5.13g), AUM-19 (5.12g) and Mung-04 (5.15g) are at par. Minimum 100-seed weight was recorded in AUM-31 (4.97g) and among radiation doses D₁ (25kR), 5.28g pods/plant perform best followed by the D₃ (45kR), 5.20g. D₂ (35kR), 5.12g and D₀ (Control), 4.77g have

got the minimum pods 100-seed weight. As regard the interaction results, AUM-19 (34.05g pods/plant) AUM-18 (32.0g pods/plant), AUM-31 and Mung-04 (30.0g pods/plant) are at par at D₁. For dose level D₂ D₃ all genotypes are at par. The result indicated that the genotypes showed similar behavior due to which it may be difficult to select better genotype on the basis of 100-seed weight. The genotypes should be continued for further selection procedure to improve grain yield. Table 4.12 revealed positive and highly significant phenotypic correlation of 100-seed weight with biological yield and seed yield per plant. Genotypic correlation ranged for this trait was (0.961). High genotypic correlation of seed per pod was found with seed yield per plant however low correlation of seeds per pod was observed with 100-seed weight. The results were not agreed with Gill *et al.* (2000) and Kumar *et al.* (2003).

4.9 Biological yield (g)

The table 4.13 showed that the value of coefficient of variance was 4.57%, phenotypic and genotypic coefficient were 25.82% and 25.85% respectively for biological yield. Heritability estimates was 93.68% with genetic advance 4.874. The result were in agreement with Gill *et al.* (2000), Arshad *et al.* (2002), Khan *et al.* (2004), Sadiq (2005) Hakim *et al.* (2006) and Jagadeesan *et al.* (2008) who reported high heritability. The result were in agreement with Singh (2004), Sadiq (2005), Kapoor *et al.* (2005) Hussain *et al.* (2005), Hakim *et al.* (2006), Idrees *et al.* (2006), Tadele *et al.* (2006) Sadiq *et al.* (2007), Gul *et al.* (2007), Khan and Goyal (2009), Jagadeesan *et al.* (2008) and Gill *et al.* (2000) who reported high heritability. Table 4.10 showed that the maximum biological yield was obtained by AUM-31 (8.53g) followed by the AUM-18 (8.15g) minimum biological yield was obtained by AUM-19 (6.53g) and among radiation doses D₁ (25kR), 8.65g perform best followed by the D₂ (35kR), 7.45g. D₃ (45kR), 7.06g and D₀ (Control), 7.13g have got the minimum biological yield. As regard the interaction results, AUM-18 (9.6g) produced maximum biological yield followed by AUM-31 (9.28g) whereas third position was occupied by Mung-04 (8.23g) and minimum seed biological yield was gained by the (7.5g) by AUM-19 at D₁. For dose level D₂, genotypes AUM-31 (9.05g) produced maximum seed yield per plant followed by AUM-18 (8.2g), AUM-19, (6.3g) was ranked at third position whereas minimum (6.27g) was observed for Mung-04. At dose level D₃ the results of genotypes, AUM-19 (6.32g) AUM-18 (6.7g), Mung-04 (7.43g) and AUM-31 (7.81g) were at par. The genotype AUM-31 showed better performance and indicated that it may be useful for the improvement of crop yield following mutation breeding program. Results presented in table 4.12 had positive and significant

phenotypic correlation of biological yield with seed yield per plant. Genotypic correlation ranged for biological yield with seed yield per plant was 0.871. The results were agreed with Arshad *et al.* (2004) and Ali and Ahsan (2011).

4.10 Seed yield per plant (g)

The table 4.13 showed that the value of coefficient of variance was 5.39%, phenotypic and genotypic coefficient were 29.58% and 28.58% respectively for seed yield per plant. Heritability estimates was 98.39% with genetic advance 4.425. The result were in agreement with Sinha *et al.* (1996), Islam *et al.* (1999); Gill *et al.* (2000); Ahmad *et al.* (2012); Ali *et al.* (2011a,b,c); Ali *et al.* (2012a,b); Ahsan *et al.* (2013) and Ahsan *et al.* (2014) who reported high heritability and genetic advance for plant height but differ from Loganathan *et al.* (2001). The results about the interaction of genotypes and treatments and averages are given in the table 4.11. Table showed that the maximum seed yield per plant was obtained by AUM-31 (6.39g) followed by the AUM-18 (6.04g) minimum seed yield per plant was obtained by AUM-19 (4.60g) and among radiation doses D₁ (25kR), 6.67g perform best followed by the D₂ (35kR), 5.48g. D₃ (45kR), 4.91g and D₀ (Control), 5.45g have got the minimum seed yield per plant. As regard the interaction results, AUM-18 (7.61g) produced maximum seed yield per plant followed by AUM-31 (7.28g) whereas third position was occupied by Mung-04 (6.23g) and minimum seed yield per plant was gained by the (5.57g) by AUM-19 at D₁. For dose level D₂, genotypes AUM-31 (7.05g) produced maximum seed yield per plant followed by AUM-18 (6.28), AUM-19, (4.33g) was ranked at third position whereas minimum (4.27g) was observed for Mung-04. At dose level D₃ the results of genotypes, AUM-19 (4.3g) AUM-18 (4.73 g), Mung-04 (5.43 g) and AUM-31 (5.18 g) are at par. The genotype AUM-31 showed higher seed yield per plant and indicated that it may be useful for the improvement of crop yield through mutation breeding program.

5. Conclusion

Genetic diversity estimates revealed that significant genetic diversity developed among the genotypes at different levels of radiations. High heritability estimates for all characters indicated that selection could be more effective for genetic improvement. From the present studies, it may be concluded that germination rate and plant height at first pod maturity exerted great positive influence both directly and indirectly on yield. It was concluded that plant length, first pod maturity, germination rate, cluster per plant, seed per pod and biological yield may be useful for selection of higher yielding mungbean genotype following mutation breeding

program.

Table 4.12: Estimation of genotypic (rg) and phenotypic (rp) correlation coefficients of various character combinations

Traits		plant height	Branches per plant	clusters perplant	Pods per plant	pod length	seeds per pod	100-seed weight	biological yield	seed yield per plant
Germination	r(g)	-0.276	-0.266	-0.115	0.501	-0.305	0.121	0.601	0.431	0.815
	r(p)	-0.277ns	-0.280ns	-0.151ns	0.504ns	-0.312ns	0.113ns	0.608*	0.370ns	0.775**
Plant height	r(g)		0.898	0.909	-0.468	0.970	0.107	-0.888	-0.671	-0.671
	r(p)		0.991**	0.855**	-0.373ns	0.954**	0.107ns	-0.885**	-0.630ns	-0.752*
Branches per plant	r(g)			0.926	-0.479	0.970	0.096	-0.887	-0.673	-0.751
	r(p)			0.855**	-0.470ns	0.965**	0.095ns	-0.884**	-0.641ns	-0.751*
Cluster per plant	r(g)				-0.706	0.991	-0.387	-0.886	-0.981	-0.642
	r(p)				-0.714*	0.904**	-0.295ns	-0.806**	-0.770*	-0.563ns
Pods per plant	r(g)					0.803	0.784	0.979	0.672	
	r(p)					-0.659*	0.730*	0.766**	0.879**	0.672*
Pod length	r(g)						-0.177	-0.934	-0.838	-0.651
	r(p)						-0.142ns	-0.930**	-0.810*	-0.714*
Seeds per pod	r(g)							0.207	0.696	0.031
	r(p)							0.192ns	0.649ns	0.041ns
100-seed weight	r(g)								0.961	0.863
	r(p)								0.981**	0.838**
Biological yield	r(g)									0.871
	r(p)									0.571*

*= Significant at 5% probability level, **=Highly Significant at 1% probability level; ns=Non Significant

Table 4.13: Various genetic parameters for different traits

Plant Traits	Heritability (h ²)%	Genetic advance (GA)	Coefficient of variance (CV)	Genotypic coefficient of variance (GCV)	Phenotypic coefficient of variance (PCV)
GP	95	3.83	1.07	3.58	3.93
PH	95.56	14.50	1.50	14.45	16.19
C/P	92.49	4.46	5.51	21.56	22.29
P/P	97.85	10.415	2.70	18.85	19.30
S/Pd	97.81	5.28	3.74	32.57	31.45
PL	90.54	7.111	4.410	12.07	12.49
B/P	83.49	2.375	2.88	10.83	11.85
100-SW	97.85	10.415	7.32	8.37	8.47
SY/P	98.3	4.425	5.39	28.58	29.58
BY	93.68	4.874	4.57	25.82	25.85

GP= Germination percentage, PH=Plant height. B/P= Branches per plant, C/P= Clusters per plant, P/P=Pods per Plant, PL= Pod Length, G/P= Grains per pod, 100SW= 100 seed weight, BY= Biological yield, SY/P= Seed yield per plant

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