*Turk J
Field Crops
2018, 23(2), 173-179
DOI: 10.17557/tjfc.485605*

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND QUALITY TRAITS IN M_{2-4} GENERATIONS OF BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES

Alpay BALKAN[*]

Tekirdağ Namık Kemal University, Faculty of Agriculture, Department of Field Crops, Tekirdağ, TURKEY
[*]Corresponding author: abalkan@nku.edu.tr

Received: 17.09.2018

ABSTRACT

The purpose of the study was to investigate genetic variability, heritability and genetic advance for grain yield and quality characters in the M_2, M_3 and M_4 populations of bread wheat (*Triticum aestivum* L.) in a Randomized Complete Block Design with 3 replicates during the 2011-12, 2012-13 and 2013-14 periods. Analysis of variance indicated that the mean squares for treatments were significant for all the characters except harvest index in the M_2; plant height, grain weight per spike, harvest index and gluten index in the M_3; sedimentation value and gluten index in the M_4. For the genotype, mean squares were also were significant for all the characters except gluten content in the M_3. The M_2 and M_3 showed a response to selection for grain yield and its components in bread wheat, while the M_4 generation was a response to selection for quality traits. Moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimated for the grain yield, the number of grains per spike, the grain weight per spike, the gluten index and the sedimentation value in three mutant generations indicated that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters in the early mutant generations. Heritability for the plant height, the number of grains per spike and the sedimentation value could be due to additive gene effects, and selection might be effective for these characters due to high heritability with high genetic advance. The harvest index, the gluten content and the gluten index could be used in the early generation stages with their high to medium values of heritability estimates associated with moderate expected gain, but would be more effective if postponed to late generations.

Keywords: GCV, heritability, mutant, PCV, population, wheat

INTRODUCTION

The variation of all present forms of life has been driven by three main forces: i) mutation, the fundamental source of heritable variation; ii) environment, which influences the selection of mutations that survive and reproduce; and iii) time, during which the genotype and the environment constantly interact and evolutionary change is realized (Czyczyło-Mysza et al., 2013). To a start proper wheat breeding program to improve yield and quality, the source populations should possess sufficient genetic variability suitable for selection. Unfortunately, with present distribution of improved high yielding, pure line cultivars in all of the world’s wheat growing areas, selection from established cultivars would rarely isolate a new genotype (Poehlman and Sleper, 1995). Genetic variation in major crops such as wheat has been successfully unlocked, shuffled, recombined, and sometimes created, by plant breeders over the last century to achieve yield increase. The success of induced variation will mainly depend on the precision in selection techniques (MacKey, 1984; Konzak, 1987). The expected response to selection can be measured by determining the parameters like mean, coefficient of variation, standard deviation, heritability and genetic advance (Ibrahim and Sharaan, 1974; Scossiroli, 1977; Shabana et al., 1994; Amer et al., 2001).

Two breeding procedures, i.e., mutation and hybridization are used to induce new genetic variation. Controversy exists among the breeders on the relative incidence of induced polygenic variations (through induced mutagenesis) in negative or positive direction and shift of the mean in the M_2 and later generations (Rao et al., 1988; Siddiqui and Singh, 2010). Since mutagen derived variability for quantitative characters in crop plants is heritable and the response of the selection seems good, henceforth, many workers hold the view that induced mutations can be used to generate useful variation in the quantitatively inherited traits where appropriate selection is applied for improvement (Scossiroli, 1964; Brock, 1970; Chakrabarthi, 1975; Khan, 1984; Tickoo and

Chandra, 1999; Kozgar et al., 2009; MacKay, 2011; Mba, 2013). Changes in morphological, physiological and quality characters after mutagen application are common, and therefore it has been demonstrated that induced mutation can increase yield as well as other agronomic characters such as stiffness of straw, time of maturity, adaptability, shattering resistance, disease resistance, protein content, baking quality, malting quality and numerous other characters (Ibrahim and Sharaan, 1974; Borojevic, 1990; Brunner, 1991). Several achievements in crop improvement through mutation breeding have resulted in two major outcomes: improved varieties that are directly used for commercial cultivation and new genetic stocks with improved characters or with better combining ability of traits (Roychowdhury and Tah, 2013). More than 3,200 mutant varieties have been directly or indirectly derived through mutation induction, nearly 80 % of these crop varieties are seed propagated, almost half of which (48 %) are cereals (Jankowicz-Cieslak et al., 2017) including 274 bread wheat varieties (International Atomic Energy Agency, IAEA, 2018) are being grown in different countries of the worldwide. Considering the improvements in mutation breeding in the world, unfortunately, there is no mutant wheat variety in our country yet.

The aim of this study was to study the mutational genetic variation .Knowledge of high value of heritability and predicted genetic advance clarifies that the selection among genotypes would be effective for yield and yield components (Shabana et al., 1994, Tammam et al., 2000, Kashif and Khaliq, 2004; Baloch et al., 2013). High heritability in broad sense associated with high genetic advance reveals strong contribution of additive genetic variance for expression of the traits and the selection based on these traits could play a vital role in improving grain yield (Laghari et al., 2010). Therefore, the present work was planned to estimate genetic variation, heritability (h_{bs}^2) and genetic advance (% mean).

MATERIALS AND METHODS

Plant material

Three bread wheat (*Triticum aestivum* L.) genotypes, Bezostaja 1 (tall, mid-early, awnless, superior in flour quality for bread making, but inferior in lodging resistance and yield capacity), Kate A-I (tall, mid-early, awnless and inferior in flour quality for bread making, lodging and disease resistance and superior in yield capacity) and IBWSN4 (tall, early, awned and inferior in flour quality for bread making, disease resistance and superior in lodging and yield capacity) were used as the experimental material.

Gamma ray irradiation

The moisture contents of seeds of wheat (*Triticum aestivum* L.) genotypes used in this study were 11.4% for the Bezostaja 1, 11.7% for the Kate A-I and 12.0% for the IBWSN4. Each seed sample for the each genotype were divided into six groups (A, B, C, D, E and F), which contain 2000 grains. From them group A was kept un-irradiated (control), while the other groups were irradiated with various levels of gamma ray (100, 200, 300, 400 and 500 Gy). Gamma treatment was obtained from ^{60}Cobalt, Ob-Servo Sanguis Co-60 Research Irradiator with isotope model, while the dose rate was 2.190 kGy h^{-1} in before the 2010-2011 growing season sowing at the Turkish Atomic Energy Authority, Sarayköy Nuclear Research and Training Center, Ankara, Turkey. After the irradiation, the experiment was set up using with 15 M_0 combination seeds along with the un-irradiated (control) in the experimental field of the Field Crops Department of the Faculty of Agriculture of Tekirdağ Namık Kemal University during the 2009-2010. The experiment was carried out in a randomized complete block design (RCBD) with 3 replicates. Plots were sown on Nov.15, 2010 by hand at the rate of 350 seeds per m^2 into the 2 m in length x 1.0 m wide, with 6 rows 0.2 m on row distance. Nitrogen and P_20_5 at 160 and 50 kg ha^{-1}, respectively, were incorporated into the soil as compound fertilizer (20-20-0) before sowing, urea during tillering and ammonium nitrate before heading stage. The crop was kept free of weeds by hand hoeing as the necessary. The remaining seeds were sown in the greenhouse in order to guarantee the work. The seeds obtained from the harvested plants in M_1 generation were sown to be able to get of the M_2 in 2011-12; to be able to get of the M_3 in 2012-13 and to be able to get of the M_4 in 2013-14 from the plots which are 20 cm row distance in 5 meters of 6-row parcels as 400 seeds in the each row with 4 replicates. Morphological and yield characters were recorded on 15 randomly selected plants to study the effect of irradiation doses on the studied genotypes. Grain yield (GY) and some yield components such as plant height (PH), spike length (SL), number of grains per spike (NGPS), grain weight per spike (GWPS) and harvest index (HI) were measured (Gençtan, 1988).

After harvest, the grain samples were cleaned. Physical characteristics of the grain such as thousand kernel weight (TKW) and test weight (TW) were determined following the official methods of the Approved Methods of the American Association of Cereal Chemists (AACC, 2000). The quantity of grain protein content (PC) (ICC, 1995) was determined by a near infrared reflectance spectrophotometer calibrated against Kjeldahl data. Gluten content (GC) and gluten index (GI) of wheat flours were analyzed according to the revised standard ICC method No. 155 (ICC, 1994) by using the Glutomatic 2200 system (Perten Instruments AB, Huddinge, Sweden). Sedimentation value (SV) was determined following ICC method No: 166/1 (ICC, 1972).

Statistical analyses

All data obtained were subjected to analysis of variance (ANOVA) by using JUMP 5.0.1 statistical software. The genotypic and phenotypic variances and their corresponding coefficients of variations were estimated, using the pertinent mean square expectations, according to the method, suggested by Johnson et al. (1955). In addition, broad-sense heritability (h_{bs}^2), genetic advance (GA) as % of mean were calculated following Hanson et al. (1956) and Allard (1999).

Mean squares were used to estimate;

$\boldsymbol{\sigma}_g^2 =$ (MSS-MSE)/r

$\boldsymbol{\sigma}_{ph}^2 = \boldsymbol{\sigma}_e^2 + \boldsymbol{\sigma}_g^2$, where broad-sense heritability (h_{bs}^2)was estimated as follows:

$h_{bs}^2 = (\boldsymbol{\sigma}_g^2 / \boldsymbol{\sigma}_{ph}^2)$ x 100 and the phenotypic (PCV) and genotypic (GCV) coefficients of variation were computed as follows:

PCV = $100\ x \sqrt{\sigma_{\mathrm{ph}}^2}/\bar{\mathrm{X}}$

GCV = $100\ x \sqrt{\sigma_g^2}/\bar{\mathrm{X}}$

Expected genetic advance (GA): Expected genetic advance from direct selection for all studied traits was calculated according to Singh and Chaudhary (1999) as follows:

GA% at 10% (selection intensity) = $100\, x\, \mathrm{k}\, x\, h_{bs}^2\ x\ \sigma_{\mathrm{ph}}/\bar{\mathrm{X}}$,

Where, $\bar{\mathrm{X}}$: general mean and k is selection differential (k= 1.76 for 10% selection).

RESULTS AND DISCUSSION

The significances of variance components obtained from the analysis of variance (ANOVA) for all of the characters in the bread wheat mutated populations of the M_2, M_3 and M_4 is presented in Table l. ANOVA results show that the mean squares for treatments were significant for all the characters except HI in the M_2, PH, GWPS, HI and GC in the M_3, and SV and GI in the M_4 (Table 1). Regarding the genotype, mean squares were also were significant for all the characters except GC in the M_3. This indicates that genotypes and treatments under study varied significantly for all the quantitative characters. Highly significant mean squares attributable to genotypes also revealed that significant genetic variability existed among the used genotypes. Treatment x genotype interaction mean squares were significant for all the characters except the PH, GWPS, TW, SV and PC in the M_2, PH, GY, TW and PC in the M_3 and SL and SV in the M_4, indicating that genotype did not perform uniformly across different gamma rays. Non-significant interaction for the PH, SL, GWPS, TW, SV and PC in mutated population generations indicated a consistency in performance of each genotype across different irradiation treatments.

Table 1. ANOVA results of the 12 examined characters in theM_2, M_3 and M_4

Characters	Replication d.f.= 2			Treatments (T) d.f.= 5			Genotype (G) d.f.= 2			T x G d.f.= 10		
	M_2	**M_3**	**M_4**	**M_2**	**M_3**	**M_4**	**M_2**	**M_3**	**M_4**	**M_2**	**M_3**	**M_4**
PH (cm)	*	ns	**	*	ns	**	**	**	**	ns	ns	**
SL (cm)	ns	ns	*	**	**	**	*	**	*	**	**	ns
NGPS (no)	ns	ns	ns	**	**	**	**	**	**	**	**	**
GWPS (g)	ns	ns	ns	**	ns	**	**	**	**	ns	**	**
HI (%)	ns	ns	ns	ns	ns	**	**	**	**	*	**	**
GY (kg da^{-1})	ns	ns	ns	**	**	**	**	**	**	**	ns	*
TGW (g)	*	ns	ns	*	**	*	**	**	**	**	*	**
TW (kg hl^{-1})	ns	ns	*	**	**	**	**	**	**	ns	ns	**
GC (%)	**	ns	ns	**	**	*	**	ns	**	**	**	**
GI (%)	ns	ns	ns	*	ns	ns	**	**	**	*	*	**
SV (ml)	*	ns	*	**	**	ns	**	**	**	ns	*	ns
PC (%)	**	ns	ns	**	**	**	**	**	**	ns	ns	*

d.f.: degrees of freedom, ** and *: Significant at 0.01 and 0.05s, ns: Non-significant

The pool of genotypes was therefore, assessed for variability analysis. The existence of wide diversity among the constituent genotypes with regard to characters under study was confirmed through various statistical parameters. The basic material, therefore, offers positive opportunities for investigation furtherance of the aforesaid objectives. The general range, grand mean, coefficient of variation along with genotypic and phenotypic coefficient of variation, heritability and genetic advance for the GY and its components and some quality characters in the M_2, the M_3 and the M_4 generations are presented in Tables 2 and 3.

The ranges obtained in the M_2 generation were wider than that in the other both generations for the PH (77.6-115.5 cm), the SL (8.7-11.9 cm), the NGPS (31.0-60.0), the GWPS (1.570-3.070 g), the TGW (26.5-36.5 g), the TW (68.0-78.5 kg hl^{-1}) and the PC (9.10-13.90 %), while the M_3 and the M_4 generations showed wider ranges for generation for HI (27.27-41.10) and the GY (453.0-795.0 kg da^{-1}), and the GC (31.5-42.0 %), the GI (45.0-80.0 %) and the SV (33.0-63.0 ml) respectively (Table 2 and Table 3). The wider range of variation observed for all the characters suggested enough variation to be exploit the variability. These results indicated that the M_2 and M_3 mutated generations showed a response to selection for grain yield and its components in the bread wheat, while the M_4 generation was a response to selection for quality traits. As mentioned by Rao and Siddiq (1977) the increase of variation of quantitative characters for given generations can depend on the trait investigated.

Table 2. Range, mean, PCV, GCV, heritability and the expected genetic advance (GA) for investigated characters in the M_2, M_3 and M_4

Characters	Generations	Range	Grand mean	Coefficient of variation (%)		h_{bs}^2 (%)	GA mean (10%)
				PCV	GCV		
PH (cm)	M_2	77.6-115.5	92.9	9.74	7.42	58.1	90.02
	M_3	94.5-124.7	111.1	7.36	6.56	79.5	84.20
	M_4	77.3-114.0	99.1	9.19	8.69	89.4	131.58
SL (cm)	M_2	8.8-12.1	10.3	6.93	5.61	65.6	5.71
	M_3	8.7-11.9	10.2	6.10	4.54	55.3	3.69
	M_4	8.8-11.7	10.3	6.62	5.62	72.2	5.74
NGPS (no)	M_2	31.0-60.0	42.0	18.13	16.50	82.8	201.24
	M_3	29.5-53.2	41.5	14.94	14.00	87.8	143.21
	M_4	33.3-57.3	46.3	11.28	10.20	81.8	84.79
GWPS (g)	M_2	1.570-3.070	2.210	16.00	12.96	65.6	6.53
	M_3	1.080-2.140	1.546	18.86	15.31	66.1	6.40
	M_4	0.740-1.750	1.322	15.69	11.47	53.9	3.09
HI (%)	M_2	28.65-40.30	35.37	7.78	6.09	61.3	23.09
	M_3	27.27-41.10	35.54	10.63	9.93	87.3	61.69
	M_4	35.81-45.12	41.85	5.08	4.39	74.9	14.22
GY (kg da^{-1})	M_2	326.0-632.0	468.2	15.12	11.65	59.4	1119.64
	M_3	453.0-795.0	619.3	14.61	11.21	58.8	1368.43
	M_4	553.0-824.0	663.8	10.82	8.16	56.9	777.66

Genetic variability is the tendency of individuals in a population, to vary from one another. Variability is different from genetic variation, which is the actual amount of phenotypic variation seen in a particular population. Genetic variability in a population is very important because, without variability, it becomes difficult for a population to adapt to environmental changes and plays a very important role in any crop breeding program. Frey (1969) reported that mutagen derived variability for quantitative characters in crop plants was heritable and that the response to selection was good. Statistically, the total variability was expressed in terms of the PCV and the genotypic variability is expressed in terms of the GCV. The GCV and PCV values were categorized as low (<10%), moderate (10 to 20%) and high (>20%) as indicated by Subramaniam and Menon (1973). The GCV and PCV values obtained in our study were moderate and low for the grain yield and quality characters. Accordingly, the moderate PCV and GCV were estimated for the GY, NGPS, GWPS, GI and SV in three mutated generations (Table 2 and Table 3). This indicated that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters in early mutated generations. Report of Birhanu et al. (2016) is in line with the occurrence of GCV and PCV media in this study. Low estimates of the GCV were recorded for the PH, SL, HI, TGW, TW, GC, GI and PC. The result indicated that the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these characters by direct selection of high performing genotypes. This was in agreement with report of Naik et al. (2015). On the other hand, the values of phenotypic coefficient of variation (PCV) were slightly higher than their corresponding values of the GCV for all traits which reflect somewhat environmental influence on the expression of characters in mutated generations. These results indicated that the selection would be effective to improve these traits among the tested genotypes. However, the NGPS, GWPS and GY revealed high difference between the GCV and the PCV in comparison to other characters, suggested that environmental effect was prominent for the NGPS, GWPS and GY.

Table 3. Range, mean, PCV, GCV, heritability and the expected genetic advance (GA) for the quality characters in the M_2, M_3 and M_4

Characters	Generations	Range	Grand mean	Coefficient of variation (%)		h^2_{bs} (%)	GA mean (10%)
				PCV	GCV		
TGW (g)	M_2	26.5-36.5	30.6	8.45	7.73	83.6	32.17
	M_3	31.5-40.9	35.8	5.86	4.86	68.9	14.90
	M_4	39.7-49.0	44.2	4.88	4.33	78.6	14.54
TW (kg hl^{-1})	M_2	68.0-78.5	73.3	3.39	2.62	60.0	8.88
	M_3	70.2-78.2	75.5	2.59	2.32	80.1	7.16
	M_4	77.9-84.1	81.5	1.99	1.83	84.6	4.81
GC (%)	M_2	18.0-29.1	24.0	8.39	6.92	67.9	20.20
	M_3	31.5-42.0	35.9	5.37	3.91	53.1	9.66
	M_4	37.1-49.0	43.9	6.83	4.66	46.6	16.78
GI (%)	M_2	77.0-94.0	86.5	5.78	5.26	83.0	42.18
	M_3	55.0-85.0	70.3	12.52	9.62	59.0	114.51
	M_4	45.0-80.0	62.6	15.17	11.60	58.5	148.35
SV (ml)	M_2	30.4-50.90	37.5	12.96	11.73	81.9	90.76
	M_3	33.0-55.0	44.3	16.44	15.03	83.6	176.16
	M_4	33.0-63.0	46.7	17.67	15.35	75.5	193.82
PC (%)	M_2	9.10-13.90	11.19	6.95	5.04	52.6	5.00
	M_3	12.20-14.90	13.70	4.88	4.14	72.0	4.13
	M_4	13.20-15.40	14.39	3.59	2.99	69.7	2.28

The variation in 3 mutated populations for grain yield and quality traits indicated that selection for these traits might be effective. However, the high PCV or the GCV did not provide a clear picture of the extent of genetic gain to be achieved from selection, for the phenotypic traits unless the heritable fraction of the trait was known (Kumar et al., 2017). Since, the efficiency of selection would depend upon the magnitude of variability that is heritable and caused by genetic factors the higher values, therefore, heritability accompanied by high genetic advance for the characters studied should be quite valuable (Johnson et al., 1955). According to Singh (2001), heritability of a trait was considered as high when the value is 80% or moderate when it ranged from 40-80% and when it was less than 40%, it was low. Deshmukh et al. (1986) classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). In our study, moderate to high estimates of heritability were estimated for characters studied. High heritability was coupled with high genetic advance as percent of mean observed for the PH (89.4%), the NGPS (87.8 %) and the SV (83.6 %) (Table 2 and Table 3). This indicated that most likely the heritability of these characters was due to additive gene effects, and selection might be effective for these characters (Salman et al., 2014; Rahman et al., 2016). High to medium values of heritability estimates were found associated with moderate expected and actual gain for the HI (14.22-61.69 %), the GC (9.66-20.20 %) and the GI (42.18-148.35 %). These obtained results indicated that, these traits could be used in the early generation, but would be more effective if postponed to late generation (Kumar et al., 2017). As in many other crops, GY had the lowest heritability estimate with a relatively low value for expected genetic advance (Budak, 2000 and Kashif and Khaliq, 2004). The variations were observed of value of heritability and genetic advance for the SL (55.3-72.2 % and 3.69-5.74 %), GWPS (53.9-66.1 % and 3.09-6.53 %), GY (56.9-59.4 % and 777.66-1368.43 %), TW (60.0-84.6 % and 4.81-8.88 %) and PC (52.6-72.0 % and 2.28-5.00 %) (Table 2 and Table 3). The variations of the values of heritability and genetic advances were found to be independent for almost all the yield and quality attributing traits in the mutagenized population, thereby reflecting that high heritability was not always associated with high genetic advance (Najeeb et al., 2009; Ali et al., 2012).

As a conclusion, ANOVA indicating significant variability among the genotypes for all traits; the mean sum squares for 12 characters were highly significant thereby suggesting the presence of considerable amount of heritability in bread wheat mutated populations of the M_2, M_3 and M_4. The M_2 and M_3 generations can be useful from point of view for selecting higher yielding plants in early generation, while the M_4 generation is appropriate for quality characters. Non-gradual increases in genetic parameters were observed in consecutive mutated generations. Heritability estimates and genetic advance showed considerable increase indicating that the PH, NGPS, HI, and GC, GI and SV can be transmitted to advance generations and significant gain could be gained by selection method(s) in the early generations with multidisciplinary (particularly plant physiology, mutation breeding, agronomy etc.) under the greenhouse and field conditions in the long and near future.

LITERATURE CITED

AACC, 2000. Approved Methods of the American Association of Cereal Chemists. Methods 38-12 and 46-13, tenth ed. American Association of Cereal Chemists, St. Paul, MN.

Ali, A., S. Khan and M.A. Asad. 2012. Drought tolerance in wheat : Genetic variation and heritability for growth and ion relations. Asian J. Plant Sci. 1: 420-422.

Allard, R.W. 1999. Principals of Plant Breeding. 2. ed. New York: John Wiley & Sons.

Amer, I.M., R. Shabana, A.A.H. Allah and C.R. Azzam. 2001. Evaluation of sunflower irradiated populations in M_4 and M_5 generations. Second Plant Breeding Conference, Agronomy Dep. Faculty of Agric. Assuit University. 41-60.

Baloch, M.J., E. Baloch, W.A. Jatoi and N.F. Veesar. 2013. Correlations and heritability estimates of yield and yield attributing traits in wheat (*Triticum aestivum* L.). Pak. J. Agri. Eng. Vet. Sci. 29(2): 96-105.

Birhanu, M., A. Sentayehu, A. Alemayehu, A. Ermias and D. Dargicho. 2016. Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes. Glob. J. Sci. Front. Res. 16(7):12-15.

Borojevic, S. 1990. Mutations in Plant Breeding. In: Borojevic, S. (Eds.), Principles and Methods of Plant Breeding. Elsevier Science Publishing Co. Inc. New York, 252-262.

Brock, R.D. 1970. Mutations in quantitatively inherited traits induced by neutron irradiation. Radiation Botany 7: 193-203.

Brunner, H. 1991. Methods of Induction of Mutations. In: Mandal, A. K., Ganguli, P. K., Banerjee, S.P. (Eds.), Advances in Plant Breeding. CBS Publishers and Distributors, Delhi, 187-220.

Budak, N. 2000. Heritability, correlation and genotype x year interactions of grain yield, test weight and protein content in durum wheat. Turk J Field Crops 5(2): 35-40.

Chakrabarthi, S.N. 1975. Effects of combined X-rays and dES treatments on mutation frequencies in rice (*Oryza sativa* L.). Radiation Botany 15: 417-421.

Czyczyło-Mysza, I., I. Marcińska, J. Jankowicz-Cieślak and F. Dubert. 2013. The effect of ionizing radiation on vernalization, growth and development of winter wheat. Acta Biologica Cracoviensia Series Botanica 55(1):1-6.

Deshmukh, S.N., M.S. Basu and P.S. Reddy. 1986. Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric. Sci. 56: 816-821.

Frey, K.J. 1969. Release of mutagen-induced genetic variablity in oats by outcrossing. Japan J. Genet. 44: 396-403.

Gençtan, T. 1988. Buğdayda başlıca verim komponentlerinde F_1 melez gücünün (Heterosis) saptanması. Trakya Üniv. Tekirdağ Ziraat Fakültesi Yayın No:59, Araştırma No:14, 53s.

Hanson, G.H., H.F. Robinson and R.E. Comstock. 1956. Biometrical studies on yield in segregating populations of Korean Lespidiza. Agorn. J. 48:268-272.

Ibrahim, A.F. and A.N. Sharaan. 1974. Studies on certain early barley mutants in M_3 and M_4 generations after seed irradiation with gamma rays. Plant Breeding 73: 44-57.

ICC, 1972. ICC standart Method 166/1: Determination of the Sedimentation Value (according to Zeleny) as an approximate measure of baking quality.

ICC, 1994. ICC Standard No 155: Determination of wet gluten quantity and quality (Gluten Index ac. To Perten) of whole wheat meal and wheat flour.

ICC, 1995. ICC Standard No 159: Determination of protein by near infrared reflectance (NIR) spectroscopy.

International Atomic Energy Agency (IAEA). 2018. Mutant Varieties Database. https://mvd.iaea.org (Accessed 6 April 2018)

Jankowicz-Cieslak, J., C. Mba and B.J. Till. 2017. Mutagenesis for Crop Breeding and Functional Genomics. In: Biotechnologies for Plant Mutation Breeding, ed. Jankowicz-Cieslak, J., Tai, T. H., Kumlehn, J. and Till, B. J., 3-18, Springer, New York.

Johnson, H.W., H.F. Robinson and R.E. Comstock. 1955. Estimation of genetic and environmental variability in soybean. Agron. J. 47:314-318.

Kashif, M. and I. Khaliq. 2004. Heritability, correlation and path coefficient analysis for some metric traits in wheat. Int. J. Agri. Biol. 6 (1):138-142.

Khan, I.A. 1984. Mutations induced by gamma irradiation, ethylmethane sulphonate and hydrazine hydrate in mungbean (*Phaseolus aureus* Roxb.). Botanical Bulletin of Academia Sinica 25(1): 103-110.

Konzak, C.F. 1987. Mutations and Mutation Breeding. In: E.G. Heyne (ed.), Wheat and Wheat Improvement, Second Edition, 428-443, ASA. CSSA. SSSA. Inc. Press, Madison, WI, USA.

Kozgar, M.I., S. Khan and N. Jabeeen. 2009. Mitotic studies in chickpea raised in lead nitrate supplemented Murashige and Skoogs basal media. D.I.E. Journal of Science and Engineering Research 15 (1&2): 9-12.

Kumar, D., R.K. Srivastava, P.K. Yadav, A. Kumar and R.S. Yadav. 2017. Studies on variability, heritability and genetic advance in some quantitative characters in bread wheat (*Triticum aestivum* L.). Int. J. Curr. Microbiol. App. Sci. 6(7): 873-877.

Laghari, K.A., M.A. Sial, M.A. Arain, A.A. Mirbahar, A.J. Pirzada, M.U. Dahot and S.M. Mangrio. 2010. Heritability studies of yield and yield associated traits in bread wheat. Pak. J. Bot. 42(1): 111-115.

MacKay, T.F.C. 2011. Mutations and quantitative genetic variation: lessons from *Drosophila*. Philosophical Transactions of the Royal Society B. 365: 1229-1239.

MacKey, J. 1984. Selection Problems and Objectives in Mutation Breeding. Joint FAO/IAEA Div. of Isotope and Radiation Applications of Atomic Energy for Food and Agricultural Development, Vienna (Austria). Panel proceedings series. 35-48.

Mba, C. 2013. Induced mutations unleash the potentials of plane genetic resources for food and agriculture. Agronomy 3: 200-231.

Naik, V.R., S.S. Biradar, A. Yadawad, S.A. Desai and B.A. Veeresha. 2015. Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. Res. J. Agric. Sci. 6(1): 123-125.

Najeeb, S., A.G. Rather, A.G. Parray, F.A. Sheikh and S.M. Razvi. 2009. Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under the high altitude temperate conditions of Kashmir. Maize Genet. Cooperation News l: 83-46.

Poehlman, J.M. and D.A. Sleper. 1995. Breeding Field Crops. 4th Iowa State University Press, Ames, USA.

Rahman, M.A., M.L. Kabir, M. Hasanuzzaman, R.H. Rumi and M. Afrose. 2016. Study of variability in bread wheat (*Triticum aestivum* L.). Int. J. Agric. Res. 8: 66-76.

Rao, D.M., T.P. Reddy and T. Kinoshita. 1988. Characterization of induced polygenic variability in pigeonpea (*Cajanus cajan* L). J. Faculty Agric. Hokkaido University 63(4): 387-395.

Rao, G.M. and E.A. Siddiq. 1977. Induced variation for yield and its components in rice. Indian J. Genet. Plant Breed. 37: 12-21.

Roychowdhury, R. and J. Tah. 2013. Mutagenesis A Potential Approach For Crop Improvement. In: Crop improvement: New Approaches and Modern Techniques, ed. Hakeem, K.R., P. Ahmad and M. Ozturk, 149-187, Springer, New York.

Salman, S., S.J. Khan and R. Ullah. 2014. Genetic variability studies in bread wheat (*Triticum aestivum* L.) accessions. Pak. J. Agric. Res. 27 (1): 2-6.

Scossiroli, R.E. 1964. Wheat mutagenesis in quantitative traits. In Proceedings of the 2nd. Wheat Genetics Symposium, pp. 85-101, Lund.

Scossiroli, R.E. 1977. Mutations in Characters With Continuous Variation. In: Manual On Mutation Breeding. 2nd ed., IAEA, Tech. Rep. Ser. No: 119, 118-123, Vienna.

Shabana, R., I.M. Amer, R.S. Taha and C.R. Azzam. 1994. Variability, heritability and expected genetic advance in irradiated and non-irradiated populations of sunflower after two cycles of mass selection for short stature. Annals Agric. Sci. 39 (1): 249-256.

Siddiqui, S.A. and S. Singh. 2010. Induced genetic variability for yield and yield traits in basmati rice. World Journal of Agricultural Sciences 6(3): 331-337.

Singh, B.D. 2001. Plant Breeding: Principles and Methods, 1-896, Kalyani Publishers, New Delhi, India.

Singh, R.K. and B.D. Chaudhary. 1999. Biometrical methods in quantitive genetics analysis, 1-318, Kalyani Publishers, New Delhi, India.

Subramaniam, S. and M. Menon. 1973. Inheritance of short stature in rice. Madras Agriculture Journal 60: 1129-1133.

Tammam, A.M., S.A. Ali and E.A.M. El-Sayed. 2000. Phenotypic, genotypic correlation and path coefficient analysis in some bread wheat crosses. Assiut. J. Agric. Sci. 31(3): 73-85.

Tickoo, J.L. and N. Chandra. 1999. Mutagen induced polygenic variability in mungbean (*Vigna radiata* (L.) Wilczek). Indian Journal of Genetics and Plant Breeding 59(2): 193-201.