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Impact of irradiation with gamma rays on genetic behavior of potato plant (*Solanum tuberosum* L.)

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Abstract

The study was conducted under the conditions of Nineveh Governorate, Iraq, to investigate the inheritance patterns of some growth and yield traits in five imported potato cultivars of the E grade (Arizona, Fajah, Paradiso, Riviera, and Vogue) under the influence of Gamma Rays exposure for varying durations: untreated, 30 minutes, 45 minutes, and 60 minutes. The study was carried out during the spring growing season of 2024/2025 in the Agricultural Research Field at the College of Agriculture and Forestry in the forest region of Mosul. The experiment was set as a factorial trial of 20 treatments using a randomized complete block design (RCBD) with three replicates.

The results of the variance analysis indicated that the mean squares for the five cultivars were significant for all studied traits, except for the carbohydrate percentage in the tubers. Meanwhile, the mean squares for radiation treatments were significant only for the percentage of dry matter and starch in the tubers. The values for genetic and environmental variance were significant for all studied traits. Moreover, the genetic variance values were higher than the environmental variance values for plant height, total tuber count per plant, phosphorus percentage in tubers, and potassium percentage in tubers, but lower for the remaining traits.

The broad-sense heritability values were high for plant height and the percentages of phosphorus and potassium in the tubers. A high heritability percentage for any trait offers a good opportunity for breeders to enhance these traits through direct selection. The expected genetic improvement values, as a percentage of the trait mean, were moderate for most of the studied traits.

Keywords: Gamma Rays, variance and heritability, genetic improvement, potatoes.

INTRODUCTION

Potato (Solanum tuberosum L.) is one of the most important vegetable crops worldwide, belonging to the Solanaceae family. It ranks fourth among the most widely cultivated crops, following wheat, rice, and maize. The potato originates from South America and later spread to Europe and North America. It has high nutritional value due to its rich content of essential nutrients, proteins, vitamins, carbohydrates, fats, sugars, and organic acids (Hassan, 2003). In Iraq, the total cultivated area of potatoes in 2022 was approximately 440.50 dunams, with an average yield of 5,364.5 kg/dunam, producing a total of 270,591 tons (Central Statistics Bureau, 2023).

Most potato varieties cultivated in the Arab region are of European origin. High-yielding and well-adapted cultivars play a key role in determining productivity (Taha, 2007). The interaction between genetic and environmental factors largely influences the quality and quantity of yield (Kumar et al., 2000).

Achieving high yields in crops requires an understanding of genetic variation and its extent in plant materials since genetic differences are essential for plant breeders. The success of any breeding program depends on desirable genetic variations within the plant population. Without such variations, superior plant types with improved yield and quality characteristics would not exist.

Environmental differences can sometimes obscure genetic variations. When phenotypic differences within a genetic composition arise due to environmental factors, selecting genetic differences becomes difficult. However, if environmental influence on trait variation is minimal compared to genetic differences, selection becomes more effective, ensuring that selected traits are passed on to subsequent generations (Mufarriji, 2006).

This necessity led to the use of heritability (Heritability Broad Sense) as a quantitative measure to assess the extent of environmental influence on traits. Heritability expresses the proportion of genetic variance in a trait relative to its total phenotypic variance. High heritability values indicate that direct selection is effective for breeding and trait improvement. Genetic enhancement estimation (Genetic Advance) plays a crucial role in breeding programs (Kamar, 1999).

To accelerate genetic variation and broaden genetic diversity, various techniques have been employed to create new plant varieties with desirable traits. One of the most efficient and cost-effective methods for developing genetic structures in a short time is radiation treatment. Seeds contain essential nutrients and energy for growth, but they sometimes require stimulation to activate these stored materials, and radiation serves as one such stimulant (Piri et al., 2011). Ionizing radiation is defined as energy transmitted via photons (X-rays and Gamma rays) or particles (Alpha, Beta, Neutrons, and Protons) (Lemus et al., 2002).

Gamma rays have been widely used to induce genetic variation in various plant species (Moussa, 2011). These rays impact plant growth and development by triggering genetic, cellular, biochemical, and physiological changes in tissues and cells. The extent of these effects depends on the radiation levels applied (Ikram et al., 2010). Low doses of gamma rays have shown positive effects on chemical, morphological, and physical characteristics, demonstrating the potential to develop new plant varieties (Anne & Jin, 2020).

Study Objectives

This study, as a novel contribution to vegetable crop research in Iraq—particularly in Nineveh Governorate—focuses on potatoes:

1. Investigating the effects of different Gamma Ray exposure durations on vegetative growth and quantitative and qualitative yield traits of potatoes.
2. Assessing the genetic performance of five potato cultivars under various radiation treatments to select the most productive and high-quality varieties.
3. Estimating genetic and phenotypic variance for key yield components and evaluating cultivar selection potential in breeding and improvement programs.
4. Determining heritability and expected genetic improvement of yield and its components.

MATERIALS AND METHODS

This study was conducted in the vegetable field of the Department of Horticulture and Landscape Engineering, College of Agriculture and Forestry, University of Mosul, Mosul City. The field is located at a latitude of 36.35° N and longitude of 43.15° E, with an elevation of 223 meters above sea level (Guest, 1966). The research aimed to estimate certain genetic parameters under the conditions of Nineveh Governorate for five imported potato cultivars of E grade (Arizona, Fajah, Paradiso, Riviera, and Vogue) exposed to Gamma Rays for varying durations: untreated, 30 minutes, 45 minutes, and 60 minutes. The irradiation of the five potato cultivars under study was performed in lead-shielded chambers at the Physics Department laboratories, College of Science, University of Mosul.

The tubers of the five cultivars were planted on 13/02/2024 in furrows aligned east-west. Each experimental unit consisted of three furrows, each 1.50 meters long and 0.75 meters wide, resulting in a total area of 3.375 square meters per experimental unit. The study was implemented as a factorial experiment with three replicates following a Randomized Complete Block Design (RCBD). The total number of treatments was 20 (5×4=20), and the total number of experimental units was 180 (5×4×3×3=180). Agricultural services were uniformly applied across all treatments (Matloub et al., 1989).

The data were statistically analyzed using the SAS program (2010), and Duncan's multiple range test was used to compare mean values at a significance level of 0.05. After collecting, categorizing, and tabulating data for the studied traits, a genetic analysis was performed to estimate certain genetic parameters from the variance analysis table of the experiment design. The genetic estimations were calculated using the mathematical model equation mentioned by (Al-Rawi and Khalaf Allah, 2000).

$$y_{ijk} = \mu + R_k + A_i + B_j + AB_{ij} + e_{ijk}\{i = 1, 2, \dots A; j = 1,2, \dots B; k = 1,2, \dots R\}.$$

Table (1): Analysis of Variance (ANOVA) Table for the Experimental Design Used

S.O.V	**d.f**	**SS**	**MS**	**Cal. F**
Reps	**r – 1 = 2**	**(SSr) = R-CF**	**MSr**	F_r
A	**a – 1= 4**	**(SS_A) =A–CF**	MS_A	F_A
B	**b – 1 = 3**	**($SS_{B)}$ =B–CF**	MS_B	F_B
AB	**(a-1) (b–1) = 12**	**(SS_{AB}) = AB-A-B+CF**	MS_{AB}	F_{AB}
Error	**(ab-1) (r-1) = 38**	**(SSe) = ABR-AB-R+CF**	MS_e	
Total	**abr – 1 = 59**	**SST = ABR-CF**		

Where:

A: Cultivars = 5.

B: Radiations treatments = 4.

R: Replications = 3.

The components of phenotypic variance (σ^2p), genetic variance (σ^2g), and environmental variance (σ^2e) were estimated from the Analysis of Variance (ANOVA) Table (Table 1). The significance of both genetic (σ^2g) and environmental (σ^2e) variance relative to zero was tested following Kempthorne's method (1957). This was achieved by calculating the variance for each and extracting their square roots to obtain the standard errors, as follows:

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

Where:

$$\sigma_p^2 : Phenotypic\ variance$$

$$\sigma_g^2 : Genotypic\ variance$$

$$\sigma_e^2 : Enrionmental\ variance$$

$$\sigma_g^2 = \frac{MS_g - MS_e}{r\ b}$$

Where:

MS_g: Means of Squares of Cultivars.

MS_3: Error Mean Squares

r: Number of Replications.

b: Numbers of Radiation treatments.

The variance for both genetic variance (σ^2g) and environmental variance (σ^2e) was calculated as follows:

$$V(g) = \frac{1}{r^2 b^2} \{\frac{2(Msg)^2}{gen.df.+2} + \frac{2(Mse)^2}{error\ df.+2}\}$$

$$V(e) = \frac{2(Mse)^2}{error\ \ df.+2}$$

The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were estimated using the following equations proposed by Burton (1952) for GCV and Dudle & Moll (1969) for PCV:

$$GCV\% = \frac{\sqrt{\sigma_g^2}}{\bar{y}} \times 100$$

$$PCV\% = \frac{\sqrt{\sigma_g^2}}{\bar{y}} \times 100$$

Where:

- ($\bar{y}$): Represents the arithmetic mean of the trait.

- σ^2g: Refers to the genotypic standard deviation.

- σ^2p: Refers to the phenotypic standard deviation.

The broad-sense heritability values (H^2b.s.) were estimated using the equation provided by Falconer and Mackay (1996), which is as follows:

$$H^2 b.s. = \frac{\sigma_g^2}{\sigma_p^2}$$

The significance of broad-sense heritability values was expressed based on the scale provided by Ali (1999):

- Less than 40%: Low

- 40–60%: Moderate

- More than 60%: High

Expected Genetic Advance (EGA) , referred to by Falconer and Mackay (1996) as the response to selection, measures the difference between the mean of the offspring population resulting from selection and the mean of the original population. EGA was estimated for each trait using the equation proposed by Allard (1960), as follows:

$$E.G.A = \left(K\,H^2 b.s.\sqrt{\sigma_p^2}\right)$$

Where:

E.G.A = Expected Genetic Advance

K = 2.06 , representing the selection intensity for the top 5% of plants.

H^2b.s. = Broad-Sense Heritability

σ^2p = Phenotypic Standard Deviation

The expected genetic advance was estimated as a percentage of the mean trait value using the method described by Kempthorne (1969), which is as follows:

$$E.G.A\% = \left[\frac{KH^2 b.s.\sqrt{\sigma_p^2}}{\bar{y}}\right] \times 100$$

Where:

$$\bar{y}: the\ average\ of\ triat$$

The expected genetic improvement thresholds, as outlined by Agarwal and Ahmed (1982), are as follows:

- Less than 10%: Low

- 10–30%: Moderate

- More than 30%: High

RESULTS AND DISCUSSION

The results of the variance analysis for the studied potato traits are presented in Table (2). They reveal that the mean squares of the five cultivar compositions were significant for all studied traits except for the carbohydrate percentage in tubers. Significance was observed at the 1% probability level for traits including plant height, the number of aerial stems, the percentage of dry

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matter in the vegetative growth, the total number of tubers per plant, the total yield per plant, the total tuber yield, the percentage of soluble solids in tubers, the percentage of phosphorus in tubers, and the percentage of potassium in tubers. Significance was observed at the 5% probability level for traits such as the average total tuber weight, the percentage of dry matter in tubers, the percentage of starch in tubers, the percentage of protein in tubers, and the percentage of nitrogen in tubers.

Meanwhile, the mean squares for the irradiation treatments were significant at the 1% probability level for traits including the percentage of dry matter in tubers and the percentage of starch in tubers, while the differences did not reach significance for other traits.

For the interaction between cultivars and irradiation treatments, significance was observed at the 1% probability level for traits such as the percentage of dry matter in tubers, the percentage of starch in tubers, the percentage of carbohydrates in tubers, the percentage of phosphorus in tubers, and the percentage of potassium in tubers. Significance was observed at the 5% probability level for other traits, except for the number of aerial stems, where the differences did not reach the significance threshold.

Table (2): Variance Analysis for the Studied Potato Traits Representing Mean Square Values

S.O.V.	d.f.	Mean Squares				
		Plant hight (cm)	Stems No. (stem. plant^{-1})	Vegetative Dry matter percentage	Total tubers (tuber. plant^{-1})	Mean of total tubers (g. plant^{-1})
Replications	**2**	201.876	0.629	35.720	0.303	2683.006
Cultivars	**4**	913.626 **	2.699 **	17.892 **	34.801 **	949.006 *
Radiation treatments	**3**	3.512	0.981	4.343	1.120	79.638
Cultivars×R. treatments	**12**	51.248 *	0.439	6.169 *	4.518 *	329.155 *
Error	**38**	37.146	0.220	1.694	2.649	122.493

*,** Significant at a probability level of 0.05 and 0.01, respectively.

Continuation of Table (2): Variance Analysis for the Studied Potato Traits Representing Mean Square Values

S.O.V.	d.f.	Mean Squares				
		Total Yield (g. plant^{-1})	Total Tubers Yield (ton. ha^{-1})	Dry matter in Tubers (%)	Starch percentage in Tubers (%)	(TSS)
Replications	2	126090.517	358.864	2.387	0.996	1.456
Cultivars	4	641364.642 **	1823.204 **	1.365 *	1.075 *	1.212 **
Radiation treatments	3	18288.778	52.076	4.789 **	3.778 **	0.027

Cultivars×R. treatments	12	97534.431 *	277.314 *	5.806 **	4.598 **	0.393 *
Error	38	49427.505	362.744	0.325	0.120	0.107

*,** Significant at a probability level of 0.05 and 0.01, respectively.

Continuation of Table (2): Variance Analysis for the Studied Potato Traits Representing Mean Square Values

S.O.V.	d.f.	Mean Squares				
		Tubers Protein percentage (%)	Tubers Carbohydrate percentage (%)	Tubers Nitrogen percentage (%)	Tubers Phosphorus percentage (%)	Tubers Potassium percentage (%)
Replications	2	16.353	0.866	0.418	0.0002	0.351
Cultivars	4	2.366 *	1.206	0.060 *	0.021 **	0.444 **
Radiation treatments	3	0.663	0.521	0.016	0.006	0.012
Cultivars×R. treatments	12	2.977 *	10.363 **	0.076 *	0.013 **	0.372 **
Error	38	0.419	0.325	0.011	0.001	0.019

*,** Significant at a probability level of 0.05 and 0.01, respectively.

This aligns with the findings of Mishra et al. (2017), Rohit et al. (2022), Naiem et al. (2022), Seid et al. (2023), and Singh et al. (2024), which reported significant differences among cultivars in growth and yield traits of potatoes.

The results presented in Table (3) illustrate the values of phenotypic variations and their genetic and environmental components, along with genetic parameters for the studied potato traits. It is evident that the genetic and environmental variance values were significantly different from zero for all studied traits, which is in agreement with the conclusions of Luthra et al. (2018), Hu et al. (2022), Shetty et al. (2023), and Singh et al. (2024), who reported significant genetic and environmental variance for certain potato traits.

The results indicate that genetic variance values exceeded environmental variance values for traits such as plant height, total tuber count per plant, phosphorus percentage in tubers, and potassium percentage in tubers, while they were lower for the remaining traits.

The highest values for genotypic coefficient of variability (GCV) were recorded for total plant yield at 20.409 . Meanwhile, the highest values for phenotypic coefficient of variability (PCV) were observed for aerial stem count (25.152), total tuber count per plant (26.703), total plant yield (28.877), and total tuber yield (37.923). These findings align with the reports of Prajapati *et al.*

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(2020), Zeleke *et al.* (2021), Tessema *et al.* (2022), and Likeng-Li-Ngue *et al.* (2023), which documented variable genotypic and phenotypic variability coefficients across different potato traits.

Table (3): General Mean and Components of Phenotypic Variance (Genetic and Environmental) and Genetic Parameters for the Studied Potato Traits

Genetic Parameters	Traits				
	Plant hight (cm)	Stems No. (stem. Plant^{-1})	Vegetative dry matter percentage	Total Tubers in plant (tuber. Plant^{-1})	Mean of total Tuber weight (g. plant^{-1})
Genetic Variance	73.040 43.972±	0.206 0.130±	1.349 0.862±	2.679 1.676±	68.876 45.821±
Environmental Variance	37.146 14.039±	0.220 0.083±	1.694 0.640±	2.649 1.001±	122.493 46.298±
Phenotypic variance	110.186	0.426	3.043	5.328	191.369
Genetic Coefficient variance	12.852	17.490	4.787	18.935	6.620
Phenotypic Coefficient variance	15.786	25.152	7.190	26.703	11.034
Broad Heritability	0.662	0.484	0.443	0.503	0.359
Expected Genetic improvement	14.315	0.651	1.592	2.392	10. 231
Expected Genetic improvement as (%)	21.528	25.086	6.562	27.672	8.161
General mean	**66.495**	**2.595**	**24.262**	**8.644**	**125.364**

Continuation of Table (3): General Mean and Components of Phenotypic Variance (Genetic and Environmental) and Genetic Parameters for the Studied Potato Traits

Genetic Parameters	**Traits**				
	Total Plant yield (g. plant^{-1})	Total tubers yield (ton. ha^{-1})	Tubers dry matter (%)	Tubers Starch (%)	(TSS)
Genetic Variance	49328.094 30896.920±	121.705 88.45989±	0.086 0.066±	0.079 0.051±	0.092 0.058±
Environmental Variance	49427.505 18681.840±	362.744 137.104±	0.325 0.122±	0.120 0.045±	0.107 0.040±
Phenotypic variance	98755.599	484.449	0.411	0.199	0.199
Genetic Coefficient variance	20.409	19.008	1.953	2.993	7.199
Phenotypic Coefficient variance	28.877	37.923	4.271	4.751	10.588
Broad Heritability	0.499	0.251	0.209	0.397	0.462
Expected Genetic improvement	323.034	11.381	0.276	0.365	0.425

Expected Genetic improvement as (%)	29.684	19.609	1.838	3.887	10.088
General mean	**1088.233**	**58.038**	**15.010**	**9.389**	**4.213**

Continuation of Table (3): General Mean and Components of Phenotypic Variance (Genetic and Environmental) and Genetic Parameters for the Studied Potato Traits

Genetic Parameters	**Traits**				
	Tubers Protein percentage (%)	Tubers Carbohydrate percentage (%)	Tubers Nitrogen percentage (%)	Tubers Phosphorus percentage (%)	Tubers Potassium percentage (%)
Genetic Variance	0.162 0.114±	0.073 0.058±	0.004 0.002±	0.002 0.001±	0.035 0.021±
Environmental Variance	0.419 0.158±	0.325 0.122±	0.011 0.004±	0.001 0.0003±	0.019 0.007±
Phenotypic variance	0.581	0.398	0.015	0.003	0.054
Genetic Coefficient variance	4.378	1.461	4.299	14.907	6.557
Phenotypic Coefficient variance	8.291	3.413	8.325	18.257	8.145
Broad Heritability	0.279	0.183	0.266	0.666	0.648
Expected Genetic improvement	0.438	0.237	0.067	0.075	0.310
Expected Genetic improvement as (%)	4.764	1.282	4.554	25.000	10.865
General mean	**9.193**	**18.484**	**1.471**	**0.300**	**2.853**

The findings indicate that the values of the phenotypic coefficient of variability (PCV) were considerably higher than those of the genotypic coefficient of variability (GCV) for all traits. This reflects the environmental influence—specifically the gamma radiation treatments—on the studied traits at varying levels, as most of these traits are quantitative. Consequently, selection based on external phenotype proves effective for these traits (Mukhtar, 1988).

The broad-sense heritability values ranged between 0.183 for carbohydrate percentage in tubers and 0.666 for phosphorus percentage in tubers. High heritability was observed for plant height (0.662), phosphorus percentage (0.666), and potassium percentage in tubers (0.648). Meanwhile, moderate heritability was noted for the number of aerial stems (0.484), dry matter percentage in vegetative growth (0.443), total number of tubers per plant (0.503), total plant yield (0.499), and soluble solids percentage in tubers (0.462). The remaining traits exhibited low heritability values. Previous studies have reported varying heritability estimates (low, moderate, and high) for different traits, including findings from Asefa et al. (2016), Hunde et al. (2022), Rohit et al. (2022), and Singh et al. (2024). A high heritability percentage in any trait provides breeders with a strong opportunity for direct selection to improve that trait (Allard, 1960).

The results presented in Table (3) indicate that the expected genetic improvement , expressed as a percentage of the mean trait value, ranged from low for:

- Dry matter percentage in vegetative growth (6.562%)

- Average total tuber weight (8.161%)

- Dry matter percentage in tubers (1.838%)

- Starch percentage in tubers (3.887%)

- Protein percentage in tubers (4.764%)

- Carbohydrate percentage in tubers (1.282%)

- Nitrogen percentage in tubers (4.554%)

The expected genetic improvement was moderate for the remaining traits. Researchers such as Singh et al. (2020), Al-Ajili (2021), Zeleke et al. (2021), Seid et al. (2023), and Likeng-Li-Ngue et al. (2023) have similarly reported variations between low, moderate, and high genetic improvement estimates for studied traits.

The correlation between genetic parameters (GCV, PCV, heritability, and expected genetic improvement) reveals that their values were consistent in either increasing or decreasing across most studied traits, reflecting strong relationships among them. Given this strong correlation, it is possible to predict future genetic improvements in selection cycles using phenotypic variability values . In such cases, mass selection can be an effective strategy for improving crop yield (Welsh, 1981).

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