Int.J.Curr.Microbiol.App.Sci (2023) *12*(10): 1-14

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 12 Number 10 (2023)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2023.1210.001

Assessment of Variability Induced by Gamma Rays in M2 Generation Mutants of three Genotypes of Okra (*Abelmoschus esculentus* (L.) Moench) in Burkina Faso

Alphonse Yakoro[1*], Mahamadi H. Ouédraogo[1], Windpouiré V. Tarpaga[2], Kiswendsida R. Nanema[1], Karidiatou Traoré[3] and Mahamadou Sawadogo[1]

[1]Équipe Génétique et Amélioration des Plantes/ Laboratoire Biosciences, École Doctorale Sciences et Technologies, Université Joseph KI-ZERBO, 03 BP 7021, Ouagadougou 03, Burkina Faso
[2]Institut de l'environnement et de Recherches Agricoles (INERA), Centre national de spécialisation en fruits et légumes (CNSL-FL), Farako-Bâ, 01 BP 910, Bobo-Dioulasso, Burkina Faso
[3]Institut de l'environnement et de Recherches Agricoles (INERA), CNRST, Ouagadougou, Burkina Faso

**Corresponding author*

Keywords

Okra, mutants, quantitative traits, M2, yield, *Abelmoschus esculentus* (L.) Moench

Article Info

Received:
19 August 2023
Accepted:
30 September 2023
Available Online:
10 October 2023

A B S T R A C T

In Burkina Faso, M2 mutants and their three Okra (*Abelmoschus esculentus* (L.) Moench) control genotypes seeds irradiated with gamma rays, were grown and care taken in pots. Twenty-six quantitative traits were evaluated and all the M2 genotypes revealed some significant differences compared to the control. No stem branching and multiple fruits at a same node were recorded in M2 and control lines, as previously in M1. However, three interesting lines, L32, L33 and L55, were identified from UAE22, having reduced plant height and higher or same fruits traits than control. In KbG535, one M2 line, L48, showed an increased plant height associated with higher stem diameter, fruit length, weight and number of seeds. One more line, L61, had reduced height without difference from control for yield traits. For KBG24, line L34 showed a reduction of first fruit node height and an increase in fruit weight and seed number per fruit; while line L43 had a high fruit length associated with decrease in first fruit node height. All these lines came from irradiation with doses ranged from 200 to 600Gy, confirming that this interval of doses was more suitable for mutation inducing in okra.

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) is an economically important common vegetable crop cultivated throughout the tropical and warm temperate regions of the world (Surendran and Udayan, 2017). Its fruits and leaves have low amount of calories, are rich in calcium, phosphorus, ascorbic acid and contain proteins, fats, carbohydrates, fibres, iron, b-carotenes, thiamine,

riboflavin, niacin (Tindall, 1983). The World data atlas 2020, states that okra production in the world in 2020 was 10,548,942 tons, from which Burkina Faso contributed with 22,543 tons, being the 11th best producer among African countries.

Okra genetic diversity still worth an improvement, since some consumer needs related to yield and nutritional properties are not satisfied. The nature and extent of genetic variability available within the species form the basis for an effective selection for agro-economic traits under improvement (Amin *et al.*, 2019).

Morphological mutations, having desirable traits, play a key role in plant breeding. The development of new varieties and making of ideotype are the result of modifications of plant parts during morphological mutations (Khursheed *et al.*, 2019).

Induced mutation is highly effective in enhancing natural genetic resources and has been used in developing improved cultivars of cereals, fruits and other crops (Lee *et al.*, 2002).

Among the mutant varieties in the FAO/IAEA 2022 database, 2001 concerned 6 species viz. Rice, Barley, Chrysanthemum, Wheat, Soybean and Maize. No okra mutant was registered yet (MVD iaea.org).

Nevertheless, there are few reports in okra where mutants have been isolated through mutation breeding. The examples of such mutant varieties are Punjab-8, Pusa Swani, and Parbhani Tillu (Ashwini and Rajaram, 2019).

In order to enhance variability and allow selection, experimentations using gamma rays irradiation have been performed on some genotypes in Burkina Faso. The gamma radiation revealed to have significant effect on agromorphological traits of okra M1 generation (Yakoro *et al.*, 2022 and 2023). Since most mutations are recessive in nature and are not expressed in the first generation. M1 generation may show variation in the growth of individual plants due to physiological effects, with the plants showing lethality at various stages of growth and development. (Suprasanna *et al.*, 2015; Kalpande, *et al.*, 2020))

The aim of the present study is to evaluate the effect of gamma ray on inducing M2 interesting mutants which could be selected and used in a breeding program. M2 generations may express heritable traits and allow further selection.

Materials and Methods

Plant material

It was made with the M1 seeds of 3 genotypes (UAE22, KBG535 et KBG24) previously irradiated with gamma radiation in 2020 in Burkina Faso. The list of M1 seeds constituting the M2 generation lines is in table I below. Every line comes from a single M1 plant.

Experimentation in pots

Seeds from every M1 plant of the three genotypes and control were sown in plastic pots containing heat sterilized soil, at the "Plant Protection" facilities in Bobo-Dioulasso. The method of M1 plant to row (Sharma, 2014) was used. Each row consisted of plants in at least 4 plastic pots depending on availability of seeds, and in each pot, at most 5 seeds were sown. Plants were then thinned to no more than 2 plants per pot. Water was provided and grass removed on demand. Phytosanitary treatment and NPK fertilizer were also applied.26 quantitative traits (Table II) were measured and data were collected on three plants per row i.e. per line. The plants in M2 generation were thoroughly screened in order to identify mutations affecting any part of the plant.

Data analysis

Data analysis, i.e. ANOVA and AHC, was performed by genotype, using XLSTAT2016. Differences comparing means of control with each M2 mutant line of the same genotype were evaluated through DUNETT bilateral test at 95%

confidence interval. Dissimilarities between groups were assessed using Euclidian distance and Ward aggregation method. When exploiting matrix of correlation results, traits with high correlation coefficient have been considered redundant when they were a same trait measured at different times. In those cases, only one trait was retained for AHC.

Results and Discussion

According to the present study, it can be stated that in M2 plants, irradiation has induced changes in quantitative agromorphological characters for all three genotypes (Tables III, IV and V).

For UAE22 genotype, among the twenty-six (26) traits evaluated, significant variation was noticed for plant height, height of first fruit node, stem diameter, internode length, peduncle length, first fruit length, fruit diameters, first fruit weight, weight of seeds per fruit, total fruits weight per plant, number of seeds per fruit, number of seeds per plant, weight of seeds per plant, ratio plant height/fruit length.

For KBG535 genotype, the characters which showed significant difference from the control were plant height, height of first fruit node, stem diameter, internode length, first fruit length, fruit diameters, number of internodes, number of ridges per fruit, ratio plant height/fruit length.

For KBG24, height of first fruit node, first fruit weight, number of seeds per fruit, number of ridges per fruit and ratio plant height/fruit length were significantly different from control

Indeed, variation occurred but the number of characters concerned was different from one genotype to another. UAE22 showed the highestradiation induced variation, followed by KBG535 then KBG24. Mainly, in UAE22 some lines made interest by their good characteristics. They are lines with reduced height without reduction of stem vigour, fruit traits and yield characters compared to control or with increase of these characters. As results of this study, we can identify the following mutant lines as significantly interesting: The traits may have been induced by mutation of the associated genes.

For UAE22

Line 32 (400Gy) had a small height, a short peduncle and a small plant height/1st fruit length ratio.

Line 33 (400Gy) had a small height, short peduncle and internode, a small plant height/1st fruit length ratio.

Line 55 (500Gy) showed reduction of peduncle length and plant height.

For KBG535

Line 48 (200Gy): increase of plant height, stem diameter, first fruit length, weight and number of seeds.

Line 61 (500Gy): reduction of plant height, internode length, height of first fruit node and plant height/1st fruit length ratio.

For KBG24

Line 34 (400Gy): decrease in height of first fruit node, and increase in first fruit weight and seed number.

L43 (600Gy): decrease in height of first fruit node and plant height/1st fruit length ratio due to a greatest fruit length.

Furthermore, the Ascendant hierarchical classification (AHC) results showed, for UAE22 lines, 3 groups as mentioned in figure 1. The first group contained the control and 2 lines. Then, one of the other two groups contained the preferred lines 32, 33 and 55.

For KbG535, 7 groups applied. The group with the

control is made by only 2 lines, with L08. Then other lines formed the other 6 groups (Figure 2), with 3 groups containing only one line.

Finally, KbG24 lines were arranged within 4 groups. The control formed one of them with lines 04 and 56associated with lines 35, 42, 43 and 53(Figure 3).

For all the three genotypes lines, the lines previously considered interesting were in groups different from the one of the controls. However, groups were not arranged according to irradiation doses. In the same group, many lines originated from different doses occurred.

Significant reduction of plant quantitative traits was recorded for UAE22 and KBG535 lines while irradiation doses increase starting from 400Gy to 1000Gy. The reduced height of most of the mutants was due to reduction of internode length or number of nodes.

Then, significant increase was observed in lower dose (200Gy) mainly for KBG535 line. This statement is similar to Khursheed (2019) findings in Okra where they identified M2 tall mutants at 100Gy and dwarf mutants at 400Gy.

Jadhav *et al.,* (2013) then Reddy and Dhaduk (2014) reported significant differences between the treatments for all the characters they studied in M2 generation of okra. The lower doses of mutagens i.e. 15 kR and 30kR gamma rays and 0.2 and 0.4 per cent Ethyl methane sulfonate (EMS) increased germination rate, plant height, number of fruits per plant, fruit length, number of seeds per fruit and yield per plant. Significant decrease was recorded for yield per plant at 45 kR and 60 kR gamma rays and 0.8% and 1.00% EMS in M2 generation.

Amin *et al.,* (2019) also reported a wider magnitude of variability induced by mutagenic treatment on black cumin concerning some quantitative traits such as plant height, number of fertile branches per plant, number of capsules per plant, number of seeds per capsules and 1000-seeds weight in M2. In their study, plant height increased with lower concentrations of EMS and gamma rays.

Kharkwal *et al.,* (2004) stated that dwarf and semi-dwarf mutants with reduced plant height belong to the most frequently arising types in mutation experiments. In addition, Yashvir (1975) reported that, in the irradiated okra M2 generation, plant height decreased. Saleem *et al.,* (2014), working on gamma rays induced variations in some cotton genotypes, also reported that, as compared to the control, significant reduction in plant height was observed for all the varieties under the influence of all the gamma rays' doses they've used (10, 15, 20 and 25kR).

The results of this study are similar to those of Rao (1991) on M2 plants, for plant height fruit length, number of seeds per fruit. They got different from the same results with 100 seeds weight which was not significantly different from control in our study. In addition, dwarf lines (25 t0 45cm) that they reported were also recorded in our study for UAE22 lines L32 and L33 (400Gy) and all the 4 lines at 800 and 1000Gy, then KBG535 line L61 (500Gy).

Also, the tall lines with long fruits that they identified were observed for KBG535 line 48-200Gy. In addition, Fayad *et al.,* (2020) reported a decrease in fruit length, number of fruits per plant and fruit yield characters in M2 generation okra plants, under irradiation from 10 to 40kR.

Mohite and Gurav (2019) observed that M2 lines of okra didn't show significant difference from the control at 10, 20, 30 and 40kR for number of nodes, length of internodes, number of fruits per plant, number of seeds /fruits and 100 seeds weight. At 50kR, only the number of seeds / fruits got a significant reduction. Finally, Elangovan and Pavadai (2015) obtained results in their study on okra that demonstrated significant differences between the seed yield parameters such as a number of pods per plant, pod length, weight of seeds per plant, and seed yield per plant.

Table.1 List of the three genotypes M2 lines in relation with the irradiation doses

Doses (Gy)	0	200	400	500	600	800	1000
UAE22	L45	L31 L49 L50	L32 L33 L54	L55 L60	L12 L57	L07 L59	L13 L24
KBG535	L40	L47 L48 L51	L08 L11 L20	L18 L21 L61 L62	L37 L58		
KBG24	L46	L10 L15 L16 L42 L52 L53	L34 L35	L04 L09 L30 L56	L17 L23 L43		

Table.2 Traits studied

N°	Traits	N°	Traits
1	Plant height at 55DAS (PHI)	14	Fruit base diameter at 55DAS (DBI)
2	Plant height at maturity (PHM)	15	Fruit middle diameter at 55DAS (DMI)
3	Stem diameter at 55DAS (SDI)	16	Fruit base diameter at maturity (DBM)
4	Height first fruit node at 55DAS (HNI)	17	Fruit narrow part diameter at maturity (DNM)
5	Height first fruit node at maturity (HNM)	18	Fruit middle diameter at maturity (DMM)
6	Peduncle length at 55DAS (PLI)	19	Weight of first fruit at maturity (WFF)
7	Length of internode at 55DAS (LII)	20	Weight of total fruits per plant (WFP)
8	Length of internode at maturity (LIM)	21	Number of seeds per fruit (NSF)
9	Number of internodes above first fruit (NIA)	22	Number of seeds per plant (NSP)
10	Number of fruits per plant (NFP)	23	Weight of seeds per fruit (WSF)
11	Number of ridges per fruit (NRF)	24	Weight of seeds per plant (WSP)
12	First fruit length at 55DAS (FLI)	25	Weight of hundred seeds (WHS)
13	First fruit length at maturity (FLM)	26	Ratio PHM/FLM

Table.3 Dunnett bilateral genotypes test – Analysis of differences between Control L45 and other lines with 95% confidence interval: UAE22

Lines	PHI	HNI	SDI	LII	PLI	FLI	DBI	DMI	HNM
L45	58,64	29,66	8,99	8,501	3,50	17,50	22,97	22,78	30,02
L31	65,02	35,99	7,64	9,982	2,77	13,66*	20,81	21,72	37,14
L49	60,31	38,66	7,50	7,825	2,67	16,50	21,92	21,81	41,50*
L50	65,73	38,35	9,01	11,013	2,67	15,50	25,27	25,93	41,45*
L32	39,71***	26,02	9,02	6,678	2,50*	17,17	24,82	26,20	26,59
L33	33,06****	21,01	7,37	3,507***	2,17***	15,50	22,37	22,44	22,86
L54	50,03	33,01	7,52	7,838	2,17***	16,67	22,51	22,32	33,70
L55	46,999	30,165	8,37	6,000	2,17***	16,83	21,81	21,91	30,34
L60	48,658	29,812	8,20	6,149	2,82	14,83	20,32	21,10	30,56
L12	60,311	32,322	9,60	9,328	3,00	16,17	22,52	22,18	32,72
L57	50,628	28,982	8,49	6,993	3,00	15,50	22,06	21,59	29,68
L07	49,984	30,991	7,47	5,327	2,33**	12,17***	18,22**	19,19	31,37
L59	36,384****	25,018	7,39	5,345	2,33**	13,83	20,07	20,56	26,89
L13	42,551*	22,524	9,90	6,019	3,00	8,25****	19,78	19,88	29,96
L24	30,345****	20,336*	6,37**	4,169**	2,17***	13,50*	21,91	22,30	19,53*
Pr>F	0,000	0,000	0,002	0,000	0,001	0,000	0,000	0,003	0,000
Sign.	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

Table.3 (continued)

Lines	PHM	LIM	NIA	NFP	WFF	FLM	NSF	WSF	DBM
L45	61,977	8,860	7,643	2,34	5,90	17,66	49,42	3,10	18,46
L31	68,186	10,789	4,976	2,00	**4,19***	**14,49***	36,36	2,12	17,72
L49	62,265	7,350	4,255	2,00	4,66	15,66	36,91	2,32	17,25
L50	68,399	10,579	5,326	2,00	6,20	**14,17***	65,15	3,79	20,43
L32	**41,380******	6,985	4,970	2,00	5,20	16,67	46,26	2,29	19,99
L33	**34,669******	**3,388*****	4,619	2,34	4,55	15,001	52,16	2,47	18,95
L54	51,662	7,845	4,206	2,00	5,32	16,17	45,33	2,83	18,17
L55	**46,308*****	5,628	4,584	2,34	5,28	16,50	44,99	2,78	18,02
L60	49,575	5,989	5,361	2,35	**3,77****	14,70	34,34	2,02	16,19
L12	62,621	9,056	7,818	2,00	**4,26***	15,50	43,32	**1,90***	18,49
L57	57,943	6,492	9,599	2,34	**4,07***	15,16	29,92	1,94	17,31
L07	**47,602****	5,462	4,968	2,34	**2,85******	**12,99****	30,99	**1,66****	**14,01******
L59	**34,701******	6,362	4,207	2,03	**2,55******	**13,67****	31,93	**1,33****	**14,30*****
L13	**42,591*****	6,467	5,504	2,00	**3,58****	**13,00****	**22,44***	**1,15****	16,81
Pr>F	0,000	0,000	0,008	0,831	0,000	0,005	0,000	0,000	0,000
Signt	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes

Table.3 (end)

Lines	DNM	DMM	NRF	WFP	NSP	WSP	WHS	PHM/FLM
L45	16,098	17,737	5,002	9,466	82,988	4,750	6,262	3,521
L31	16,869	17,079	5,334	6,938	36,437	2,132	5,874	**4,707***
L49	15,960	16,658	5,001	6,915	60,700	3,431	6,146	4,007
L50	18,021	19,519	5,001	10,491	109,710	6,159	5,886	**4,843****
L32	17,146	16,929	5,002	6,356	55,020	2,805	4,887	**2,486***
L33	16,632	16,934	5,002	8,090	74,111	3,896	3,932	**2,312***
L54	16,950	17,920	5,002	7,998	68,386	4,121	6,230	3,209
L55	15,800	16,927	5,002	7,780	67,034	3,959	6,169	2,808
L60	14,218	16,724	5,647	7,390	71,113	3,858	6,028	3,425
L12	15,539	16,720	5,001	8,513	85,690	3,786	4,425	4,048
L57	15,807	17,638	5,001	8,105	65,336	3,995	6,545	3,832
L07	**12,395****	**14,566*****	5,669	5,372	60,720	3,047	5,378	3,677
L59	**12,711***	**14,751****	5,002	**3,397****	46,382	**1,739***	4,670	2,582
L13	14,542	17,904	5,002	7,453	68,498	2,952	5,076	3,314
L24	15,216	17,890	5,002	**4,760***	**40,707***	2,138	5,704	**2,011****
Pr> F	0,000	0,000	0,639	0,003	0,001	0,004	0,330	0,000
Significant	Yes	Yes	No	Yes	Yes	Yes	No	Yes

Table.4 Dunnett bilateral genotypes test – Analysis of differences between Control L40 and other lines with 95% confidence interval: KBG535

Lines	PHI	HNI	SDI	LII	PLI	FLI	DBI	DMI	HNM
L40	63,017	32,449	7,876	7,679	2,674	14,327	23,525	24,625	31,615
L47	58,042	26,966	8,668	7,660	3,499	17,033	19,239	20,560	27,046
L48	74,599	23,561	**11,216***	7,253	3,760	13,775	18,457	20,252	24,455
L51	52,386	31,035	7,756	9,328	3,006	10,862	23,292	26,629	31,365
L08	57,501	24,777	9,067	8,686	3,518	13,028	**16,836****	20,390	25,687
L11	**38,324****	**19,350****	7,329	6,331	2,002	**6,662***	22,142	25,179	**19,520****
L20	51,374	**22,976***	9,132	5,157	2,333	13,518	**18,261***	19,055	24,651
L18	50,044	26,662	7,598	4,996	2,668	14,359	**17,436***	20,646	26,345
L21	**45,062***	22,449	8,386	4,832	2,340	14,350	22,079	22,978	24,982
L61	**34,942*****	**19,350***	9,346	**3,169***	2,341	18,166	25,668	24,338	24,617
L62	44,051	**22,976***	**11,877****	3,500	2,259	16,010	26,564	23,648	22,937
L37	60,463	25,843	8,395	6,500	3,601	13,144	**16,689****	19,447	26,194
L58	49,745	**23,693***	8,865	5,993	2,673	14,028	20,372	22,304	23,967
Pr> F	0,000	0,009	0,008	0,002	0,001	0,011	0,000	0,023	0,022
Significant	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

Table.4 (continued)

Lines	PHM	LIM	NIA	NFP	WFF	FLM	NSF	WSF	DBM
L40	60,422	8,513	5,404	2,329	5,055	12,971	49,647	2,807	18,706
L47	59,710	7,656	7,674	2,002	4,550	15,168	70,294	2,952	**14,051***
L48	**86,216***	8,245	**11,710******	2,999	8,045	**18,774***	84,398	3,917	17,033
L51	52,493	8,331	4,927	2,001	5,186	10,789	73,941	3,443	16,732
L08	58,919	8,997	5,410	2,328	3,966	15,515	43,518	2,296	**13,646***
L11	41,357	6,670	6,991	2,000	4,086	8,706	44,934	2,088	18,061
L20	60,044	6,658	8,012	2,002	2,887	13,244	32,025	1,250	**13,768***
L18	52,743	4,992	8,038	2,334	3,134	14,145	31,631	1,660	**13,846***
L21	47,128	**4,657***	6,707	2,666	4,444	14,632	51,924	2,325	16,722
L61	**36,975***	**3,827****	5,041	2,326	6,220	17,162	49,007	2,693	21,672
L62	46,135	**3,741***	6,042	3,499	4,468	15,730	16,355	1,126	20,580
L37	71,485	6,721	**9,270***	2,680	3,182	14,071	28,647	1,279	**13,954***
L58	53,489	6,153	7,729	2,668	4,037	13,620	40,699	2,226	**14,327***
Pr> F	0,000	0,002	0,000	0,336	0,019	0,000	0,001	0,032	0,000
Significant	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes

Table.4 (end)

Lines	DNM	DMM	NRF	WFP	NSP	WSP	WHS	PHM/FLM
L40	17,633	19,269	6,008	9,439	102,642	5,047	5,715	4,743
L47	**11,238****	16,356	**8,368***	10,421	127,086	5,666	4,0	3,946
L48	**12,541***	18,556	7,535	**17,381**	203,916	8,340	4,689	4,618
L51	17,874	19,099	7,019	7,966	117,907	4,998	4,642	4,859
L08	**11,176***	15,850	5,652	8,723	104,994	4,974	5,300	3,838
L11	18,112	20,330	5,998	5,405	55,721	2,548	4,710	4,763
L20	**13,008***	**15,092***	5,320	8,309	93,334	3,490	3,530	4,535
L18	**10,099*****	**15,221***	7,015	7,332	74,554	4,099	5,316	3,738
L21	15,229	15,881	4,993	8,975	102,469	4,419	4,378	**3,198***
L61	18,124	17,729	4,998	11,536	92,603	4,902	5,498	**2,139*****
L62	16,240	17,637	4,997	**18,210**	99,895	6,630	6,610	**2,921***
L37	**11,456****	15,711	6,660	7,477	57,407	2,667	4,506	5,108
L58	**12,074****	16,559	5,670	8,279	91,799	4,540	5,417	4,018
Pr> F	0,000	0,004	0,000	0,052	0,047	0,357	0,275	0,000
Significant	Yes	Yes	Yes	No	Yes	No	No	Yes

Table.5 Dunnett bilateral genotypes test – Analysis of differences between Control L46 and other lines with 95% confidence interval: KBG24

Lines	PHI	HNI	SDI	LII	PLI	FLI	DBI	DMI	HNM
L46	58,320	36,717	8,292	6,315	2,344	13,975	20,868	22,199	35,362
L10	70,467	31,636	10,455	6,147	2,344	15,659	22,947	24,370	32,017
L15	56,981	**25,280***	8,463	7,164	2,679	15,172	18,295	18,703	26,341
L16	56,997	31,322	8,542	8,471	1,996	11,809	17,101	17,810	33,983
L42	47,550	**24,954****	7,800	4,467	1,498	13,661	20,525	22,385	25,673
L52	48,904	27,635	7,521	5,987	1,666	13,318	21,662	20,837	29,335
L53	52,951	26,280*	8,206	5,309	1,329	14,326	20,836	22,033	27,331
L34	54,955	**23,959****	8,638	6,491	2,258	10,963	20,208	19,872	24,032
L35	47,218	**26,984***	6,898	6,998	1,497	11,639	19,703	19,946	27,678
L04	57,325	30,307	8,363	5,813	2,173	14,997	18,866	20,223	30,667
L09	48,239	30,020	7,801	4,982	1,494	10,959	22,092	21,707	32,343
L30	69,101	31,642	10,141	5,979	1,670	13,123	19,987	19,841	33,692
L56	68,793	30,661	10,488	8,851	2,510	16,517	20,169	21,063	32,668
L17	52,113	27,560	8,322	4,956	2,446	11,878	15,932	17,127	28,878
L23	47,885	**22,255*****	8,965	5,821	1,497	9,947	20,654	19,060	**22,672****
L43	45,894	**23,405****	10,043	5,735	2,761	15,505	25,342	24,141	**23,497***
Pr> F	0,001	0,007	0,029	0,092	0,001	0,165	0,012	0,048	0,015
Significant	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes

Table.5 (continued)

Lines	PHM	LIM	NIA	NFP	WFF	FLM	NSF	WSF	DBM
L46	58,938	6,159	5,330	2,001	4,173	12,829	45,657	2,517	16,480
L10	64,367	6,326	6,373	3,003	4,673	14,150	51,410	2,582	15,696
L15	58,981	7,523	6,369	2,334	3,815	15,998	38,666	2,106	15,721
L16	60,643	8,404	5,602	2,007	3,680	15,926	43,234	2,060	14,445
L42	47,841	4,966	5,667	2,334	3,777	13,496	45,123	2,176	16,478
L52	51,175	6,162	4,967	2,001	3,396	13,099	36,079	1,776	15,567
L53	51,493	4,826	6,023	2,001	4,221	13,663	43,134	2,287	17,262
L34	56,236	7,005	7,065	1,996	**7,585***	15,751	**76,588***	4,523	21,590
L35	47,592	5,988	5,314	1,999	4,424	13,826	49,524	2,606	16,490
L04	57,679	6,338	5,675	2,004	2,915	15,168	40,386	1,725	13,227
L09	54,430	6,673	5,306	2,331	3,181	10,344	31,186	1,625	18,208
L30	67,157	6,662	6,724	3,002	3,880	13,486	45,797	2,205	17,971
L56	70,373	9,061	6,368	2,335	4,370	16,165	37,720	2,383	16,296
L17	53,374	5,445	7,757	2,320	2,698	13,392	**16,598***	0,826	12,999
L23	53,790	6,264	6,859	2,665	2,474	10,829	28,341	0,976	17,199
L43	48,572	5,733	6,010	2,500	5,177	17,989	36,353	2,092	20,670
Pr> F	0,009	0,151	0,267	0,440	0,023	0,016	0,001	0,004	0,007
Significant	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes

Table.5 (end)

Lines	DNM	DMM	NRF	WFP	NSP	WSP	WHS	PHM/FLM
L46	13,928	15,940	4,995	7,720	86,431	4,622	5,604	4,706
L10	14,301	15,683	4,997	10,711	123,850	5,397	4,971	4,579
L15	11,844	14,497	4,996	7,078	74,678	3,939	5,470	3,688
L16	11,510	13,764	4,996	5,654	65,351	3,045	4,708	**2,689***
L42	13,044	15,898	**6,345***	6,566	83,902	3,615	4,800	3,556
L52	14,367	15,324	4,996	6,134	71,902	3,171	4,922	3,910
L53	13,993	15,180	6,008	6,991	77,342	3,656	5,158	3,828
L34	18,275	19,034	4,995	13,683	143,496	7,688	5,901	3,536
L35	14,144	15,607	5,333	6,460	81,569	3,640	5,327	3,414
L04	11,677	14,085	5,671	5,749	84,289	3,410	4,381	3,841
L09	15,356	15,434	4,996	8,315	66,444	3,436	5,143	5,269
L30	15,241	16,028	5,037	10,890	127,435	5,228	4,752	5,136
L56	13,776	15,244	4,996	9,835	90,041	5,428	6,291	4,378
L17	11,124	13,457	5,046	6,044	59,609	2,843	4,759	4,009
L23	14,445	15,575	4,997	6,982	69,838	3,103	3,437	4,945
L43	17,679	17,678	4,997	11,997	96,707	4,501	4,967	**2,667***
Pr> F	0,006	0,015	0,010	0,066	0,016	0,098	0,224	0,005
Significant	Yes	Yes	Yes	No	Yes	No	No	Yes

** Significant, ** highly significant, *** very highly significant, ****...*

Fig.1 Dendrogram of UAE 22 genotype lines

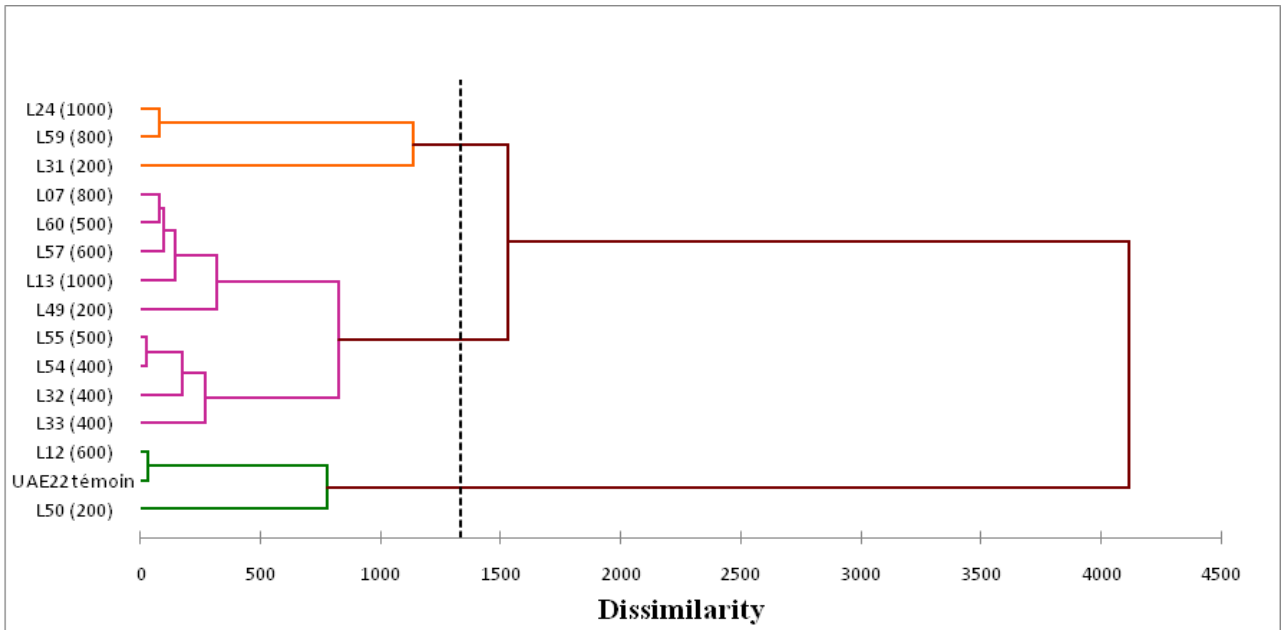


Fig.2 Dendrogram of KbG 535 genotype lines

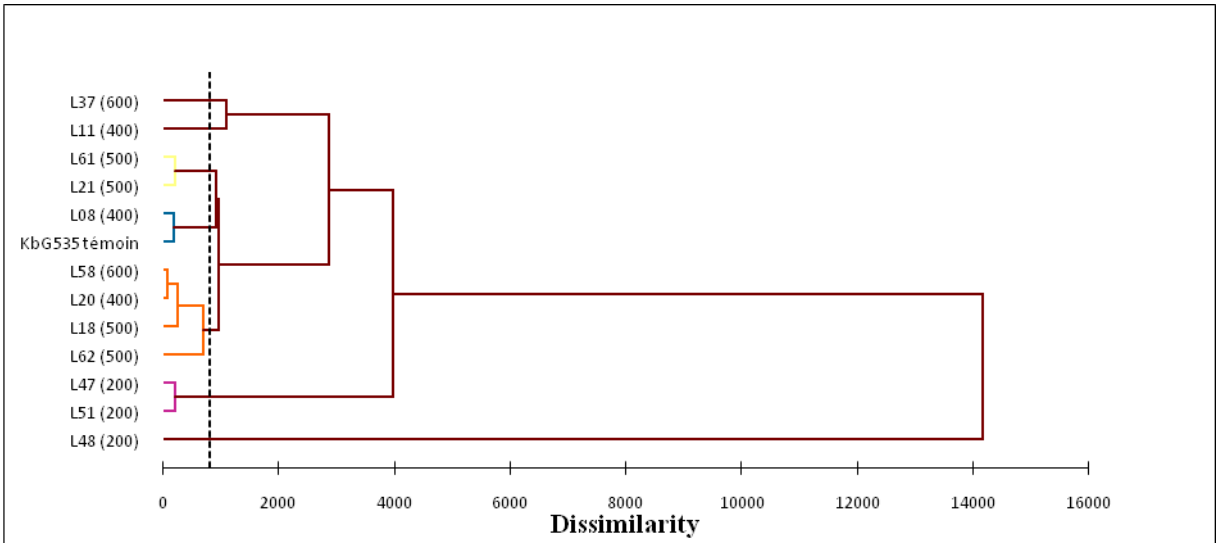
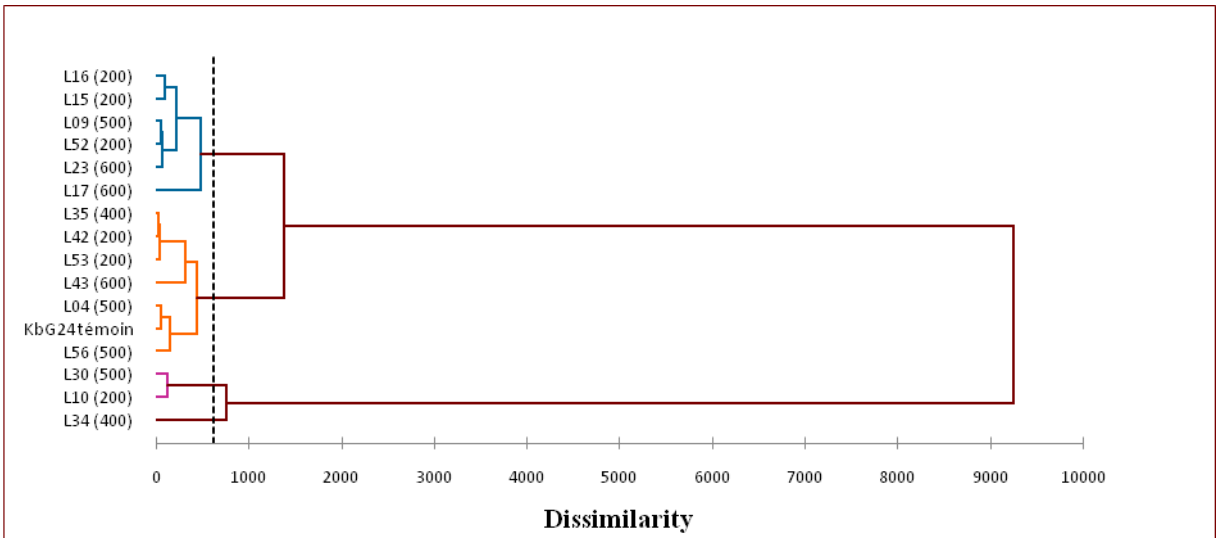


Fig.3 Dendrogram of KbG24 genotype lines



Stem branching observed in M1 plants didn't appear in M2 lines. One can state that this trait is morphological change due to radiation without heritable pattern or is a result of polygenic interaction.

The importance of identification of our seven (07) mutant lines on the basis of their traits comes as follow. Small plant height prevents from lodging. As stated by Jency *et al.*, (2020), lodging is usually referred to as a condition in which the stem of a crop bends at or near the surface of the ground, which could lead to the collapse of the canopy. Sruba and Amitava (2017) stated that, to start a breeding program of any crop wind should be taken into consideration due to possibility of lodging. Generally, tall plants bearing high capsules are prone to lodging, whereas, dwarf plants are more suitable in these conditions. When small height is associated with no difference of yield traits from the control, the small plants should be preferred because they resist to some abiotic factors, consume less

nutrients and produce good yield. This justifies the preference for small plant height/first fruit length ratio. According to Aamir *et al.*, (2019), the prime objective of any mutation breeding programme(s) is to develop varieties that would be high yielding coupled with short stature, early maturing and disease resistant.

Also, small peduncle strengthens the fixation of fruit at the node and prevent it from falling or anatomic damaging. At the reverse side, plant height increase needs to be associated with increased stem diameter and fruit traits in order to be selected compared to control. Also, small height of first fruit node may mean precocity and opportunity to produce more fruits since the fruits are harvested fresh.

Bhatia and Swanminathan (1962) in Yashvir (1975), in their work on bread wheat, emphasized that if in a particular character, no selection in the past had been exercised, the mean value would go down as a result of mutagenic treatment.

This can explain the mean significant reduction of some of the traits studied in this work, particularly for UAE22. Nevertheless, the opposite effect was recorded in KBG535 lines with some increase in means.

Irradiation effects varied according to the doses and also according to genotypes. Further, within the same dose, irradiation produced mutants with various patterns. Similarly, Gupta *et al.*, (2018), while working on mutagenesis on okra, stated that at M2 generation, all the mutagenic treatments were not equally effective in generating variability.

In conclusion, M2 mutant lines from three okra genotypes previously irradiated with gamma rays showed a significant variation for all the 26 quantitative traits assessed. The variability created was higher in UAE22 lines, then in KBG535 lines and finally KBG24 lines. No stem branching was reproduced in M2 lines like in M1. Interesting lines were identified with suitable traits for climatic adaptation and yield attributing traits.

Since mutations have a high probability not to appear in M1 generation, mainly due to their recessive nature, the mutant's patterns identified are produced by mutations of genes.

The few M2 interesting mutants reported show that mutation breeding on Okra is possible in Burkina Faso. The range of gamma rays' doses which produced these mutants should be used to produce more M1 plants in order to allow wider expression of genes. Thus, in M2 some more mutants can be selected due to the aleatory nature of mutation occurrence.

Also, M3 generations need to be grown in field conditions in order to assess the plants heritable traits and ability to express their genotypes in normal growing conditions.

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How to cite this article:

Alphonse Yakoro, Mahamadi H. Ouédraogo, Windpouiré V. Tarpaga, Kiswendsida R. Nanema, Karidiatou Traoré and Mahamadou Sawadogo. 2023. Assessment of Variability Induced by Gamma Rays in M2 Generation Mutants of three Genotypes of Okra (*Abelmoschus esculentus* (L.) Moench) in Burkina Faso. *Int.J.Curr.Microbiol.App.Sci.* 12(10): 1-14. **doi:** https://doi.org/10.20546/ijcmas.2023.1210.001