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Studies on gamma radio-sensitivity and identification of seed-borne pathogens in beans

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Abstract

A study investigated radio-sensitivity (LD50) and seed-borne pathogens in five Tanzanian common bean varieties (UYOLE 16, SELIAN 13, TARIBEAN 6, JESCA, and CALIMA UYOLE) and two Pakistani mung bean genotypes (MH20106 and AVMV8601). Seeds were irradiated at doses of 0, 100, 150, 200, 250, and 300 Gy and planted in a wire house under a Completely Randomized Design at the Nuclear Institute for Agriculture and Biology (NIAB) in Faisalabad, Pakistan. The LD50 values for common bean varieties were 219 Gy (UYOLE 16), 192 Gy (SELIAN 13), 190 Gy (TARIBEAN 6), 196 Gy (JESCA), and 154 Gy (CALIMA UYOLE). For mung bean, LD50 was 223 Gy (MH20106) and 218 Gy (AVMV8601). Overall, LD50 values ranged from 150 to 250 Gy for both types. Additionally, fungal pathogen isolation revealed that TARIBEAN 6 was infected with Rhizoctonia solani, while the mung bean showed infection from Macrophomina phaseolina. Pathogenicity tests confirmed susceptibility in common bean varieties TARIBEAN 6, JESCA, and CALIMA UYOLE. These findings underscore the importance of using fungicides on seeds and selecting tolerant varieties for improved cultivation outcomes.

Keywords: Common bean, LD50 dose, Mung bean, Gamma radiation, Germination, Seed-borne fungi.

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Contents

Contribution of this paper to the literature
This study contributes to the existing literature on bean mutation breeding. The paper's primary finding is that LD50 values ranged between 150 to 250 Gy. Seeds were susceptible to fungal infections. The study documents the obtained LD50 as a benchmark for bean mutation breeding and the need for seed pre-treatment.

1. Introduction

Common bean (*Phaseolus vulgaris* L.) and mung bean (*Vigna radiata* (L.) R. Wilczek) are a group of legume crops that are an essential source of protein, dietary fiber, and other nutrients in many parts of the world [1]. Common beans are largely grown in Latin America, Asia, and Africa. In Africa, common beans are the second staple food after cereals [2]. Its production in Sub-Saharan Africa is mostly carried out by small-scale farmers for food and as a cash crop [3]. In Tanzania, common beans are mainly cultivated in the Southern Highland Zone, Lake Zone, and Northern Zone, and are mostly intercropped with maize or with permanent crops such as banana or coffee [4, 5]. Typically, production is carried out by small-scale farmers with farming areas of less than 2 hectares, who account for approximately 80% of the total pulses produced in Tanzania [6]. Mung bean is largely produced and consumed in Southeast Asia and South Asian countries [7]. In Pakistan, it is a major summer legume produced in Punjab Province, contributing about 88% of the country's area. About 60% of the produce is utilized by the human population, with an average consumption of 4.18 kg per person annually [8]. Apart from having high nutritional content, it is also available at a low cost for most people in developing countries compared to animal proteins, which are not affordable. Beans also play an important role in improving soil and environmental health through symbiotic nitrogen fixation [9, 10].

In Pakistan and Tanzania, as in other developing countries, the production of common beans and mung beans is hindered by several biotic and abiotic factors [11]. Biotic factors contributing to significant yield loss include diseases caused by various agents such as fungi (*Rhizoctonia* and *Macrophomina* spp.), viruses (yellow mosaic virus), bacteria, nematodes, and insect pests (aphids and pod borers) [12]. Recently, more than 200 diseases that are causing significant losses in bean yield have been reported [10]. Abiotic factors also contribute to poor production of beans; these include salinity, drought, and temperature extremes. These factors (soil and climatic change) hinder farmers' willingness to invest or cultivate large areas [9, 13]. In Tanzania, prolonged drought periods have rigorously impacted the yield of common beans, while in Pakistan, issues such as salinity and extreme heat affect mung bean production. These biotic and abiotic factors compel the development of more resilient varieties that can withstand climate change conditions, diseases, and pests in both countries. Advanced studies in genetic diversity are important for plant breeders because they provide an opportunity to develop new varieties with desirable characteristics for improving crop production and food security.

Over the years, breeding programs for common beans and mung beans have been ongoing, aiming to improve yield, disease and pest resistance, drought tolerance, and adaptation to different soil types [12, 14]. Conventional breeding techniques, such as mass selection, pure line selection, and hybridization, have been employed to enhance crop performance [15]. In Tanzania, breeding efforts have focused on drought-resistant and disease-tolerant varieties [16], while in Pakistan, there has been progress in developing mung bean varieties that are more tolerant to heat and salinity through mutation breeding, where mutations are artificially induced through physical or chemical agents, and have been successfully employed to create genetic diversity that can be harnessed to develop improved varieties [17]. Marker-assisted selection has also been utilized to accelerate the breeding process by identifying specific genes linked to desirable traits [18]. Additionally, mutation breeding has led to the development of higher-yielding and stress-tolerant crops, especially in regions where genetic diversity in the natural gene pool is limited [19]. Despite these efforts, advanced breeding techniques, such as genome editing (e.g., CRISPR-Cas9), can further enhance the introduction of novel traits, improving the efficiency of breeding programs [18]. Coupling mutation breeding with these advanced techniques could significantly boost the productivity of common beans and mung beans in Pakistan and Tanzania.

A mutation is a heritable change in genetic makeup, resulting in new traits that are passed on from parent to offspring. It can be caused by errors in the replication of deoxyribonucleic acid (DNA), naturally, or it can be induced by gamma rays or other physical and chemical mutagens [20]. Mutations induced by gamma rays can affect plant growth by changing the genetic, biochemical, physiological, and morphological features of the cells [18]. The isotopes cobalt-60 (60Co) and caesium-137 (137Cs) are the main sources of gamma rays usually used. Caesium-137 is used mostly due to its longer half-life of 30.17 years compared to cobalt-60, which is 5.26 years [20]. In this study, mutation was induced through caesium-137 (137Cs) gamma radiation, which has been employed for plant breeding programs in Pakistan and has contributed to the release of various new varieties of mung beans, wheat, chickpeas, and other crops. The radiation level achievement is determined by the dosage concentration since plant material and genotypes have sensitivity to radiation (radio-sensitivity) [21]. Radiation energy absorbed by an object is measured in Gray (Gy) units. To determine the appropriate dosage, a radio-sensitivity study must be conducted, depending on the type of varieties or species, environmental conditions, and genetic factors such as chromosome number before and after gamma radiation treatment. After species or variety radiation induction, the sensitivity of the seedling is estimated by calculating the lethal dose (LD) value, which is the dose that causes 50% mortality of irradiated plants. LD50 is considered the optimal dose that can induce the greatest mutant genetic diversity [22]. Additionally, regression in the growth parameters of seedlings obtained from treated seeds is usually an indicator of genetic damage to the plant. Therefore, the appropriate dose determination can be achieved by comparing first-generation seedlings (M1) and untreated seedlings in terms of plant growth parameters and survival percentages. The data obtained from these comparisons are then used to determine the LD50 dose [23]. The objective of this joint study is to evaluate the radio-sensitivity of common beans and mung beans to determine the optimal radiation doses for inducing favorable mutations and to study different seed pathogens and their pathogenicity effects on seed germination. This study aims to enhance the effectiveness of mutation breeding and contribute to the development of more resilient bean varieties, supporting agricultural sustainability and food security in both countries.

2. Materials and Methods

2.1. Irradiation of the Seeds

Pure seeds of five Tanzania market-class common bean varieties (UYOLE 16, SELIAN 13, TARIBEAN 6, JESCA, and CALIMA UYOLE) and two mung bean genotypes from Pakistan (AVMV 8601 and MH 20106) were irradiated at six different doses of gamma radiation (0, 100, 150, 200, 250, and 300 Gy) using Caesium-137 (Cs137). Sixty seeds for each dose in each common bean variety and 10 g of seeds of the mung bean for each dose were irradiated. The treatments were then used for further experiments.

2.2. Germination Experiment

The germination experiment was conducted in a wire house of the Plant Breeding and Genetic Division at the Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan. For this purpose, two irradiated common bean seeds were sown in each glass measuring 9.5cm in height, 8.0cm in width, and containing 400g of pure and clean sand. Each dose had ten glasses with three replications. Plants were irrigated every two days to ensure adequate moisture levels in the glasses. At fourteen days after sowing, data on germination were collected, and the germination percentage was calculated using the formula.

$$Germination\ \% = \frac{Number\ of\ germianted\ seeds}{Total\ number\ of\ seeds} \times 100 \quad (1)$$

Then, plants were uprooted, and data on growth parameters, including seedling length (cm), fresh and dry seedling weight (g), shoot length (cm), and root length (cm), were recorded. The root-shoot ratio was determined by dividing the root length by the shoot length. The Vigour index was calculated using the formula explained by.

$$Vigor\ index = Germination\ percentage\ \times (mean\ shoot\ length + mean\ root\ length) \quad 2$$

The data were entered into an Excel sheet and managed for analysis.

2.3. Pathological Studies

2.3.1. Isolation of Fungus from Bean Seeds

All pathological studies were performed in the laboratory of the Plant Pathology Group, Plant Protection Division, NIAB Faisalabad, Pakistan. Under this study, 15 seeds from each variety of common bean and mung bean were surface sterilized using 5% NaOCl for 5 minutes [11]. These seeds were then washed three times in sterilized distilled water to remove the detergent. The rinsed seeds were then blot-dried for 30 minutes under a laminar airflow, and five seeds were placed in Petri dishes containing Potato Dextrose Agar (PDA) medium, followed by incubation at 25°C. After 5 days, growing fungal hyphal tips were transferred onto new PDA plates for preservation and future work. Morphological identification of isolated fungal pathogens was performed under a compound microscope with the help of published literature of Alsohaili and Bani-Hasan [24] and Thilagam et al. [25].

2.3.2. Molecular Characterization of Fungus

To verify the identity of isolated pathogenic fungal pathogens following molecular characterization, a modified CTAB-based DNA extraction method was used to obtain whole genomic DNA from a seven-day-old culture of each test fungus isolated from common bean and mung bean seeds [26]. Using primer pairs ITS-1/4, the internal transcribed spacer (rDNA-ITS) region was amplified, and the bands were characterized.

2.3.3. Pathogenicity Test of the Isolated Fungus

The agar plate method was employed to confirm the pathogenicity of seed-borne fungi isolated from common bean and mung bean varieties [11]. For this study, fifteen surface-sterilized seeds of each common bean variety were incubated on seven-day-old fungi cultured from each species. There were three replicates (5 seeds per replicate) for each variety and test fungus. A negative control, with the same number of seeds per variety, incubated on water agar plates, was also included (Figure 1). Data was recorded following the rating system given in Table 1 as described by Sajjad et al. [11]. Seed germination was recorded after five and fifteen days following inoculation. Final data, including seedling length, mortality percentage, etc., were collected after 15 days to assess disease response.

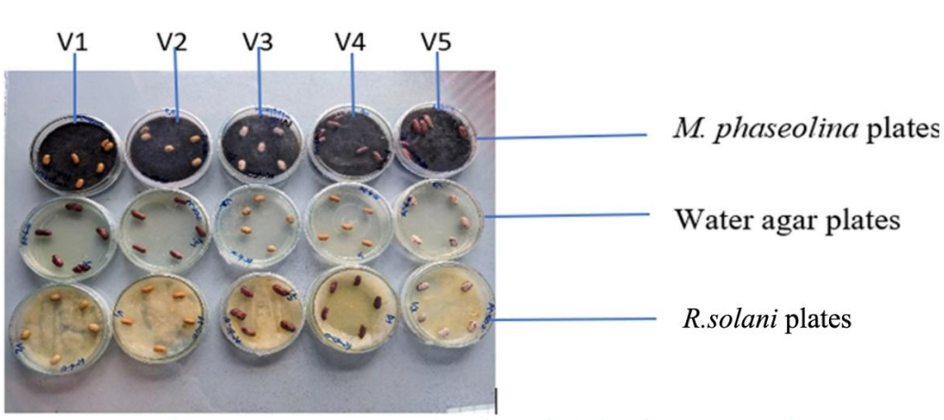

Figure 1. A pathogenicity test experiment of *R. solani* and *M. phaseolina* on common bean varieties.

The disease rating scale for the tested common bean and mung bean genotypes is indicated in Table 1.

Table 1. Disease severity rating scale used to assess the pathogenicity of fungi *R. solani* and *M. phaseolina* seeds under laboratory conditions.

Disease rating	Root/Shoot necrosis %	Disease severity index	Disease response
0	No lesions (Healthy hypocotyl and or radicle)	0	Highly resistant
1	Small, light brown lesions affecting 1-25% of the hypocotyl and/or radical.	0.1-1.4	Resistant
2	Brown lesions affecting 26-50% of the hypocotyl or radical	1.5- 2.4	Moderately resistant
3	Brown lesions affecting 51-75% of the hypocotyl or radical	2.5-3.4	Moderately susceptible
4	Brown lesions affecting 75-100 of the hypocotyls or radicals, followed by complete necrosis or wilting	3.5-4.5	Susceptible
5	Seeds are completely covered by fungus, followed by no germination.	4.5-5.0	Highly susceptible

2.4. Data Analysis

Collected data on germination percentage was used to calculate the percentage mortality (MP) and then corrected percentage mortality (CMP); these values were subjected to probit analysis using OPSTAT software. Then, R software was used to perform regression analysis between the doses against CMP. Two-way analysis of variance (ANOVA) was performed in R software to assess the variability of germination among varieties, and means were separated using the Honestly Significant Difference (HSD) test at P=0.05. The disease rating for the five seeds was averaged, and the value obtained was used to indicate the disease severity index.

3. Results

3.1. Optimal LD_{50}

The results indicated that for common beans, the optimal LD_{50} was 219Gy, 192Gy, 190Gy, 196Gy, and 154Gy, respectively, for UYOLE 16, SELIAN 13, TARIBEAN 6, JESCA, and CALIMA UYOLE. For mung beans, the optimal LD_{50}> values were 223Gy and 182Gy for the AVMV 8601 and MH20106 varieties, respectively. It was observed that the LD_{50} values for both common beans and mung beans ranged between 150Gy and 250Gy (Table 2).

Table 2. LD_{50} values for five common bean varieties and mung bean genotypes.

Variety	LD_{50}(Gy)
Common bean varieties	
UYOLE16	219
SELIAN 13	192
TARI 6	190
JESCA	196
CALIMA UYOLE	154
Mung bean genotypes	
AVMV 8601	223
MH20106	182

3.1.1. Analysis of Variance for Common Bean Varieties

The results indicated that there was a significant difference in germination among different radiation doses of various varieties, and their interaction was also significantly different at $p<0.05$ (Table 3).

Table 3. ANOVA for corrected mortality control (CMP) for common bean varieties.

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Varieties	4748.889	4	1187.222	14.308	0.000	2.525
Doses	96349.87	5	19269.97	232.231	0.000	2.368
Interaction	5650.578	20	282.529	3.405	0.000	1.748
Within	4978.667	60	82.978			
Total	111728	89				

3.1.2. Analysis of Variance for Mung Bean Genotypes

The results indicate that there was a significant difference in germination between the two varieties; similarly, the effect of doses was significantly different, while the interaction of radiation doses and varieties was not significantly different at $p\leq0.05$ (Table 4).

Table 4. ANOVA for Corrected Mortality control (CMP) for common bean varieties.

Source of variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Varieties	571.248	1	571.248	6.666	0.016364	4.260
Doses	19234.05	5	3846.811	44.886	0.000	2.621
Interaction	225.5288	5	45.106	0.526	0.754	2.621
Within	2056.824	24	85.701			
Total	22087.65	35				

3.1.3. Effect of Radiation Doses on Germination Percentage

It was recorded that for UYOLE 16, there was a significant difference in germination percentage between 0 and 100 Gy and also between 150 and 200 Gy. For SELIAN 13, there was no significant difference in seed germination at 0, 100, and 150 Gy radiation doses. For TARI6, a non-significant difference in germination was recorded between 0 and 100 Gy, while the rest of the doses were significantly different. For JESCA, there was no significant difference in germination at 0 and 100 Gy, but also between 150 and 200 Gy. For variety 5, all six doses were significantly different from one another at $p\leq0.05$ (Table 5).

For mung bean, AVMV8601, a significant difference in seed germination was recorded among all six radiation doses, while for MH20106, no significant difference was observed between 200 and 250 radiation doses, whereas other doses showed significant differences at p≤0.005 (Table 5).

Table 5. Effect of radiation doses on germination percentage.

Doses (Gy)	Common bean varieties					Mung bean genotypes	
	UYOLE 16	SELIAN 13	TARI 6	JESCA	CALIMA UYOLE	AVMV8601	MH20106
0	100^{a}	100^{a}	100^{a}	100^{a}	100^{a}	100^{a}	100^{a}
100	100^{a}	93.3^{a}	100^{a}	90^{a}	60^{b}	81^{ab}	73.5^{b}
150	83.3^{ab}	82.3^{a}	66.7^{b}	66.7^{b}	50^{bc}	73.2^{abc}	60.3^{bc}
200	70^{ab}	51.0^{b}	46.7^{c}	53.3^{b}	$33.^{bc}$	57.4^{bcd}	48.2^{c}
250	53.3^{b}	23.3^{c}	30^{d}	30^{c}	30^{cd}	45.8^{cd}	42.3^{c}
300	6.7^{c}	6.7^{c}	0^{e}	0^{d}	0^{d}	36.1^{d}	21.7^{d}

Note: *Means followed by the same letters in a column indicate no significant differences in germination percentage among the doses

3.2. Fungal Isolation from Common Bean Seeds

The results regarding the isolation of fungal pathogens showed that the common bean variety TARIBEAN 6 was found to be infected by *Rhizoctonia solani*, while mung bean varieties were infected with *Macrophomina phaseolina*. However, seeds of the remaining four common bean varieties (UYOLE 16, SELIAN 13, CALIMA UYOLE, and JESCA) were found to be infected by the aflatoxin-producing fungus *Aspergillus flavus*. The fungal pathogens *Rhizoctonia solani* and *Macrophomina phaseolina* are emerging as common threats to bean cultivation worldwide.

3.3. Molecular Characterization of Isolated R. Solani and M. Phaseolina

The DNA isolated from fungal cultures was PCR amplified using universal fungal ITS primers (ITS1/ITS4). The results indicated that *R. solani* was found between 350 and 420 bp, while *M. phaseolina* isolates were found between 405 and 420 bp (Figure 2).

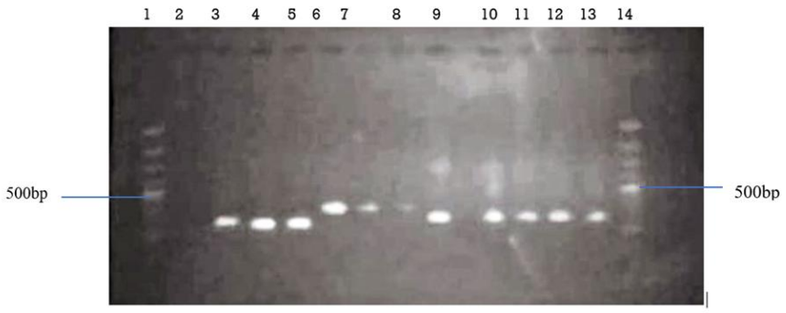

Figure 2. Bands for molecular identification of *R.solani* and *M.phaseolina.*

Note: 1=1Kbp ladder, 2=Negative control, 5=*Rhizoctonia solani* 6=*Rhizoctonia solani* 7=*Rhizoctonia solani*, 8=*Macrophomina phaseolina* 10=*Macrophomina phaseolina*

3.4. Pathogenicity Test

Pathogenicity tests were performed on five common bean genotypes (TARI 6, UYOLE 16, SELIAN 13, CALIMA UYOLE, and JESCA) using fungi *R. solani* and *M. phaseolina.*

For the *M. phaseolina* test, the *result* indicated that CALIMA UYOLE and SELIAN 13 were highly susceptible to infection, TARIBEAN 6 was susceptible, and UYOLE 16 and JESCA were moderately susceptible to infection by the fungus. UYOLE 16 and SELIAN 13 recorded 100% germination, JESCA and TARI 6 recorded 80% germination, and there was no germination in CALIMA UYOLE. There was no significant difference in seedling length between UYOLE 16, TARI 6, and JESCA; however, an important difference was recorded among those varieties and CALIMA UYOLE and SELIAN 13 (Table 6). On the susceptibility to *R. solani*, the study revealed that Tari 6 was susceptible, while UYOLE 16, SELIAN 13, and JESCA were moderately resistant, and CALIMA UYOLE was highly resistant to the infection. All five varieties except SELIAN 13 (60%) recorded 100%. No significant difference in seedling length was recorded between UYOLE 16 and SELIAN 13 (6.3 and 6.32), respectively, while the contrary was observed between JESCA, CALIMA UYOLE, and TARIBEAN 6 (6.68, 4.56, and 3.58), respectively. Generally, a higher percentage of seed germination and greater seedling length were recorded in control plates when compared to *M. phaseolina* and *R. solani*-containing plates (Table 6) (Figure 3).

Table 6. The analysis of the pathogenicity of *M. phaseolina* and *R. solani* on five common bean test varieties.

Fungus	Variety	Germination %	Seedling length (cm)	Disease severity index	Disease response
M. phaseolina	UYOLE 16	100	4.16^{a}	3.2	Moderately susceptible
	SELIAN 13	100	0^{b}	4.8	Highly susceptible
	TARI 6	80	4^{a}	4.2	Susceptible
	JESCA	80	5.5^{a}	3.2	Moderately susceptible
	CALIMA UYOLE	0	0^{b}	5	Highly susceptible
	UYOLE 16	100	6.38^{ab}	2	Moderately tolerant
	SELIAN 13	60	6.32^{ab}	2	Moderately tolerant

Fungus	Variety	Germination %	Seedling length (cm)	Disease severity index	Disease response
R.solani	TARI 6	100	3.58[c]	3.8	Susceptible
	JESCA	100	6.68[a]	2	Moderately resistant
	CALIMA UYOLE	100	4.56[bc]	1	Resistant
Control	UYOLE 16	100	5.06[a]	0	Highly resistant
	SELIAN 13	100	4.9[a]	0.8	Resistant
	TARI 6	100	4.83[a]	1	Resistant
	JESCA	100	4.48[a]	1.4	Resistant
	CALIMA UYOLE	80	4.45[a]	4.2	Susceptible

Note: *Means followed by the same letters in a column indicate no significant differences in germination percentage among the doses

Figure 3. Pathogenicity results for *R. solani* and *M. phaseolina* on common bean seeds.

4. Discussion

4.1. Optimal (LD_{50})

The LD_{50} indicates the required amount of dose to kill half of a tested plant population. The determination of the optimal LD_{50} is considered a prerequisite in mutation breeding, as a standard dose is associated with higher chances of successful mutation. The germination percentage is a crucial factor for determining the viability of an irradiation study, as it determines the extent of radiation-mediated lethal effects.

The present study evaluated the optimal LD_{50} for five Tanzanian common bean varieties (UYOLE 16, SELIAN 13, TARI 6, JESCA, and CALIMA UYOLE) and two mung bean genotypes from Pakistan (MH 20106 and AVMV 8601). The results indicated a significant difference in different doses (treatments), varieties, and interaction effects in common beans. For mung bean, there were substantial differences among doses and varieties, but their interaction effect was insignificant. However, the LD_{50} crops ranged between 150Gy and 250Gy, indicating that any dose in that range may cause significant genetic change in the crops. This finding is consistent with the range of optimal LD50 reported by FAO/IAEA [20] values for crops belonging to the Fabaceae family, i.e., pigeon pea (*Cajanus cajan*), chickpea (*Cicer arietinum*), and peanut (*Arachis hypogaea*), which range between 80 and 350 Gy. Kumar et al. [27] also found that they evaluated the LD50 of germination percentage for two French bean varieties (BL and PL) with optimal values of 248.058 Gy and 234.167 Gy, respectively. The values obtained were also not far from the optimal LD_{50} values for irradiation mutation breeding determined by Olukupi et al. [28] for common bean varieties (Elfsane and F16), i.e., 318.22 Gy and 303.7 Gy, respectively. In another experiment by Guha Mallick et al. [29] to determine the lethal dose 50 (LD_{50}) for five faba bean genotypes, the values were found to be 140 Gy, 669 Gy, 575 Gy, 386 Gy, and 158 Gy for L-2013-060, L-2013-092, Anandnagar Local, Gazipur Local, and Bangla Gangachar, respectively.

The germination optimal LD_{50} values for Mung bean genotypes in this study were 223 Gy for AVMV8601 and 201,060 Gy, which differ from the values obtained in a study conducted in Mumbai, India, on the TARM 1 variety by Bonde et al. [30], with an optimal LD_{50} of 375.52 Gy. These differences in LD_{50} may be attributable to genotypic differences within the same crop [20]. Another experiment by Thounaojam et al. [31] on the determination of LD50 in the Mung bean variety (Mung bean *var.* GAMI 8), an inconsistent LD_{50} value was recorded, i.e., 524.26 Gy. A higher LD_{50} value was also reported by Roslim and Fiatin [32], who recorded an LD_{50} of 619.875 Gy based on the number of surviving plants in the Kampar mung bean cultivar. This indicates that the cultivar was less sensitive to gamma radiation.

4.2. Pathological Studies

Rhizoctonia spp is among the major fungal pathogens affecting common bean production worldwide. It is a soil-borne pathogen that can easily be spread from plant to plant through the formation of mycelial bridges between roots and infested soil debris, but it can also survive on seeds, facilitating long-distance dispersal [10]. The current study isolated *Rhizoctonia* spp. from the TARIBEAN 6 seed variety, which was subsequently used in the pathogenicity study of common beans. *Aspergillus flavus* was also isolated from the other four isolates (UYOLE 16, SELIAN 13, JESCA, and CALIMA UYOLE). The isolated species can cause seed abortion, seed necrosis, and seed rot, reducing germination ability, as well as seedling damage, thereby resulting in the development of disease in plant growth [33]. *Macrophomina spp.* is also an emerging problem in legumes. These pathogens have previously been isolated from common beans, as indicated by several studies conducted [10, 11, 34], and it is considered a polyphagous pathogen capable of infecting several hundred plant species [35].

Pathogenicity studies reveal resistance of UYOLE 16 and SELIAN 13 bean varieties to *M. Phaseolina* and *R. solani* grown on agar plates. This suggests that these varieties may carry naturally available resistance genes; they were not induced by mutation. For breeding activities, resistant cultivars are preferable because they possess the naturally added advantage of resistance, which is an important trait of interest. These varieties are highly recommended due to their resistance advantage. This provides early indications for breeders to take further steps,

including researching other important traits such as high yield. The study conducted pathogenicity analysis based on isolated spp such as *Rhizoctonia* and *Macrophomina spp*. Additional studies, like marker-assisted breeding and mutation breeding, can complement these findings. Other common bean varieties, TARIBEAN 6, JESCA, and CALIMA UYOLE, were susceptible to *Macrophomina* but resistant to *Rhizoctonia*. Overall, most fungi that infect common beans can also infect a wide range of other plant species, which may act as pathogen reservoirs. Therefore, better control of these pathogenic fungi is essential for improving bean production, reducing yield losses, and minimizing health risks caused by fungal toxins and allergens [31, 34, 20]. Minimum germination was recorded on CALIMA UYOLE in *Macrophomina spp* and SELIAN 13 in *Rhizoctonia spp* (20%). This was due to the high pathogenic susceptibility of these varieties, though there were no significant differences between common bean varieties.

5. Conclusion

The LD_{50} values determined for the common bean and mung bean varieties from this study may be useful in further experiments for mutation breeding. *Macrophomina phaseolina* and *R. solani* are noxious seed- and soil-borne pathogenic fungi affecting common beans, mung beans, and many other pulses. Contaminated seeds may serve as the primary source of inoculum when seeds are sown. Therefore, there is a need for pre-testing for these pathogens and seed treatment before planting, as well as selecting tolerant and resistant varieties against these pathogens. Furthermore, pulse breeders should focus on breeding beans for resistance against diseases caused by *M. phaseolina* and *R. solani*.

References

[1] R. D. Semba, R. Ramsing, N. Rahman, K. Kraemer, and M. W. Bloem, "Legumes as a sustainable source of protein in human diets," *Global Food Security*, vol. 28, p. 100520, 2021. https://doi.org/10.1016/j.gfs.2021.100520

[2] J. Medendorp, D. DeYoung, D. G. Thiagarajan, R. Duckworth, and B. Pittendrigh, *A systems perspective of the role of dry beans and pulses in the future of global food security: Opportunities and challenges, Dry Beans and Pulses: Production, Processing, and Nutrition*. USA: Springer, 2022.

[3] K. Ulukapi and S. F. Ozmen, "Study of the effect of irradiation (60Co) on M1 plants of common bean (Phaseolus vulgaris L.) cultivars and determined of proper doses for mutation breeding," *Journal of Radiation Research and Applied Sciences*, vol. 11, no. 2, pp. 157-161, 2018. https://doi.org/10.1016/j.jrras.2017.12.004

[4] P. A. Ndakidemi, F. D. Dakora, E. M. Nkonya, D. Ringo, and H. Mansoor, "Yield and economic benefits of common bean (Phaseolus vulgaris) and soybean (Glycine max) inoculation in Northern Tanzania," *Australian Journal of Experimental Agriculture*, vol. 46, no. 4, pp. 571-577, 2006. https://doi.org/10.1071/EA03157

[5] M. Ndimbo *et al.*, *Variety catalogue of common beans (Phaseolus vulgaris) in Tanzania*. Tanzania: Tanzanian Agricultural Research Institute, 2022.

[6] J. J. Musimu, *Economics of small holder common beans production in Mbeya*. Tanzania: University of Mbeya, 2018.

[7] C. S. Akibode and M. K. Maredia, "Global and regional trends in production, trade and consumption of food legume crops," *Food Policy*, vol. 37, no. 4, pp. 285–294, 2012.

[8] A. Ullah, T. M. Shah, and M. Farooq, "Pulses production in Pakistan: Status, constraints and opportunities," *International Journal of Plant Production*, vol. 14, no. 4, pp. 549-569, 2020. https://doi.org/10.1007/s42106-020-00108-2

[9] T. Assefa *et al.*, "A review of breeding objectives, genomic resources, and marker-assisted methods in common bean (Phaseolus vulgaris L.)," *Molecular Breeding*, vol. 39, no. 2, p. 20, 2019. https://doi.org/10.1007/s11032-018-0920-0

[10] G. Taboada *et al.*, "Characterization of fungal pathogens and germplasm screening for disease resistance in the main production area of the common bean in Argentina," *Frontiers in Plant Science*, vol. 13, p. 986247, 2022. https://doi.org/10.3389/fpls.2022.986247

[11] M. Sajjad, K. P. Akhtar, N. Ullah, and M. J. Asghar, "Incidence, characterization and pathogenicity of seed-borne fungi of Lentil (Lens culinaris L.) in Pakistan," *Ceylon Journal of Science*, vol. 53, no. 3, pp. 333–347, 2024. https://doi.org/10.4038/cjs.v53i3.8307

[12] K. P. Akhtar *et al.*, "Field evaluation of mungbean recombinant inbred lines against mungbean yellow mosaic disease using new disease scale in Thailand," *The Plant Pathology Journal*, vol. 25, no. 4, pp. 422-428, 2009.

[13] W. F. Abobatta, E. F. El-Hashash, and R. H. Hegab, "Challenges and opportunities for the global cultivation and adaption of legumes," *Journal of Applied Biotechnology & Bioengineering*, vol. 8, no. 5, pp. 160-172, 2021. https://doi.org/10.15406/jabb.2021.08.00270

[14] M. Wasif *et al.*, "Role of mutation breeding by gamma rays to improve mung bean: A review," *Asian Journal of Biotechnology and Genetic Engineering*, vol. 6, no. 2, pp. 133–142, 2023.

[15] A. Sharma and R. Sharma, *Crop improvement and mutation breeding*. India: Scientific Publishers, 2014.

[16] A. M. Perez-de-Castro *et al.*, "Application of genomic tools in plant breeding," *Current Genomics*, vol. 13, no. 3, pp. 179-195, 2012. https://doi.org/10.2174/138920212800543084

[17] R. Solanki, R. Gill, P. Verma, and S. Singh, *Mutation breeding in pulses: An overview breeding of pulse crops*. Ludhiana: Kalyani Publishers, 2011.

[18] I. Javed, M. Ahsan, H. M. Ahmad, and Q. Ali, "Role of mutation breeding to improve Mungbean (Vigna radiata L. Wilczek) yield: An overview," *Nature and Science*, vol. 14, no. 1, pp. 63-77, 2016.

[19] M. Kharkwal, *Role of mutation breeding in crop improvement with special reference to Indian Subcontinent. In Mutation Breeding for Sustainable Food Production and Climate Resilience*. India: Springer, 2023.

[20] FAO/IAEA, *Manual on mutation breeding- Spencer-Lopes, M.M., Forster, B.P. and Jankuloski, L. (eds.)*, 3rd ed. Rome, Italy: Food and Agriculture Organization of the United Nations, 2018.

[21] F. Ahmad *et al.*, "Molecular markers and marker assisted plant breeding: Current status and their applications in agricultural development," *Journal of Environmental and Agricultural Sciences*, vol. 11, pp. 35-50, 2017.

[22] S. T. Kadam *et al.*, "Thermal neutron as a potential mutagen for induced plant mutation breeding: Radiosensitivity response on wheat and rice," *Genetic Resources and Crop Evolution*, vol. 70, no. 3, pp. 789-798, 2023. https://doi.org/10.1007/s10722-022-01461-z

[23] M. Iqbal, E. Rahmawati, and W. Puspitasari, "Effects of gamma-ray irradiation dose and dose rates on the growth and radiosensitivity of soybean varieties Grobogan and Mutiara 1," presented at the IOP Conference Series: Earth and Environmental Science, IOP Publishing, 2024.

[24] S. A. Alsohaili and B. M. Bani-Hasan, "Morphological and molecular identification of fungi isolated from different environmental sources in the Northern Eastern desert of Jordan," *Jordan Journal of Biological Sciences*, vol. 11, no. 3, pp. 329 - 337, 2018.

[25] R. Thilagam, G. Kalaivani, and N. Hemalatha, "Isolation and identification of phytopathogenic fungi from infected plant parts," *International Journal of Current Pharmaceutical Research*, vol. 10, no. 1, pp. 26-28, 2018. https://doi.org/10.22159/ijcpr.2018v10i1.24404

[26] J. J. Doyle, *The molecular basis of plant breeding: Techniques and applications*. Germany: Springer, 1987.

[27] S. Kumar *et al.*, "Induced mutants in locally adapted landraces of french bean (Phaseolus vulgaris L.), their mutagenic sensitivity and mutability for crop improvement," *Acta Scientific Agriculture*, vol. 5, no. 12, pp. 10–16, 2021. https://doi.org/10.31080/asag.2021.05.1079

[28] O. I. Olukupi, F. O. Adeyemi, and S. A. Adebayo, "The effect of irradiation on mutation breeding for crop improvement: An evaluation of LD50 values," *Journal of Agricultural Biotechnology*, vol. 12, no. 4, pp. 214–223, 2023.

[29] R. Guha Mallick *et al.*, "Radiosensitivity of seedling traits to varying gamma doses, optimum dose determination and variation in determined doses due to different time of sowing after irradiation and methods of irradiation in faba bean genotypes," *International Journal of Radiation Biology*, vol. 99, no. 3, pp. 534-550, 2023. https://doi.org/10.1080/09553002.2022.2107723

[30] P. J. Bonde, B. S. Thorat, and V. J. Gimhavnekar, "Effect of gamma radiation on germination and seedling parameters of mung bean (Vigna radiata)," *International Journal of Current Microbiology and Applied Sciences, Special Issue*, vol. 11, pp. 1582-1587, 2020.

[31] A. S. Thounaojam, K. V. Patel, R. U. Solanki, R. I. Chaudhary, and N. K. Chavda, "Response of gamma irradiation on germination and seedling growth of green gram var. GAM 8," *Environment Conservation Journal*, vol. 25, no. 1, pp. 131-137, 2024. https://doi.org/10.36953/ECJ.23552612

[32] D. I. Roslim, H. Herman, and I. Fiatin, "Lethal dose 50 (LD 50) of mungbean (Vigna radiata L. Wilczek) cultivar Kampar," *SABRAO Journal of Breeding & Genetics*, vol. 47, no. 4, pp. 409–415, 2015.

[33] S. Y. Mahmoud, M. H. Hosseny, K. A. EL-Shaikh, H. O. Ali, and Y. A. Mohamed, "Seed-borne fungal pathogens associated with common bean (Phaseolus vulgaris L.) seeds and their impact on germination," *Journal of Environmental Studies*, vol. 11, no. 1, pp. 19-26, 2013.

[34] D. Marcenaro and J. P. T. Valkonen, "Seedborne pathogenic fungi in common bean (Phaseolus vulgaris cv. INTA Rojo) in Nicaragua," *PLoS One*, vol. 11, no. 12, p. e0168662, 2016. https://doi.org/10.1371/journal.pone.0168662

[35] M. P. You, T. D. Colmer, and M. J. Barbetti, "Salinity drives host reaction in Phaseolus vulgaris (common bean) to Macrophomina phaseolina," *Functional Plant Biology*, vol. 38, no. 12, pp. 984-992, 2011. https://doi.org/10.1071/FP11137