UNIVERSITY OF CAPE COAST

EFFECT OF IONIZING IRRADIATION ON SEED QUALITY, AGRONOMIC PERFORMANCE AND YIELD OF M_1 AND M_2 MUTANT COWPEA LINES

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BY

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DECLARATION

Candidate's Declaration

I hereby declare that this thesis is the result of my own original research and that no part of it has been presented for another degree in this university or elsewhere.

Candidate's Signature:..... Date:.....

Name: Mishael Amoah Nyarko

Supervisors' Declaration

We hereby declare that the preparation and presentation of the thesis were supervised in accordance with the guidelines on supervision of thesis laid down by the University of Cape Coast.

Principal Supervisor's Signature:..... Date:.....

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ABSTRACT

The use of mutation breeding in crop improvement is becoming popular in recent times with gamma rays being among the most widely used physical mutagens. However, during gamma-irradiation of seeds to generate desirable traits, certain physiological and biochemical processes are affected. This study sought to examine the effect of irradiation on seed quality, including physiological, seed health, agronomic and yield performance of mutant cowpea lines. Twenty-five (25) cowpea lines were irradiated at five (5) doses of gamma radiation (0, 50, 100, 150 & 200 Gy) at a rate of 330 Gys^{-1}. The results showed significant differences *($p<0.05$)* among the lines in germination parameters, percentage mycoflora infection, agronomic and yield parameters. Increasing irradiation up to 200 Gy led to an increase in percentage hard seeds, mean germination time and uncertainty of germination. However, increasing irradiation led to a decrease in coefficient of variation of germination time, mean germination rate and synchronization index. Irradiation doses up to 200 Gy did not show a significant lethal effect on percentage infections for *Cladosporium sphaerospermum*, *Penicillium* and *Fusarium moniliforme*. The pre-treated irradiated cowpea seeds recorded relatively lower mycoflora infections for saprophytic fungi. Increasing irradiation up to 200 Gy showed decreasing plant height at 21 days after planting and at flowering as well as decreasing pod length and seeds per pod but led to an increase in 100 seed weight. Low doses of irradiation up to 200 Gy affected germination time and synchrony, agronomic performance and yield parameters of both M_1 and M_2 mutant generations but relatively higher doses would be required to reduce seed-borne mycoflora.

KEYWORDS

Crop improvement

Mutation

Irradiation

Seed-borne mycoflora

Seed quality

Vigna unguiculata

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DEDICATION

This study is dedicated to my parents, Mr. Kweku Nyarko and Madam Araba Bosuwa for their prayers, love and support during the entire period of my studies.

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100SW	100 seed weight
D50%G	Days to 50% germination
%DcS	percentage decayed seeds
%DfS	percentage deformed seedlings
%G	percentage germination
%HS	percentage hard seeds
ANOVA	Analysis of variance
BNARI	Biotechnology and Nuclear Agricultural Research Institute
cm	centimetre
CRD	Completely Randomized Design
CRI	Crops Research Institute
CSIR	Council for Scientific and Industrial Research
CVG	coefficient of velocity of germination
CVt	coefficient of variation of germination time
DAP	days after planting
DLG	day to last germination
DtF	Days to Flowering
Dt50F	Days to 50% flowering
EMS	ethyl methane sulfonate
FAO	Food and Agriculture Organization
g	gram
GAEC	Ghana Atomic Energy Commission
GI	germination index
GY	grain yield

Gy	gray
Gys^{-1}	gray per second
IITA	International Institute for Tropical Agriculture
IPPC	International Plant Protection Convention
ISTA	International Seed Testing Association
Kg	kilogram
MoFA	Ministry of Food and Agriculture
MGR	mean germination rate
MGT	mean germination time
Mt/ha	metric tonnes per hectar
NaDCC	sodium dichloro-s-triazinetrione
NaOCl	Sodium hypochorite
NUV	Near ultra violet
NVRRC	National Variety Release and Registration Committee
nB	number of branches
nPed/Pl	number of peduncles per plant
nPo/Pe	number of pods per peduncle
nPo/Pl	number of pods per plant
OECD	Organization for Economic Co-operation and Development
PH@21	Plant height @21DAP
PH@F	Plant height at Flowering
PL	pod length
RCBD	Randomised Complete Block Design
SI	synchronization index
S/P	seeds per pod

SRID	Statistics Research and Information Directorate
TSG	time spread of germination
UCC	University of Cape Coast
UG	uncertainty of germination
UV-B	ultraviolet-beta

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background

Cowpea (*Vigna unguiculata* (L) Walp) (2n=2x=22), a member of the *Fabaceae* family, has been identified to have the potential to feed sub-Saharan Africa's malnourished population with cheap protein source (Boukar *et al.*, 2018). This attribute has contributed greatly to its nickname, the "poor man's meat" (Dube & Fanadzo, 2013). It is a prominent crop in the nutrition of sub-Saharan Africans and its cultivation also improves soil fertility (Yirzagla *et al.*, 2016). This makes cowpea a potential crop for leveraging Africa's basic nutrition, especially protein requirements. People consume different parts of the cowpea plant; the immature and young pods, leaves and grains are consumed in sub-Saharan Africa (Akpan & Mbah, 2016).

Cowpea production is popular in the tropics (Timko & Singh, 2008) and Africa is the world's leading producer with Nigeria and Niger producing contributing over 50% of world cowpea production (Akpan & Mbah, 2016; Boukar *et al.*, 2016; FAOstat, 2017). There is a vibrant market for cowpea in and out of the West African sub-region and this has greatly contributed to employment, poverty alleviation and revenues to governments (Langyintuo *et al.*, 2003). Cowpea's drought tolerance makes it adaptable to the Savannah and Sahel Regions of Africa (Timko *et al.*, 2007; Boukar *et al.*, 2016).

Cowpea is a versatile African crop because of its uses as food, feed and as soil amendment (Mshelmbula *et al.*, 2019). The forage and fodder of cowpea are used as animal feed (Timko & Singh, 2008). The grain is the most important part (OECD, 2016) and it is used in various dishes in West and

Central Africa (Langyintuo *et al.*, 2003). The leaves and green pods have significant dietary uses and can be served as a vegetable at all stages of development (Ahenkora *et al*., 1998). Cowpea has the capacity to fix atmospheric nitrogen into soils through its symbiotic relationship with nitrogen-fixing bacteria such as *Rhizobia* when cowpea is introduced in a crop rotation system (Timko *et al.*, 2007; Gwata, Shimels, & Motova, 2016). These multiple uses and potential make cowpea a food security crop (Dube & Fanadzo, 2013).

Cowpea is the second most consumed legume in Ghana (MoFA; SRID, 2017). Current production levels do not meet consumption demands (Egbadzor *et al.*, 2013). Cowpea production by land area has slightly declined in the past decade but the tonnage has increased (MoFA; SRID, 2017). This can be attributed to improved farming practices and better performing genotypes available to farmers (Dugje, Omoigui, Ekeleme, Kamara, & Ajeigbe, 2009; Egbadzor *et al.*, 2013; Gwata *et al.*, 2016). The on-farm rain-fed productivity of cowpea is 1.41 Mt/ha. However, the potential yield is 2.5 Mt/ha (MoFA; SRID, 2017).

Cowpea consumers prefer large cream seeds that are sweet and easy to cook, whereas farmers prefer varieties with insect pest resistance, yield and drought tolerance (Egbadzor *et al.*, 2013). In addition, farmers prefer cowpea varieties with distinctive growth habits that satisfy their markets, cropping system and environmental conditions (Singh, Raj, & Dashiell, 1997). Thus, farmers may prefer varieties with specific photosensitivity and classified as early, medium or late-maturing to be used as grain type, fodder type or dual-purpose varieties that are in harmony with the farmer's cropping system: sole

cropping or intercropping (Boukar *et al.*, 2018). This implies that there is the need for the development of cowpea varieties with morpho-physiological traits that satisfy farmer's cropping systems as well as the nutritive, culinary and physical qualities preferred by consumers (Etwire, Ariyawardana, & Mortlock, 2016).

Cowpea production in Ghana is limited by a number of factors; critical among these, is disease incidence. These diseases include cercospora leaf spot (*Cercospora canescens*), cowpea fusarium wilt (*Fusarium oxysporum* f. sp. *tracheiphilum*), soft stem rot (*Pythium aphanidermatum*) and anthracnose (*Colletotrichum lindemuthianum*). These diseases are seed borne and seed transmitted (Gupta & Singh, 2010) and cause great losses to cowpea production (Van Gastel, Bishaw, & Gregg, 2002).

Mutagenic agents have simplified the induction of genetic variability in crops (Horn, Ghebrehiwot, & Shimelis, 2016). These agents may be physical or chemical (Mba *et al.*, 2010). Optimal mutagenic treatment has been used for creating new genetic variability in plant propagules such as seeds, tissues and organs (Horn *et al.*, 2016). Sometimes, lower levels of radiation exposure can only cause morphological aberrations in phenotypes (Amjad & Anjum, 2002). Mutation can be spontaneous or induced artificially to produce large genetic variability in a short time interval (Gnanamurthy *et al.*, 2019). This evolutionary change in plant genetic research is potent for enhancing variability for crop improvement (Girija *et al.*, 2013) and has been a significant breakthrough in genetics. Seed germination characteristics have been reported to be influenced by exposure of seeds to ionising radiation (Amjad & Anjum, 2003).

A germination test is one of the most effective ways of predicting the field establishment and the performance (yield and quality) of farmers' harvests (ISTA, 2011). High-quality seeds have faster, better and more uniform establishment on the field (FAO & AfricanSeeds, 2018). In angiosperms, germination is confirmed when the radicle or plumule emerges from the seed coat (Kader, 2005). The germination dynamics (proportions and rates) of a seed lot is influenced by the seed's complex physiological mechanisms as well as environmental conditions (ISTA, 2011). The measurements of the germination properties of a seed lot are essential for seed quality assessments (FAO & AfricanSeeds, 2018).

The seed of any crop is an indispensable factor for agricultural production in every country. The poor access to good quality seeds by most sub-Saharan African farmers has contributed greatly to the low productivity of agricultural systems in the sub-region (Asare *et al*., 2016). The notion that the seed is the most important input in any cropping system paves the way for the development of an efficient seed system where institutions involved in the sustainability of the enterprise mutually coordinate till good quality seeds are eventually released to the grain farmer (Etwire *et al.*, 2016).

1.2 Problem Statement

The production of cowpea in Ghana is lower than its consumption and the problem is multi-faceted (Egbadzor *et al.*, 2013; MoFA; SRID, 2017). Research by Egbadzor *et al.* (2015) showed that farmers preferred varieties that were drought and pest resistant, less vegetative, high yielding and early maturing. Consumers also preferred cowpea varieties which had large cream seeds, high swelling abilities, sweet taste and easy to cook (Langyintuo *et al.*,

2003; Egbadzor *et al.*, 2013). According to Egbadzor *et al.* (2013), cowpea traders think that cowpea varieties in Ghana are limiting and these consumer preferences hence the need to explore other markets in the sub-region to satisfy consumer demands. This lack of coordination between farmer' production needs and consumers' preferences contribute to Ghana becoming a net importer of cowpea. This is an economic disincentive to the Ghanaian economy in the cowpea trade.

Cowpea has varying growth patterns, which invariably always affects the type of crop production system adopted by a farmer. For example, indeterminate cowpea varieties will produce pods with varying days to maturity and this a major disadvantage to mechanized harvesting. This constraint limits the farmer's choice of cropping system in terms of mono-cropping or mixed cropping cowpea with other species. Also, the diversity of growth habits of cowpea influences its adaptability and use among farmers (Timko & Singh, 2008; Boukar *et al.*, 2018). For example, cowpea varieties with late maturity and high vegetative growth are used as vegetables and the fodder is used to feed animals. When a farmer has access to only such varieties but he may have problems with increased production cost and/or marketing when the seeds produced do not appeal to his customers.

Cowpea varieties released in Ghana are comparatively few and they have their unique characteristics (yield, growth pattern, disease and pest resistance etc.) (NVRRC, 2019), which may not altogether satisfy the preferences of farmers and consumers alike. This may be partly attributed to the non-availability of assorted cowpea lines (narrow gene pool) from which breeders could research to improve the crop to suit both farmer and consumer

preferences simultaneously. In effect, this makes farmers' preferred production and cropping systems less flexible with available cowpea genotypes at their disposal.

The use of conventional breeding and crossing techniques to generate variations in available cowpea lines as a means of cowpea improvement is cumbersome and time-consuming (Gwata *et al.*, 2016). In self-pollinated crops like cowpea, the correct timing for controlled crossing can be nearly impractical, and therefore, make the induction of genetic variability among genotypes less effective. Even with mutation breeding, inducing genetic variation with chemical mutagens have been reported to have its own practical dysfunctions, including safety, handling and disposal (Olasupo, Ilori, Forster, & Bado, 2016).

In a seed lot, germination is not always perfect under optimal conditions of light, water and temperature (Kameswara Rao *et al.*, 2006). Even in the case where all seeds germinate, there is the probability of deformed seedlings (Mathur *et al*., 2003). Different species vary in their response to physiological quality testing, which is mainly based on viability and vigour (Marcos-Filho, 2015). The proportion of seeds that germinate and the time dynamics of the germination process are influenced when seeds are exposed doses of irradiation (Ariraman *et al*., 2014; ISTA, 2010).

The seed can serve as a biome for pathogens (Cross, 1979). The pathogens of some plant diseases are seed-borne and or seed transmissible (Aveling, 2016) and, therefore, reduce the quality of the seed or propagules (Cross, 1979). Seed-borne infections are the leading cause of epiphytotics (De Tempe & Binnerts, 1979) and have significant impact on field seed

establishment, seedling growth, development, and ultimately, yield (FAO & AfricanSeeds, 2018).

1.3 Justification

The demand to feed the increasing population of the world has been the focus of most crop improvement exercises. Cowpea's protein and nutritional benefits make it a better candidate for research in improving the health of the populace of the West African sub-region through the provision of a cheaper source of protein (Boukar *et al.*, 2018). More so, cowpea is second to groundnut in most consumed legumes, yet its production is plagued with problems of disease and pest incidence, drought, storability, grain quality, farming systems, adoption rate, and many others (Egbadzor *et al.*, 2013, 2015; MoFA; SRID, 2017). These problems have compelled researchers to breed for better genotypes that serve both farmer and consumer preferences.

Cowpea can be used as food, feed and soil amendment in poor soils (Akpan & Mbah, 2016; Mshelmbula *et al.*, 2019) and therefore, it suitably serves as a food security crop because of its versatility in uses (Dube & Fanadzo, 2013; Boukar *et al.*, 2016). The availability of market for cowpea makes it a potential tool for poverty alleviation in West and Central Africa (Langyintuo *et al.*, 2003), yet Ghana has achieved 56 % of its production potential (MoFA; SRID, 2017). The increased production of quality cowpea in Ghana can take advantage of the regional market demand and hence contribute to foreign exchange for the country.

The plethora of benefits of cowpea production and uses has informed the breeding of cowpea through diverse crop improvement strategies to continually serve the needs of farmers and consumers (Boukar *et al.*, 2016,

2018). Optimal mutagenesis has been very effective in generating variability in crop species (Mba *et al.*, 2010). Achievements through mutation of cowpea include varieties with better yield and produce quality (Olasupo *et al.*, 2016). Harnessing the safe use of ionising irradiation in mutagenesis is a better and quick tool to induce genetic variability in crops than conventional breeding and crossing techniques (Mba *et al.*, 2010; Olasupo *et al.*, 2016). Induced mutation using ionising irradiation to select for lines preferred by farmers and consumers in terms of cowpea's morphological and physiological attributes without jeopardizing its yield and nutritional qualities is highly achievable (Horn *et al.*, 2016; Gnanamurthy, Dhanavel, & Girija, 2019). Mutation breeding has proved to be a successful tool in transmitting improvements in self-pollinated crops (Gnanamurthy & Dhanavel, 2014) because it offsets the cross incompatibility mechanisms, high crossing barrier and poor seed setting of some self-pollinated species.

The physiological quality testing for a seed is determined by the characteristics of its germination. The germination capacity is a measure of the proportion of live seeds that can produce normal seedlings without defect (Mathur *et al*., 2003; FAO & AfricanSeeds, 2018). A germination test is carried out to ascertain the portion of a seed lot that will germinate and grow into healthy seedlings (Kameswara Rao *et al.*, 2006) and therefore, it is the best predictor for field establishment and performance. Seed physiological potential is determined by germination and viability and these control the capacity of seeds to express their vital functions under different environments (Marcos-Filho, 2015). Hence, various indices have been introduced to assess the nature of the germination process to predict the quality of seeds (Kader,

2005; Ranal & De Santana, 2006). Adequate knowledge of the germination properties of seeds will go a long way to help farmers in their productions.

The control of seed-borne infections is the first step in any successful crop protection and production program (Van Gastel, Bishaw, & Gregg, 2002). Seed health is of utmost priority in the value chain of crop production (International Rice Rsearch Institute, 1994) because it informs on the treatment to be given to seeds to be used for production (Shahat *et al*., 2017). The use of ionising irradiation has been successful in controlling pathogens in foods and other products (Radomyski, Murano, Olson & Murano 1994; Shathele, 2009; Jeong, Shin, Chu, & Park 2015). This implies that the growth and development of seed-borne fungi can be investigated in irradiated seeds.

1.4 Objectives

1.4.1 General objective:

The objective of this experiment was to assess the impact of different doses of ionising radiation on the physiological and health of cowpea seeds and hence the yield of the cowpea genotypes. These will generate knowledge that will contribute towards the development of improved varieties through mutagenesis.

1.4.2 Specific objectives

The specific objectives were to:

1. determine the effect of irradiation on physiological qualities of cowpea seeds
2. determine the effect of irradiation on seed health of cowpea

3. assess the agronomic and yield performance of M_1 and M_2 irradiated seeds

1.4.3 Test of Hypotheses

1. H_0: No significant differences exist in the effect of different doses of irradiation on seed physiological qualities.

   H_1: Significant differences exist in the effect of different doses on seed physiological qualities.

2. H_0: Irradiation does not significantly affect the seed health of cowpea.

   H_1: Irradiation has significant effect on the seed health of cowpea.

3. H_0: Irradiation has no significant effect on the agronomic and yield performances of the different varieties.

   H_1: Irradiation has significant effect on the agronomic and yield performances of cowpea.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Cowpea genetics and breeding

Cowpea (*Vigna unguiculata* (L) Walp) (2n=2x=22) belongs to the *Fabaceae* family. It is considered a short day or day-neutral plant (Timko & Singh, 2008). Cowpea is self-pollinated and that outcrossing is minimal and varies with the environment (Boukar *et al.*, 2016). This implies that most varieties are pure lines (Timko *et al.*, 2007). Based on pod and seed characteristics, cultivated cowpea can be divided into five cultivars (Timko *et al.*, 2007); Unguiculata, Sesquipedalis (yard-long-bean), Biflora, Textilis (long peduncles), and Melanophthalmus. West and Central Africa have maximum diversity in cultivated cowpea and landraces (Boukar *et al*., 2018).

Over 1500 cultivated cowpea from almost 90 countries worldwide is under preservation at the genebank of IITA in Nigeria (Timko *et al.*, 2007). Out of this total, core collections that represent the entire genetic diversity have been established to aid scientists to develop breeding programs (Boukar *et al.*, 2018). Although there are rich germplasm collections accessible by various national and international breeding programs and the IITA, the genetic base for most self-pollinated crops such as cowpea is narrow for economic traits such as yield components, grain yield, drought and disease and pest tolerance (Mudibu *et al*., 2012) cited by Horn & Shimelis, 2013).

Classically, most cowpea breeding programs involve pedigree, backcross or bulk breeding methods to study segregating populations (Boukar *et al.*, 2016).

Another potential tool used in generating genetic variation in crops is mutation breeding, where physical and or chemical mutagens are used (Mba *et al.*, 2010). The general strategy of most cowpea breeding programs is to develop a collection of high yielding varieties adapted to different agro-ecological zones that possess preferred traits for growth habit, plant type, days to maturity and seed type (Timko & Singh, 2008). In effect, the target for most breeding programs in cowpea is grain yield, quality and resistance to major diseases and pests (Timko *et al.*, 2007; Olasupo *et al.*, 2016).

2.2 Global cowpea production

The production of cowpea is popular in the tropical regions of the world (Timko & Singh, 2008) and hence Africa contributes over 50% of world cowpea production (Akpan & Mbah, 2016; FAOstat, 2017). Nigeria is the highest producer of cowpea with an annual production of approximately 2.14 million metric tonnes with a domestic consumption greater than 3.0 metric tonnes (FAOstat, 2017). Other important cowpea producers in sub-Saharan Africa are Burkina Faso and Niger; 0.57 and 1.59 million metric tonnes annual production respectively (Boukar *et al.*, 2018). The yield of cowpea in most sub-Saharan African countries is lower than 1000 kg/ha. Among the top 20 world producers, Serbia has the highest per area yield of cowpea (3,389 kg/ha) and Mozambique has the lowest, 275 kg/ha (FAOstat, 2017). Ghana, however, has a yield per area of cowpea to be 1.41 Mt/ha with a total production of 206,380 Mt in 2016 (MoFA; SRID, 2017).

2.3 Importance of cowpea production

The cowpea plant forms a major staple in the diet of many sub-Saharan Africans, especially those of the savannah agro-ecologies (Dugje *et al.*, 2009). Cowpea seeds are frequently harvested and stored for later consumption, as wholly cooked or in the form of flour after milling because the seed is considered in most countries as the most important part (Timko & Singh, 2008; Akpan & Mbah, 2016). The seeds contain a total protein content that is about two to four times higher than most cereals and tubers (Timko & Singh, 2008) and therefore provides a cheap protein source to complement the dietary requirements of most sub-Saharan Africans (Dube & Fanadzo, 2013; Gnankambary *et al.*, 2019).

The young and tender leaves of cowpea are consumed in various African cultures in diverse cuisines (Boukar *et al.*, 2016). In East Africa, the fresh leaves of cowpea are also used as pot herb (Boukar *et al.*, 2018). The forage and fodder of cowpea usually after harvest are used as animal feed (Timko & Singh, 2008). The fodder is said to contain up to 18.6 g protein per 100 g dry weight and therefore, cowpea haulm can be a good source of income for farmers in livestock rearing communities (Boukar *et al.*, 2018).

The cultivation of cowpea improves soil fertility through biological nitrogen fixation by the symbiosis of root nodules and nitrogen-fixing bacteria such as rhizobia (Gwata *et al.*, 2016; Yirzagla *et al.*, 2016). The drought tolerance of cowpea makes it adaptable to the Savannah and Sahel regions of Africa (Timko *et al.*, 2007; Boukar *et al.*, 2016). The availability of different varieties with distinct growth habits (erect, semi-erect and creeping) influences the cropping

systems (mono-cropping or mixed cropping) practised by most small scale farmers (Dugje *et al.*, 2009; Boukar *et al.*, 2018). The versatility of cowpea in the provision of food, feed and as a soil amendment (Mshelmbula *et al.*, 2019) completes its potential as the "poor man's crop" (Dube & Fanadzo, 2013).

The value chain of cowpea production has largely contributed to employment, poverty alleviation and revenues to governments in sub-Saharan Africa (Langyintuo *et al.*, 2003; Dube & Fanadzo, 2013). Cowpea has also defined the formal and informal regional market systems in sub-Saharan Africa (Langyintuo *et al.*, 2003). Thus, the multiple benefits derived from cowpea best qualify it as a food security crop (Dube & Fanadzo, 2013).

2.4 Cowpea production in Ghana

Cowpea is the second most important legume under cultivation in Ghana. In the past decade, cowpea production by land area has decreased but the production per unit area has intensified (MoFA; SRID, 2017). This is attributable to the availability of better-performing genotypes and or better farming practices such as intensification by farmers (Dugje *et al.*, 2009; Egbadzor *et al.*, 2013; Gwata *et al.*, 2016). The on-farm rain-fed productivity of cowpea has been reported to be 1.4 Mt/ha but the potential is pegged at 2.5 Mt/ha (MoFA; SRID, 2017). There is a wide range of diversity of cultivated cowpea in Ghana just like the sub-region and these have distinctive morphological, physiological and yield traits that can be developed to suit the preference of farmers and consumers alike (Timko & Singh, 2008; Etwire *et al.*, 2016).

2.5 Production constraints

In Ghana, cowpea production is limited by several factors. These constraints may apply to a farmer's production system or depend on the consumers' preferences. The constraints limited to the farmer include inadequate genotypes, diseases and pests and poor-performing genotypes (Egbadzor *et al.*, 2013).

Comparatively, cowpea varieties released in Ghana are fewer than other countries of the sub-Saharan Africa and these varieties have their unique characteristics of yield, growth pattern as well disease and pest resistance (NVRRC, 2019). This may be partly attributed to the narrow gene pool from which breeders could research to improve the crop to suit both farmer and consumer preferences simultaneously. This affects farmers' preferred cropping systems where available varieties may fit for monocropping, mixed cropping or can be used as a dual type (Timko & Singh, 2008; Boukar *et al.*, 2018). For example, cowpea varieties with late maturity and high vegetative growth are used as vegetables and the fodder is used to feed animals. When a farmer has access to only such varieties, he may have problems with increased production cost and/or marketing when the seeds produced do not appeal to his customers. Therefore, the farmer needs varieties that will simultaneously satisfy his field production preferences as and the market demand.

The average yield of cowpea in Ghana is a little above 50% of its potential (MoFA; SRID, 2017). This may be as a result of poor performing genotypes or factors such as drought, soil fertility, diseases and pests. Variation among

genotypes is a critical prerequisite in breeding for disease resistant varieties with desired morphological traits for the farmer and the consumer alike. The disease incidences include Cercospora leaf spot (*Cercospora canescens*), cowpea fusarium wilt (*Fusarium oxysporum* f. sp. *tracheiphilum*), soft stem rot (*Pythium aphanidermatum*) and anthracnose (*Colletotrichum lindemuthianum*). These diseases are seed-borne and seed transmitted (Gupta & Singh, 2010) and they cause great losses to cowpea production hence the need for pathogen-free seeds (Van Gastel, Bishaw, & Gregg, 2002).

Consumers' preferences for a cowpea variety influences the marketing of cowpea (Langyintuo *et al.*, 2003). Cowpea traders always try to meet the market demand for specific varieties to the extend of importing when such prefences are not available locally. According to Egbadzor *et al.* (2013), consumers in Ghana prefer cowpea varieties which have large cream seeds, high swelling abilities, sweet taste, easy to cook and long storability. Most Ghanaian varieties lack some of these seed qualities and hence seed traders tend to import from other countries in the sub-region to meet the market demand (Langyintuo *et al.*, 2003; Egbadzor *et al.*, 2013).

2.6 Mutagenesis and Mutation breeding

Mutation refers to the heritable change to the genetic constituents of an individual and it can occur naturally or be induced artificially (Mba *et al.*, 2010). Thus, mutation is a sudden heritable change in an organism's genetic structure and it can be produced by a change in the sequence of base genes (Bind & Dwivedi, 2014; Gnanamurthy *et al.*, 2019). Mutagenesis has been used as a tool

for crop improvement (Olasupo *et al.*, 2016). The optimal mutagenic treatment has been used for creating new genetic variability in plant propagules such as seeds, tissues, and organs (Horn, Ghebrehiwot, & Shimelis, 2016; Olasupo *et al.*, 2016).

Mutation breeding has been a significant breakthrough in plant breeding programs (Horn, Ghebrehiwot, & Shimelis, 2016; Dhanavel & Girija, 2019). Globally, more than 3200 mutant cultivars in over 220 cultivated crops have been developed and released to farmers in recent times (Olakunle *et al*., 2018). Various achievements have been recorded with respect to mutagenesis in different plant growth stages, physiology and or yield (Amjad & Anjum, 2002; Horn *et al.*, 2016; Olasupo *et al.*, 2016; Kusmiyati, Sutarno, Sas, & Herwibawa, 2018; Dhanavel & Girija, 2019).

2.6.1 Types of mutagens

A genetic mutation in plants can be done by the use of physical or chemical mutagens. Examples of physical mutagens include ionising and non-ionising radaiton (gamma rays, X-rays, UV light, etc.) whereas chemicals such as ethyl methane sulfonate (EMS) and ethydium bromide (Mba *et al.*, 2010; Horn & Shimelis, 2013). The duration of exposure of plant propagules to radiation sources can be classified as acute or chronic. According to guidelines by Mba *et al.*, (2010), chronic irradiation refers to exposures at relatively low doses for extended periods (up to months), whereas acute irradiation refers to exposures at relatively higher doses for very short times (seconds or minutes).

High doses of mutagenic applications may destroy growth promoters, increase growth inhibitors and metabolic status of plant propagules and also induce chromosomal aberrations (Amjad & Anjum, 2002). These will in effect, render few plants suitable for selection because of the increased lethality (Horn & Shimelis, 2013). Thus high irradaition doses negatively affect the success of identifying and selecting useful mutants during induced mutation exercises. For these reasons, low doses of irradiation may be effective in ensuring that the maximum population of mutants survive after irradiation and thereafter exhibit variability in their traits for enhanced selection (Olasupo *et al.*, 2016).

With chemical mutagens, several practical dysfunctions have been identified and they include soaking of seeds, penetration of the relevant target cells, the safety of handling and disposal and many more (Mba *et al.*, 2010; Olasupo *et al.*, 2016). This makes mutagenesis through irradiation safer and more preferable to the use of chemical mutagens.

2.6.2 Effects of Mutagenesis

2.6.2.1 *Effect of irradiation on germination and seedling characteristics*

Exposure of cowpea seeds to UV irradiation (260 nm) for durations up to 15 h does not affect measured germination parameters (Mshelmbula *et al.*, 2019). In soybean, enhanced UV-B irradiation decreased plant traits such as plant height, the number of nodes, the diameter of basal node and dry weight of stem (Liu, Liu, Li, & Herbert, 2013). Also, Brodie, Ryan, & Lancaster (2012) experimented with microwave radiation and found that it was lethal to paddy melon seeds and

seedlings. The authors concluded that the microwaves caused internal steam explosions in the seeds and seedlings and that resulted in their death.

With chemical mutagens, 25 mM of EMS produced mutants in leaves (pentafoliate and tetrafoliate), long pod, single-seeded pod, variants of pink flower colour and chlorophyll II spectrum mutants (albino, virescence and xantha) (Gnanamurthy & Dhanavel, 2014). Generally, increasing the concentration of EMS decreased germination parameters such as percentage germination, epicotyl and hypocotyl lengths, seedling vigour and seedling survival in pigeon pea (Ariraman *et al.*, 2014).

According to Horn and Shimelis (2013); gamma irradiation doses greater than 300 Gy significantly reduced the germination percentage of cowpea seeds. The authors also reported that epicotyl length and hypocotyl length generally decreased with increasing dosage of gamma irradiation. These seed abnormalities were linked to the destruction of the plant hormone, auxin and a possibility of chromosomal aberration due to the ionising radiation. Similar results have been reported by Dhanavel & Girija, (2019); Gwata *et al.* (2016) Gnanamurthy *et al.* (2019). Kusmiyati *et al.* (2018) also reported that higher irradiation doses significantly reduced measured germination parameters such as first and final germination count, germination rate index, and germination index and epicotyl and hypocotyl lengths among others in soybean.

In barley seeds, Rozman (2014) found that gamma irradiation doses from 400 Gy and beyond showed significantly decreased germination percentage compared to lower doses. However, irradiation doses lower than 300 Gy were not

significantly different from the control. Also, samples irradiated with ≥200 Gy recorded lower germination percentage with age but in the fifth year, the 100 Gy irradiated seeds recorded higher germination percentage than the control and other treatments. In rice, similar results have been documented (Harding *et al*., 2012). It was observed that increasing irradiation dose up to 800 Gy had no significant effect on germination up to the 7^{th} day when sowing was done under laboratory conditions but seedlings survival and heights were decreased under field conditions for doses ≥300 Gy in the M_1 mutants (Harding *et al*., 2012).

In recent times, percentage germination is an unsatisfactory indicator when used solely to assess germination in seeds (El-Bialee & Nawito, 2020). Hence, other derivatives of percentage germination that better predict the temporal dynamics that characterise the germination process is required to a wholesome evaluation. These derivatives may include measurements of germination rates, uniformity and synchrony (Ranal & De Santana, 2006).

2.6.2.2 *Effect of irradiation on vegetative and yield traits*

Studies by Singh, Surabhi, Gao and Reddy (2008) revealed that there was significant genotypic variability among plant characteristics measured when they were exposed to projected UV-B radiation. Specifically, most of the vegetative traits measured showed a positive response to the UV-B radiation, whereas the reproductive traits such as flower length and seed yields were lowered by the same radiation.

Increasing gamma irradiation generally decreased both vegetative and yield traits in cowpea when irradiation doses up to 500 Gy were applied

(Gnanamurthy *et al*., 2019). Vegetative growth traits such as plant height, the number of leaves, the number of branches and the number of clusters decreased with increasing doses up to 500 Gy. Kusmiyati *et al*., (2018) also reported that gamma irradiation had varied effects on leaf anatomical properties such as stomata density, width and length in soybean. Yield traits such as pod number and seed yield per plant decreased with increasing gamma irradiation doses (Gnanamurthy *et al*., 2019). However, mutations are random events and hence responses to irradiation may vary for different genotypes.

2.6.2.3 *Effect of irradiation on pathogens*

Studies on the effectiveness of gamma irradiation against certain fungal species were conducted by Jeong, Shin, Chu and Park (2015). The results showed that spore germination, germ tube elongation, and mycelia growth of *Penicillium digitatum* were completely inhibited at 1000 Gy. However, the interaction of 400 Gy and 10 ppm of sodium dichloro-*s*-triazinetrione (NaDCC) achieved the same inhibitory results. Similar results have been published (Jeong *et al*., 2015). Irradiating wheat at 3000 Gy was able to reduce the presence of *Aspergillus*, *Alternaria* and *Fusarium* by about 10-fold (Calado *et al*., 2014). More so, 5000 Gy of irradiation achieved similar results in rice. Similar results have been reported in lotus seed (Bhat *et al*., 2010) and in cowpea (Lima *et al*., 2011).

Fungal genera such as *Aspergillus*, *Rhizopus*, *Penicillium* and *Fusarium* were eliminated at varying irradiation doses up to 10000 Gy (Lima *et al*., 2011). In barley, irradiation at 4000 Gy has been effective in reducing fungal infection without negatively affecting its germination (Kottapalli, Wolf-Hall, Schwarz,

Schwarz, & Gillespie, 2003). There is limited evidence on the effect of low dose irradiation on seed-borne mycoflora. However, there is evidence of susceptibility of microbes at the logarithmic growth phase to low dose irradiation than during the stationary growth phase (Radomyski *et al.*, 1994).

2.7 Seed and Seed Quality

The seed of a crop is an indispensable factor for agricultural production in any country (Van Gastel, Gregg, & Asiedu, 2002; Etwire *et al.*, 2013). Seed quality is a concept that expresses the extent to which given seeds meet set standards for known attributes that determine the quality status of seeds (FAO & AfricanSeeds, 2018). Thus, a high-quality seed is essential to enhancing agricultural productivity, safeguarding food security, and improving rural livelihoods (Zhou, 2016; Vijay, Kumar, Yadava, & Kumar, 2017). According to Etwire *et al.* (2016), an improved seed could be well-thought-out as the most significant technology that significantly contributes to crop productivity regardless of other input factors. The seed is seen as a medium for disseminating technology, both the technology embedded in the seed itself (for example, short-straw feature of rice and wheat) and the technology that accompanied the new genes (Louwaars, 2002). Hence, the results of irradiation in cowpea can be explored for new genes that satisfy the needs of farmers and consumers.

2.8 Determinants of Seed Quality

Quality seeds are sometimes referred to as standard seeds because regular inspections have been conducted on them (Wekundah, 2012). These inspections are mainly genetic purity, seed physiological quality test (germination tests) and

seed health test (FAO, 2004; ISTA, 2012). Thus, seed quality has evolved from simple visualizations to comprehensive measurements at all stages of seed production and marketing (Van Gastel *et al.*, 2002). These tests usually lead to varietal purity and identity (Atilaw *et al.*, 2011) and the ability to establish properly in the field (Van Gastel *et al.*, 2002).

2.8.1 Seed Purity Test

Seed purity tests typically include physical purity and genetic (varietal) purity. Physical purity is mostly achieved by the removal of debris, other seeds and inert materials such that by physical observation, the seeds look clean and uniform in shape, size and colour. For a certified seed, the proportion of pure seed, weed seeds, other crop seeds, inert materials and other possible physical contaminants must be clearly labelled (Kameswara Rao *et al.*, 2006; Sanne, Vodouhe, Halewood, & De Jonge, 2017; FAO & AfricanSeeds, 2018).

It is technically difficult to test for genetic purity in seeds. This is because the genetic differences in seeds are easily detectable when grown in the field (Van Gastel *et al.*, 2002). The major observation for genetic purity is trueness-to-type, usually determined by checking seedling/plant characteristics to verify the source and history of the seed (FAO & AfricanSeeds, 2018). This is usually time-consuming since seedling characteristics within species are minimal in the early growth stage of plant life. However, recent advances in biotechnology have made it possible to detect genetic variation in seeds in laboratories but this approach can be cumbersome and expensive (ISTA, 2012).

2.8.2 Seed Physiological Quality

The physiological quality of a seed refers to the performance of the seed in terms of viability and vigour which characterise its germination (ISTA, 2010). Germination is a process initiated by imbibition and culminates in the elongation of the embryonic axes; plumule and radicle (Bhatla & Lal, 2018). The germination capacity is a measure of the proportion of live seeds that can produce normal seedlings without defect (Mathur *et al.*, 2003; FAO & AfricanSeeds, 2018). A germination test is carried out to ascertain the fraction of a seed sample that will germinate and produce healthy seedlings (Kameswara Rao *et al.*, 2006). A vigour test, however, assesses directly or indirectly the physiological and physical basis of prospective seed lot performance in a range of environments and provides a more profound differentiation between seed lots of acceptable germination than does the germination test (ISTA, 2010).

The commonly used substrates in germination tests include paper, sand and sometimes soil. The growth medium and apparatus are sterilized to minimize non-seed source contaminations. The use of paper is more accustomed to small sized seeds (example, onion) while sand is often used for relatively large seeds such as maize. In a working sample, 100 seeds in 4 replications are the standard for a germination test. The set-up is usually left to stand for a week. Germination count can be daily and destructive or non-destructive and cumulative (Mathur *et al.*, 2003; ISTA, 2010).

A normal seedling should have the ability to grow into a satisfactory plant under good environmental conditions of moisture, light and temperature. The

normal seedling should be healthy and well developed with all the essential structures complete and also in proportion (Mathur *et al.*, 2003). The essential structures should be balanced for both root and shoot systems (Bhatla & Lal, 2018). Some of the deformities that may characterise an abnormal seedling include features in either or both of the root and shoot systems: seedlings being stunted, stubby, retarded, missing structures, broken, constricted, spindly, etc. (Mathur *et al.*, 2003).

2.8.3 Seed Health Quality

Seed health test refers to the presence or absence of disease-causing organisms that determine the disease status of a seed sample (ISTA, 2010; Kameswara Rao *et al.*, 2006). Seeds may be contaminated by microscopic inoculum during seed collection. These infections are generally in four groups; fungi, bacteria, insects and viruses (Kameswara Rao *et al.*, 2006). In other scopes, seed health testing may involve physiological conditions such as trace element deficiency (ISTA, 2010). The control of seed-borne infections is the first stage in any effective crop protection and production programme (Van Gastel, Bishaw, & Gregg, 2002).

Different methods have been classified for use in seed health test. The most common are the standard blotter method and the agar method. The methods are dependent on the sensitivity and reproducibility of the results, as well as the equipment required. The method used also depends on the pathogen or condition to be investigated, the purpose of the test and the species of the seed. Selection of the method and assessment of the results requires mastery of the methods

available. In effect, the choice of the method ensures that the presence or absence of disease inoculum, pests and damaging physiological conditions specified by the client is estimated as accurately as the method used permits (ISTA, 2010).

Seed health quality is essential because on the field, seed-borne inoculum may give rise to progressive disease development and thus reduce the crop's commercial value. Also, seed health test may explain seedling performance and the causes for poor germination or field establishment and consequently supplement germination test. More so, the results of seed health test may/can be the cause for seed treatment in order to eliminate seed-borne pathogens or to lessen the risk of disease transmission (Kameswara Rao *et al.*, 2006; ISTA, 2010). Seed health test may be carried out as a requirement for phytosanitary certificates that conform to the International Plant Protection Convention (IPPC) standards (Aveling, 2014; Zhou, 2016). In summary, seed health is of utmost significance in the value chain of crop production (International Rice Rsearch Institute, 1994).

2.9 Effect of quality seeds on seed system

The poor access to good quality seeds by most sub-Saharan African farmers has contributed greatly to the low productivity of agricultural systems in the sub-region (Asare *et al.*, 2016). The notion that the seed is the most important input in any cropping system paves the way for the development of an efficient seed system where institutions involved in the sustainability of the enterprise mutually coordinate till good quality seeds are eventually released to the grain farmer (Etwire *et al.*, 2016). This is because a competitive seed system is a key to

ensure that high-quality seeds and appropriate varieties are made available to farmers (Mabaya *et al*., 2017).

It should be noted that both high and low-quality seeds can be found in both the formal and informal seed systems of every country (FAO, 2004). Since most countries are trying to formalise their seed systems, there is the risk of genetic erosion of farmer varieties when these varieties have not been collected to be kept in genebanks and later used in other participatory plant breeding programs (Wekundah, 2012). Understanding the seed system of any crop is the surest way to monitor the response of the associative stakeholders (breeders, farmers, extension officers, etc.) for a more effective seed delivery system for enhanced agricultural productivity.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Cowpea genetic materials

Twenty-five (25) genotypes of cowpea (Table 1) were used for the experiment. These genotypes included five improved varieties from Crops Research Institute- Council for Scientific and Industrial Research (CRI-CSIR, Ghana), three inbred lines from the International Institute for Tropical Agriculture (IITA, Nigeria) and 17 genotypes from Uganda out of which one was an improved variety, three landraces and 13 inbred lines at F_9 generation. The genotypes were selected based on their differences in yield, seed physical properties and growth habit, as well as their sources (countries of origin).

3.2 Sampling and radiation

Three thousand, five hundred (3500) seeds of each genotype were sampled. These were further allotted into 700 seeds replicates to be irradiated according to genotype for the respective objectives; seed physiological quality testing (400 seeds), seed health testing (200 seeds) and agronomic performance (100 seeds). Five different doses of irradiation were used in this study. These doses were the control (0 Gy), 50, 100, 150 and 200 Gy, at a dose rate of 330 Gys^{-1}. These dose ranges are not lethal to cowpea (Horn & Shimelis (2013; Liu *et al.* (2017). The irradiation was carried out at the Biotechnology and Nuclear Agricultural Research Institute (BNARI) of the Ghana Atomic Energy Commission (GAEC).

Table 1: Details of genotypes used in the study

Genotype	Yield (kg/ha)	Seed colour	Growth habit	Country/ source	Cultivar type
Agyenkwa	1060.6	White	semi-erect	Ghana	Improved
Asontem	1662.7	Red	semi-erect	Ghana	Improved
Hansadua	1009.4	White	semi-erect	Ghana	Improved
Nketewadea	1564.9	White	semi-erect	Ghana	Improved
Soronko	1760.5	Red	semi-erect	Ghana	Improved
IT889	1596.3	Mottled	semi-erect	IITA	Inbred line
IT91	1868.9	Brown	semi-erect	IITA	Inbred line
IT97K819	1694.2	Brown	semi-erect	IITA	Inbred line
Sunshine1M	1865.0	Brown	semi-erect	Uganda	Inbred line
ACC122W*NE48	1768.3	Brown	semi-erect	Uganda	Inbred line
Secow5T	2175.8	Brown	semi-erect	Uganda	Improved
ACC122W*NE51	1729.9	Brown	semi-erect	Uganda	Inbred line
ACC122W*WC10	1986.8	Brown	semi-erect	Uganda	Inbred line
ACC122W*WC36	2662.5	Black	semi-erect	Uganda	Inbred line
Alegi*NE51	1821.6	Brown	semi-erect	Uganda	Inbred line
Ebelate	1901.2	Brown	semi-erect	Uganda	Inbred line
F258T2E	1700.2	Brown	Erect	Uganda	Inbred line
H24	2111.4	Black	semi-erect	Uganda	Inbred line
NE15*WC35B	2843.6	Brown	semi-erect	Uganda	Inbred line
WC10*WC36	3047.6	Brown	semi-erect	Uganda	Inbred line
Alegi	1871.0	Brown	semi-erect	Uganda	Landrace
NE21	2356.2	Mottled	semi-erect	Uganda	Landrace
Sunshine	2237.1	Brown	semi-erect	Uganda	Landrace
WC10	1539.4	Brown	semi-erect	Uganda	Landrace
WC36	1359.7	Brown	semi-erect	Uganda	Landrace

3.3 Experiment One - Seed Physiological Quality Test

3.3.1 Location of the Experiment

The experiment was conducted at the Crop Science laboratory at A.G. Carson Technology Centre (School of Agriculture), University of Cape Coast. The mean daily temperature of the germination room was 26 °C.

3.3.2 Substrate and growth conditions

Sea sand was used as the substrate. The sand was put in a sack and drenched under running water for 1 h to dissolve the salt (minerals) to an alkaline pH of 8.3 on a pH meter. It was then air-dried on a concrete floor for three days, during which the sand was intermittently turned to hasten the drying. This was then followed by sieving through a 2 mm Tyler sieve to obtain uniform particle size (ISTA, 2010). The sieved substrate was then heat sterilized at 150 ^{O}C for 3 h (ISTA, 2010) in an oven (Memmert oven, UNE 700 3N - 400V 50/60Hz DIN 12880-K1) using aluminium trays of dimensions 35×25×5(cm^3) [length, breadth and height respectively]. The sand was then allowed to cool and stored in clean airtight sacks to minimize contamination and kept on a bench.

The seed trays and plastic sheets were also sterilized with bleach; sodium hypochlorite (1% NaOCl). The sand was moistened with distilled water and used to fill the seed trays. Fifty (50) holes of 2 cm depth were made in the trays and the seeds sown singly per hole in each tray. The holes were 5 cm apart so that exudative effects between adjacent seeds were minimized (Figure 1). The setup was arranged on the floor overlaid with black plastic sheets in randomized complete block design due to differences in ventilation and light in the

germination room. The trays were covered with plain polythene sheets (Figure 2) to maintain the moisture content of the medium for the entire duration of the experiment. The set up was observed for 14 days.

Figure 1: Seed trays showing how holes were made and seeds sown

Figure 2: Seed trays covered with polythene sheet to minimize evaporation

3.3.3 Measurement of germination parameters

Germination was recorded based on recommendations from (ISTA, 2010). A seed was said to have germinated when any of its essential structures (epicotyl or hypocotyl) emerges above the medium. The setup was observed from day 1 after sowing till day 8 but was further observed till day 14 for late germinations. Germination count was done daily and germinated seedlings were recorded. After recording germination, seedlings were examined as normal or abnormal based on the presence or absence of essential structures of the root or shoot portions and then discarded. The parameters were computed as follows:

Day to first germination (DFG): This was the day on which the first germination event was observed within the 14-day period.

Day to last germination (DLG): This was the day on which the last germination event was observed within the 14-day period.

Time spread of germination (TSG): This was the difference in days between the first and last germination events (Kader, 2005) occurring within the 14 days (Equation 1).

$$\mathbf{TSG} = \mathbf{DLG} - \mathbf{DFG} \qquad \text{Equation 1}$$

Germination percentage (G %): This was the percentage of the total seeds that germinated within the 14 days of observation (Equation 2). It was based on the binary answer of germinated or non-germinated (Ranal & De Santana, 2006).

$$\mathbf{G\ \%} = \frac{\boldsymbol{number\ of\ seed\ germinated}}{\mathbf{Total\ number\ of\ seeds\ sown}} \text{ x } 100 \qquad \text{Equation 2}$$

Percentage decayed seeds (%DcS): This was the proportion of seeds that were decayed, mouldy or showed mycelial growth (Olembo, 1985; ISTA, 2010) within the 14 days (Equation 3).

$$\mathbf{\%\ DcS} = \frac{\boldsymbol{number\ of\ decayed\ seeds}}{\mathbf{Total\ number\ of\ seeds\ sown}} \text{ x } 100 \qquad \text{Equation 3}$$

Percentage deformed seedlings (%DfS): This was the proportion of the total sown seeds that germinated with abnormal root and or shoot organs. Any seed that had one or a combination of the following seedling defects was classified as deformed: stunted, stubby, retarded, missing, broken, constricted, spindly or glassy (Mathur *et al.*, 2003).

$$\%DfS = \frac{number\ of\ deformed\ germinats}{\text{Total number of seeds sown}} \text{ x } 100 \qquad \text{Equation 4}$$

Percentage hard seeds (%Hs): This was the proportion of sown seeds that remained intact after the 14 days. These seeds did not show signs of decay/rot nonetheless, they failed to germinate (ISTA, 2010).

$$\%Hs = \frac{number\ of\ ungerminated\ seeds}{\text{Total number of seed sown}} \text{ x } 100 \qquad \text{Equation 5}$$

Days to 50 % germination (T50%G): This is the taken for 50 % of seeds to germinate. If the germination has symmetric frequency distribution, the mean time and the median time can be used to show central tendency of the data (Ranal & De Santana, 2006).

Coefficient of Velocity of Germination (CVG): This was a measure of the rapidity of the germination event (Kader, 2005). It was calculated by

$$CVG = \left(\frac{\sum_{i=1}^{k} f_i}{\sum_{i=1}^{k} f_i x_i}\right)100 \qquad \text{Equation 6}$$

Where, f_i: newly germinating seeds on day i; x_i: number of days from sowing, and k: last day of germination.

Coefficient of Variation of Germination time (CV_t): This was used to evaluate the germination variability or uniformity in relation to the mean germination time (Equation 7). It served as a relative dispersion measurement that permitted comparisons, independently of the extent of the mean germination time (Ranal & De Santana, 2006).

$$CV_t = \frac{S_t}{\bar{t}} 100 \quad \text{Equation 7}$$

Where S_t: standard deviation of the germination time and $\bar{t}$: mean germination time

Germination index (GI): This was used to place emphasis on the percentage germination and its corresponding speed (Kader, 2005).

$$\mathbf{GI} = (20xN_1) + (19xN_2) + \ldots + (1xN_{20}) \quad \text{Equation 8}$$

Where N_1, N_2 ...N_{20} is the number of germinated seeds on the first, second and subsequent days until 20th day and the multipliers (*e.g.* 20, 19 ... *etc.*) are weights given to the days of the germination.

Mean Germination Rate (MGR) was computed as the reciprocal of the mean germination time (Equation 9). It was a measure of the speed of germination (Ranal *et al.*, 2009).

$$MGR = \frac{\sum_{i=1}^{k} n_i}{\sum_{i=1}^{k} n_i t_i} \quad \text{Equation 9}$$

Where t_i: time from the start of the experiment to the i^{th} observation; n_i: number of seeds germinated in the i^{th} time and k: last time of germination.

Mean Germination Time (MGT): This was a measure of the time taken for the seeds to germinate (Equation 10). It was dominated by the day when most germination events occurred (Kader, 2005).

$$\bar{t} = \frac{\sum_{i=1}^{k} n_i t_i}{\sum_{i=1}^{k} n_i}$$ Equation 10

Where t_i: time from the start of the experiment to the i^{th} observation; n_i: number of seeds germinated in the i^{th} time and k: last time of germination.

Synchronization Index (Z) was used to calculate the degree of overlapping between germinating seeds (Ranal & De Santana, 2006).

$$Z = \frac{\sum_{i=1}^{k} Cn_{i,2}}{C_{\sum n_i,2}};$$ Equation 11

$$Cn_{i,2} = n_i(n_i\text{-}1)/2$$

Where $Cn_{i,2}$: combination of the seeds germinated in the i^{th} time, two by two, and n_i, number of seeds germinated in the i^{th} time.

Uncertainty of the Germination process (*U*) was used to measure the degree of uncertainty in predicting the uncertainty associated with the distribution of the relative frequency of germination (Ranal & De Santana, 2006). It was calculated as

$$U = -\sum_{i=1}^{k} log_2 f_i$$ Equation 12

$$f_i = \frac{n_i}{\sum_{i=1}^{k} n_i}$$

Where n_i: number of seeds germinated on the i^{th} time, and k: last day of observation.

3.4 Experiment Two- Seed Health Test

3.4.1 Study Area

The experiment was carried out at the Seed Pathology laboratory of Crop Research Institute (CRI) under the Council for Scientific and Industrial Research (CSIR), Fumesua-Kumasi.

3.4.2 Experimental Set-up

The experiment was laid out in a completely randomised design (CRD). The seed testing method was the Standard Blotter Method; where seeds were plated and observed for their mycoflora after 7days of incubation.

3.4.3 Standard Blotter Method (ISTA, 2010)

3.4.3.1 *Preparation of Petri dishes*

For each treatment, 40 Petri dishes of 90 mm diameter were conditioned for use. The Petri dishes were sterilized with 70% ethanol. Each dish was labelled with the treatment name and the date of plating. Three blotter papers were together dipped in distilled water and placed in each Petri dish.

3.4.3.2 *Sample size*

Out of the 200 seeds sampled, two sub-samples of 100 seeds each were obtained. Thus, each sub-sample consisted of two replicates of 50 seeds each making 100 seed sub-sample total. These sub-samples were plated separately as pre-treated and untreated samples with appropriate labels for the seed health test.

3.4.3.3 *Pre-treatment*

One sub-sample of 100 seeds was pre-treated with 1% NaOCl for 5 minutes, after which they were dried on autoclaved blotter paper in a fume hood and then plated. The pre-treatment was meant to suppress the rapid growth of saprophytic fungi while enhancing the growth of pathogenic seed-borne fungi. The pre-treatment also served as a basis for comparison between the sub-samples for the specific fungi that will grow on the pre-treated and untreated seeds (Afutu, 2012).

3.4.3.4 *Seed plating*

Ten (10) cowpea seeds were plated in each Petri dish of 90 mm diameter. The seeds were arranged radially such that adjacent seeds were almost equidistant from each other (Figure 3) in order to minimize cross-contamination of seeds by the growing pathogens during incubation.

3.4.3.5 *Incubation of seeds*

The labelled Petri dishes were put in seed trays and conveyed to the incubation room according to their randomizations (Completely Randomized Design) (Figure 4). The transit was gently done such that the plated seeds were not displaced in the dishes. The incubation room had a temperature of 22 °C. The seeds were incubated for 7 days under alternating 12 hours of light and darkness regimes. The light was provided by fluorescent tubes 20 cm apart that hang horizontally. The tubes (Philip TL-D 36W/08) provided light rays of near-ultraviolet (NUV) with photosynthetic radiation range of 340 – 410 nm with a peak intensity of 270 μWcm^{-2} at 365 nm (Yin *et al*., 2014). The distance between the light source and

the dishes was 40 cm. The NUV light source was intended to enhance sporulation; which improves the identification of the mycoflora (Alam *et al*., 2014).

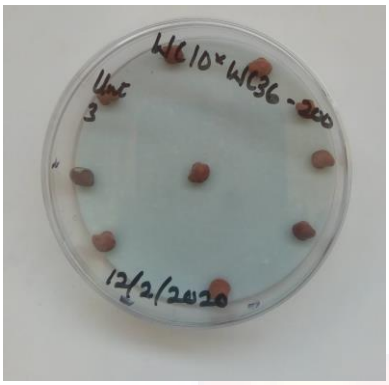

Figure 3: Radial arrangement of seeds on blotter paper

Figure 4: Plated seeds under NUV light during incubation at CSRI-CRI

3.4.4 *Examining the incubated seeds*

Guidelines for the examination and identification of seed-borne fungi described in the first edition of Common Laboratory Seed Health Testing Methods for Detecting Fungi (ISTA, 2010) were followed.

After 7 days of incubation, the plated seeds were examined. Among the sub-samples (treated or untreated seeds), the 20 Petri dishes were serially numbered; 1, 2, 3, 4 …20). To examine each seed, a horizontal line was drawn from the centre of the blotter to the edge and used as a guide for the completion of the rotation. The radially plated seeds were examined singly in a clockwise pattern using the drawn line. The examination was carried out under different magnifications (X^{16} - X^{25}) using a stereoscopic microscope to ascertain the habit character of each fungus observed (Bhuiyan *et al.*, 2013). In situations of

uncertainty about the identification of a fungus, slides of the fruiting structures were prepared and viewed under a compound microscope. The mycoflora were identified using mycological literature (ISTA, 2010).

During the examination, a seed was counted as infected if an identifiable fructification was observed. For example, the presence of a single conidiophore with the conidia of *Alternaria* and *Bipolari*, an acervulus of *Colletotrichum*, sporodochium of *Fusarium*, a Pycnidium of *Ascochyta*, *Botryodiplodia* and *Macrophomina* implies that a seed was infected (ISTA, 2010).

When the species identification of a fungus is successful with the aid of a compound microscope, the abbreviation of the scientific name of the fungus was written on the blotter; for example, '**An**' for *Aspergillus niger*, **Fm**' for *Fusarium moniliforme* and '**Fo**' for *Fusarium oxysporum*.

3.4.5. *Recording of infection*

The abbreviation of each fungus observed was crossed with a different colour pencil to enable easy counting during the final check. This was done to guarantee that all marked abbreviations were counted. After the examination of each plate, the final count of each fungus was immediately recorded in a Working Recording Sheet (ISTA, 2010) (Appendix 1).

3.5 Experiment Three – Field Evaluation

3.5.1 Study area

The experiment was conducted at the Alex Carson Teaching and Research Farm of the School of Agriculture, University of Cape Coast, Ghana. The location was characterized by a bimodal rainfall pattern from May to June and August to October. The annual mean rainfall of the area ranges between 750 and 1000 mm (Asare-Bediako *et al*., 2014) and a mean temperature of 27.6^{O}C (Asare-Bediako *et al*., 2017). The soil type was an Acrisol and the location falls within the Coastal Savannah Zone of Ghana and within latitude 05°-03'N and 05°-5'N, longitude 01°-13'W and 01°-13'W (Armah, 2011). Rainfall and temperature data were also collected for the duration of the field experiment (Appendix 2). The site was previously cropped with cassava and then left to fallow for a year before the experiment was conducted.

3.5.2 Land preparation

An area of 1430 m^2 (22 m × 65 m) was cleared, ploughed and harrowed to a fine tilth. The plain field was then set out and pegged for sowing.

3.5.3 Soil sampling and analysis

The field was zoned into three blocks and soil samples were collected in each block by cores in a Z-pattern. The samples were air-dried and bulked. Three sub-samples were taken from the bulk for physical and chemical properties of the field. The physical and chemical properties determined included bulk density, particle density, pH, total nitrogen (N), available phosphorus (P), calcium (Ca)

and exchangeable K (potassium), and cation exchange capacity (CEC) (Appendix 3). These physico-chemical properties give an indication of the fertility status of the soil and its complementary impact on crop yield (Belay *et al*., 2002).

3.5.4 Field experimental design

A randomised complete block design (RCBD) with three replications was laid out for the field experiment. Each replication had 125 treatment combinations. These consisted of 5 rows of 25 plots totalling 125 plots per block. The treatments were assigned to their respective plots within the block up to the 125th. Each plot measured 3.0 m × 0.8 m. An inter plot distance of 0.8 m was allowed and within a plot, a distance of 0.3 m between plant stands and 1 m between replications. Each plot had 10 plants in two rows of 5 each. Two seeds were sown per hill but thinned to 1 after field establishment.

3.5.5 Agronomic practices

The field was sprayed with "*Glycot"* which is a pre-emergence herbicide with glyphosate as active ingredient. The rate of application was 75 ml per 15 litre knapsack sprayers. Insecticide application was done at the 3rd, 5th and 8th week after germination. The insecticide used was "*PAWA 2.5EC*" with lamba-cyhalothrin as active ingredient at a rate of 50 ml/15 litre. No fertilizer or fungicide was applied to the plants during the course if the experiment. The field was weeded with hoe 3 times before the final harvest.

3.5.6 Data collection

The six central plants were tagged for field data collection. Data on the days to first flowering, days to 50% flowering, number of branches per plant, number of peduncles per plant, number of pods per peduncle and number of pods per plant were taken on the field. At harvest, pods were selected at random from the plants tagged and further yield data were taken; pod length (cm), seeds per pod and 100 seed weight (g). These were used to estimate the grain yield (kg ha^{-1}) per plot for each treatment.

General observations were also made for differences in plant morphology among the mutants and insect's infestations on the field.

3.6 Data and statistical analysis

The major statistical software used for the data analyses were Microsoft excel and GenStat Release 10.3DE, Discovery Edition 4, 2016 (VSN International Limited, Rothamsted Experimental Station, Hemel Hempstead, UK). IBM SPSS Statistics for Windows, Version 20.0 was also used for Principal Component Analysis (PCA) and correlations.

Means of the germination parameters, grain yield and yield related parameters were computed in Microsoft Excel 2010 and then subjected to analysis of variance (ANOVA) in Genstat to test for statistical significance. The treatment factors for the two-way ANOVA were genotype, dose of irradiation and the genotype and dose interaction. For the seed health testing, mean percentage mycoflora infections were Arcsine transformed. Differences between the treatments were compared by least significant difference (*lsd*) at P = 0.05.

Chi-square tests for interdependence between six selected traits from all three experiments were performed. Excerpts from Nikolić *et al.*, (2020) was used to establish the threshold for decayed and hard seeds. The mycoflora infection guide was adopted from Department of Environment and Primary Industries (2013). Yield potential for cowpea in Ghana was used to establish the ranges for yield in the chi-square test rankings (MoFA; SRID, 2017) whereas the germination thresholds followed recommendations in ISTA (2010). The set ranges for measured traits used for the Chi-square tests for interdependence are summarised in Appendix 4.

The structure of the interrelationships between the 25 genotypes irradiated at five different levels was analysed with Principal Component Analysis (PCA) to explain their common underlying measurements. The PCA involved Varimax rotation and Kaiser-Meyer Normalization done in SPSS version 20.

CHAPTER FOUR

4.0 RESULTS

4.1 Experiment One: Seed Physiological Quality

The results of analysis of variance of the various seed physiological quality parameters of the cowpea genotypes as affected by the doses of irradiation showed that there were significant ($P < 0.001$) differences on all measured germination traits among the genotypes. Similarly, there were significant ($P < 0.001$) differences among the doses of irradiation on percentage hard seeds, percentage decayed seeds, days to 50% germination, mean germination time, mean germination rate, coefficient of velocity of germination, coefficient of variation of germination time, uncertainty of germination and synchronization index.

There were significant ($P < 0.001$) interactions between the genotypes and doses on all measured traits. There were also significant ($P = 0.044$) genotype-dose interactions on day to last germination, time spread of germination and percentage of deformed seedlings. Details of these are shown in Figures 5 to 26 and Tables 3 to 6.

Table 2: Combined ANOVA for mean sum of squares for seed physiological quality parameters of irradiated cowpea seeds

	Mean sum of squares						
Source of variation	Day to Last Germination	Time Spread of Germination	Days to 50% Germination	Percentage Germination	Percentage Decayed seeds	Percentage Hard seeds	Percentage Deformed Seedlings
Genotype (G)	2.92***	2.924***	0.812***	1843.24***	323.58***	636.27***	11.694***
Dose (D)	1.32	1.32	0.080***	10.92	273.71***	355.43***	5.28
G × D	1.01*	1.001*	0.054***	177.73***	33.66***	80***	4.03*
Residual	0.74	0.737	0.004	82.99	14.56	30.23	2.95

* and *** show significance at P < 0.05 and P < 0.001 respectively

Table 2 continued

	Mean sum of squares						
Source of variation	Coefficient of Velocity of Germination	Coefficient of Variation of Germination time	Germination Index	Mean Germination Rate	Mean Germination Time	Synchronization index	Uncertainty of germination
Genotype (G)	93.43***	2.94***	52.17***	0.0032***	0.056***	0.021***	0.454***
Dose (D)	15.92	32.12***	0.21	0.0002***	0.658***	0.044***	0.152***
G × D	27.13***	2.20***	3.58***	0.0002***	0.046***	0.007***	0.060***
Residual	11.95	0.38	1.20	0	0.009	0.002	0.029

* and *** show significance at P < 0.05 and P < 0.001 respectively

4.1.1 Genotypic effect of irradiation on cowpea seed physiological quality

The results of mean number of days to last germination showed significant ($P < 0.001$) differences among the genotypes as shown in (Figure 5). The following genotypes; NE48*SecowIT, Ebelate, Hansadua, H24 and IT889 took 5 days to last germination and were significantly lower than Soronko, WC36 and NE15*WC36B which took 6 – 7 days to last germination (Figure 5). However, the remaining genotypes were not significantly different from both extremes. The range for mean number of days to last germination was 5 – 7 days (Figure 5).

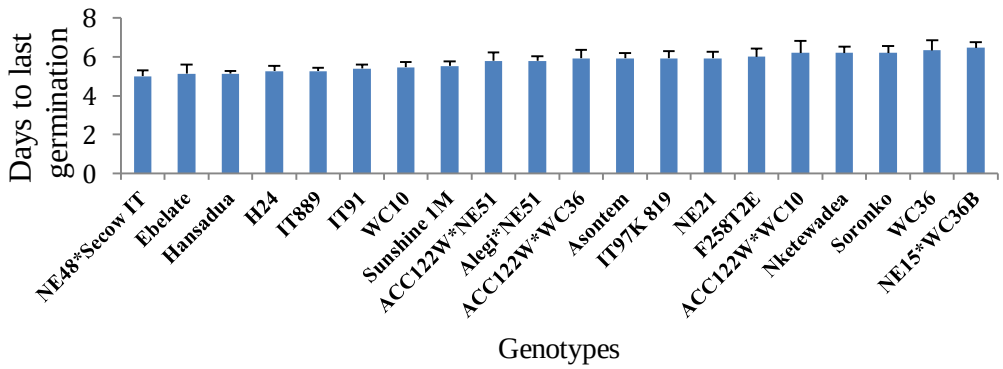

Figure 5: Genotypic response of irradiated cowpea seeds on day to last germination

Similarly, the results of time spread of germination exhibited significant ($P < 0.001$) differences among the genotypes (Figure 6). Time spread of germination ranged between 2 and 4 days (Figure 6). Genotypes ACC122W*WC36, Nketewadea, Soronko, WC 36 and NE15*WC36 were the topmost five genotypes with in time spread of germination. Conversely, NE48*SecowIT, Ebelate, Hansadua, H24 and IT889 had the lowest time spread of germination (Figure 6). The mean time spread of germination was ≈3 days.

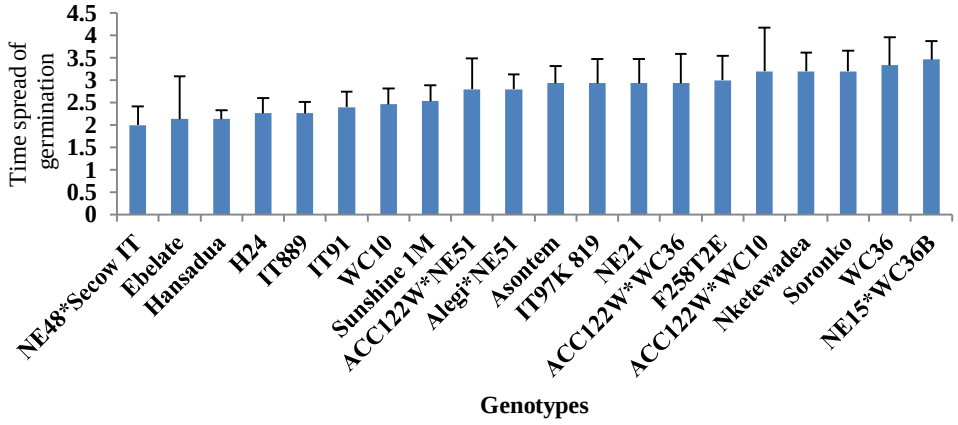

Figure 6: Genotypic response of irradiated cowpea seeds on time spread of germination

There were significant ($P < 0.001$) differences among the genotypes on days to 50% germination as shown in (Figure 7). Genotypes WC10 and Ebelate took the shortest days to 50% germination (≈3 days) and were significantly different from the remaining genotypes. However, genotypes ACC122W*WC36B, Sunshine 1M and ACC122W*NE51 took ≈4 days to attain 50% germination and they were the slowest genotypes to attain 50% germination. Although days to 50% germination ranged from 3 – 4 days, about 85% of the genotypes used ≈3 days to attain 50% germination (Figure 7).

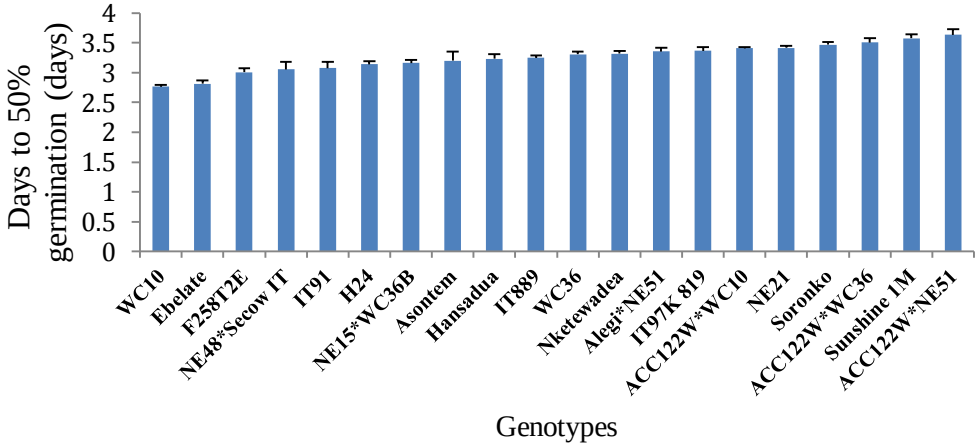

Figure 7: Genotypic response of irradiated cowpea seeds on days to 50% germination

The results for percentage germination showed significant ($P < 0.001$) differences among the genotypes (Figure 8). The percentage germination ranged from 59 - 96% with a mean of 80% (Figure 8). Genotypes NE15*WC36B, Nketewadea, Sunshine 1M and Alegi*NE51 were the poorest (59 – 63%) in percentage germination and were significantly lower than IT889, Ebelate and H24 (93 - 96%) which were the best performers in percentage germination (Figure 8). Only 15% of the genotypes recorded over 90% in percentage germination among the genotypes (Figure 8).

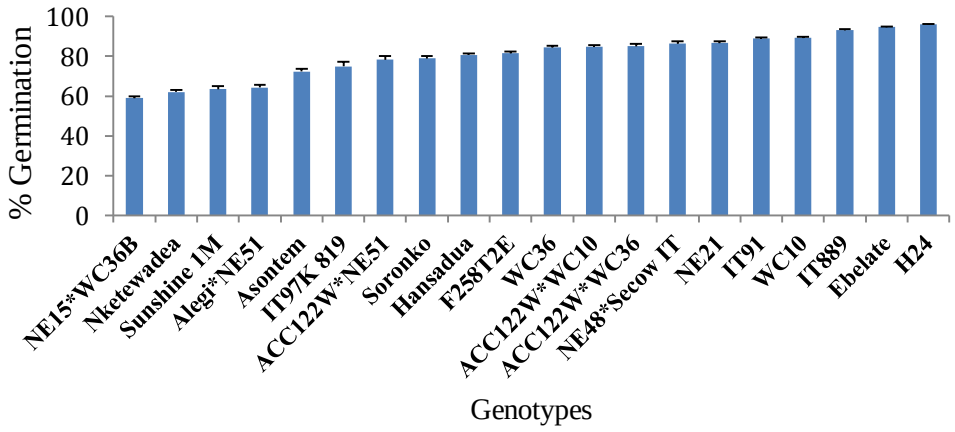

Figure 8: Genotypic response of irradiated cowpea seeds on percentage germination

Percentage decayed seeds showed significant ($P < 0.001$) differences among the genotypes as shown in (Figure 9). Genotype NE15*WC36B had the highest proportion of decayed seeds (17%) while H24 recorded just about 1% decayed seeds (Figure 9). The top four genotypes with the highest proportion of decayed seeds were NE15*WC36B (17%), Nketewadea (16%), Sunshine 1M (15%) and Alegi*NE51 (14%) while H24, Ebelate and IT889 had the lowest (1 - 3%) decayed seeds Figure 9). The mean percentage decayed seeds were 8 among the genotypes.

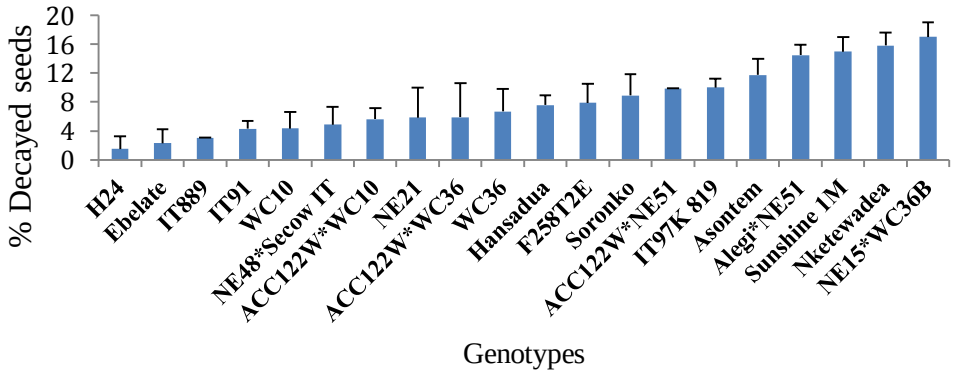

Figure 9: Genotypic response of irradiated cowpea seeds on percentage decayed seeds

The results for percentage hard seeds showed significant ($P < 0.001$) differences among the genotypes (Figure 10). Genotypes H24, Ebelate and IT889 recorded between 3% and 4% hard seeds as the genotypes with the least percentage hard seeds. Also, Alegi*NE51, Sunshine 1M, Nketewadea and NE15*WC36B recorded between 21% and 24% as the highest proportion of hard seeds. The mean percentage hard seeds among the genotypes was 12%. About 50% of the genotypes recorded at least 10% hard seeds (Figure 10).

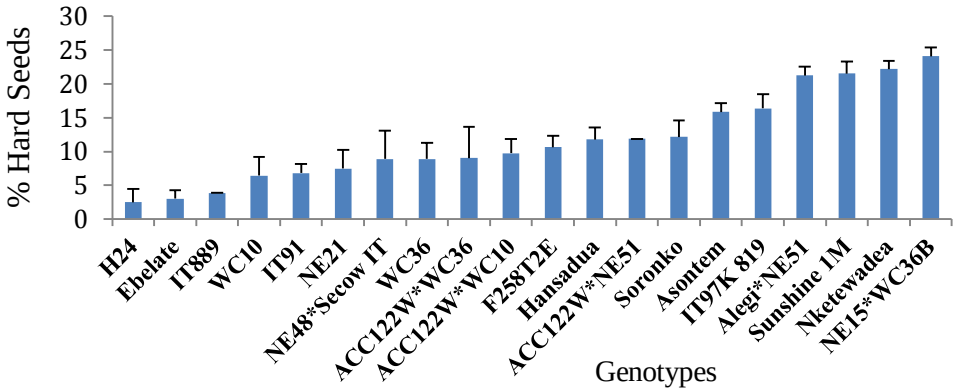

Figure 10: Genotypic response of irradiated cowpea seeds on percentage hard seeds

There were significant ($P < 0.001$) differences among the genotypes on percentage deformed seedlings (Figure 11). The range for percentage deformed seedlings among the genotypes was 10 – 13%. Nearly all the

genotypes had at least 10% deformed seedlings (Figure 11). Genotypes NE48*SecowIT, Ebelate, Hansadua and H24 had the lowest proportion of deformed seedlings (≈10%) and were significantly lower than WC36 and NE15*WC36B (Figure 11).

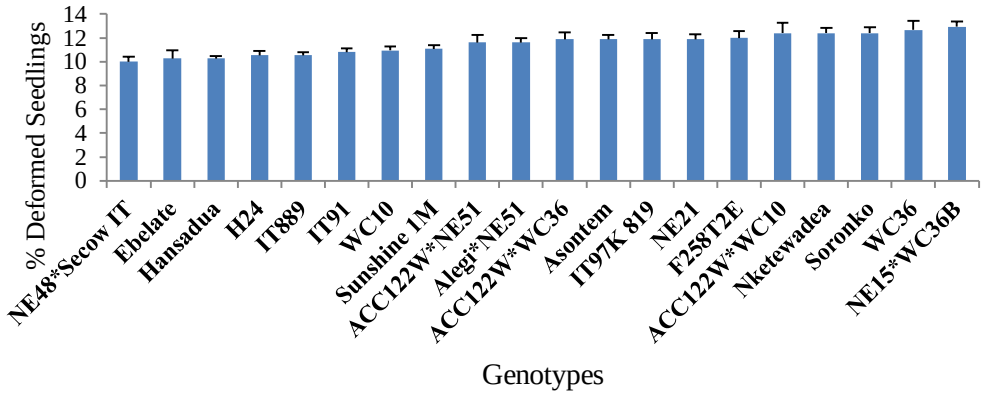

Figure 11: Genotypic response of irradiated cowpea seeds on percentage deformed seedlings

The genotypic response for coefficient of velocity of germination exhibited significant ($P < 0.001$) differences as shown in (Figure 12). The range for coefficient of velocity of germination was 16 – 24. The genotypes NE48*SecowIT and H24 had the least (16) coefficient of velocity of germination whereas WC10, NE15*WC36B, F248T2E and Nketewadea recorded the highest (23) for coefficient of velocity of germination with a mean of 19.9 (Figure 12). About 45% of the genotypes recorded a value less than 20 for coefficient of velocity of germination (Figure 12).

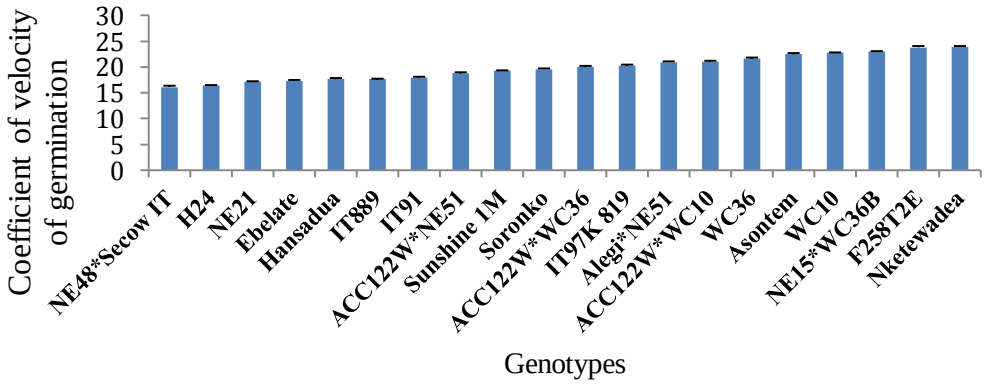

Figure 12: Genotypic response of irradiated cowpea seeds on coefficient of velocity of germination

The coefficient of variation of germination time showed significant ($P < 0.001$) differences among the genotypes as shown in (Figure 13). Among the genotypes, more than 50% recorded coefficient of germination velocity values between 24 and 26 (Figure 13). The highest coefficient of variation of germination time was recorded by Ebelate and WC10 (≈29) while ACC122W*NE51 and Sunshine 1M recorded the least (24) as shown in (Figure 13). The mean coefficient of variation of germination time was 26.3.

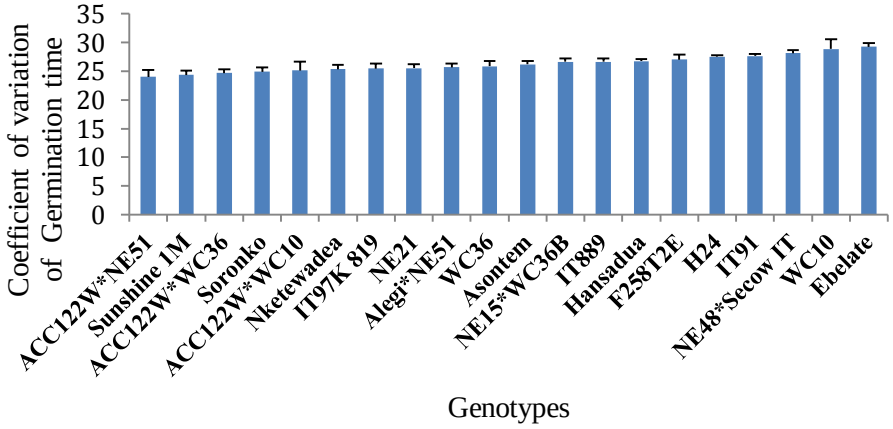

Figure 13: Genotypic effect of irradiated cowpea seeds on coefficient of variation of germination time

The results for germination index showed significant ($P < 0.001$) differences among the genotypes (Figure 14). The mean germination index was 10.9 and the ranged between 8 and 14.2 (Figure 14). Genotypes IT889,

WC10, H24 and Ebelate recorded the highest germination index (12.8 – 14.2) and where significantly different (P < 0.001) from genotypes Sunshine 1M, NE15*WC36B, Nketewadea and Alegi*NE51 which recorded the lowest range (8 – 8.6) of germination index.

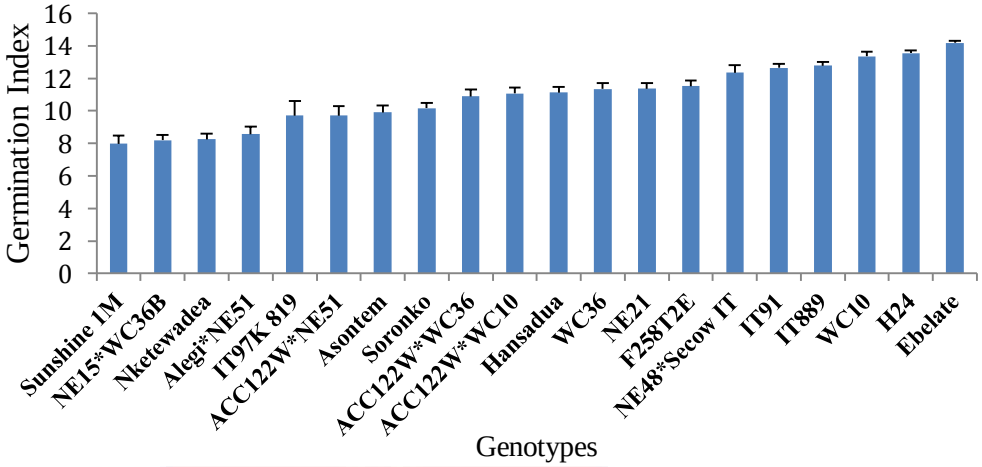

Figure 14: Genotypic response of irradiated cowpea seeds on germination index

The genotypes exhibited significant (P < 0.001) differences on mean germination rate among the genotypes (Figure 15). The mean germination rate ranged from 0.24 – 0.29 seeds per day. Except for genotype ACC122W*NE51 and Sunshine 1M, all the genotypes recorded at least 0.25 seeds per day (Figure 15). Genotypes WC10 and Ebelate recorded the highest mean germination rate and were significantly different from the remaining genotypes except for NE48*SecowIT (Figure 15).

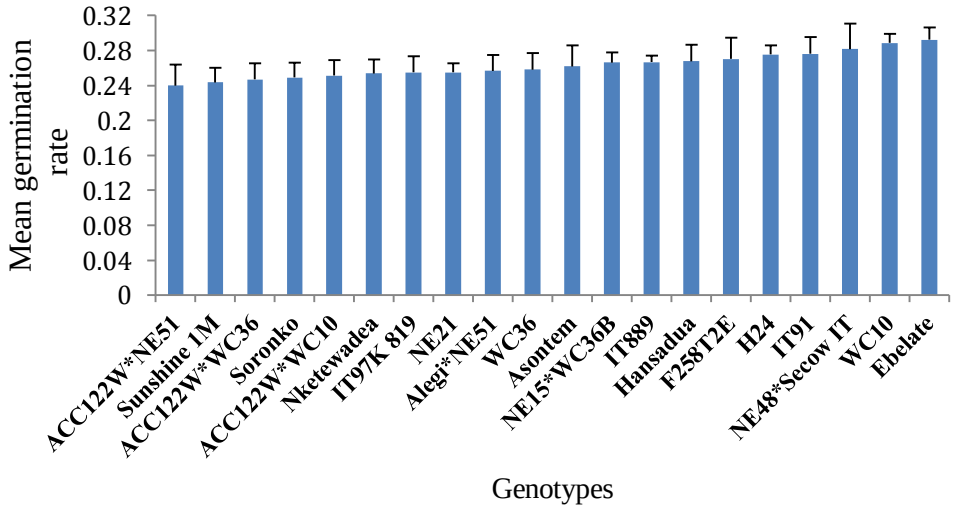

Figure 15: Genotypic response of irradiated cowpea seeds on mean germination rate

The results for mean germination time showed significant ($P < 0.001$) differences among the genotypes assessed (Figure 16). On the average, the genotypes took ≈4 days to germinate. The range for mean germination time was 3 – 4 days. Only two genotypes; Ebelate and WC10, took ≈3 days while the remaining genotypes took about 4 days as mean germination time (Figure 16). The top three genotypes with the highest mean germination time were ACC122W*WC36B, Sunshine 1M and ACC122W*NE51 while Ebelate and WC10 had the least mean germination time (Figure 16).

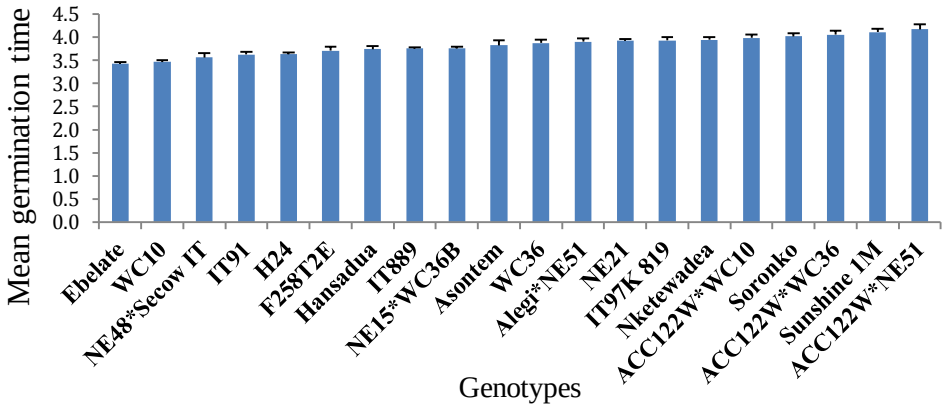

Figure 16: Genotypic effect of irradiated cowpea seeds on mean germination time

The results of synchronization index showed significant (P < 001) differences among the genotypes (Figure 17). The following genotypes recorded the least synchronization index; Nketewadea (0.32), Sunshine 1M (0.34) and Asontem (0.35) and were significantly lower than WC10 (0.49), NE48*SecowIT (0.50) and Ebelate (0.50). The synchronization index ranged between 0.32 and 0.5 with a mean of 0.4 (Figure 17). About 50% of the genotypes recorded synchronization index values ≥ 0.40.(Figure 17).

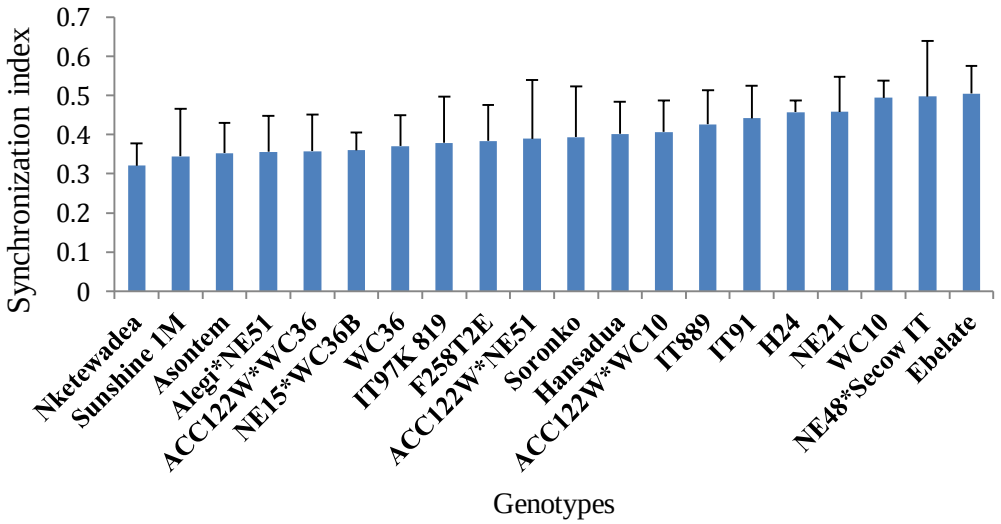

Figure 17: Genotypic response of irradiated cowpea seeds on synchronization index

There were significant (P < 0.001) differences among the genotypes on uncertainty of the germination process as shown in (Figure 18). The range was 1.1 – 1.7 bit with a mean of 1.4 bit. Genotypes Ebelate, NE48*SecowIT, H24, WC10 and IT91 had the lowest uncertainty of germination values (1.1 – 1.2 bit) which were significantly lower than Sunshine 1M, ACC122W*WC36 and Nketewadea (1.6 – 1.7 bit) as shown in (Figure 18). About 60% of the genotypes recorded uncertainty of germination values ≥1.5 bit (Figure 18).

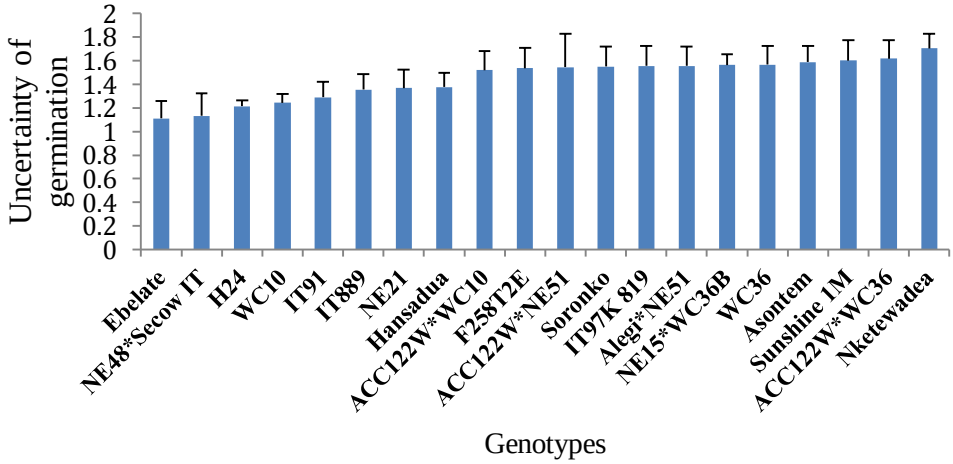

Figure 18: Genotypic response of irradiated cowpea seeds on uncertainty of the germination process

4.1.2 Irradiance effect on cowpea seed physiological quality

The results for irradiance effect on the cowpea genotypes showed significant ($P < 0.001$) differences on days to 50% germination (Figure 19). Although all the doses of irradiation took about 3 days to attain 50% germination, the control (0 Gy) was significantly lower than the remaining doses. The 50 Gy irradiance was the highest but was only significantly different from 0 Gy and 100 Gy irradiation doses (Figure 19).

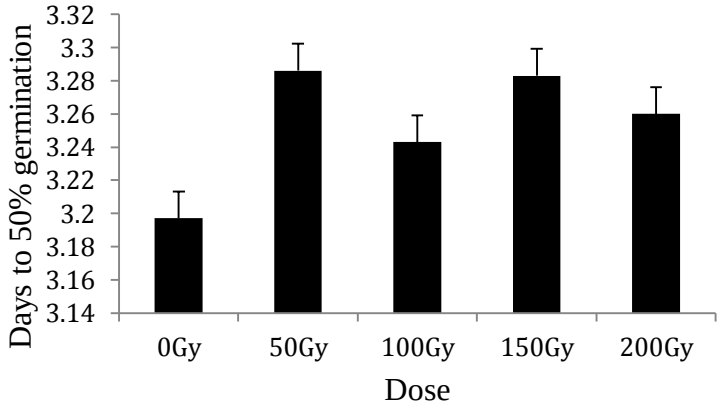

Figure 19: Irradiance effect of irradiated cowpea seeds on days to 50% germination

Similarly, there were significant ($P < 0.001$) differences on percentage decayed seeds among the doses of irradiation as shown in (Figure 20). The mean percentage decayed seeds among the irradiation doses were 8 while the range was 6 – 11%. The control had the least proportion of decayed seeds; however, it was not significantly different from 200 Gy. Generally, there was a general decline in percentage decayed seeds among the doses of irradiation with increasing irradiation from 50 to 200 Gy (Figure 20).

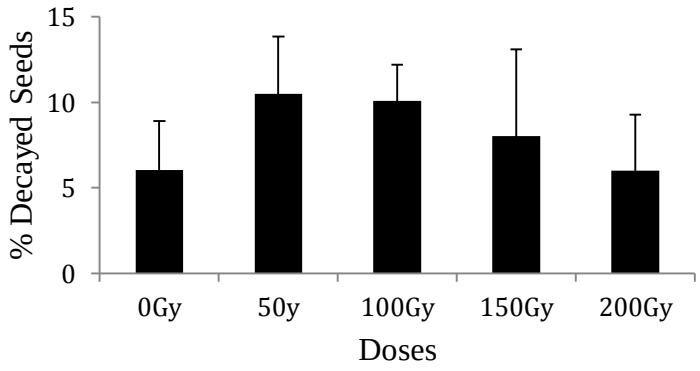

Figure 20: Irradiance effect of irradiated cowpea seeds on percentage decayed seeds

The results for percentage hard seeds showed significant ($P < 0.001$) differences among the irradiation doses (Figure 21). The control (0 Gy) was significantly different from 50 Gy and 100 Gy. The range for percentage hard seeds among the irradiation doses was 9 – 14%. There was a general increment in percentage hard seeds among the doses of irradiation (50 – 200 Gy) as shown in (Figure 21).

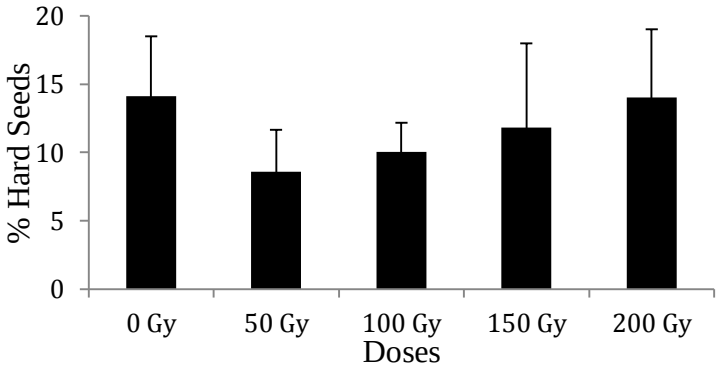

Figure 21: Irradiance effect of irradiated cowpea seeds on percentage hard seeds

There were significant ($P < 0.001$) differences among the doses of irradiation on coefficient of variation of germination time (Figure 22). The range for coefficient of variation of germination time was between 26.1 and 26.6 with a mean of 26.3. The control recorded the highest coefficient of variation of germination time and was significantly different from the remaining doses (Figure 22).

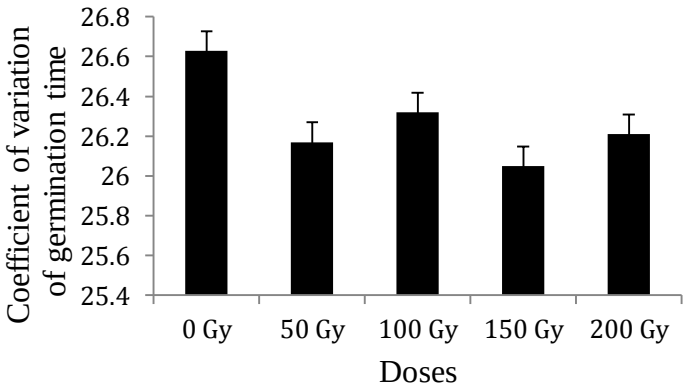

Figure 22: Irradiance effect of irradiated cowpea seeds on coefficient of variation of germination time

Similarly, mean germination rate showed significant ($P < 0.001$) differences among the irradiances (Figure 23). The range for mean germination rate was 0.26 – 0.27 seeds per day. All the irradiation doses recorded 0.26 seeds per day as mean germination rate and were significantly lower than the control which recorded 0.27 seeds per day (Figure 23).

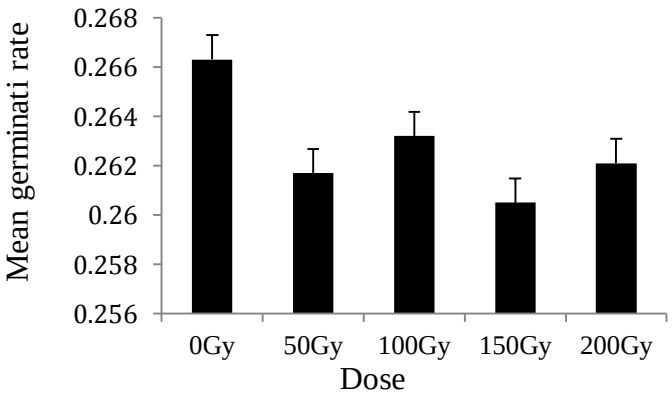

Figure 23: Irradiance effect of irradiated cowpea seeds on mean germination rate

The results for mean germination time among the doses of irradiation showed that there existed significant ($P < 0.001$) differences among doses of irradiation on mean germination time (Figure 24). All the doses of irradiation used ≈4 days as mean germination time. However, the control was significantly lower than the doses of irradiation from 50 to 200 Gy (Figure 24).

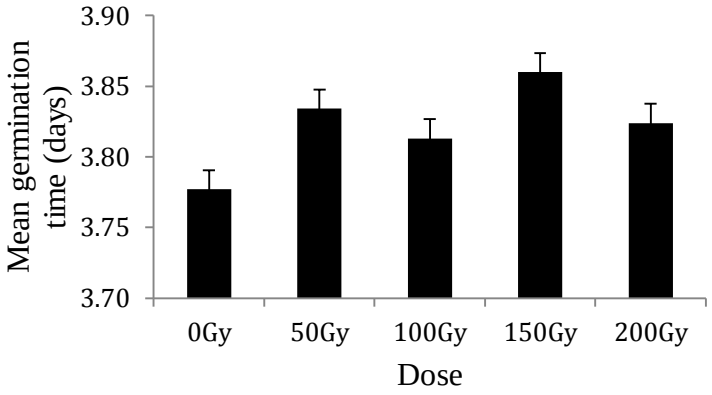

Figure 24: Irradiance effect of irradiated cowpea seeds on mean germination time

The results for synchronization index also showed significant ($P < 0.001$) differences between the control and the irradiation doses from 50 to 200 Gy (Figure 25). The mean for synchronization index was 0.4 and ranged

between 0.4 and 0.44. All the doses of irradiation (50 – 200 Gy) were significantly lower than the synchronization index of the control (Figure 25).

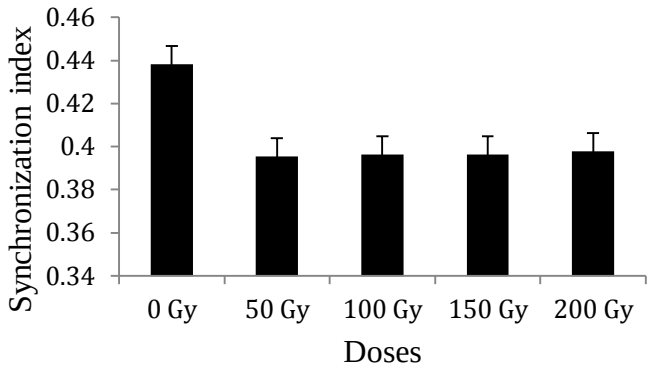

Figure 25: Irradiance effect of irradiated cowpea seeds on synchronization index

Equally, there were significant ($P < 0.001$) differences between the control and the irradiation doses on uncertainty of the germination process (Figure 26). The least uncertainty of germination was recorded by the control (1.36 bit) and was significantly lower than the other doses. The mean of uncertainty of germination was 1.45 bit and ranged from 1.36 to 1.49 bit. Generally, increasing irradiation led to increasing uncertainty of germination from 50 to 150 Gy before declining at 200 Gy (Figure 26).

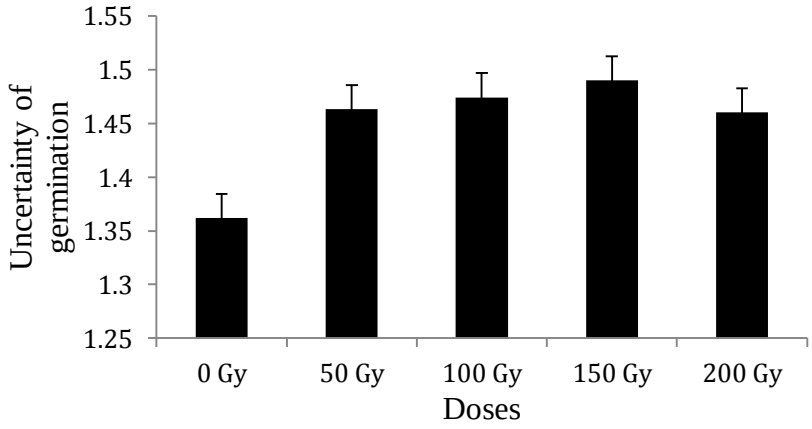

Figure 26: Irradiance effect of irradiated cowpea seeds on uncertainty of the germination process

4.1.3 Genotype-dose interaction effect on cowpea seed physiological quality

The results of means of the various seed physiological parameters of the cowpea genotypes as affected by the doses of irradiation are shown in Table 2. The results show that for days to last germination, ACC122W*WC10, Ebelate, NE48*SecowIT and WC36 were significant ($P < 0.05$) in their mean responses to the effect of the different doses of irradiation applied. For ACC122W*WC10, the least days to last germination was recorded by dose 200 Gy while the highest was recorded by the control (0 Gy) and the value was 7.7 days ≈8 days (Table 3). For Ebelate, the least days to last germination (≈4 days) was recorded by both 0 Gy and 200 Gy and were significantly lower than the 100 Gy (≈6 days and 150 Gy (≈7 days).

Also, the control and 50 Gy of NE48*SecowIT both recorded ≈4 days and were significantly lower than 200 Gy (≈ 6 days). In WC36, 200 Gy (≈ 8 days) was significantly different from the other doses (5 – 6 days). The remaining genotypes showed no significant ($P < 0.05$) differences in their mean days to last germination (Table 3).

The results for means of time spread of germination showed that significant ($P < 0.05$) differences existed only in ACC122W*WC10 and WC36 (Table 3). The remaining genotypes showed no significant differences in their time spread of germination when irradiated at different doses. For ACC122W*WC10, the highest time spread of germination was recorded for 0 Gy (5 days) and was significantly different from dose 200 Gy (2 days). For WC10, dose 50 Gy (2 days) was significantly lower than the time spread of germination of dose 200 Gy (5 days).

Table 3: Means of physiological quality parameters; days to last germination, time spread of germination, days to 50% germination (days) and percentage germination of irradiated cowpea seeds

Genotype	Days to last germination					Time spread of germination					Days to 50% germination					Percentage germination				
	Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
ACC122W*NE51	5.0	6.3	6.3	6.3	5.0	2.0	3.3	3.3	3.3	2.0	3.7	3.7	3.8	3.6	3.4	81.0	77.0	73.0	66.0	94.0
ACC122W*WC10	7.7	6.3	6.3	5.7	5.0	4.7	3.3	3.3	2.7	2.0	3.4	3.5	3.4	3.5	3.4	74.0	95.0	88.0	85.0	81.0
ACC122W*WC36	6.3	5.7	6.3	6.3	5.0	3.3	2.7	3.3	3.3	2.0	3.4	3.5	3.6	3.7	3.4	74.0	91.0	83.0	88.0	90.0
Alegi*NE51	5.7	5.7	5.7	5.7	6.3	2.7	2.7	2.7	2.7	3.3	3.2	3.4	3.4	3.5	3.3	69.0	61.0	69.0	69.0	53.0
Asontem	5.7	5.7	6.3	5.7	6.3	2.7	2.7	3.3	2.7	3.3	3.2	3.5	2.9	3.5	3.0	78.0	61.0	73.0	79.0	71.0
Ebelate	4.3	5.0	6.3	5.7	4.3	1.3	2.0	3.3	2.7	1.3	2.7	2.8	2.9	2.8	3.0	93.0	93.0	94.0	96.0	97.0
F258T2E	5.0	6.3	6.3	6.3	6.0	2.0	3.3	3.3	3.3	3.0	2.8	3.1	2.9	3.1	3.1	87.0	75.0	85.0	76.0	84.0
H24	5.0	5.0	5.0	5.0	6.3	2.0	2.0	2.0	2.0	3.3	3.1	3.1	3.2	3.1	3.3	94.0	99.0	98.0	93.0	96.0
Hansadua	5.0	5.0	5.0	5.0	5.7	2.0	2.0	2.0	2.0	2.7	3.0	3.2	3.3	3.2	3.5	79.0	86.0	83.0	81.0	75.0
IT889	5.0	5.0	5.7	5.0	5.7	2.0	2.0	2.7	2.0	2.7	3.3	3.3	3.1	3.3	3.3	95.0	89.0	94.0	93.0	95.0
IT91	5.0	5.7	5.7	5.7	5.0	2.0	2.7	2.7	2.7	2.0	3.2	3.2	3.0	2.8	3.2	91.0	93.0	93.0	85.0	83.0
IT97K 819	5.7	5.7	5.7	7.0	5.7	2.7	2.7	2.7	4.0	2.7	3.5	3.4	3.3	3.5	3.2	86.0	85.0	78.0	77.0	49.0
NE15*WC36B	7.0	6.3	6.3	6.3	6.3	4.0	3.3	3.3	3.3	3.3	3.0	3.3	3.1	3.2	3.2	59.0	62.0	55.0	49.0	69.0
NE21	6.3	5.7	6.3	5.7	5.7	3.3	2.7	3.3	2.7	2.7	3.4	3.4	3.5	3.5	3.4	87.0	85.0	77.0	91.0	93.0
NE48*Secow IT	4.3	4.3	5.7	5.0	5.7	1.3	1.3	2.7	2.0	2.7	2.6	3.2	3.1	3.2	3.2	59.0	91.0	95.0	96.0	90.0
Nketewadea	6.3	5.7	6.3	6.3	6.3	3.3	2.7	3.3	3.3	3.3	3.4	3.2	3.4	3.3	3.3	69.0	63.0	57.0	58.0	63.0
Soronko	6.3	5.7	6.3	6.3	6.3	3.3	2.7	3.3	3.3	3.3	3.5	3.4	3.5	3.6	3.5	81.0	74.0	77.0	82.0	81.0
Sunshine 1M	5.7	5.7	5.7	5.7	5.0	2.7	2.7	2.7	2.7	2.0	3.7	3.7	3.4	3.5	3.6	73.0	65.0	66.0	54.0	59.0
WC10	5.7	5.7	5.0	5.7	5.3	2.7	2.7	2.0	2.7	2.3	2.7	2.8	2.8	2.7	2.8	79.0	89.0	88.0	95.0	94.0
WC36	5.7	5.0	6.3	6.3	8.3	2.7	2.0	3.3	3.3	5.3	3.2	3.3	3.3	3.4	3.4	88.0	85.0	74.0	88.0	87.0
L.S.D			1.4					1.4					0.1					14.7		
S.E.			0.9					0.9					0.1					3.3		
% C.V.			14.9					31.2					1.9					11.4		

The results of means of days to 50% germination showed that all the genotypes had significant ($P < 0.001$) interactions in their mean responses to the effect of the irradiation doses applied (Table 3). For genotypes ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Alegi*NE51, Asontem, Hansadua, IT97K819, NE21, Soronko and Sunshine 1M, there was only about a day difference (3 - 4 days) among their means for days to 50% germination as affected by their exposure to the different doses of irradiation. However, the remaining genotypes all had ≈3 days as their mean for days to 50% germination (Table 3).

Percentage germination showed significant ($p < 0.001$) interaction in its mean responses of the genotypes upon exposure to different irradiation doses as shown in Table 3. For the following genotypes; ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Alegi*NE51, Asontem, IT97K819, NE15*WC36B, NE15*SecowIT, NE21, Sunshine 1M, and WC10, there were significant ($P < 0.001$) differences in their means for percentage germination (Table 3). For ACC122W*NE51, dose 200 Gy recorded the highest (94%) percentage germination which was significantly different from dose 150 Gy. Contrarily, 150 Gy recorded the highest percentage germination (95%) in WC10 and was significantly different from the control (79%) but not the other doses (Table 3).

The results for percentage decayed seeds exhibited significant ($P < 0.001$) interaction in their means for genotypes and doses (Table 4). The following genotypes; ACC122W*NE51, Alegi*NE51, Asontem, F258T2E, IT97k819, NE15*WC36B, NE21, NE48*SecowIT, Nketewadea, Soronko, Sunshine 1M and WC36 showed significant differences in their mean

percentage decayed seeds. The remaining genotypes showed no significant differences in their mean percentage decayed seeds upon irradiation (Table 4). For Alegi*NE51 and Asontem, the control recorded 9% and 7% and they were significantly lower than their respective irradiation at 50 Gy (21% and 22%). For Nketewadea, both 50 Gy and 100 Gy recorded 21% mean decayed seeds which were significantly higher than 0 Gy and 200 Gy Table 4).

The results for percentage hard seeds showed significant ($P < 0.001$) genotype-dose interaction in the means of the irradiated cowpea seeds (Table 4). Significant differences were found among the means of ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Alegi*NE51, Hansadua, IT91, IT97k819, NE15*WC36B, NE48*SecowIT, Sunshine 1M and WC10. For ACC122W*WC36, the 0 Gy (18%) recorded significantly higher percentage decayed seeds than the other doses of irradiation. For NE48*SecowIT, the control recorded 28% hard seeds and were significantly different from the other doses. However, dose 200 Gy for Alegi*NE51 (33%) and IT97K819 (41%) recorded significantly higher percentage hard seeds than the other doses (Table 4). The remaining genotypes were not significant in their means for percentage hard seeds.

The results for the means of percentage deformed seedlings showed significant ($P < 0.001$) genotype-dose interaction in ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Ebelate, F258T2E, H24, IT97k819, and WC36 (Table 4). The highest percentage deformed seedlings were recorded for dose 200 Gy of WC36. It was significantly different from the other doses. For ACC122W*WC10, doses 150 Gy (11%) and 200 Gy (10%) were significantly lower than the 0 Gy (15%) irradiation dose. However, all

the doses recorded 11% in IT97K819 and significantly lower than 150 Gy (Table 4).

Table 4: Means of physiological quality parameters; percentage decayed seeds, percentage hard seeds, percentage deformed seedlings and coefficient of velocity of germination of irradiated cowpea seeds

Genotype	Percentage decayed seeds					Percentage hard seeds					Percentage deformed seedlings					Coefficient of velocity of germination				
	Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
ACC122W*NE51	6.0	12.0	14.0	15.0	2.0	13.0	10.0	13.0	19.0	4.0	10.0	13.0	13.0	13.0	10.0	15.3	22.3	18.9	22.5	14.9
ACC122W*WC10	8.0	3.0	6.0	6.0	6.0	18.0	2.0	6.0	9.0	14.0	15.0	13.0	13.0	11.0	10.0	30.0	19.6	18.4	18.6	18.7
ACC122W*WC36	8.0	5.0	9.0	5.0	3.0	18.0	4.0	9.0	7.0	7.0	13.0	11.0	13.0	13.0	10.0	21.6	18.7	20.3	20.2	19.3
Alegi*NE51	9.0	21.0	16.0	12.0	14.0	22.0	17.0	16.0	18.0	33.0	11.0	11.0	11.0	11.0	13.0	18.3	18.9	22.5	21.7	23.2
Asontem	7.0	22.0	14.0	8.0	9.0	15.0	18.0	14.0	12.0	20.0	11.0	11.0	13.0	11.0	13.0	21.6	21.6	25.7	20.3	23.2
Ebelate	2.0	4.0	3.0	2.0	1.0	5.0	3.0	3.0	2.0	2.0	9.0	10.0	13.0	11.0	9.0	15.1	16.5	20.1	19.5	15.5
F258T2E	4.0	14.0	7.0	10.0	5.0	9.0	11.0	7.0	14.0	11.0	10.0	13.0	13.0	13.0	12.0	18.1	26.5	25.7	21.9	26.9
H24	2.0	1.0	1.0	3.0	1.0	4.0	1.0	1.0	4.0	3.0	10.0	10.0	10.0	10.0	13.0	16.7	15.8	15.3	16.9	17.5
Hansadua	6.0	8.0	9.0	8.0	7.0	15.0	6.0	9.0	12.0	17.0	10.0	10.0	10.0	10.0	11.0	18.3	17.4	17.8	15.4	19.3
IT889	2.0	6.0	3.0	3.0	1.0	4.0	5.0	3.0	4.0	3.0	10.0	10.0	11.0	10.0	11.0	13.8	19.0	19.7	17.5	18.3
IT91	3.0	4.0	4.0	6.0	5.0	7.0	3.0	4.0	9.0	12.0	10.0	11.0	11.0	11.0	10.0	14.7	18.6	19.8	18.7	17.8
IT97K 819	4.0	8.0	11.0	9.0	17.0	10.0	7.0	11.0	14.0	41.0	11.0	11.0	11.0	14.0	11.0	16.8	18.7	18.8	24.0	22.9
NE15*WC36B	12.0	21.0	22.0	20.0	9.0	29.0	17.0	22.0	30.0	21.0	14.0	13.0	13.0	13.0	13.0	25.5	19.7	21.8	25.1	23.0
NE21	4.0	8.0	12.0	4.0	2.0	9.0	7.0	12.0	6.0	5.0	13.0	11.0	13.0	11.0	11.0	19.1	17.8	18.5	14.6	15.7
NE48*Secow IT	12.0	5.0	3.0	2.0	3.0	28.0	4.0	3.0	2.0	7.0	9.0	9.0	11.0	10.0	11.0	14.7	14.5	18.1	15.7	17.5
Nketewadea	9.0	21.0	21.0	17.0	11.0	22.0	17.0	21.0	25.0	26.0	13.0	11.0	13.0	13.0	13.0	25.0	21.3	22.3	25.8	25.2
Soronko	6.0	14.0	12.0	7.0	6.0	13.0	12.0	12.0	11.0	14.0	13.0	11.0	13.0	13.0	13.0	18.7	18.0	18.5	19.1	23.6
Sunshine 1M	8.0	19.0	17.0	18.0	12.0	19.0	16.0	17.0	28.0	28.0	11.0	11.0	11.0	11.0	10.0	18.0	16.5	21.1	22.9	17.8
WC10	6.0	6.0	6.0	2.0	2.0	14.0	5.0	6.0	3.0	4.0	11.0	11.0	10.0	11.0	11.0	34.7	22.1	17.4	20.2	19.6
WC36	4.0	8.0	13.0	5.0	4.0	8.0	7.0	13.0	7.0	9.0	11.0	10.0	13.0	13.0	17.0	20.3	17.2	20.6	23.7	26.5
L.S.D			6.1					8.9					2.8					5.6		
S.E.			3.8					5.5					1.7					3.5		
% C.V.			46.9					46.9					14.9					17.4		

The results of coefficient of velocity of germination showed significant ($P < 0.001$) genotype-dose interaction in their mean responses to the effect of the irradiation applied on the cowpea seeds (Table 4). Eight genotypes namely ACC122W*NE51, ACC122W*WC10, F258T2E, IT97k819, NE15*WC36B, Soronko, Sunshine 1M, WC10 and WC36 showed significant differences in their mean responses to coefficient of velocity of germination (Table 4). For ACC122W*WC10, the control (30) was significantly different from the remaining doses (18.4 – 19.6) for coefficient of velocity of germination. Similar trend was observed for WC10 whereas the highest (26.9) coefficient of velocity of germination for F258T2E was recorded for dose 200 Gy and was significantly different from the control. The remaining genotypes showed no significant differences in their means for coefficient of velocity of germination (Table 4).

Similarly, the genotype-dose interaction was significant ($P < 0.001$) for coefficient of variation of germination time on the irradiated cowpea seeds (Table 5). All the genotypes showed significant differences in their mean coefficient of variation of germination time responses. For NE48*SecowIT, the highest coefficient of variation of germination was recorded for the control (31) and it was significantly different from the other doses. Likewise, the control for Ebelate recorded a mean of 30.1 which was significantly different from doses 100 Gy (28.5), 150 Gy (29.1) and 200 Gy (28.7). For IT91, dose 200 Gy. However, dose 200 Gy for ACC122W*NE51 recorded mean coefficient of variation of germination time to be 25.5 and was significantly higher than the other doses of irradiation which ranged from 23.3 to 24.2 (Table 5).

Table 5: Means of physiological quality parameters; coefficient of variation of germination time, germination index and mean germination rate of irradiated cowpea seeds

Genotype	Coefficient of variation of germination time					Germination Index					Mean Germination Rate				
	Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
ACC122W*NE51	24.2	23.5	23.3	23.6	25.5	10.0	9.5	8.7	8.1	12.3	0.24	0.24	0.23	0.24	0.26
ACC122W*WC10	24.2	25.0	25.6	25.2	25.8	9.6	12.3	11.6	11.1	10.8	0.24	0.25	0.26	0.25	0.26
ACC122W*WC36	24.8	25.2	24.2	23.6	25.7	9.6	11.8	10.4	10.8	12.0	0.25	0.25	0.24	0.24	0.26
Alegi*NE51	27.1	25.5	25.0	24.9	25.8	9.6	8.1	9.0	9.0	7.2	0.27	0.26	0.25	0.25	0.26
Asontem	26.3	24.7	27.3	25.1	27.5	10.7	7.8	10.4	10.3	10.2	0.26	0.25	0.27	0.25	0.28
Ebelate	30.4	29.5	28.5	29.1	28.7	14.5	14.0	13.9	14.4	14.3	0.30	0.30	0.29	0.29	0.29
F258T2E	28.8	25.7	27.1	27.3	26.2	12.9	10.2	12.2	10.8	11.6	0.29	0.26	0.27	0.27	0.26
H24	28.1	28.0	27.2	27.7	26.7	13.6	14.2	13.6	13.3	13.2	0.28	0.28	0.27	0.28	0.27
Hansadua	27.7	27.0	26.5	27.4	25.2	11.2	12.0	11.3	11.3	9.8	0.28	0.27	0.27	0.27	0.25
IT889	26.7	26.2	27.2	26.7	26.5	12.9	12.0	13.2	12.7	13.0	0.27	0.26	0.27	0.27	0.26
IT91	27.1	27.0	27.8	29.4	26.8	12.6	12.9	13.3	12.9	11.5	0.27	0.27	0.28	0.29	0.27
IT97K 819	25.2	25.9	26.4	24.0	26.0	11.1	11.3	10.6	9.7	5.7	0.25	0.26	0.26	0.24	0.26
NE15*WC36B	26.9	26.1	27.1	26.6	26.4	8.3	8.4	7.8	6.9	9.6	0.27	0.26	0.27	0.27	0.26
NE21	25.6	26.0	24.9	25.0	26.0	11.6	11.4	9.9	11.6	12.4	0.26	0.26	0.25	0.25	0.26
NE48*Secow IT	31.0	27.6	27.9	27.4	26.9	9.4	12.9	13.6	13.5	12.5	0.31	0.28	0.28	0.27	0.27
Nketewadea	25.0	26.2	25.2	25.1	25.4	9.0	8.6	7.6	7.7	8.5	0.25	0.26	0.25	0.25	0.25
Soronko	24.9	25.9	24.9	24.4	24.4	10.5	9.9	9.9	10.3	10.3	0.25	0.26	0.25	0.24	0.24
Sunshine 1M	23.8	23.5	25.3	24.4	24.7	9.0	7.8	8.7	6.9	7.6	0.24	0.24	0.25	0.24	0.25
WC10	28.2	28.5	29.1	29.6	29.0	11.9	13.2	13.1	14.5	14.1	0.28	0.29	0.29	0.30	0.29
WC36	26.7	26.6	25.8	25.0	25.1	12.2	11.7	9.9	11.5	11.4	0.27	0.27	0.26	0.25	0.25
L.S.D			1.0					1.8					0.01		
S.E.			0.6					1.1					0.01		
% C.V.			2.3					10.0					2.30		

Germination index also showed significant (P <. 0.001) genotype-dose interactions in the responses when the genotypes were exposed to different irradiation doses (Table 5). Genotypes ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Alegi*NE51, Asontem, F258T2E, H24, Hansadua, IT91, IT97K819, NE15*WC36B, NE21, NE48*SecowIT, Sunshine 1M, WC10 and WC36 all showed significant differences in their means but the other genotypes showed no significant differences in their responses for germination index when exposed to the irradiances (Table 5). The remainder of the genotypes showed no significant differences in their means for germination index. For IT97K819, dose 200 Gy (5.7) was significantly lower than the remaining doses of irradiation. However, dose 150 Gy for WC10 (14.5) was only significantly different from the control (11.9) as shown in Table 5.

The results for mean germination rate showed that there were significant (P < 0.001) interaction for the genotypes and doses in the mean responses to the irradiation as shown in Table 5. All the irradiated cowpea genotypes showed significant differences in mean germination rate. For NE48*SecowIT, the control recorded 0.31 seeds per day as the highest mean germination rate and it was significantly different from the irradiation doses (50 – 200 Gy). Similar observations were found in the mean responses of F258T2E and Hansadua upon irradiation. However, the control for WC10 was significantly lower (0.28 seeds per day) than the remaining doses of irradiation in the mean responses of mean germination rate (Table 5). For Ebelate, the mean responses both 0 Gy and 50 Gy and were equal and were both significantly different from the other doses. The means of genotype WC36 showed similar trend as Ebelate on mean germination rate (Table 5).

The results of means for mean germination time showed significant ($P < 0.001$) genotype-dose interactions in all the genotypes except for NE15*WC36B (Table 6). Although the means for mean germination time showed significant differences, all the doses for the different genotypes had mean germination time values of ≈4 days with the exception of Ebelate, F258T2E, IT91, NE48*SecowIT and WC10. For Ebelate, the 100 Gy dose had mean germination time of ≈4 days while the other doses had ≈3 days. Also, the control for F258T2E and 100 Gy dose for IT91 both had mean germination time of ≈3 days while the other doses recorded ≈4 days. However, both the control and 50 Gy of WC10 had mean germination time of ≈4 days while the remaining doses recorded ≈3 days as mean germination time (Table 6).

There were significant ($P < 0.001$) genotype-dose interactions for synchronization index in all the assessed genotypes except for H24, NE15*WC36B and Nketewadea (Table 6). For NE48*SecowIT, the mean synchronization index was 0.67 for 0 Gy and was significantly higher than the remaining doses. Similarly, the control (0 Gy) for Ebelate and IT889 were significantly different from the other doses of irradiation. However, 200 Gy recorded the highest (0.49) mean synchronization index for ACC122W*NE51 and was significantly different from the other doses but not the 0 Gy (0.44). For Soronko, the 200 Gy (0.33) irradiation dose was significantly lower than 0 Gy (0.41), 50 Gy (0.4) and 100 Gy (0.44) but not 150 Gy (0.39) as shown in Table 6.

Table 6: Means of physiological quality parameters; mean germination time, synchronization index and uncertainty of germination of irradiated cowpea seeds

Genotype	Mean germination time					Synchronization index					Uncertainty of germination				
	Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
ACC122W*NE51	4.1	4.3	4.3	4.3	3.9	0.44	0.30	0.35	0.37	0.49	1.32	1.83	1.66	1.68	1.24
ACC122W*WC10	4.2	4.0	3.9	4.0	3.9	0.37	0.42	0.46	0.38	0.41	1.67	1.52	1.39	1.55	1.47
ACC122W*WC36	4.0	4.0	4.1	4.3	3.9	0.41	0.37	0.31	0.33	0.37	1.51	1.56	1.72	1.75	1.56
Alegi*NE51	3.7	3.9	4.0	4.0	3.9	0.42	0.36	0.29	0.30	0.41	1.34	1.55	1.75	1.73	1.42
Asontem	3.8	4.1	3.7	4.0	3.6	0.34	0.30	0.40	0.32	0.40	1.59	1.73	1.51	1.66	1.45
Ebelate	3.3	3.4	3.5	3.4	3.5	0.59	0.51	0.46	0.49	0.47	0.92	1.10	1.23	1.23	1.09
F258T2E	3.5	3.9	3.7	3.7	3.8	0.46	0.32	0.39	0.41	0.35	1.24	1.77	1.60	1.42	1.65
H24	3.6	3.6	3.7	3.6	3.7	0.44	0.46	0.47	0.43	0.49	1.23	1.17	1.19	1.28	1.19
Hansadua	3.6	3.7	3.8	3.7	4.0	0.41	0.41	0.39	0.46	0.34	1.35	1.36	1.41	1.18	1.59
IT889	3.7	3.8	3.7	3.8	3.8	0.53	0.40	0.41	0.40	0.40	1.07	1.47	1.41	1.38	1.45
IT91	3.7	3.7	3.6	3.4	3.7	0.49	0.40	0.41	0.51	0.40	1.13	1.41	1.40	1.11	1.39
IT97K 819	4.0	3.9	3.8	4.2	3.9	0.46	0.41	0.38	0.34	0.30	1.37	1.46	1.48	1.80	1.66
NE15*WC36B	3.7	3.8	3.7	3.8	3.8	0.37	0.36	0.39	0.35	0.35	1.56	1.55	1.46	1.62	1.63
NE21	3.9	3.9	4.0	4.0	3.8	0.42	0.41	0.44	0.53	0.49	1.46	1.44	1.46	1.23	1.25
NE48*Secow IT	3.2	3.6	3.6	3.7	3.7	0.67	0.49	0.44	0.46	0.44	0.78	1.07	1.28	1.21	1.32
Nketewadea	4.0	3.8	4.0	4.0	3.9	0.31	0.33	0.33	0.34	0.30	1.77	1.61	1.68	1.67	1.79
Soronko	4.0	3.9	4.0	4.1	4.1	0.41	0.40	0.44	0.39	0.33	1.51	1.45	1.46	1.59	1.74
Sunshine 1M	4.2	4.3	4.0	4.1	4.1	0.37	0.40	0.32	0.28	0.36	1.59	1.49	1.68	1.77	1.47
WC10	3.6	3.5	3.4	3.4	3.5	0.51	0.46	0.48	0.55	0.49	1.29	1.35	1.18	1.16	1.24
WC36	3.7	3.8	3.9	4.0	4.0	0.36	0.41	0.39	0.31	0.39	1.53	1.37	1.54	1.79	1.60
L.S.D			0.2					0.07					0.28		
S.E.			0.1					0.44					0.17		
% C.V.			2.5					10.70					11.80		

The results showed significant ($P < 0.001$) genotype-dose interactions on uncertainty of the germination process in genotypes ACC122W*NE51, ACC122W*WC10, Alegi*NE51, Asontem, Ebelate, F258T2E, Hansadua, IT889, IT91, IT97K819, NE48*SecowIT, Soronko, Sunshine 1M and WC36 (Table 6). However, genotypes ACC122W*WC36, H24, NE15*SecowIT, Nketewadea and WC10 showed no significant differences in their mean responses to uncertainty of germination. For ACC122W*NE51, uncertainty of germination recorded by dose 50 Gy was 1.83 and it was significantly different from the control (1.32) and dose 200 Gy (1.24). For F258T2E, dose 150 Gy was significantly different from the control and 150 Gy (Table 6).

4.2 Experiment Two: Seed Health Test

Six (6) different mycoflora were observed on the irradiated cowpea seeds. They were *Aspergillus flavus, Aspergillus niger, Cladosporium sphaerospermum, Penicillium, Rhizopus* and *Fusarium moniliforme*. Different genotypes showed different mycoflora. Similarly, different irradiation doses showed different mycoflora during observation.

The results of the combined analysis of variance for the different mycoflora observed showed significant ($P < 0.001$) differences both among the genotypes and doses for all 6 mycoflora. Also, there were significant ($P < 0.001$) differences between the seed treatments (pre-treated and untreated seeds) for all the mycoflora identified except for *Rhizopus sp.* which showed no significant difference between the seed treatments. Both 2 – way and 3 – way interactions were significant ($P < 0.001$) for all the mycoflora identified. The details of the findings are presented in Figures 27 to 38 and Tables 8 and 9.

Table 7: Combined ANOVA for mycoflora infection on irradiated cowpea seeds

		Mean sum of squares					
Source of variation	Degree of freedom	*Aspergillus flavus*	*Aspergillus niger*	*Cladosporium sphaerospermum*	*Penicillium sp.*	*Rhizopus sp.*	*Fusarium moniliforme*
Genotype (G)	23	3269.01***	144.03***	280.04***	179.59***	396.63***	229.02***
Dose (D)	4	143.92***	17.42***	85.04***	163.18***	76.46***	64.42***
Treatment (T)	1	696.30***	16.46***	3730.26***	1026.34***	0.025	37.00***
G × D	92	113.67***	22.72***	41.58***	74.57***	49.84***	479.57***
G × T	23	239.90***	40.86***	184.64***	120.04***	32.03***	194.20***
D × T	4	219.56***	2.93***	43.65***	12.97***	22.38***	61.61***
G × D × T	92	137.36***	12.13***	29.99***	41.34***	36.84***	377.30***
Residual	240	21.31	0.5	0.59	1.27	0.66	51.6

*** = significant at P < 0.001

4.2.1 Genotypic effect of irradiation on cowpea seed health quality

The results showed that there were significant ($P < 0.001$) differences among the genotypes in their mean responses to the percentage infection of *Aspergillus flavus* (Figure 27). The *Aspergillus flavus* mycoflora was present on all the examined genotypes. Nearly 60% of the genotypes recorded < 10% infection for the mycoflora. Secow5T recorded 76.6% [61.4] mean percent *Aspergillus flavus* infection as the highest infection rate and was significantly different from the remaining genotypes. The genotypes WC36, NE48*SecowIT and Sunshine 1M recorded 1.5% [8.1] mean percent *Aspergillus flavus* infection among the irradiated genotypes and were significantly lower than the remaining genotypes (Figure 27).

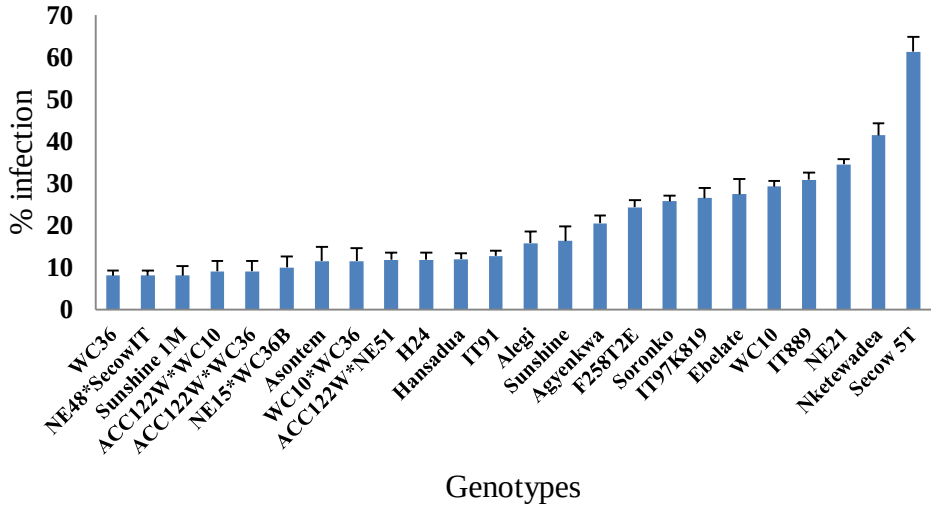

Figure 27: Genotypic response of mean percent Aspergillus flavus infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.

Similarly, the results of mean percent *Aspergillus niger* infection showed significant ($P < 0.001$) differences among the genotypes when exposed to different irradiation doses (Figure 28). Genotypes Alegi, NE21 and Secow5T recorded the highest mean percent infection of *Aspergillus niger*

among the genotypes and were significantly different from the remaining genotypes. Genotypes Ebelate, Soronko, Sunshine, WC10, WC36 and WC10*WC36 recorded 0.3% [5.1] mean percent *Aspergillus niger* infection but were not significantly different from ACC122W*WC10 and ACC122WC36 which recorded 0.6% [6.02]. The remaining genotypes recorded 0% [4.05] infection for *Aspergillus niger* among the irradiated genotypes (Figure 28).

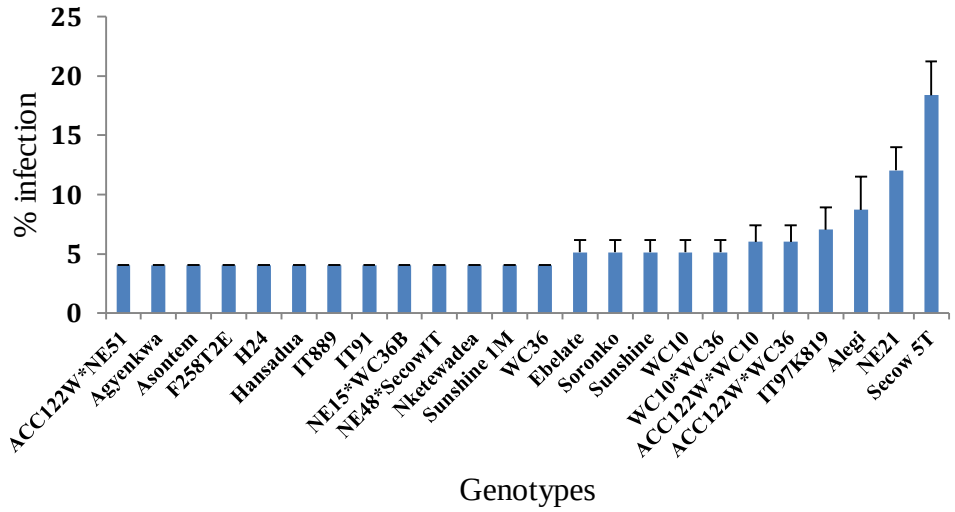

Figure 28: Genotypic response of mean percent Aspergillus niger infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.

The results of means of genotypic responses to irradiation showed significant ($P < 0.001$) differences in percent *Cladosporium sphaerospermum* infection as shown in Figure 29. The top three genotypes with the highest infection of *Cladosporium sphaerospermum* were ACC122*WC36 (6.3%)[15.1], ACC122W*WC10 (7.7%)[16.64] and Ebelate (9.5%)[18.43]. About 45% of the genotypes recorded mean percentage *Cladosporium sphaerospermum* infection range between 1.7% [6.55] and 7.7% [16.64] as shown in Figure 29. Genotypes ACC122W*NE51, Agyenkwa, F258T2E,

H24, IT97K819, NE21, Nketewadea, Secow5T and WC10*WC36 recorded no incidence of *Cladosporium sphaerospermum* mycoflora (Figure 29).

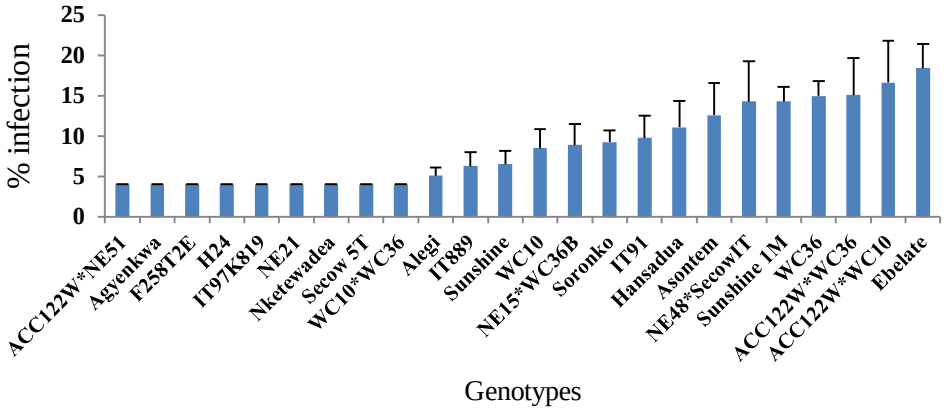

Figure 29: *Genotypic response of mean percent Cladosporium sphaerospermum infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.*

The results of means of genotypic responses of the irradiated cowpea seeds showed significant ($P < 0.001$) differences in the mean percentage infection of *Penicillium sp.* as shown in Figure 30. Genotypes NE15*WC35B, ACC122W*WC10, ACC122W*WC36, Hansadua, Alegi, Sunshine and WC10 recorded about 5% [13.56] mean percent infection for *Penicillium sp.* However, genotypes F258T2E, IT97K819, NE21, NE48*SecowIT, Nketewadea, Secow5T and Sunshine 1M recorded 0% [4.05] mean percentage *Penicillium sp.* infection and were significantly lower than remaining genotypes except Ebelate, IT91, WC10*WC36 and WC36 (Figure 30).

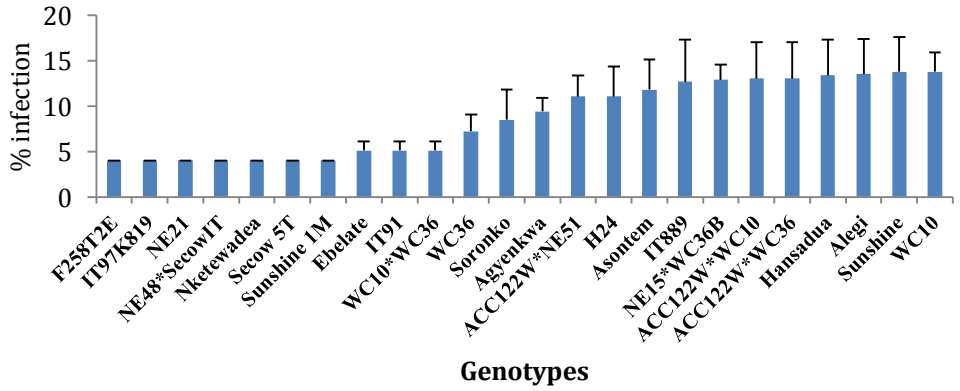

Figure 30: Genotypic response of mean percent Penicillium sp. infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.

There were significant ($P < 0.001$) differences among the genotypes for the mean percentage infection of *Rhizopus sp*. on the irradiated seeds (Figure 31). Genotypes Agyenkwa, Nketewadea, IT97K819, NE21 and Secow5T were the only genotypes to record incidence for the mycoflora of *Rhizopus sp*. The remaining genotypes did not record incidences for *Rhizopus sp*. Genotypes IT97K819, NE21 and Secow5Trecorded mean percent *Rhizopus* infection of 1.35% [7.82], 5.3% [1.87] and 22.3% [28.52] respectively and were significantly higher than Agyenkwa and Nketewadea which both recorded a mean of 0.3% [5.13] (Figure 31).

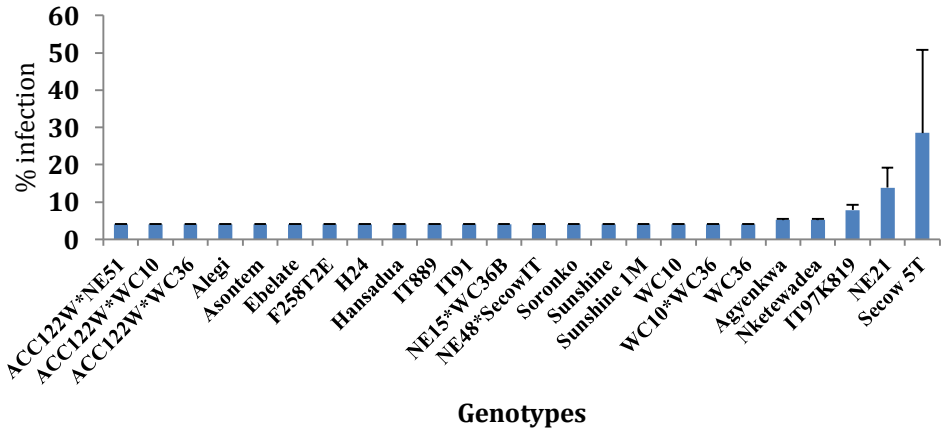

Figure 31: *Genotypic response of mean percent Rhizopus sp. infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.*

Similarly, there were significant ($P < 0.001$) differences in the mean percentage infection of *Fusarium moniliforme* among the irradiated cowpea seeds (Figure 32). Seven genotypes showed incidence of *Fusarium moniliforme* mycoflora among the genotypes. These were NE15*WC36B, IT91, Sunshine, WC10, Soronko, WC10*WC36 and ACC122W*WC10. The top three genotypes with the highest incidence of *Fusarium moniliforme* mycoflora were Soronko 0.9% [6.79], WC10*WC36 (0.9%) [6.79] and ACC122W*WC10 (1.2%) [7.49] and were significantly different from the remaining genotypes (Figure 32)

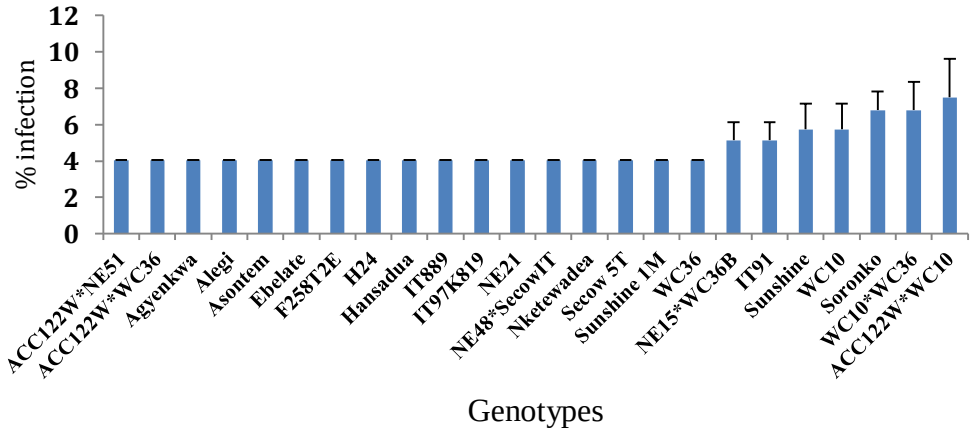

Figure 32: Genotypic response of mean percent Fusarium moniliforme infection on irradiated cowpea seeds. Means represent Arcsine transformed infection rates.

4.2.2 Effect of irradiation on cowpea seed-borne mycoflora

There were significant ($P < 0.001$) differences in the irradiance effect of mean percent *Aspergillus flavus* infection on the cowpea seeds as influenced by the irradiation (Figure 33). Dose 100 Gy recorded the highest (15.2%) [23.34] mean percentage *Aspergillus flavus* infection and it was significantly different from doses 50 Gy and 150 Gy. The range for mean *Aspergillus flavus* infection among the doses ranged from 12.9% [21.49] to 15.2% [23.34] as shown in Figure 33.

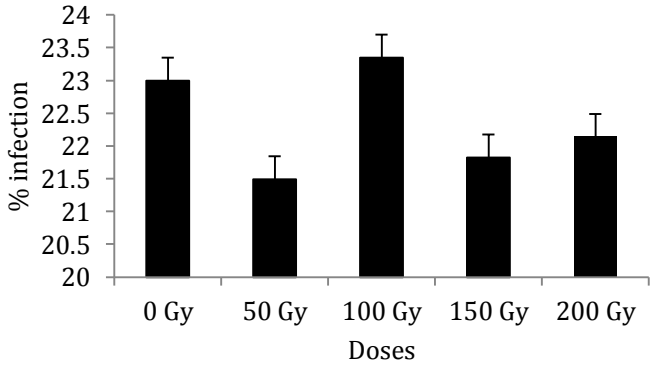

Figure 33: Mean effect of irradiation on Aspergillus flavus. Means represent Arcsine transformed infection rates.

The results of irradiance effect on *Aspergillus niger* infection on the irradiated cowpea seeds showed significant (P <. 001) differences among the doses of irradiation (Figure 34). The highest mean percentage *Aspergillus niger* infection was recorded for dose 100 Gy (1.2%) [7.6] and it was significantly different from the other doses. Dose 50 Gy recorded the least (0.4%) [5.3] mean percent *Aspergillus niger* infection and was significantly lower than the other irradiation doses. The range for percentage *Aspergillus niger* mycoflora among the doses was 0.4% [5.3] to 1.2% [7.6] as shown in Figure 34. From dose 100 Gy to 200 Gy, there was a general decline in percentage *Aspergillus niger* infection on the seeds (Figure 34).

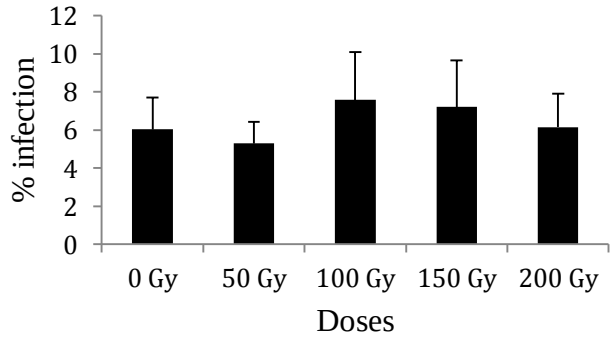

Figure 34: Mean effect of irradiation on Aspergillus niger. Means represent Arcsine transformed infection rates.

The results for mean percentage *Cladosporium sphaerospermum* infection on the irradiated cowpea seeds showed significant (P < 0.001) differences (Figure 35). The percentage infection ranged between 1.7% [8.5] and 3.2% [11.1] among the doses and had an average of 2.4% [9.8]. The control and dose 150 Gy recorded 1.7% [8.4] and 1.8% [8.8] respectively and were significantly lower than the remaining doses. Generally, increasing irradiation led to increasing *Cladosporium sphaerospermum* infection up to 100 Gy (Figure 35).

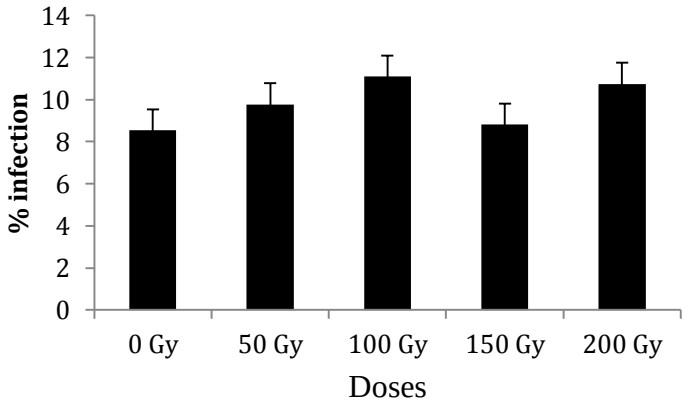

Figure 35: Mean effect of irradiation on Cladosporium sphaerospermum. Means represent Arcsine transformed infection rates.

Similarly, the results of mean percentage *Penicillium sp*. infection showed significant (P < 0.001) differences among the doses of irradiation (Figure 36). Generally, increasing irradiation dose (50 – 200 Gy) resulted in increased *Penicillium sp*. infection on the irradiated seeds although the control recorded 3.1% [11]. The 150 Gy irradiation dose recorded the highest (3.2%) [11.1] mean percentage *Penicillium sp*. infection and it was significantly different from the other doses except the control (Figure 36)

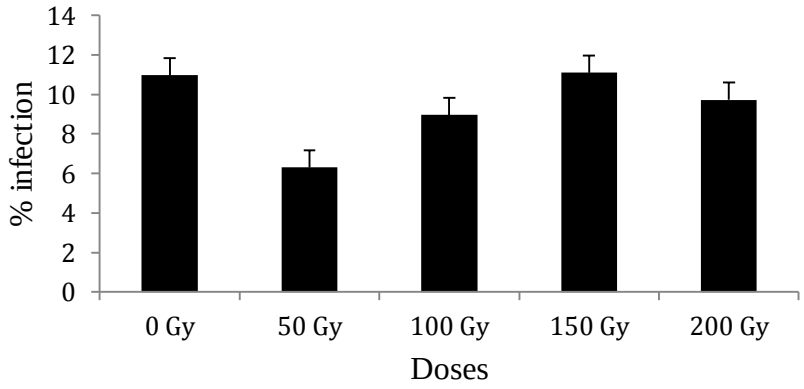

Figure 36: Mean effect of irradiation on Penicillium sp. Means represent Arcsine transformed infection rates.

The results of mean percentage *Rhizopus sp*. infection on the irradiated seeds showed significant (P <.001) differences among the doses of irradiation (Figure 37). Doses 0 Gy and 150 Gy recorded almost equal (0.2%) [4.9] mean

percentage infection for *Rhizopus sp*. infection and were significantly lower than the means of the remaining doses. The highest mean percentage infection of *Rhizopus sp*. on the seeds was recorded by 50 Gy (2.4%) [9.8] and showed significant differences with the other doses (Figure 37).

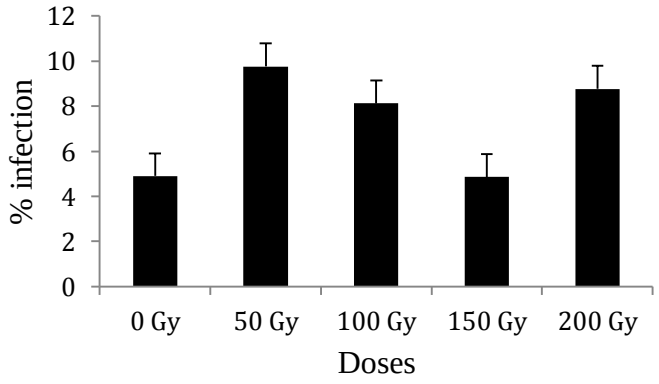

Figure 37: Mean effect of irradiation on Rhizopus sp. Means represent Arcsine transformed infection rates.

The irradiance effect of *Fusarium moniliforme* infection on the cowpea seeds showed significant ($P < 0.001$) differences among the different doses applied (Figure 38). Seeds irradiated at doses 100 Gy and 200 Gy were the top most infected by *Fusarium moniliforme* mycoflora and both recorded 0.4% [5.6] mean percentage *Fusarium moniliforme* infection (Figure 38).

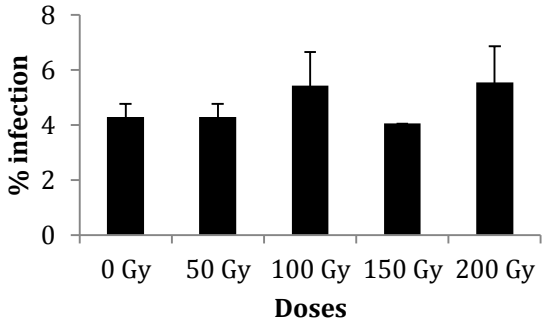

Figure 38: Mean effect of irradiation on Fusarium moniliforme. Means represent Arcsine transformed infection rates.

4.2.3 Interaction between genotypes and dose of irradiation on cowpea seed-borne mycoflora

The results for mean percentage *Aspergillus flavus* infection on the cowpea seeds as affected by the doses of irradiation showed that there were significant ($P < 0.001$) interactions in their mean responses as shown in Table 8. The results showed that only Nketewadea, Agyenkwa, WC10, F258T2E, Ebelate, IT889, Secow5T, N21, Soronko and IT97K819 showed significant ($P < 0.001$) differences in their mean responses to the effect of the irradiation (Table 8). The remaining genotypes showed no significant differences in the mean responses of percentage *Aspergillus flavus* infections on the seeds. For Secow5T, 0 Gy recorded the highest (94.8%) *Aspergillus flavus* infection and was significantly different from 50 Gy and 200 Gy. However, dose 200 Gy of IT889 was significantly different from the other doses (Table 8).

The results of means of *Aspergillus niger* infections on the seeds to the effect of the irradiation doses showed that there were significant ($P < 0.001$) interactions among Secow5T and NE21. For Secow5T, dose 150 Gy recorded 18.8% mean percentage *Aspergillus niger* infection and was significantly different from 0 Gy (9.5), 50 Gy (1.5) and 200 Gy (1.5%). For NE21, 200 Gy (10%) was significantly different from the remaining genotypes (Table 8).

The results of means of *Cladosporium sphaerospermum* infection as affected by the irradiation doses showed significant ($P < 0.001$) genotype-dose interactions in Asontem, Ebelate, NE48*SecowIT, Sunshine IM, WC36, Hansadua, ACC122W*WC10 and ACC122W*WC36 (Table 8). The remaining genotypes had no significant different differences in their mean infections of *Cladosporium sphaerospermum*. For NE48*SecowIT, 200 Gy

recorded 11% *Cladosporium sphaerospermum* infection and was significantly different from doses 0 Gy (4.5%), 50 Gy (2.5%) and 100 Gy (2.5%). Similar proportions of *Cladosporium sphaerospermum* infections were recorded for Sunshine 1M.

There were significant ($P < 0.001$) genotype-dose interactions in the mean infections of *Penicillium sp*. on the cowpea seeds as affected by the doses of irradiation (Table 8). The means of genotypes Sunshine, Asontem, NE15*WC36B, Agyenkwa, WC10, Alegi, NE48*SecowIT, Hansadua, H24, Soronko and ACC122W*NE51 showed significant differences. The means of the remaining genotypes showed no significant differences in percentage infection of *Penicillium sp*. For Hansadua, the control (1.5%) was significantly lower than 100 Gy (11%) and 150 Gy (8.5%) while the control (11%) of H24 was significantly different from the other doses (Table 8).

The results of means of *Rhizopus sp*. infection on the irradiated cowpea seeds showed significant ($P < 0.001$) interactions in genotypes Secow5T and NE21 as shown in Table 8. The remaining genotypes did not show significant differences in the mean percentage *Rhizopus sp*. infections among the irradiated cowpea seeds. For Secow5T, the 50 Gy irradiated samples recorded mean percentage infection of 43.8% and was significantly different from the other doses. Also, the 50 Gy irradiation dose for NE21 recorded 11% infection of *Rhizopus sp*. and was only significantly different from the control and 150 Gy (Table 8).

The results of means of *Fusarium moniliforme* infections on the irradiated seeds showed significant ($P < 0.001$) genotype-dose interactions among genotypes Sunshine, NE15*WC36B, WC10, IT91, WC10*WC36,

ACC122W*WC10 and Soronko as shown in Table 8. Samples irradiated at a dose of 200 Gy for ACC122W*WC10 recorded 3.5% as the highest percentage infection for *Fusarium moniliforme* and was significantly different from the other doses (Table 8).

Table 8: Mean percentage mycoflora on irradiated cowpea seed

Genotype	*Aspergillus flavus*					*Aspergillus niger*					*Cladosporium sphaerospermum*				
	Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
Sunshine	11.00	2.50	7.00	10.00	6.50	0.00	0.00	0.00	1.50	0.00	0.00	2.50	1.50	0.00	0.00
Nketewadea	36.25	37.50	56.75	52.00	34.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Asontem	1.50	6.50	6.50	1.50	1.50	0.00	0.00	0.00	0.00	0.00	0.00	5.75	4.50	1.50	9.50
NE15*WC36B	6.50	1.50	1.50	1.50	1.50	0.00	0.00	0.00	0.00	0.00	0.00	4.50	3.50	1.50	0.00
Agyenkwa	11.00	15.00	19.00	0.00	14.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
WC10	18.00	18.00	23.00	37.00	21.00	0.00	0.00	0.00	0.00	1.50	0.00	2.50	2.50	0.00	3.50
F258T2E	26.00	17.00	18.50	7.00	14.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alegi	4.00	10.00	10.00	6.00	4.50	3.50	0.00	5.50	0.00	0.00	1.50	0.00	0.00	0.00	0.00
Ebelate	20.50	25.75	27.00	15.50	15.00	0.00	0.00	0.00	1.50	0.00	5.50	4.50	10.50	19.00	8.00
IT91	5.00	6.00	1.50	3.50	6.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.50	4.00	5.50
NE48*SecowIT	1.50	0.00	0.00	0.00	6.00	0.00	0.00	0.00	0.00	0.00	4.50	2.50	2.50	7.50	11.00
WC10*WC36	4.50	3.50	4.50	1.50	3.50	0.00	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sunshine 1M	1.50	0.00	0.00	0.00	6.00	0.00	0.00	0.00	0.00	0.00	4.50	2.50	2.50	7.50	11.00
WC36	4.50	1.50	0.00	0.00	1.50	0.00	0.00	0.00	0.00	0.00	4.50	4.50	8.50	0.00	13.50
Hansadua	3.50	5.50	1.50	2.50	6.00	0.00	0.00	0.00	0.00	0.00	2.50	7.50	2.50	3.50	0.00
IT889	15.00	24.00	14.50	32.00	43.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.50
Secow 5T	94.75	61.00	86.25	86.50	55.00	9.50	1.50	16.00	18.75	1.50	0.00	0.00	0.00	0.00	0.00
H24	0.00	1.50	8.00	5.50	3.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ACC122W*WC10	1.50	1.50	7.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	9.50	9.50	15.00	0.00	4.50
NE21	31.50	41.00	25.00	21.25	39.25	1.50	4.00	2.25	1.50	10.00	0.00	0.00	0.00	0.00	0.00
Soronko	19.00	11.00	9.00	24.00	29.00	0.00	1.50	0.00	0.00	0.00	0.00	4.50	2.50	0.00	3.50
IT97K819	36.00	17.00	23.50	7.00	14.00	0.00	0.00	0.00	2.50	2.50	0.00	0.00	0.00	0.00	0.00
ACC122W*WC36	1.50	1.50	7.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	8.50	6.50	13.00	0.00	3.50
ACC122W*NE51	0.00	1.50	8.00	5.50	3.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
L.S.D.			12.7					3.2					6.6		
S.E.			9.2					2.3					4.5		
%C.V.			25.0					13.5					10.3		

Table 8 continued

Genotype	*Penicillium sp.*					*Rhizopus sp.*					*Fusarium moniliforme*				
	Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
Sunshine	15.00	0.00	7.00	1.50	2.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.50
Nketewadea	0.00	0.00	0.00	0.00	0.00	0.00	0.75	0.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Asontem	0.00	0.00	5.50	10.50	2.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NE15*WC36B	3.50	0.00	4.50	0.00	14.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.00	0.00
Agyenkwa	0.00	0.00	0.00	11.00	0.00	0.00	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
WC10	10.00	0.00	3.50	11.00	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	0.00
F258T2E	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alegi	7.00	5.00	0.00	13.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ebelate	0.00	0.00	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IT91	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.00	0.00	0.00
NE48*SecowIT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
WC10*WC36	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.00	1.50	0.00	1.50
Sunshine 1M	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
WC36	0.00	1.50	0.00	1.50	2.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Hansadua	1.50	3.50	11.00	0.00	8.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IT889	0.00	0.00	8.75	6.50	6.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Secow5T	0.00	0.00	0.00	0.00	0.00	0.00	43.75	28.00	3.75	36.00	0.00	0.00	0.00	0.00	0.00
H24	11.00	0.00	1.50	3.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ACC122W*WC10	6.50	3.50	0.00	7.50	5.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	3.50
NE21	0.00	0.00	0.00	0.00	0.00	0.00	11.00	6.00	1.50	7.75	0.00	0.00	0.00	0.00	0.00
Soronko	0.00	0.00	1.50	0.00	7.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.00	3.00
IT97K819	0.00	0.00	0.00	0.00	0.00	5.50	0.00	1.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ACC122W*WC36	6.50	3.50	0.00	7.50	5.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ACC122W*NE51	11.00	0.00	1.50	3.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
L.S.D.			5.4					6.7					1.0		
S.E.			3.9					4.8					0.7		
%C.V.			15.3					15.0					10.4		

4.2.4 Interaction between genotypes, dose of irradiation and pre-treatment on cowpea seed-borne mycoflora

The results of mean percentage *Aspergillus flavus* infections for pre-treated and untreated irradiated cowpea seeds showed significant ($P < 0.001$) interactions among genotypes ACC122W*NE51, Agyenkwa, Asontem, Ebelate, F258T2E, Hansadua, Nketewadea Secow5T, Sunshine and WC10 as shown in Table 9. The remaining genotypes recorded no significant differences in the mean percentage *Aspergillus flavus* between the pre-treated and untreated seeds although the proportions of infections were greater in the untreated than the pre-treated seeds. The untreated seeds of Secow5T (0 Gy) recorded 98.5% mean percentage *Aspergillus flavus* and was significantly higher than the pre-treated seeds which recorded 76%. For Ebelate, there were significant differences between the mean percentage *Aspergillus flavus* infections on both pre-treated and untreated seeds among all the doses of irradiation. For Secow5T, such differences were found among all the doses except between the pre-treated and untreated seeds of the control (Table 9).

Similarly, the results of mean percentage *Aspergillus niger* infections between pre-treated and untreated irradiated cowpea seeds as affected by the irradiation showed significant ($P < 0.001$) interaction among genotypes Alegi, Ebelate, IT97K819, NE21, Secow5T, Soronko, WC10 and WC10*WC36 (Table 9). The remaining genotypes showed no significant differences between the pre-treated and untreated seeds. For Secow5T, doses 50 Gy, 100 Gy and 150 Gy recorded 40%, 28% and 32% respectively for the untreated irradiated seeds and were significantly different from their corresponding pre-treated seeds which recorded 3%, 4% and 5.5% respectively. For NE21, only

the 0 Gy did not show significant differences between the pre-treated and untreated seeds as affected by the different irradiation doses (Table 9).

The results of percentage *Cladosporium sphaerospermum* infections for pre-treated and untreated irradiated cowpea seeds showed significant ($P < 0.001$) interactions among genotypes ACC122W*WC10, ACC122W*WC36, Alegi, Asontem, Ebelate, Hansadua, IT889, IT91, NE15*WC36B, NE48*SecowIT, Soronko, Sunshine, Sunshine 1M, WC10 and WC36 as shown in Table 9. Genotype Ebelate and Sunshine 1M recorded significant differences between the untreated and pre-treated seeds for all the doses of irradiation. The untreated seeds of Ebelate (150 Gy) recorded 35% as the highest mean infection of *Cladosporium sphaerospermum* while the pre-treated seeds recorded only 3% infection (Table 9).

Table 9: Comparison of individual mycoflora for pre-treated and untreated irradiated cowpea seeds

		Pathogen											
		Aspergillus flavus		*Aspergillus niger*		*Cladosporium sphaerospermum*		*Penicillium sp.*		*Rhizopus sp.*		*Fusarium moniliforme*	
Genotype	Dose	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.
ACC122W*NE51	0	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	4.050.0 [4.0	0.0 [4.05]	0.0 [4.05]	7.0 [15.8]**	15.0 [23.17]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	9.0 [17.93]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	11.0 [19.80]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	7.0 [15.86]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
ACC122W*WC10	0	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	19.0 [26.19]**	0.0 [4.05]	13.0 [21.54]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	19.0 [26.19]**	0.0 [4.05]	7.0 [15.58]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	7.0 [15.86]	7.0 [15.86]	3.0 [10.67]	3.0 [10.67]	25.0 [30.32]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]**	5.0 [13.5]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	15.0 [23.17]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	11.0 [19.80]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]**	7.0 [15.8]
ACC122W*WC36	0	3.0 [10.6]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	17.24 [24.7]**	0.0 [4.05]	13.0 [21.5]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.6]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	13.0 [21.5]**	0.0 [4.05]	7.0 [15.5]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	7.0 [15.86]	7.0 [15.86]	3.0 [10.67]	3.0 [10.67]	21.0 [27.62]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	15.0 [23.1]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [15.8]**	0.0 [4.05]	11.0 [19.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Alegi	0	5.0 [13.51]	3.0 [10.67]	7.0 [15.86]**	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	9.0 [17.93]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	15.0 [23.17]	7.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	15.0 [23.17]	7.0 [13.51]	11.0 [19.80]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	9.0 [17.93]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	23.0 [28.99]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Agyenkwa	0	11.0 [19.80]	11.0 [19.8]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	27.0 [31.62]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.7]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	21.0 [27.62]	17.0 [24.72]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	19.0 [26.19]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	15.0 [23.17]	13.0 [21.54]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
L.S.D.		9.1		1.4		1.5		2.2		1.6		0.9	
S.E.		4.6		0.7		0.8		1.1		0.8		0.5	
%CV		25.0		13.5		10.3		15.3		15.0		10.4	

** shows significance at P < 0.001. Figures in parenthesis were Arcsine transformed.Unt. = Untreated, Pre. = Pre-treated

Table 9 continued

		Pathogen											
		Aspergillus flavus		*Aspergillus niger*		*Cladosporium sphaerospermum*		*Penicillium sp.*		*Rhizopus sp.*		*Fusarium moniliforme*	
Genotype	Dose	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.
Asontem	0	0.0 [4.05]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	13.0 [21.54]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	19.0 [20.2]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	13.0 [21.54]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	11.0 [19.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	11.5 [27.6]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	19.0 [26.2]**	0.0 [4.05]	0.0 [4.05]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Ebelate	0	32.0 [34.74]**	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	11.0 [19.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	44.5 [42.12]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	41.0 [40.10]**	13.0 [21.54]	0.0 [4.05]	0.0 [4.05]	21.0 [27.62]**	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	31.0 [34.14]**	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	35.0 [36.56]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	27.0 [31.62]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	13.0 [21.54]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
F258T2E	0	42.0 [40.7]**	10.0 [18.83]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	15.0 [23.17]	19.0 [26.19]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	34.0 [35.93]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	7.0 [15.86]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	17.0 [24.72]	11.0 [19.80]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
H24	0	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]	0.0 [4.05]	15.0 [23.1]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	9.0 [17.93]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	11.0 [19.80]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	0.0 [4.05]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Hansadua	0	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	3.0 [10.67] **	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	11.0 [19.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	15.0 [23.17]**	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	15.0 [23.2]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	7.0 15.86**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	7.0 [15.86]	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	17.0 [24.7]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
L.S.D.		9.1		1.4		1.5		2.2		1.6		0.9	
S.E.		4.6		0.7		0.8		1.1		0.8		0.5	
%CV		25.0		13.5		10.3		15.3		15.0		10.4	

** shows significance at P < 0.001. Figures in parenthesis were Arcsine transformed.Unt. = Untreated, Pre. = Pre-treated

Table 9 continued

		Pathogen											
		Aspergillus flavus		*Aspergillus niger*		*Cladosporium sphaerospermum*		*Penicillium sp.*		*Rhizopus sp.*		*Fusarium moniliforme*	
Genotype	Dose	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.
IT889	0	19.0 [26.19]	11.0 [19.80]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	39.0 [38.93]**	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	29.0 [32.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.50 [14.1]	0.0 [4.05]	12.0 [19.5]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	35.0 [36.5]**	29.0 [32.8]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	13.0 [21.5]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	45.0 [42.4]	42.0 [40.6]	0.0 [4.05]	0.0 [4.05]	7.0 [15.8]**	0.0 [4.05]	13.0 [21.5]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.0]	0.0 [4.05]
IT91	0	7.0 [15.86]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	9.0 [17.93]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]**	3.0 [10.67]
	100	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	6.0 [14.60]	6.0 [14.60]	0.0 [4.05]	0.0 [4.05]	11.0 [19.8]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
IT97K819	0	62.0 [52.24]**	10.0 [18.83]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	11.0 [19.80]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	19.0 [26.19]	15.0 [23.17]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	44. 0 [41.83]**	3.0 [10.6]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	2.50 [9.94]	0.0 [4.05]	0.0 [4.05]
	150	7.0 [15.86]	7.0 [15.86]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	17.0 [24.72]	17.0 [24.72]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
NE15*WC36B	0	13.0 [21.54]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]
	150	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	29.0 [32.9]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
NE21	0	50.0 [45.28]**	13.0 [21.54]	0.0 [4.05]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	53.0 [47.0]**	29.0 [32.89]	5.0 [13.51]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	19.0 [26.19]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]
	100	29.0 [32.89]	21.0 [27.62]	4.50 [12.9]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]
	150	23.50 [29.18]	19.0 [26.19]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	39.50 [39.23]	39.0 [38.93]	17.0 [24.72]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	7.0 [15.33]	0.0 [4.05]	0.0 [4.05]
L.S.D.		9.1		1.4		1.5		2.2		1.6		0.9	
S.E.		4.6		0.7		0.8		1.1		0.8		0.5	
%CV		25.0		13.5		10.3		15.3		15.0		10.4	

** shows significance at P < 0.001. Figures in parenthesis were Arcsine transformed.Unt. = Untreated, Pre. = Pre-treated

Table 9 continued

		Pathogen											
		Aspergillus flavus		*Aspergillus niger*		*Cladosporium sphaerospermum*		*Penicillium sp.*		*Rhizopus sp.*		*Fusarium moniliforme*	
Genotype	Dose	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.
NE48*SecowIT	0	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	15.0 [23.17]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	9.0 [17.93]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	15.0 [23.2]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Nketewadea	0	41.0 [40.10]**	31.5 [34.4]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	38.5 [38.64]	36.5 [37.46]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	1.5 [7.42]	0.0 [4.05]	0.0 [4.05]
	100	64.5 [53.73]**	49.0 [44.71]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	1.5 [7.42]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	87.5 [69.82]**	16.5 [24.33]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	55.0 [48.15]**	13.5 [21.97]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
Secow5T	0	98.5 [84.4]	90.5 [72.6]	9.5 18.90	9.0 [17.9]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.0]	0.0 [4.05]
	50	63.0 [52.8]**	59.0 [50.4]	40.0 [4.05]**	3.0 [10.6]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	83.0 [66.5]**	4.5 [12.7]	0.0 [4.0]	0.0 [4.05]
	100	94.5 [77.5]**	78.0 [62.39]	28.0 [32.25]**	4.0 [12.17]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	41.5 [40.39]**	14.5 [22.76]	0.0 [4.05]	0.0 [4.05]
	150	98.5 [79.69]**	76.0 [61.08]	32.0 [34.74]**	5.5 [13.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.5 [13.51]**	2.5 [9.94]	0.0 [4.05]	0.0 [4.05]
	200	79.0 [63.08]**	31.0 [34.11]	0.0 [4.05]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	50.5 [45.6]**	21.5 [27.96]	0.0 [4.05]	0.0 [4.05]
Soronko	0	31.0 [34.14]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	17.0 [24.72]**	5.0 [13.51]	3.0 [10.67]**	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	11.0 [19.80]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.6]**	0.0 [4.05]
	150	27.0 [31.62]	21.0 [27.62]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	29.0 [32.89]	29.0 [32.89]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	11.0 [19.80]**	3.0 [10.6]	0.0 [4.05]	0.0 [4.05]	3.0 [10.6]	3.0 [10.67]
Sunshine	0	15.0 [23.17]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	23.0 [29.0]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	0.0 [4.05]	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	11.30 [19.80]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	7.0 [15.86]	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	15.0 [23.17]**	5.0 [13.51]	3.0[10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	13.0 [21.54]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
L.S.D.		9.1		1.4		1.5		2.2		1.6		0.9	
S.E.		4.6		0.7		0.8		1.1		0.8		0.5	
%CV		25.0		13.5		10.3		15.3		15.0		10.4	

** shows significance at P < 0.001. Figures in parenthesis were Arcsine transformed.Unt. = Untreated, Pre. = Pre-treated

Table 9 continued

		Pathogen											
		Aspergillus flavus		*Aspergillus niger*		*Cladosporium sphaerospermum*		*Penicillium sp.*		*Rhizopus sp.*		*Fusarium moniliforme*	
Genotype	Dose	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.	Unt.	Pre.
Sunshine 1M	0	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	15.0 [23.17]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	9.0 [17.93]	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	15.0 [23.17]**	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
WC10	0	31.0 [34.14]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	7.0 [15.86]**	13.0 [21.54]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	11.0 [19.80]**	25.0 [30.32]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	25.0 [30.32]	21.0 [27.62]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	5.0 [13.51]	0.0 [4.05]
	150	41.0 [40.10]**	33.0 [35.36]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	17.0 [24.7]**	5.0 [13.51]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	17.0 [24.72]	25.0 [30.32]	3.0 [10.67]**	0.0 [4.05]	7.0 [15.86]**	0.0 [4.05]	0.0 [4.05]**	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
WC10*WC36	0	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]
	50	9.0 [15.86]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]
	150	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	7.0 [15.86]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]
WC36	0	9.0 [17.93]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	50	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	9.0 [17.93]**	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	100	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	17.0 [24.72]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	150	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	3.0 [10.67]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
	200	3.0 [10.67]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	27 [31.62]**	0.0 [4.05]	5.0 [13.51]**	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]	0.0 [4.05]
L.S.D.		9.1		1.4		1.5		2.2		1.6		0.9	
S.E.		4.6		0.7		0.8		1.1		0.8		0.5	
%CV		25.0		13.5		10.3		15.3		15.0		10.4	

** shows significance at P < 0.001. Figures in parenthesis were Arcsine transformed.Unt. = Untreated, Pre. = Pre-treated

The results of mean infections of *Penicillium sp*. on the pre-treated and untreated seeds showed significant ($P < 0.001$) interactions among the genotypes in their responses to the irradiation doses (Table 9). The genotypes that had significant differences between the pre-treatments were ACC122W*NE51, ACC122W*WC10, ACC122W*WC36, Alegi, Agyenkwa, Asontem, H24, Hansadua, IT889, NE15*WC36B, Soronko, Sunshine, Sunshine 1MWC10 and WC36. The remaining genotypes showed no significant differences between the means of the pre-treated and untreated seeds in their responses to the different doses. The highest *Penicillium sp*. percentage infection recorded was 29% for the untreated seeds of NE15*WC36B (200 Gy) while its pre-treated seeds recorded no infection for *Penicillium sp*. For WC10, the pre-treated samples recorded 13% *Penicillium sp*. Infection while it untreated samples recorded 7%. Generally, the untreated seeds recorded higher infection of *Penicillium sp*. on the different irradiated seeds (Table 9).

There were significant ($P < 0.001$) interactions in the mean infection of *Rhizopus sp*. on both the pre-treated and untreated seeds of cowpea seeds as affected by the irradiation doses as shown in Table 9. Genotypes Agyenkwa, IT97K819, NE21 and Secwo5T showed significant differences in the pre-treated and untreated seeds with respect to *Rhizopus sp*. infection. Although the 0 Gy of Secow5T recorded no incidence of *Rhizopus sp*., the other doses recorded significant differences between the seed pre-treatments. The highest *Rhizopus sp*. infection was 83% for the untreated seeds of Secow5T (50 Gy) while the pre-treated seeds recorded 4.5% infection. Similarly, the both seed pre-treatments recorded no *Rhizopus sp*. infection on NE21 but the other doses

recorded significant differences in their mean infections for *Rhizopus sp*. as shown in Table 9.

The results of mean infections of *Fusarium moniliforme* mycoflora between the pre-treated and untreated cowpea seeds as affected by irradiation showed significant ($P < 0.001$) interactions in their mean responses (Table 9). The genotypes ACC122W*WC10, IT91, NE15*WC36B, Soronko and WC10*WC36 recorded significant differences between the pre-treaed and untreated seeds. Doses 0 Gy, 100 Gy and 200 Gy of WC10*WC36 all recorded 3% mean *Fusarium moniliforme* infection among the untreated seeds while the pre-treated seeds recorded no incidence. For ACC122W*WC10, both 100 Gy and 200 Gy recorded 3% infection in the pre-treated seeds while untreated recorded no incidence. For IT91, the pre-treated seeds recorded 3% while the untreated seeds recorded 0% infection (Table 9). There were also 3% *Fusarium moniliforme* infections on the untreated seeds of NE15*WC36B (50 Gy) and Soronko (100 Gy) while their corresponding pre-treated seeds recorded no incidence of *Fusarium moniliforme* mycoflora on the irradiated seeds.

4.3 Experiment Three: Field Experiment

4.3.1 Agronomic and yield performance of M_1 mutants

The results of combined analysis of variance for the agronomic and yield related traits of the cowpea genotypes as affected by the doses of irradiation in M_1 mutants are shown in Table 10. There were significant ($P < 0.05$) differences in plant height at 21DAP among the genotypes when exposed to the different irradiation doses. Similarly, the irradiated seeds

showed significant ($P < 0.01$) differences in plant height at flowering among the cowpea genotypes. The genotypes (M_1 mutants) showed significant ($P < 0.001$) differences on number of days to flowering, days to 50% flowering, number of branches per plant, number of peduncles per plant, number pods per peduncle, number of pods per plant, pod length, number of seeds per pod and 100 seed weight (Table 10).

The irradiance effect among the genotypes of the M_1 mutants showed significant ($P < 0.05$) differences only on plant height at flowering (Table 10). However, the doses of irradiation showed significant ($P < 0.01$) differences on plant height at 21DAP, pod length and number of seeds pod. Significant ($P < 0.001$) differences existed among the irradiation doses on days to flowering, number branches per plant and 100 seed weight (Table 10).

The genotype-dose interactions were significant ($P < 0.001$) on number of days to flowering, number of days to 50% flower, number of branches per plant, number of seeds per pod and 100 seed weight of the M_1 mutants (Table 10).

Table 10: Combined ANOVA for agronomic and yield parameters of M_1 mutant cowpeas

		Mean sum of squares					
Source of variation	Degree of freedom	Plant Height at 21DAP	Plant Height at Anthesis	Days to Flowering	Days to 50% Flowering	No. of Branches /Plant	No. of Peduncles /plant
Genotype (G)	24	9.742*	549.8**	62.74***	83.28***	6.462***	153.7***
Dose (D)	4	10.22**	252.3*	8.904***	10.1	2.168***	7.223
G × D	96	0.9874	48.28	3.904***	3.917***	0.9108***	4.641
Residual	247	1.301	49.41	2.01E-9	2.961E-16	0.00254	4.357

, * and ******* shows significant differences at P < 0.05, P < 0.01 and P < 0.001 respectively

Table 10 continued

		Mean sum of squares				
Source of variation	Degree of freedom	Pods / peduncle	No. of Pods/Plant	Pod length	Seeds/Pod	100 Seed Weight
Genotype (G)	24	0.2629***	487.9***	23.97***	14.44**	18.86***
Dose (D)	4	0.1773	10.86	2.459**	19.4**	4.946***
G × D	96	0.06622	27.42	1.481	2.358**	3.122***
Residual	248	0.05006	41.06	1.137	1.496	0.1659

*, ** and *** shows significant difference at P < 0.05, P < 0.01 and P < 0.001 respectively

4.3.1.1 Genotypic effect of irradiation on agronomic performance and yield of M_1 mutant lines

There were significant (P = 0.02) differences among the genotypes as affected by the irradiation doses applied on plant height at 21DAP (Figure 39). The five shortest plants at 21DAP were Agyenkwa, Alegi, ACC122W*WC36, ACC122W*NE51 and Secow5T (8.9 – 9.5 cm). Genotypes F258T2E and ACC122W*WC10 were the tallest mutants at 21DAP (≈12cm) and were significantly different from the five shortest mutants. The mean plant height of the M_1 mutants was 10.3 cm with a range of 8.9 cm to 12.1 cm as shown in Figure 39.

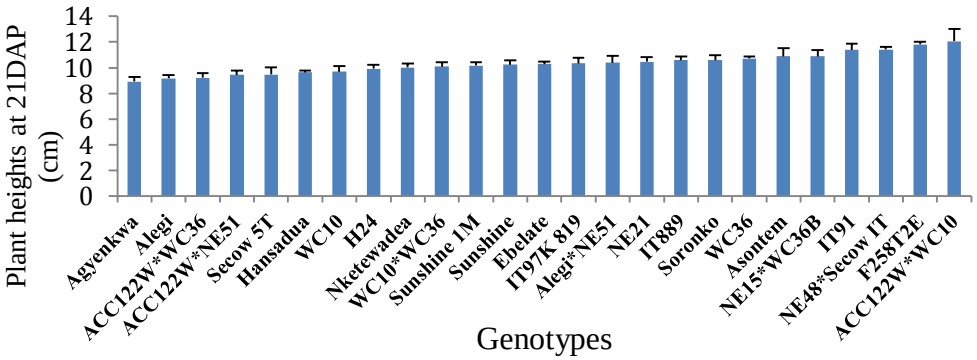

Figure 39: Genotypic responses of irradiated cowpea seeds on plant height at 21DAP of M_1 mutants

There were significant (P < 0.01) differences among the genotypes on plant height at flowering (Figure 40). The genotypes Agyenkwa, Alegi, Hansadua, Secow5T and Nketewadea recorded the least plant height at flowering and were significantly lower than the plant height of IT889, NE48*SecowIT, ACC122W*WC10 and WC36. Nearly 70% of the genotypes ranged between 40 cm to 50 cm at flowering. The range of plant height at flowering was 36cm – 59 cm (Figure 40).

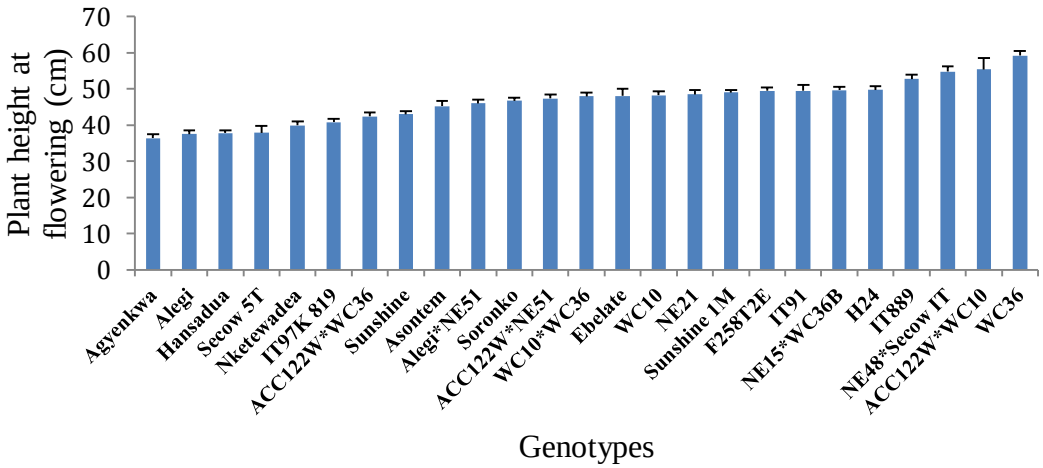

Figure 40: Genotypic responses of irradiated cowpea seeds on plant height at flowering of M_1 mutants

The number of days to flowering showed significant ($P < 0.001$) differences among the assessed genotypes (Figure 41). The three earliest genotypes to flower were Hansadua (38 days), IT91 (38 days) and IT889 (39 days). About 76% of the M_1 mutants flowered between 40 and 42 days. Genotypes ACC122W*WC36, NE15*WC36B and ACC122W*NE51 took the most days to flower (45 – 47 days) and were significantly higher than the remaining genotypes (Figure 41).

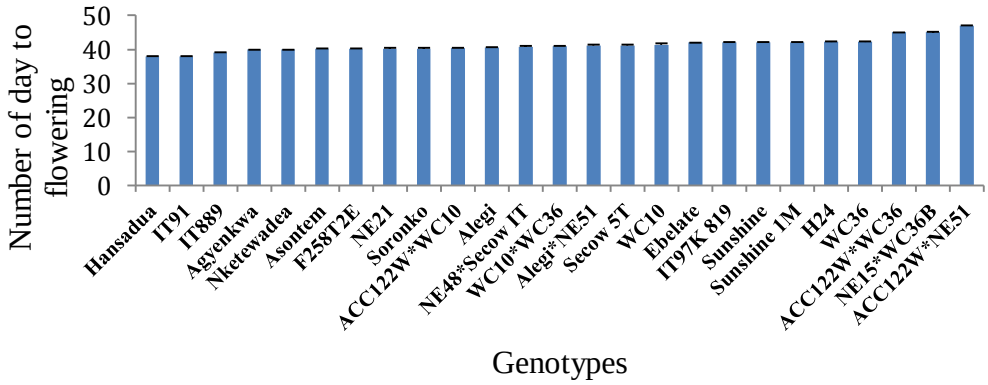

Figure 41: Genotypic responses of irradiated cowpea seeds on number of days to flowering of M_1 mutants

There were significant ($P < 0.001$) differences in the number of days to 50% flowering among the genotypes (Figure 42). Genotypes Hansadua took

less than 40 days to attain 50% flowering and was significantly lower than the remaining genotypes. Genotypes Sunshine 1M, Ebelate, ACC122W*WC36 and ACC122W*NE51 used 47 days to attain 50% flowering while ACC122W*NE51 took 48 days. The mean number of days to 50% flowering among the genotypes was 44 (Figure 42).

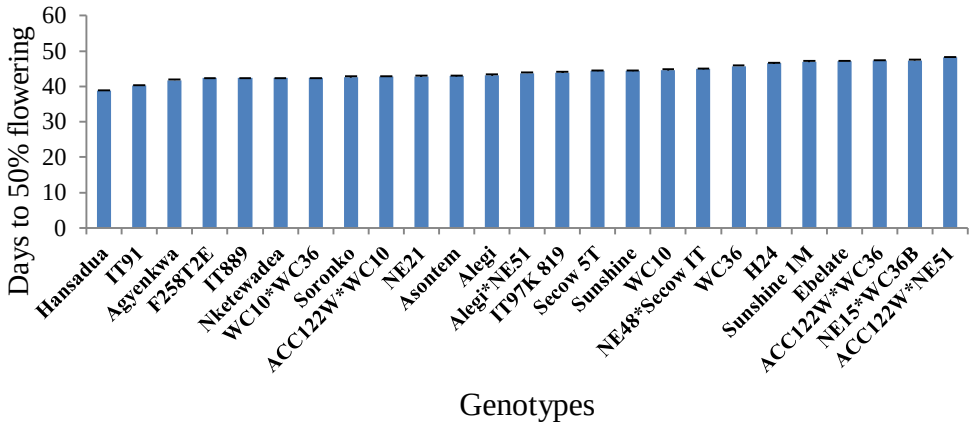

Figure 42: Figure 41: Genotypic responses of irradiated cowpea seeds on number of days to 50% flowering of M_1 mutants

There were significant ($P < 0.001$) differences among the genotypes on number of branches per plant (Figure 43). The genotypes with the least (4) number of branches per plant were Agyenkwa, WC36 and IT889 and they had significantly lower number of branches than Alegi, H24, WC10*WC36 and Sunshine which recorded 6 branches per plant. The mean number of branches per plant was 5 and the range was 4 to 6 (Figure 43).

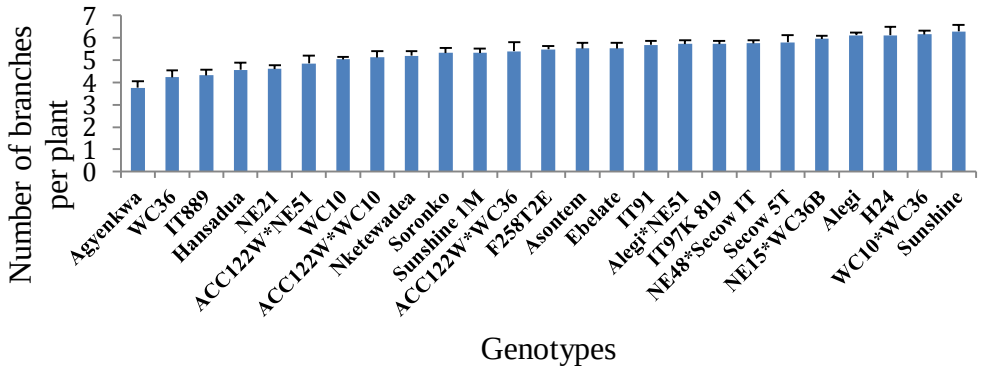

Figure 43: Genotypic responses of irradiated cowpea seeds on number of branches per plant of M_1 mutants

The results of number of peduncles per plant also showed significant ($P < 0.001$) differences among the M_1 mutants (Figure 44). ACC122W*NE51 and WC10 recorded 14 peduncles per plant and were significantly lower than the number of peduncles per plant recorded by IT91, Alegi*NE51, Sunshine 1M and ACC122W*WC36 which ranged between 23 and 25peduncles per plant. The mean number of peduncles per plant was 19 (Figure 44).

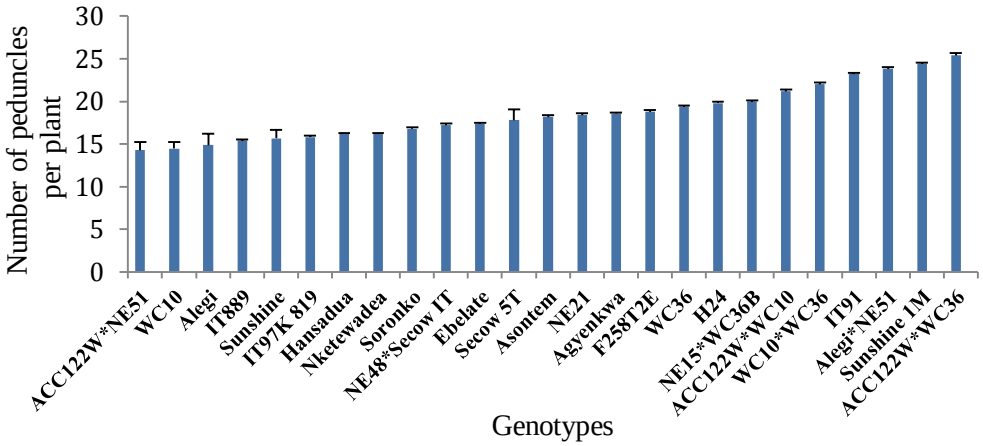

Figure 44: Genotypic responses of irradiated cowpea seeds on number of peduncles per plant of M_1 mutants

The results of the genotypic effect of the irradiation showed that there were significant ($P < 0.001$) differences in the number of pods per peduncle among the genotypes (Figure 45). About 20% of the mutants recorded more than 2 pods per peduncle. These were ACC122W*NE51, Secow5T, WC10,

Sunshine and Alegi which showed significant difference from the other genotypes with 2 pods per peduncle (Figure 45).

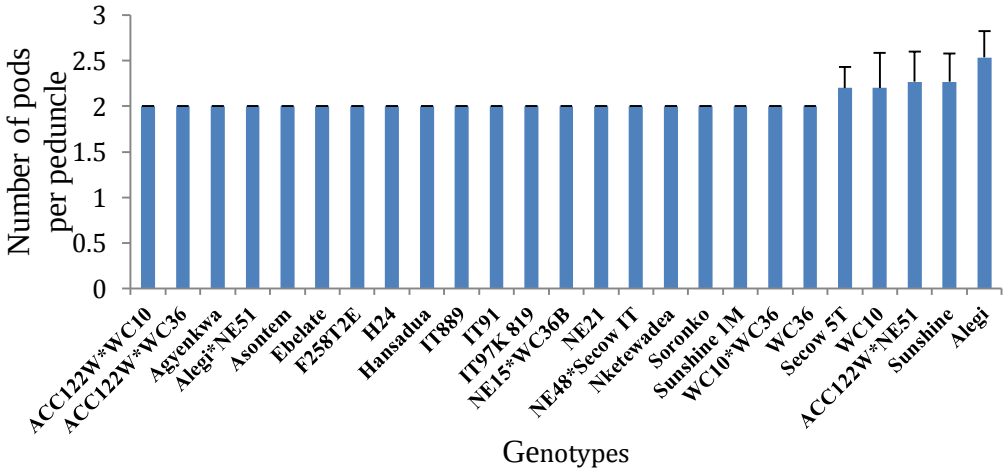

Figure 45: Genotypic responses of irradiated cowpea seeds on number of pods per peduncle of M_1 mutants

There were significant ($P < 0.001$) differences in the number of pods per plant among the genotypes as affected by the irradiation doses (Figure 46). The genotypes with the least number of pods per plant were IT889, WC10, IT97K819, ACC122W*NE51, Hansadua and Nketewadea (31 – 32 pods) while IT91, Alegi*NE51, Sunshine 1M and ACC122W*WC36 had the highest number of pods per plant (46 – 51) as shown in Figure 46. About 76% of the genotypes recorded ≤40 pods per plant in their mean responses to the irradiation doses. The mean number of pods per plant among the genotypes was 38 (Figure 46).

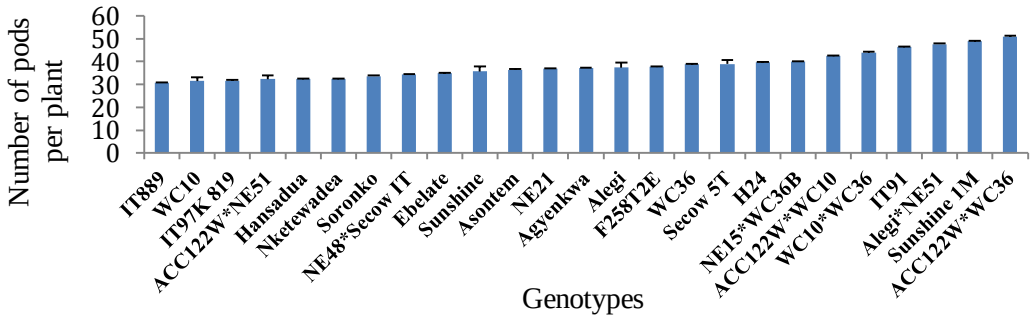

Figure 46: Genotypic responses of irradiated cowpea seeds on number of pods per plant of M_1 mutants

The results of pod lengths measured for the M_1 mutants showed significant ($P < 0.001$) differences among the genotypes (Figure 47). The topmost five genotypes with the longest pods were WC10*WC36, IT889, NE21, Sunshine and WC10 (18 – 18.7 cm) which were significantly different from genotypes NE15*WC36B, Agyenkwa, ACC122W*WC36, Nketewadea and H24 (14.7 – 15.2 cm). The mean pod length was 16.6 cm and ranged between 14.7 and 18.7 cm (Figure 47).

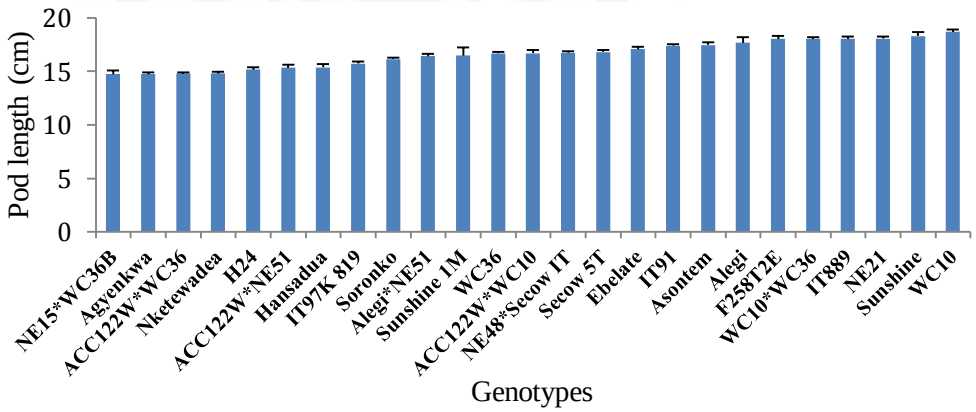

Figure 47: Genotypic responses of irradiated cowpea seeds on pod lengths of M_1 mutants

Similarly, the results of number of seeds per pod also showed significant ($P < 0.05$) differences among the genotypes (Figure 48). The genotypes with ≥18 seeds per pod were Alegi, F258T2E, WC10*WC36, IT889, NE21, Sunshine and WC10. Also, the genotypes with the least number of seeds per pod (15) were NE15*WC36B, Agyenkwa, ACC122W*WC36, Nketewadea,

H24, ACC122W*NE51 and Hansadua. The mean number of seeds per pod among the genotypes was 16.6 (≈17) as shown in Figure 48.

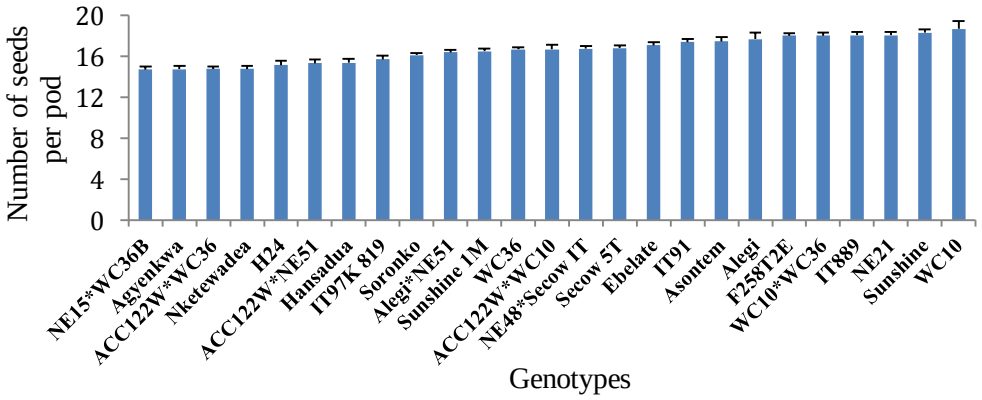

Figure 48: Genotypic responses of irradiated cowpea seeds on number of seeds per pod of M_1 mutants

The results of weight of 100 seed of the mutants showed significant ($P < 0.001$) differences among the genotypes (Figure 49). The genotypes with the highest seed weight among the M_1 mutants were Asontem, Alegi, IT889, IT91, Nketewadea and F258T2E (12.7 - 13.6 g) while ACC122W*WC36, H24 and NE15*WC36B weighed between 9.3 to 10.3 g for 100 seed. The mean 100 seed weight was 12 g (Figure 49).

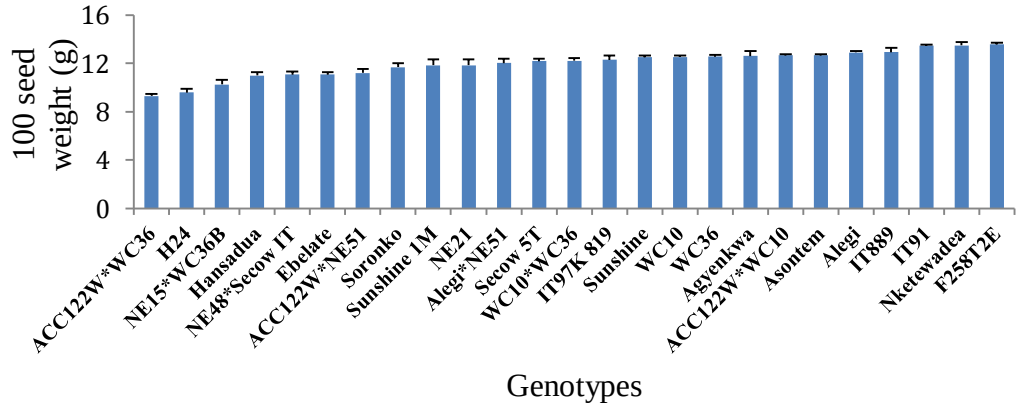

Figure 49: Genotypic responses of irradiated cowpea seeds on 100 seed weight of M_1 mutants

4.3.1.2 Effect of irradiation on agronomic performance and yield of M_1 mutant lines

The results of irradiance effect on the genotypes showed significant (P = 0.004) differences on plant height at 21DAP (Figure 50). The control (0 Gy) recorded mean plant height of 10.8 cm and was significantly different from doses 150 Gy and 200 Gy. There was no significant difference in the mean plant height among dose 0 Gy (10.8 cm), 50 Gy (10.4 cm) and 100 Gy (10.5 cm). Generally, increasing irradiation resulted in decreasing plant height at 21DAP as shown in Figure 50.

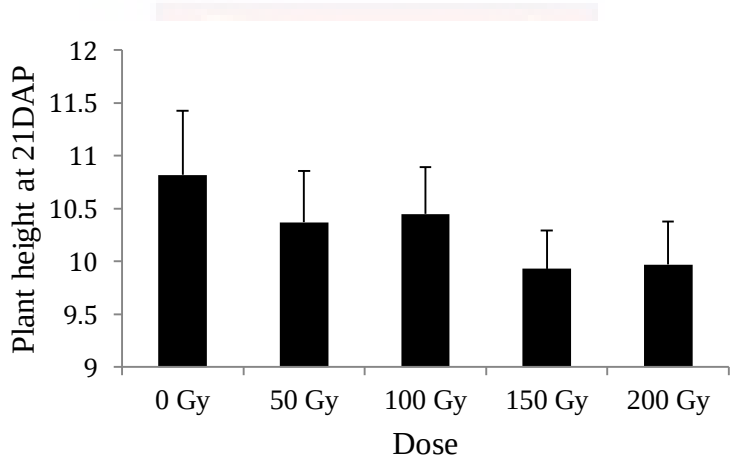

Figure 50: Irradiance effect of irradiated cowpea seeds on plant height at 21DAP of M_1 mutants

At flowering, the results of the effect of irradiation doses on the plant height showed significant (P = 0.004) differences among the doses (Figure 51). The 100 Gy irradiation dose produced the tallest (48 cm) plants at flowering but were only significantly different from the plant height of 200 Gy (43.7 cm). Increasing the irradiation dose increased plant height up to 100 Gy and then decreased with increasing dose at flowering shown in Figure 51.

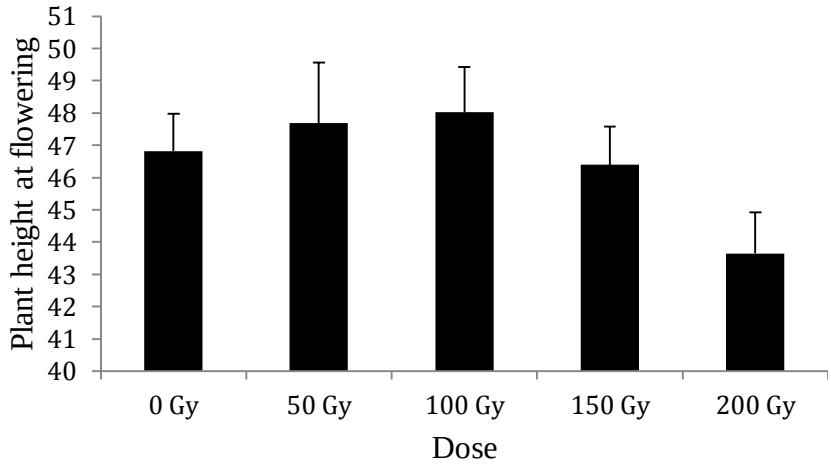

Figure 51: Irradiance effect of irradiated cowpea seeds on plant height at flowering of M_1 mutants

The results mean number of days to flowering showed significant ($P < 0.001$) differences among the irradiation doses applied (Figure 52). Although there was only a day difference among the mean number of days to flowering among the doses of irradiation, there were significant differences. Plants of the control took the most (41.7 ≈42) days to flower and were significantly different from mutants of doses 50 Gy, 100 Gy and 200 Gy. The days to flowering increased with increasing irradiation up to 150 Gy and then decreased as shown in Figure 52.

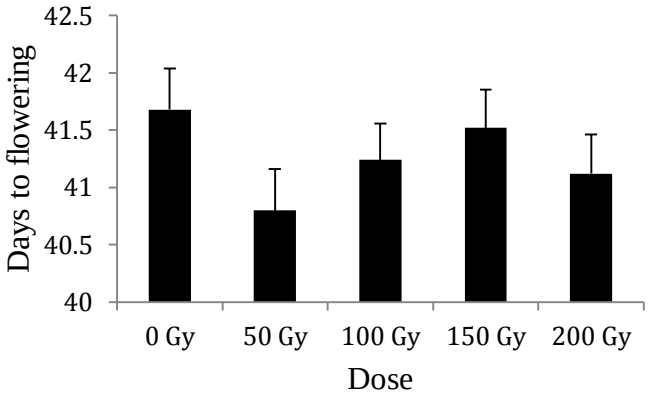

Figure 52: Irradiance effect of irradiated cowpea seeds on days to flowering of M_1 mutants

The number of branches per plant of the mutants showed significant (P < 0.001) differences among the doses of irradiation (Figure 53). The 0 Gy had 6 branches per plant and was significantly different from seeds irradiated at the other doses of irradiation. The doses of irradiation (50 Gy – 200 Gy) all had 5 branches per plant. There was a general decline in the number of branches per plant among the doses of irradiation as shown in Figure 53.

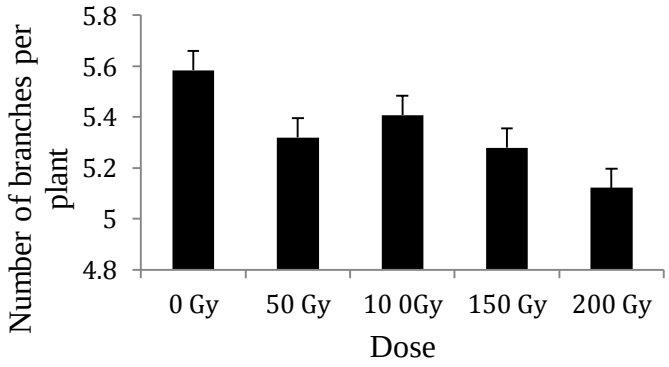

Figure 53: Irradiance effect of irradiated cowpea seeds on number of branches per plant of M_1 mutants

The results of pod lengths as affected by the irradiation doses showed significant (P = 0.003) differences among the different doses of irradiation (Figure 54). The range for pod length as affected by the irradiation doses was 16.4 cm to 16.8 cm. Seeds subjected to doses 150 Gy and 200 Gy were significantly lower than the remaining doses in pod lengths. Increasing dose of irradiation resulted in decreasing pod length up to 150 and then increased as shown in Figure 54.

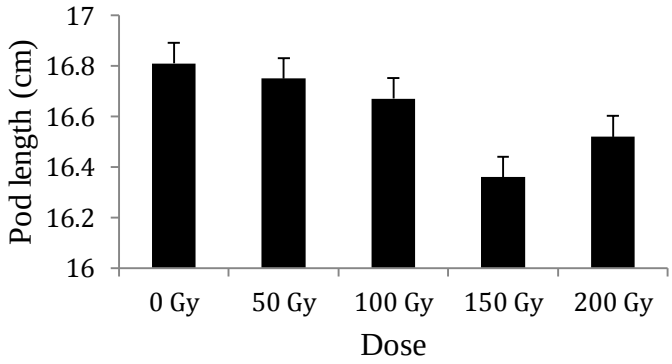

Figure 54: Irradiance effect of irradiated cowpea seeds on pod lengths of M_1 mutants

Similarly, the number of seeds per pods showed significant ($P < 0.001$) differences among the doses. The number of seeds per pod ranged between 16 and 17. There were 17 seeds per pod for the seeds of the control and mutants irradiated at 50 Gy and 100 Gy while seeds irradiated at doses 150 Gy and 200 Gy had 16 seeds per pod. The number of seeds per pod showed inverse relationship with irradiation dose as shown in Figure 55.

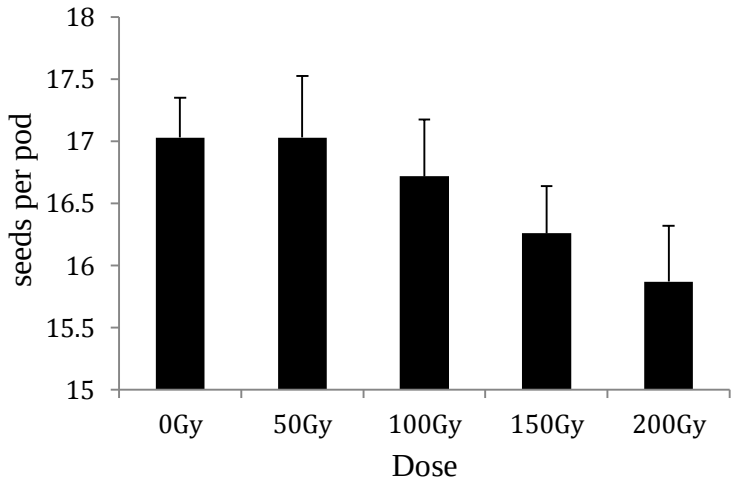

Figure 55: Irradiance effect of irradiated cowpea seeds on number of seeds per pod of M_1 mutants

The irradiation doses exhibited significant ($P < 0.001$) differences on 100 seed weight of the mutants (Figure 56). Seeds irradiated at 200 Gy had the heaviest (12.5 g) 100 seed weight and was significantly different from seeds of

the other doses of irradiation. The 100 seed weight of the mutants irradiated at 150 Gy were not significantly different from the control. The mean of 100 seed weight among the different irradiation doses was 12 g and ranged between 11.7 and 12.4 g (Figure 56).

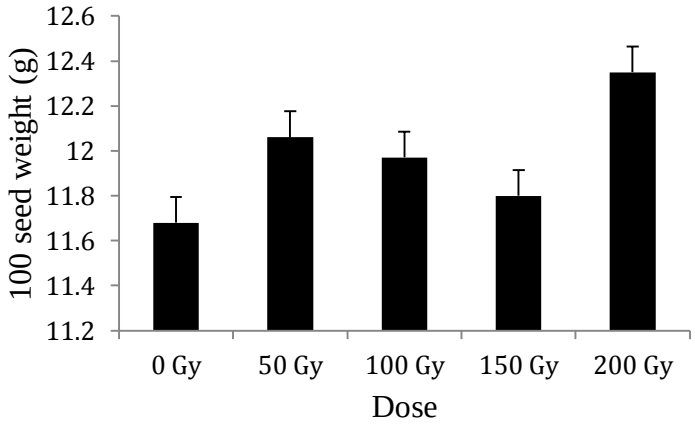

Figure 56: Irradiance effect of irradiated cowpea seeds on number of 100 seed weight of M_1 mutants

4.3.1.3 Genotype-dose interaction effect on agronomic performance and yield of M_1 mutant lines

The results of means of genotypes as affected by the irradiation doses showed significant ($P < 0.001$) interactions in the days to flowering (Table 11). All the genotypes showed significant differences in their mean number of days to flowering except for ACC122W*WC36 (45 days), Agyenkwa (40 days), Ebelate (42 days), IT91 (38 days) and Nketewadea (40 days). The longest number of days to flowering was recorded by ACC122W*NE51 (47 days); where all the irradiation doses took ≈47 days except the 200 Gy which took 46 days to flower. For IT889, the control and dose 50 Gy took 37 and 38 days to flower respectively while the other doses took 40 days. However, the number of days to flower in NE21 was least for the 200 Gy (37 days) and highest for the 0 Gy (44 days) as shown in Table 11.

The mean responses of the irradiated genotypes on number of days to 50% flowering showed significant ($P < 0.001$) interactions (Table 11). All the genotypes showed significant differences in their mean responses as affected by the doses of irradiation except for genotypes ACC122W*WC36 (47 days), IT889 (42 days), NE48*SecowIT (40 days), (Nketewadea (42 days) and WC10*WC36 (42days). The highest number of days to 50% flowering was recorded by dose 50 Gy of Sunshine IM (50 days) and it was significantly different from the other doses which ranged from 44 to 47 days. For Hansadua, all the doses of irradiation used 38 days to attain 50% flowering except the mutants irradiated at 150 Gy which took 40 days (Table 11).

There were significant ($P < 0.001$) genotype-dose interactions in the means of number of branches per plant among the genotypes in their responses to the irradiation, as shown in Table 11. The least number of branches per plant was 3 and it was recorded for mutants at 150 Gy and 200 Gy of Agyenkwa as shown in Table 11. The control and 100 Gy of genotype Sunshine recorded the highest number of branches per plant as 7 and were significantly different from the other doses of irradiation (Table 11).

There were significant ($P < 0.001$) interactions between the genotypes and doses in the means of seeds per pod among the irradiated seeds (Table 11). All the means showed significant differences on number of seeds per pod. The highest number of seeds per pods was 22 and it was recorded by mutants irradiated at 50 Gy of WC10; where it was significantly different from the other doses. Also, mutants of Nketewadea dose 100 Gy recorded the least number of seeds per pod to be 13 and was significantly lower than the means of the other doses (Table 11).

Table 11: Means of M_1 mutant responses to agronomic and yield parameters

Genotype	Days to Flowering					Days to 50% Flowering					Branches/Plant					Seeds/Pod					100 SW (g)				
	Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)				
	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
ACC122W*NE51	47.0	46.7	47.0	47.0	45.7	47.0	48.0	48.7	48.0	48.0	4.8	4.2	4.8	6.0	4.5	15.9	16.5	18.0	14.2	15.2	9.5	11.1	10.6	11.2	13.4
ACC122W*WC10	42.0	40.0	40.0	40.0	40.0	44.0	42.0	42.0	42.0	42.0	5.4	5.8	5.0	5.2	4.2	17.3	16.9	16.9	16.9	15.8	12.4	12.5	12.6	12.5	13.4
ACC122W*WC36	45.0	45.0	45.0	45.0	45.0	47.0	47.0	47.0	47.0	47.0	6.6	5.0	6.2	4.4	4.8	17.2	16.9	16.3	16.0	15.6	8.5	9.1	9.8	9.1	10.1
Agyenkwa	40.0	40.0	40.0	40.0	40.0	40.0	40.0	42.0	42.0	43.0	3.6	4.2	4.4	3.4	3.2	15.8	15.0	15.5	14.2	14.1	10.6	12.4	12.6	12.6	14.8
Alegi	40.0	41.0	42.0	40.0	40.3	42.3	43.0	45.0	42.7	42.0	6.2	6.2	6.4	6.0	5.8	17.5	17.9	18.2	17.2	15.1	12.8	12.3	12.4	13.5	13.5
Alegi*NE51	42.0	40.0	40.0	42.0	42.0	42.0	42.0	44.0	44.0	45.0	6.0	5.6	5.6	5.2	6.2	15.9	15.9	16.7	15.8	17.4	13.7	10.4	12.0	11.1	13.0
Asontem	41.0	40.0	40.0	40.0	40.0	42.0	42.0	42.0	43.0	44.0	4.6	5.6	6.0	6.2	5.2	17.3	18.8	16.4	15.3	15.4	12.2	12.7	12.6	12.7	13.2
Ebelate	42.0	42.0	42.0	42.0	42.0	46.0	47.0	47.0	48.0	46.0	6.0	5.0	5.8	6.0	4.8	17.5	16.9	17.0	17.1	17.2	10.6	11.3	11.7	10.2	11.5
F258T2E	41.0	40.0	40.0	40.0	40.0	42.0	42.0	42.0	42.0	42.0	5.0	5.6	5.6	5.8	5.4	18.2	17.7	17.5	17.4	16.3	13.3	13.2	14.0	13.5	13.8
H24	43.0	40.0	43.0	43.0	42.0	46.0	46.0	47.0	47.0	45.0	6.6	6.4	6.4	6.6	4.6	17.3	16.7	15.4	16.5	15.2	8.7	10.8	10.3	9.8	8.5
Hansadua	38.0	38.0	38.0	39.0	37.0	38.0	38.0	38.0	40.0	38.0	4.8	5.2	3.6	3.8	5.4	16.7	16.5	16.4	14.3	14.0	10.5	10.4	12.7	10.5	10.9
IT889	37.0	38.0	40.0	40.0	40.0	42.0	42.0	42.0	42.0	42.0	4.8	4.2	4.8	4.2	3.6	18.1	17.3	17.4	18.3	16.8	12.3	13.8	14.5	12.6	11.3
IT91	38.0	38.0	38.0	38.0	38.0	40.0	40.0	40.0	40.0	40.0	5.8	5.4	6.0	5.0	6.2	18.0	16.2	18.1	17.6	16.4	12.6	13.7	13.5	13.8	13.7
IT97K 819	42.0	40.0	42.0	42.0	44.0	42.0	42.0	44.0	44.0	46.0	5.8	5.2	5.8	5.6	6.2	17.3	15.6	16.1	15.8	15.2	14.5	12.6	10.4	11.7	12.2
NE15*WC36B	45.0	46.0	46.0	46.0	42.0	47.0	47.0	48.0	48.0	45.0	6.4	6.0	5.8	6.0	5.6	16.9	17.5	15.7	15.9	15.3	10.3	12.3	8.7	9.8	10.2
NE21	44.0	40.0	40.0	40.0	37.0	46.0	42.0	42.0	42.0	40.0	5.2	4.6	4.6	4.2	4.4	17.9	19.5	19.7	18.6	16.7	8.9	14.0	12.7	11.9	11.9
NE48*Secow IT	40.0	40.0	40.0	42.0	42.0	44.0	44.0	44.0	46.0	45.0	6.0	5.4	5.4	6.0	6.0	17.3	17.0	16.2	16.3	16.6	11.4	10.4	12.4	10.7	10.4
Nketewadea	40.0	40.0	40.0	40.0	40.0	42.0	42.0	42.0	42.0	42.0	5.6	5.6	5.0	4.4	5.4	14.9	15.2	13.3	14.7	13.5	11.8	14.3	13.6	13.2	14.5
Secow5T	40.0	42.0	40.0	42.0	42.0	43.0	44.0	43.0	45.0	45.0	6.6	5.0	5.6	6.6	5.2	17.3	17.3	16.9	16.2	15.8	11.3	12.5	12.8	12.8	11.5
Soronko	42.0	37.0	42.0	40.0	40.0	44.0	39.0	44.0	42.0	42.0	5.0	5.4	5.8	5.8	4.6	15.8	17.6	16.7	15.6	16.4	12.7	11.7	12.4	9.4	12.3
Sunshine	42.0	40.0	42.0	43.0	43.0	44.0	42.0	44.0	45.0	45.0	7.2	6.4	6.8	5.4	5.6	17.3	17.6	18.5	15.6	16.1	13.4	12.1	12.1	12.4	12.5
Sunshine 1M	42.0	42.0	42.0	44.0	40.0	46.0	46.0	47.0	50.0	44.0	5.8	5.8	5.2	4.8	5.0	15.7	15.5	14.3	15.8	15.4	11.9	11.9	9.4	12.6	13.5
WC10	45.0	40.0	40.7	40.0	42.0	47.0	43.0	43.0	43.0	45.0	5.2	5.2	5.2	4.8	4.8	18.7	22.2	18.0	16.8	16.6	12.4	12.7	12.2	12.5	12.8
WC10*WC36	42.0	41.0	40.0	41.0	41.0	42.0	42.0	42.0	42.0	42.0	6.2	6.4	5.6	6.6	6.0	17.9	15.8	16.9	18.1	19.3	12.7	11.3	11.6	11.9	13.5
WC36	42.0	43.0	42.0	42.0	42.0	44.0	45.0	46.0	46.0	46.0	4.4	3.6	3.8	4.0	5.4	16.3	16.0	16.2	16.2	15.8	13.2	12.4	11.8	12.9	12.6
L.S.D.			0.4					0.3					0.1					1.4					0.6		
S.E.			0.6					0.2					0.0					8.1					0.4		
%C.V.			0.6					0.4					0.9					2.2					3.3		

The mean responses of the mutants showed significant ($P < 0.001$) interactions on 100 seed weight (Table 11). The control of ACC122W*WC36 recorded the least 100 seed weight (8.5 g) and was significantly lower than the means of the other doses. For Agyenkwa, increasing irradiation led to increasing 100 seed weight. Thus, mutants of Agyenkwa (dose 200 Gy) recorded the highest 100 seed weight of 14.8 g while plants in the control recorded 10.6 g (Table 11).

4.3.2 Agronomic and yield performance of M_2 mutant cowpea

The results of combined analysis of variance for the measured agronomic and yield-related traits of the M_2 mutants are shown in Table 12. There were significant ($P < 0.001$) differences among the genotypes on plant height at 21DAP, plant height at flowering, days to first flowering, days to 50% flowering, number of branches per plant, number of peduncles per plant, number of pods per peduncle, number of pods per plant, 100 seed weight and grain yield. However, there were significant ($P < 0.01$) differences among the genotypes on pod length and seeds per pod as shown in Table 12.

There were significant ($P < 0.001$) differences among the irradiation doses on plant height at 21DAP, plant height at first flowering, number of branches per plant and 100 seed weight (Table 12). However, the doses of irradiation showed significant ($P < 0.05$) differences on grain yield (Table 12). The genotype-dose interactions of the M_2 mutants were significant ($P < 0.001$) on plant height at 21DAP, plant height at flowering, number of branches per plant, 100 seed weight and grain yield (Table 12).

Table 12: Combined ANOVA for agronomic and yield parameters of M_2 mutant cowpeas

		Mean sum of squares					
Source of variation	Degree of freedom	Plant Height at 21DAP	Plant Height at Anthesis	Days to Flowering	Days to 50% Flowering	Branches per Plant	Peduncles per plant
Genotype (G)	24	28.99***	600.24***	22.84***	32.13***	4.55***	139.84***
Dose (D)	4	2.77***	127.76***	1.74	4.56	1.66***	8.66
G × D	96	1.38***	70.70***	4.95	8.24	0.64***	5.31
Residual	248	1.83E-06	0.50	5.64	9.54	1.43E-05	4.92

*, ** and *** shows significance at P < 0.05, P < 0.01 and P < 0.001

Table 12 continued

		Mean sum of squares					
Source of variation	Degree of freedom	Pods per peduncle	Pods pod Plant	Pod length	Seeds per Pod	100 seed weight	grain yield
Genotype (G)	24	0.27***	448.05***	8.61**	7.62**	18.55***	2580256***
Dose (D)	4	0.13	34.3	2.80	2.93	4.64***	52697*
G × D	96	0.05	31.82	2.52	3.54	3.089***	67995***
Residual	248	0.05	43.86	2.40	3.98	0.11	12521

*, ** and *** shows significance at P < 0.05, P < 0.01 and P < 0.001

4.3.2.1 Genotypic effect of irradiation on agronomic performance and yield of M_1 mutant lines

The height of plants measured at 21DAP showed significant ($P < 0.001$) differences among the genotypes of the M_2 mutants (Figure 57). The five genotypes with the shortest plants at 21DAP were WC10, ACC122W*NE51, Agyenkwa, Secow5T and Alegi which ranged between 8.9 cm and 9.9 cm. Also, IT97K819, F258T2E and IT91 were the genotypes with the tallest plants at 21DAP (13.5 cm to 13.8). The mean plant height at 21DAP was 11.5 cm. Nearly 50% of the genotypes recorded plant height >11.5 cm (Figure 57).

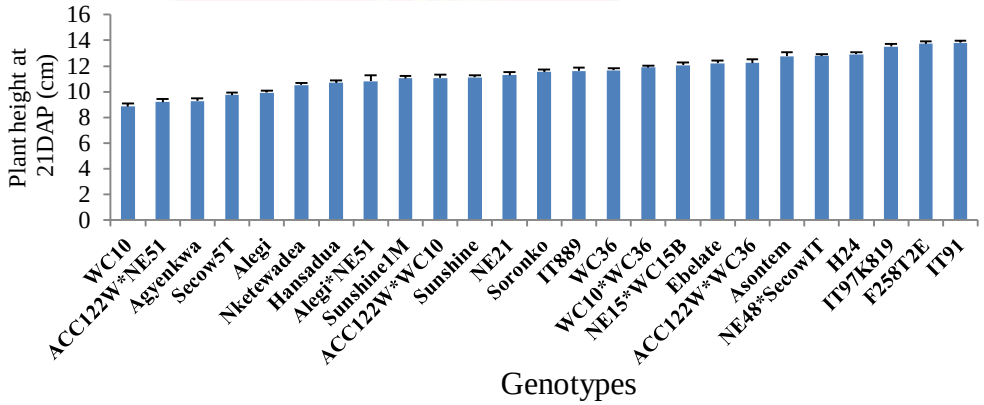

Figure 57: Genotypic responses of M_2 mutants on plant height at 21DAP

Similarly, there were significant ($P < 0.001$) differences among the genotypes on plant height at flowering (Figure 58). Genotypes NE15*WC36B (34 cm), Secow5T (37 cm) and ACC122W*NE51 (38 cm) produced the shortest M_2 mutants at flowering while WC36 (54 cm), Sunshine 1M (57 cm), NE48*SecowIT (57 cm) and WC10*WC36 (59 cm) became the four tallest mutants. These four mutants were significantly different from the other

genotypes in plant height at flowering. The average plant height at flowering among the genotypes was 45 cm (Figure 58).

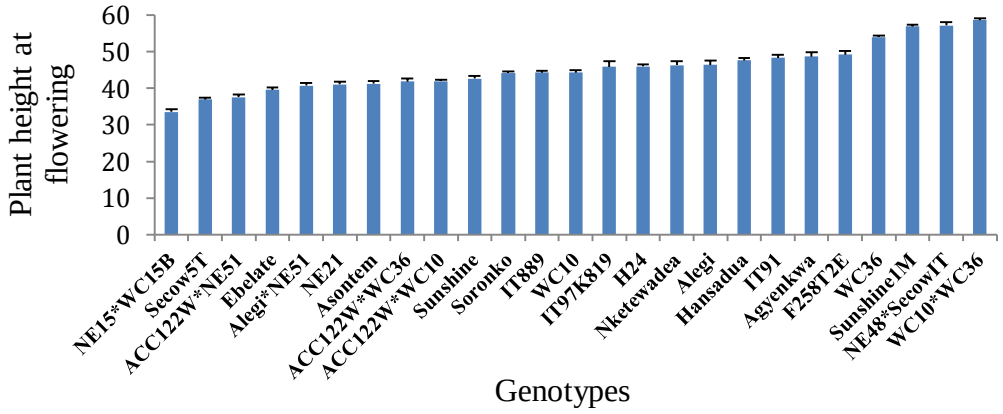

Figure 58: Genotypic responses of M_2 mutants on plant height at flowering

The effects of the irradiation showed significant ($P < 0.001$) differences among the genotypes (Figure 59). Among the genotypes, IT91, and IT889 were the earliest to flower (40 days). However, the late flowering genotypes among the M_2 mutants were Hansadua (44 days) and ACC122W*WC36 (45 days) and these were significantly different from the other genotypes as shown in Figure 59. Over 65% of the genotypes flowered between 40 and 42 days after sowing (Figure 59).

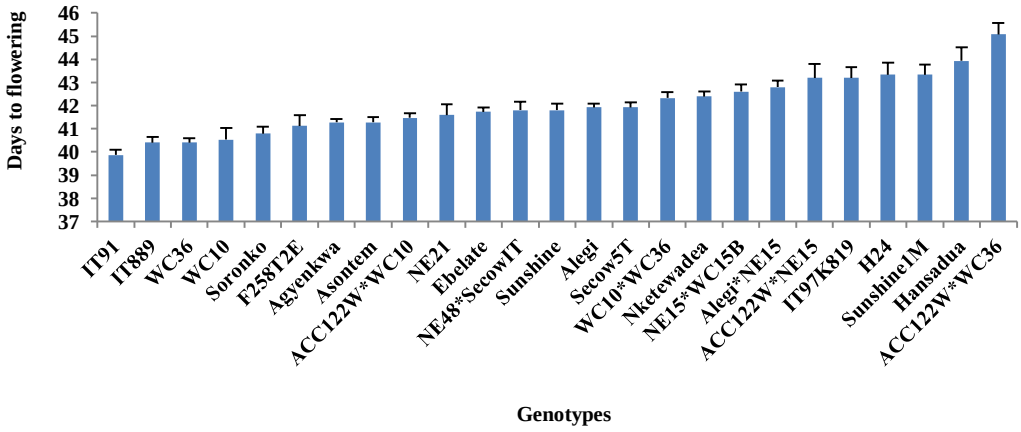

Figure 59: Genotypic responses of M_2 mutants on days to flowering

There were significant (P < 0.001) differences among the genotypes on days to 50% flowering as influenced by the irradiation doses (Figure 60). Also, genotype IT91 attained 50% flowering within 42 days while IT889 and WC36 both took 43 days and theses three were the quickest to attain 50% flowering among the genotypes. ACC122W*WC36 recorded 50% flowering within 48 days and was significantly different from the other genotypes. About 60% of the genotypes recorded 50% flowering in 44 days or less as shown in Figure 60.

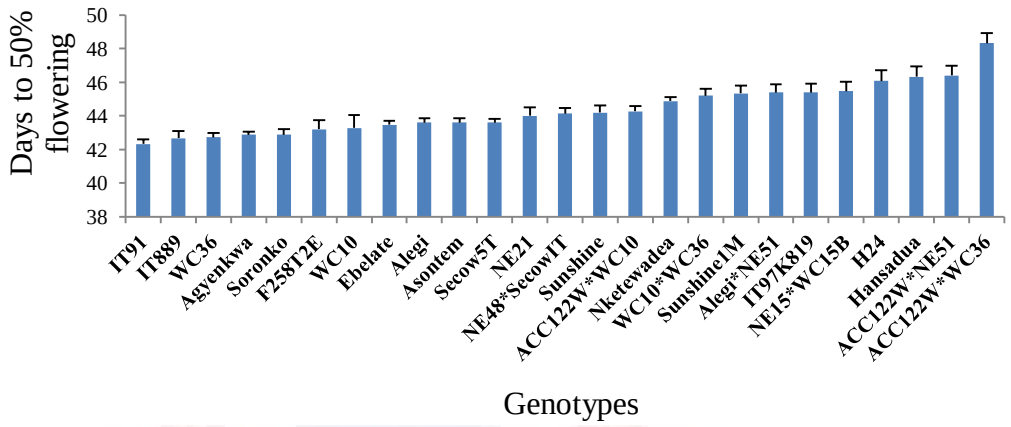

Figure 60: Genotypic responses of M_2 mutants on days to 50% flowering

There were significant (P < 0.001) differences in the number of branches per plant among the genotypes upon exposure to irradiation (Figure 61). There were 4 branches per plant for genotype Agyenkwa, WC36, IT889, Hansadua, NE21 and ACC122W*WC10. For Alegi, H24, WC10*WC36 and Sunshine, there were 6 branches per plant. About one-sixth of the genotypes had between 4 and 5 branches per plant among the genotypes (Figure 61).

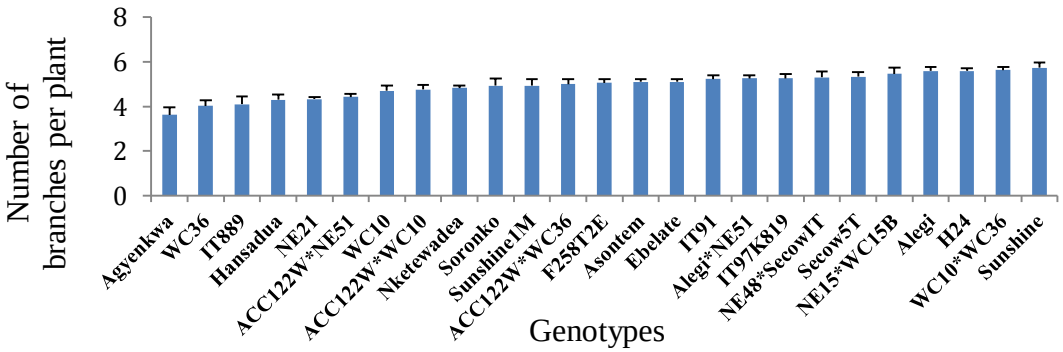

Figure 61: Genotypic responses of M_2 mutants on number of branches per plant

The number of peduncles per plant was significantly ($P < 0.001$) different among the genotypes assessed (Figure 62). The range for number of peduncles per plant was 14 – 25 among the M_2 mutants. The genotypes with the least number of peduncles per plant were ACC122W*NE51, Alegi, IT889, Sunshine, IT97K819, Hansadua and Nketewadea with a mean of 15 peduncles per plant. Also, Alegi*NE51, Sunshine 1M and ACC122W*WC36 were the genotypes with the most peduncles per plant (24 – 25) as shown in Figure 62.

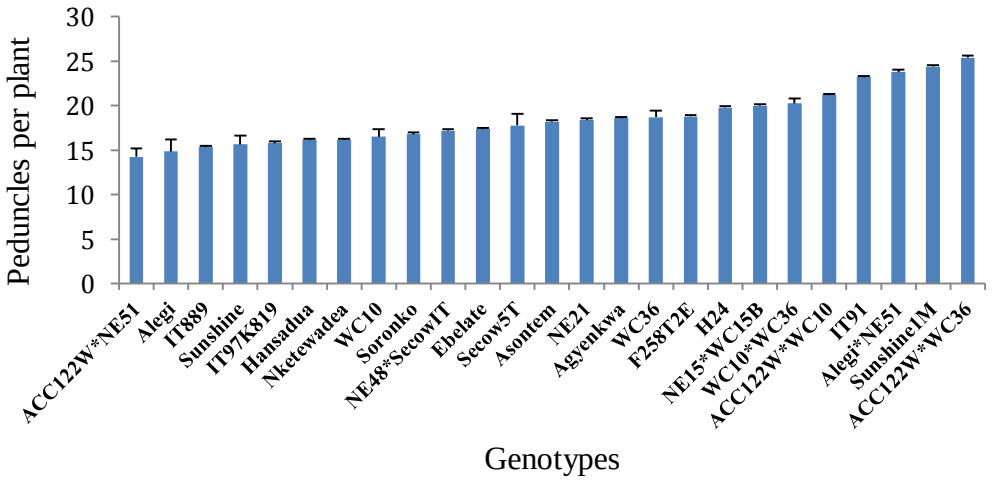

Figure 62: Genotypic responses of M_2 mutants on number of peduncles per plant

The results of genotypic responses to the irradiation showed significant ($P < 0.001$) differences on the number of pods per peduncle (Figure 63). Over 60% of the genotypes recorded 2 pods per peduncle among the genotypes. The

following genotypes recorded more than 2 peduncles per plant: Ebelate, F258T2E, Nketewadea, WC36, Sunshine, Secow5T, WC10, Alegi, and ACC122W*NE51 (Figure 63).

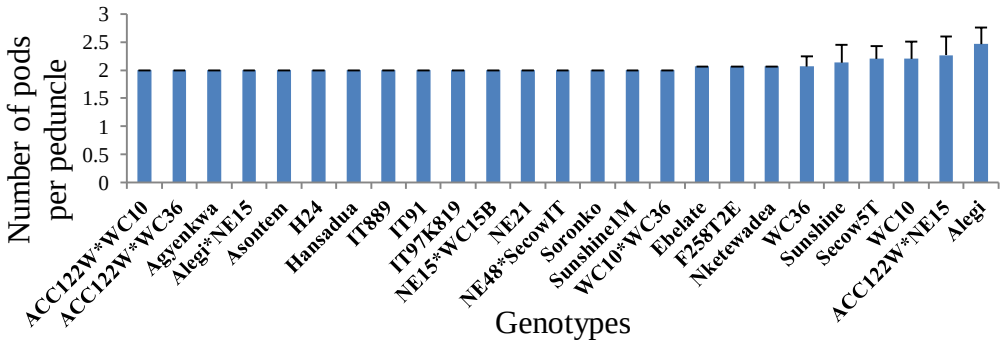

Figure 63: Genotypic responses of M_2 mutants on number of pods per peduncle

There were significant ($P < 0.001$) differences in the number of pods per plant among the genotypes (Figure 64). The number of pods per plant varied between 30 and 51 among the genotypes. About 75% of the genotypes recorded mean number of pods per plant range of 30 – 40. The top three best genotypes for mean number of pods per plant were Alegi*NE51, Sunshine 1M and ACC122W*WC36 which had an average of 49 pods per plant. Also, IT889, IT97K819, ACC122W*NE51, Hansadua and Nketewadea were the genotypes with the least (31 - 32) number of pods per plant (Figure 64).

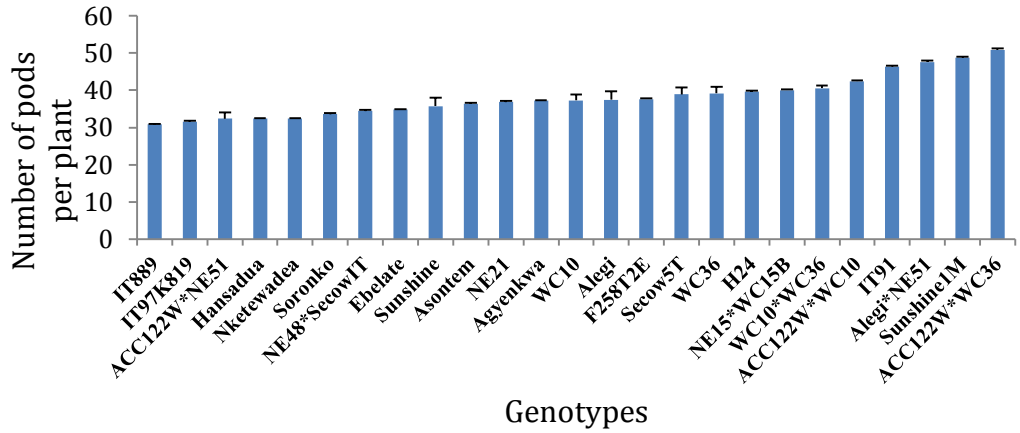

Figure 64: Genotypic responses of M_2 mutants on number of pods per plant

The pod lengths measured showed significant ($P < 0.001$) differences among the genotypes (Figure 65). The three genotypes with the shortest pods were H24, Hansadua and Asontem (16.4 - 16.9 cm) while Alegi, ACC122W8WC10 and Sunshine had the longest pods (18.7 – 18.9 cm). The mean pod length among the genotypes was 17.7 cm (Figure 65).

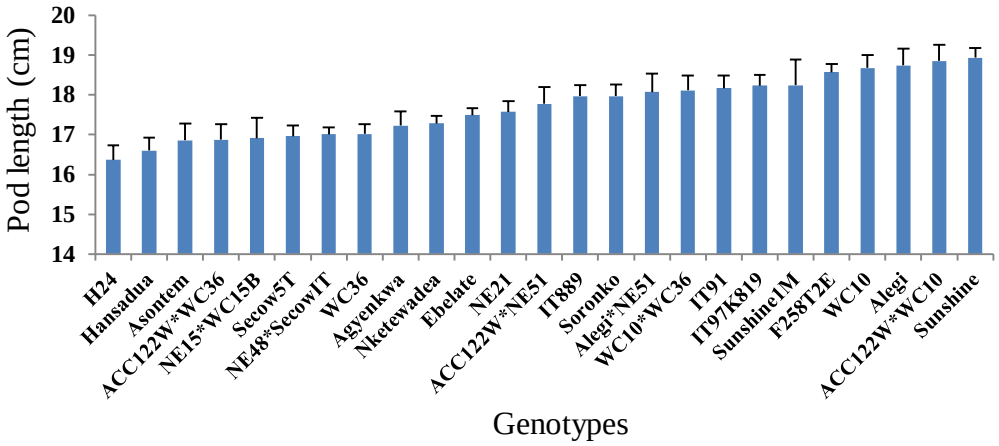

Figure 65: Genotypic responses of M_2 mutants on number of pod length

There were significant ($P < 0.01$) differences among the genotypes on the number of seeds per pod (Figure 66). The mean number of seeds per pod was 17 and ranged between 15 and 18. Asontem, Hansadua and H24 formed the trio with the least seeds per pod (15 to 16). Genotypes ACC122W*NE51, IT97K819, WC10*WC36, F258T2E, Ebelate, Alegi*NE51, Sunshine and ACC122W*WC10 had the most (18) seeds per pod among the genotypes as shown in Figure 66.

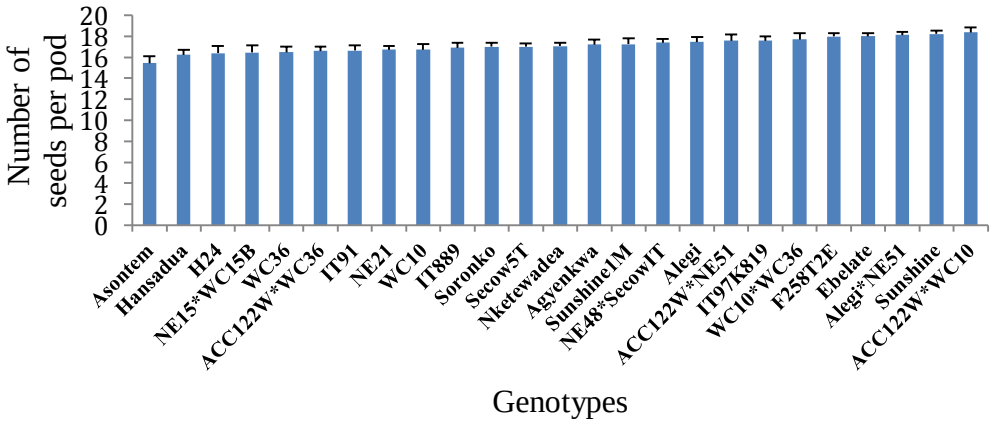

Figure 66: Genotypic responses of M_2 mutants on number of seeds per pod

There were significant ($P < 0.001$) differences in the 100 seed weight measured among the genotypes (Figure 67). ACC122W*WC36 had mean 100 seed weight of 10 g and was significantly lower than the 100 seed weight of IT91, Nketewadea and F258T2E which recorded a mean 100 seed weight of ≈14 g. The mean 100 seed weight among the genotypes was 12.6 g (Figure 67).

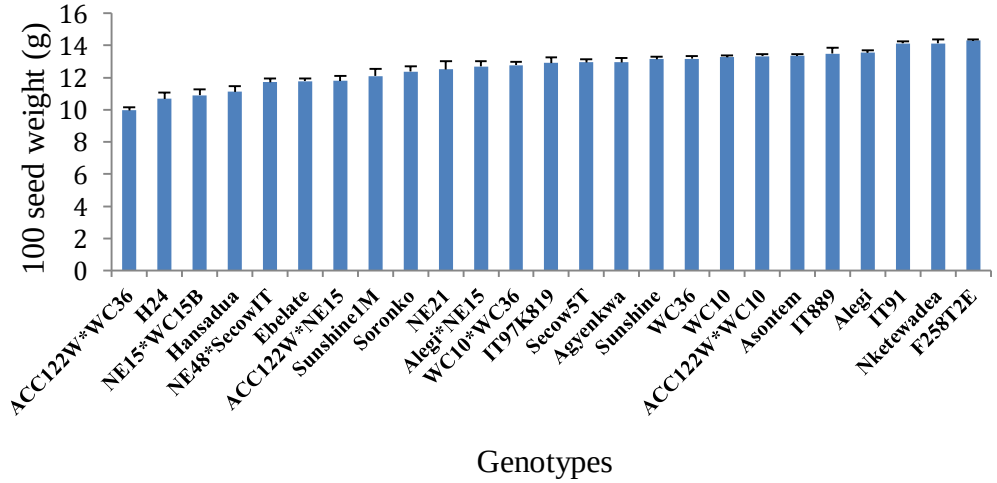

Figure 67: Genotypic responses of M_2 mutants on number of 100 seed weight

Similarly, there were significant ($P < 0.001$) differences in grain yield among the genotypes as affected the irradiation doses (Figure 68). The lowest yield was recorded by Nketewadea, Agyenkwa and Hansadua (mean – 1070

kg/ha) and they were significantly lower than the other genotypes. Genotypes NE21, NE15*WC15B, ACC122W*WC36 and WC10*WC36 had mean grain yield ≥ 2000 kg/ha. About 60% of the genotypes recorded grain yield between 1500 and 1999 kg/ha as shown in Figure 68.

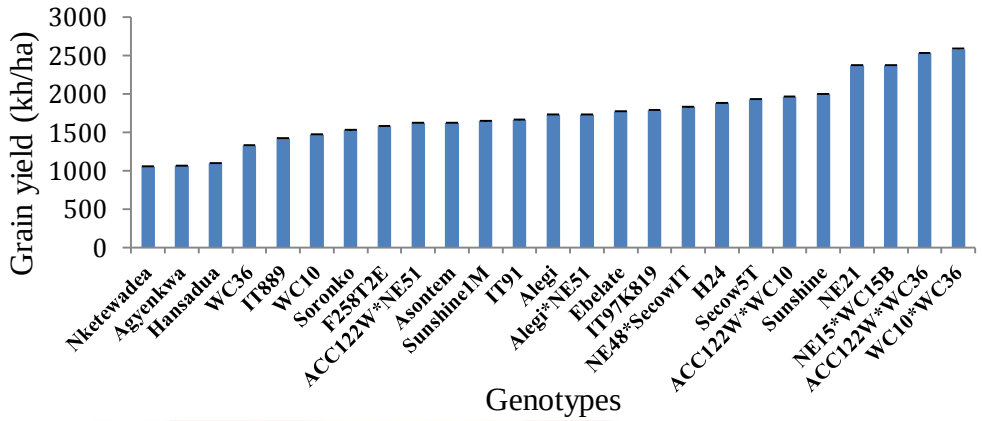

Figure 68: Genotypic responses of M_2 mutants on number of grain yield

4.3.2.2 Effect of irradiation on agronomic performance and yield of M_2 mutant lines

There were significant ($P < 0.001$) differences among the irradiation doses on plant height at 21DAP in the M_2 mutants (Figure 69). The 200 Gy irradiation dose recorded the highest plant height at 21DAP in the M_2 mutants and was significantly different from the other doses. The 150 Gy dose was significantly lower than the other doses of irradiation. The control, however, was significantly different from both 150 and 200 Gy but not dose 50 and 100 Gy in plant height at 21DAP as shown in Figure 69.

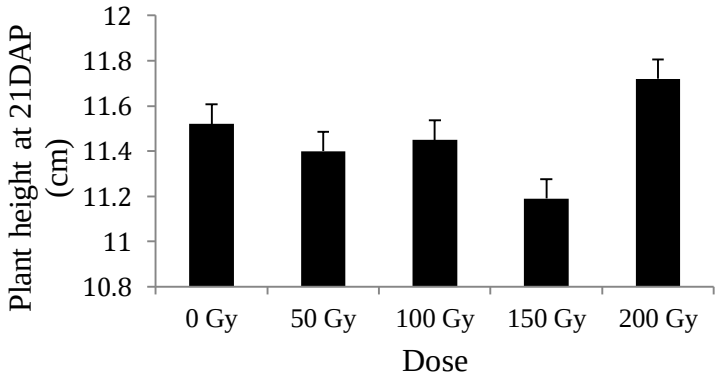

Figure 69: Irradiance effect on plant height at 21DAP in M_2 mutants

Likewise, there were significant ($P < 0.001$) differences among the doses of irradiation on plant height at flowering (Figure 70). The 100 Gy dose had the highest plant height at flowering (47 cm). However, there was significant difference between the control and 100 Gy. The mean plant height at flowering among the doses was 45.4 cm. Plants in the control were significantly different those of both dose 150 and 200 Gy but not from 50 and 100 Gy in plant height at flowering. Plant height at flowering increased with increasing irradiation dose from 50 to 100 Gy and then generally decreased with increasing irradiation (Figure 70).

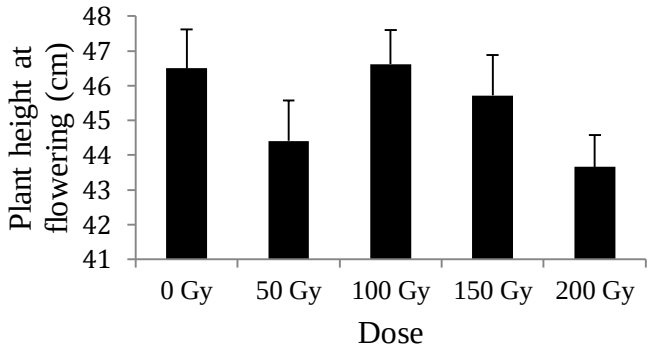

Figure 70: Irradiance effect on plant height at flowering in M_2 mutants

There were significant ($P < 0.001$) differences among the irradiation doses on the number of branches per plant (Figure 71). All the mutants of the

doses (50 to 200 Gy) recorded the same mean number of branches per plant (≈5) as the control. However, mutants of dose 200 Gy recorded significantly lower mean number of branches than the other irradiation doses. Increasing irradiation dose led to reduced number of branches per plant up to 50 Gy, increased at 100 Gy from where there was a general decline in mean number of branches per plant with increasing irradiation dose as shown in Figure 71.

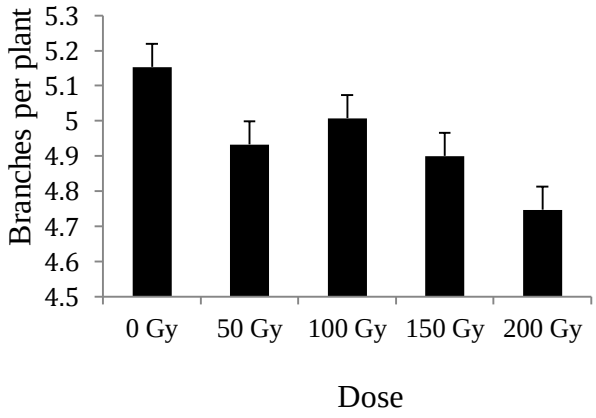

Figure 71: Irradiance effect on number of branches per plant in M_2 mutants

The results showed significant ($P < 0.001$) differences on 100 seed weight among the different doses of irradiation applied in the M_2 mutants (Figure 72). The control recorded 12.3 g for 100 seed weight and was significantly lower than the means of the other doses. The highest 100 seed weight was recorded by the mutants of dose 200 Gy (13 g) and was significantly different from the other doses of irradiation. The 100 seed weight generally increased with increasing irradiation up to 100 Gy, declined at 150 Gy and then increased up to 200 Gy (Figure 72).

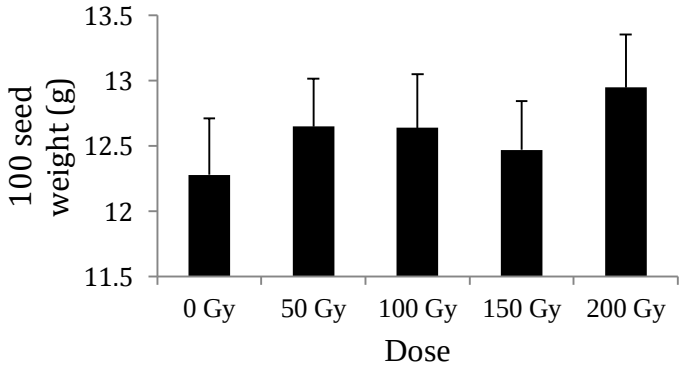

Figure 72: Irradiance effect on 100 seed weight in M_2 mutants

The grain yield showed significant (P = 0.01) differences among the doses of irradiation (Figure 73). Plants subjected to 150 Gy recorded the highest grain yield (1778 kg/ha) among the irradiation doses and was significantly different from doses 0 Gy, 100 Gy and 200 Gy. The mutants of the 100 Gy irradiation dose recorded the lowest grain yield (1714 kg/ha) among the doses. The mean grain yield among the M_2 mutants was 1742 kg/ha (Figure 73).

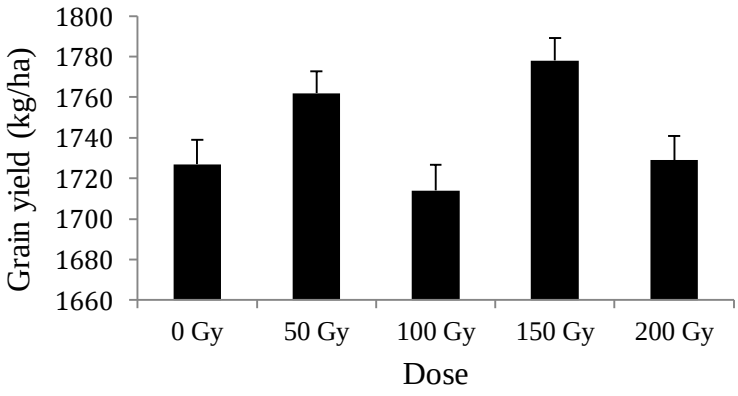

Figure 73: Irradiance effect on grain yield in M_2 mutants

4.3.2.3 Genotype-dose interaction effect on agronomic performance and yield of M_2 mutant lines

The results of means of the various agronomic and yield parameters of the cowpea genotypes as affected by the doses of irradiation in the M_2 mutants

are shown in Table 13. For plant height at 21DAP, all the genotypes showed significant ($P < 0.001$) interactions in their mean responses to the effect of the different irradiation doses applied. For IT97K819, the highest plant height at 21DAP was recorded for dose 50 Gy (14.9 cm) while the highest mean plant height was recorded for the 100 Gy dose and the value was 12.6 cm. However, the least plant height at 21DAP for ACC122W*NE51 was recorded for 50 Gy (8.4 cm) while the highest was recorded by both the control and 100 Gy as 9.9 cm. For IT91 and Sunshine, the control had the highest mean plant height at 21DAP (Table 13).

The results of means of genotypes as affected by the doses showed significant ($P < 0.001$) interactions on plant height at flowering (Table 13). For NE15*WC15B, the shortest plant at flowering was recorded for 50 Gy and the value was 29.8 cm while the 100 Gy recorded the tallest plants with mean height of 37 cm. Similar trend was seen in WC10 where the 50 Gy dose recorded mean plant height of 40 cm as the shortest while the 100 Gy recorded the tallest plants at 47.7 cm. For Sunshine 1M, the control recorded the tallest plants at flowering (61.2 cm) while the 200 Gy recorded the shortest mean plant height at flowering (52 cm). There was a decline in mean plant height at flowering among the doses of Alegi from 0 Gy (57.3 cm) to 150 Gy (37.7 cm) as shown in Table 13.

Table 13: Means of M_2 mutant cowpea responses on agronomic and yield parameters

	Genotype	Plant Height at 21DAP(cm)					Plant height at 50% (cm)					Number of Branches/Plant					100 Seed Weight (g)					Grain yield (kg/ha)				
		Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)					Dose (Gy)				
		0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200	0	50	100	150	200
1	ACC122W*NE15	9.9	8.4	9.9	8.8	9.0	41.9	33.9	38.3	39.5	34.2	4.5	4.0	4.5	5.5	3.7	10.2	11.8	11.3	12.0	13.8	1788	1533	1774	1538	1466
2	ACC122W*WC10	10.9	10.0	10.6	11.6	12.3	39.3	44.5	42.7	40.1	43.1	5.0	5.3	4.7	4.8	4.0	13.0	13.1	13.2	13.1	14.1	2047	2037	1935	1920	1870
3	ACC122W*WC36	12.1	12.9	10.9	11.9	13.5	39.2	37.2	50.9	40.0	42.0	6.0	4.7	5.7	4.2	4.5	9.2	9.7	10.4	9.8	10.7	2551	2428	2424	2765	2481
4	Agyenkwa	9.2	9.8	8.8	9.7	8.9	55.7	52.9	54.5	41.2	39.2	3.5	4.0	4.2	3.3	3.2	11.2	13.1	13.4	13.4	13.6	1088	1061	1001	1163	999
5	Alegi	9.7	9.9	9.8	10.3	10.0	57.3	52.1	44.5	37.7	40.3	5.7	5.7	5.8	5.5	5.3	13.4	12.9	13.0	14.0	14.2	1722	1966	1416	1533	2013
6	Alegi*NE15	12.7	11.8	10.9	8.9	9.8	43.9	35.9	46.3	37.1	40.3	5.5	5.2	5.2	4.8	5.7	14.4	11.1	12.7	11.7	13.6	1682	1688	1653	1966	1666
7	Asontem	13.3	10.9	13.1	12.8	13.7	45.2	39.3	42.0	34.8	44.7	4.3	5.2	5.5	5.7	4.8	12.7	13.4	13.2	13.7	13.8	1654	1766	1436	1628	1623
8	Ebelate	12.5	11.8	12.9	11.3	12.5	35.8	35.6	44.3	38.7	43.3	5.5	4.7	5.3	5.5	4.5	11.3	12.1	12.3	10.8	12.3	1689	1751	1920	1560	1945
9	F258T2E	12.9	14.1	14.5	13.3	13.8	42.5	47.2	43.0	57.9	55.4	4.7	5.2	5.2	5.3	5.0	13.9	14.3	14.6	14.2	14.4	1692	1524	1494	1638	1558
10	H24	12.5	12.4	12.9	13.2	13.5	46.2	44.5	49.7	46.6	42.9	6.0	5.8	5.8	6.0	4.3	9.8	11.3	11.8	10.6	9.8	2055	1951	1880	1561	1938
11	Hansadua	11.2	10.8	11.1	10.3	10.2	39.7	46.9	48.9	50.6	51.7	4.5	4.8	3.5	3.7	5.0	10.4	11.1	12.6	10.9	10.7	1159	993	1045	1100	1169
12	IT889	12.3	10.8	12.4	10.3	12.2	38.6	44.3	48.2	45.1	45.2	4.5	4.0	4.5	4.0	3.5	12.5	14.3	15.2	12.9	12.3	1367	1417	1436	1536	1341
13	IT91	14.3	14.1	13.5	13.0	14.1	56.2	48.0	45.2	48.9	43.2	5.3	5.0	5.5	4.7	5.7	13.2	14.3	14.1	14.6	14.4	1561	1692	1823	1705	1523
14	IT97K819	13.3	14.9	12.6	13.3	13.4	51.8	37.5	52.5	53.7	33.7	5.3	4.8	5.3	5.2	5.7	15.1	13.2	11.1	12.3	12.8	1698	1968	1809	1715	1761
15	NE15*WC15B	10.9	12.0	12.5	12.5	12.5	32.9	29.8	36.8	37.0	31.3	5.8	5.5	5.3	5.5	5.2	10.9	12.9	9.2	10.5	10.9	2135	2385	2444	2312	2594
16	NE21	11.4	11.6	10.8	10.4	12.3	41.9	35.6	39.7	43.9	44.3	4.8	4.3	4.3	4.0	4.2	9.3	14.6	13.4	12.5	12.6	2597	2329	2288	2399	2252
17	NE48*SecowIT	12.4	12.9	13.2	12.3	13.2	58.3	60.5	59.5	61.2	46.4	5.5	5.0	5.0	5.5	5.5	12.1	11.1	13.1	11.5	10.9	1886	1849	1557	1969	1863
18	Nketewadea	10.2	10.0	11.1	10.7	10.7	52.2	46.2	46.7	50.2	36.3	5.2	5.2	4.7	4.2	5.0	12.4	14.9	14.2	13.9	15.2	1061	1127	1001	1083	999
19	Secow5T	9.4	10.3	9.4	9.9	9.8	38.4	34.0	35.3	36.7	40.3	6.0	4.7	5.2	6.0	4.8	12.1	13.1	13.6	13.4	12.4	1707	2017	2183	2036	1712
20	Soronko	10.8	11.3	12.0	11.5	12.1	44.8	45.7	43.7	45.7	41.3	4.7	5.0	5.3	5.3	4.3	13.3	12.3	13.2	10.0	13.0	1589	1562	1313	1631	1541
21	Sunshine	11.7	11.4	10.7	10.8	11.0	49.1	44.9	38.3	38.1	42.7	6.5	5.8	6.2	5.0	5.2	14.1	12.7	12.7	13.1	13.1	2036	1990	2017	2091	1847
22	Sunshine1M	11.6	11.3	10.6	10.8	11.0	61.2	56.7	59.6	54.8	52.0	5.3	5.3	4.8	4.5	4.7	12.5	10.6	10.0	13.1	14.3	1383	1745	1511	1788	1776
23	WC10	8.4	8.3	8.8	9.0	9.9	40.7	40.0	46.6	47.7	46.4	4.8	4.8	4.8	4.5	4.5	13.1	13.3	12.8	13.6	13.5	1687	1346	1304	1408	1599
24	WC10*WC36	12.2	11.8	11.8	11.8	11.9	56.2	59.9	58.2	63.5	55.4	5.7	5.8	5.2	6.0	5.5	13.0	11.9	12.2	12.6	14.1	2270	2503	2861	2819	2461
25	WC36	12.2	11.7	11.8	11.2	11.6	53.7	57.3	50.5	52.3	55.9	4.2	3.5	3.7	3.8	5.0	13.8	12.9	12.3	13.5	13.3	1076	1418	1330	1575	1233
	L.S.D.			0.0					1.1					0.0					0.5					180.0		
	S.E.			0.0					0.7					0.0					0.3					111.9		
	%C.V.			0.0					1.0					0.1					2.7					6.4		

There were significant ($P < 0.001$) interactions between the genotypes and the irradiation doses on number of branches per plant (Table 13). For ACC122W*WC36, there were 6 branches per plant for doses 0 Gy and 100 Gy as the highest while there were 4 branches per plant for dose 150 Gy. For Sunshine, there were 7 branches per plant in the control while there were 6 branches for doses 50 Gy and 100 Gy. For doses 150 Gy and 200 Gy of Sunshine, there were 5 branches per plant. For Agyenkwa, there were 4 branches per plant for doses 150 Gy and 200 Gy while there were 5 branches per plant for the control, 50 Gy and 100 Gy as shown in Table 13.

There were significant ($P < 0.001$) interactions between the genotypes and doses of irradiation (Table 13). For Nketewadea, the highest 100 seed weight was recorded for dose 200 Gy (15.2 g) while the 0 Gy recorded the least 100 seed weight of 12.4 g. Similarly, the control and 200 Gy recorded the least and highest 100 seed weight of 9.2 g and 10.7 g, respectively in ACC122W*WC26. However, the highest 100 seed weight in ACC122W*WC10 was recorded for the 200 Gy dose while the other doses ranged between 13 and 13.2 g (Table 13).

The results of means of cowpea genotypes as affected by the doses of irradiation showed significant ($P < 0.001$) interactions on grain yield among the M_2 mutants (Table 13). For WC10*WC36, the highest grain yield was recorded for dose 100 Gy (2861 kg/ha) while the 0 Gy recorded the least grain yield of 2270 kg/ha. Similarly, the 100 Gy of Secow5T had the highest grain yield (2183 kg/ha) while the control recorded the least grain yield of 1707 kg/ha. However, in H24, the control recorded the highest grain yield of 2055 kg/ha while the 150 Gy produced mean grain yield of 1561 kg/ha (Table 13).

4.4 Principal Component Analysis

Based on Eigenvalues > 1 (Ho, 2006) and factor loadings of ±0.3 (Hair *et al*., 2010), four principal components were obtained and they were attributable to 70.13% of the total variance. The first principal component (PC 1) was the densest and accounted for 27.07% of the observed total variance. This was made up of the high positive factor loadings of days to first flowering and days to 50% flowering as well as the high negative factor loadings of pod length and 100 seed weight (Table 14).

The second principal component (PC 2) was largely dominated by the number of peduncles per plant and the number of pods per plant which both demonstrated high positive factor loadings. The second principal component expounded 19.37% of the total variance observed. Similarly, the third principal component (PC 3) exhibited a positive correlation with the number of branches, pod length, seeds per pod and grain yield. Pod length and grain yield contributed the least to total variance. Their high positive loadings were responsible for 13.71% of the total variance in the irradiated cowpea lines. Unlike PC 3, the fourth principal component (PC 4) showed a relatively high negative factor loading in the number of pods per peduncle and positive factor loadings in the plant height at both 21DAP and also at flowering (Table 14).

Table 14: Rotated component matrix of four model explaining 70.13% of the total variance for traits

Trait	PC 1	PC 2	PC 3	PC 4	Communalities
Plant height at 21DAP	-0.10	0.08	0.25	**0.76**	0.65
Plant height at Flowering	-0.11	0.05	0.13	**0.69**	0.51
Days to flowering	**0.88**	0.06	0.12	-0.17	0.82
Days to 50% Flowering	**0.88**	0.10	0.16	-0.10	0.82
No. of Branches	0.25	0.05	**0.64**	0.13	0.49
No. of Peduncles/plant	0.12	**0.94**	-0.02	0.26	0.96
No. pods/peduncle	-0.09	-0.11	0.25	**-0.67**	0.54
Pods/plant	0.09	**0.97**	0.06	0.00	0.96
Pod length (cm)	**-0.64**	-0.03	**0.57**	0.05	0.74
Seeds/Pod	-0.22	-0.06	**0.75**	-0.01	0.62
100 seed weight(g)	**-0.79**	-0.13	0.11	-0.10	0.66
Grain yield (kg/ha)	0.38	0.40	**0.57**	0.03	0.63
Eigen values	3.25	2.32	1.65	1.20	
Percentage of total variance	27.07	19.37	13.71	9.97	
Cumulative percentage of variance	27.07	46.44	60.15	70.13	

4.5 Correlations

4.5.1 Correlations of germination parameters

The correlations between the germination parameters are shown in Table 12. The days to 50% germination showed highly negative significant Pearson correlation with mean germination time (-0.936, $P < 0.001$) and coefficient of velocity of germination (-0.937, $P < 0.001$). Similar trend was observed in the correlation between mean germination rate and mean germination time (-0.996, $P < 0.001$) as well as the correlation of percentage germination to percentage hard seeds (-0.956, $P < 0.001$) and percentage decayed seeds (-0.925, $P < 0.001$). However, the days to 50% germination showed a weak negative significant correlation to percentage germination (-0.157, $P < 0.001$). Germination index also highly correlated negatively to percentage hard seeds (-0.910, $P < 0.001$) and percentage decayed seeds (-0.893, $P < 0.001$).

There was a highly positive significant Pearson correlation of percentage deformed seedlings to day to last germination and time spread of germination at $r = 1.000$, $P < 0.001$. The days to 50% germination highly positively correlated to mean germination time (0.930, $P < 0.001$). However, days to 50% germination showed a weak positive correlation with day to last germination, time spread of germination and percentage deformed seedlings at $r = 0.255$, $P < 0.001$. The germination index also highly correlated positively to percentage germination (0.952, $P < 0.001$) as shown in Table 15.

Table 15: Correlations of germination parameters

DLG	DLG													
TSG	1.000**	TSG												
%DfS	1.000**	1.000**	%DfS											
% HS	-0.067	-0.067	-0.067	% HS										
%DcS	-0.059	-0.059	-0.059	0.783**	%DcS									
%G	0.065	0.065	0.065	-0.956**	-0.925**	%G								
MGT	0.500**	0.500**	0.500**	0.129*	0.201**	-0.170**	MGT							
MGR	-0.488**	-0.488**	-0.488**	-0.141*	-0.215**	0.184**	-0.996**	MGR						
UG	0.691**	0.691**	0.691**	0.103	0.169**	-0.138*	0.772**	-0.773**	UG					
SI	-0.504**	-0.504**	-0.504**	-0.165**	-0.245**	0.206**	-0.693**	0.705**	-0.941**	SI				
CVt	0.765**	0.765**	0.765**	0.105	0.060	-0.091	0.339**	-0.331**	0.709**	-0.573**	CVt			
GI	-0.055	-0.055	-0.055	-0.910**	-0.893**	0.952**	-0.445**	0.459**	-.0328**	0.375**	-.0132*	GI		
CVG	-0.490**	-0.490**	-0.490**	-0.141*	-0.215**	0.183**	-0.996**	1.000**	-0.772**	0.704**	-0.331**	0.459**	CVG	
D50%G	0.255**	0.255**	0.255**	0.109	0.200**	-0.157**	0.930**	-0.936**	0.570**	-0.559**	0.012	-0.434**	-0.937**	D50%G

Values with * and ** implies that correlation is significant at P = 0.05 and P = 0.01 respectively

DLG = day to last germination (days); **TSG** = time spread of germination (days), **%G** = percentage germination (%); **%DfS** = percentage deformed seedlings (%); **%DcS** = percentage decayed (%); **%HS** = percentage hard seeds (%); **D50%G** = days to 50% germination (%), **MGT** = mean germination time (days), **MGR** = mean germination rate (seeds/day); **GI** = germination index; **CVG** = coefficient of velocity of germination; **CVt** = coefficient of variation of germination time; **UG** = uncertainty of germination (bit); **SI** = synchronization index

4.5.2 Correlations of agronomic and yield parameters

The results of correlation analysis for the agronomic and yield parameters measured on the 25 irradiated cowpea genotypes showed significant ($P < 0.001$) correlations. It was observed that the plant height at 21DAP showed highly significant positive ($P < 0.001$) correlation with plant height at flowering (0.27), number of peduncles per plant (0.15), pod length (0.15) and yield (0.22) and positively correlated with 100 seed weight (0.10, 0.008) and seeds per pod (0.08, 0.03) (Table 16).

High negative correlation ($P < 0.001$) was observed between the number of pods per peduncle and plant heights at 21DAP (-0.19) and flowering (-0.13) as well as the number of peduncles per plant (-0.21). The yield, however, showed a high positive correlation ($P < 0.001$) with traits such as days to 50% flowering (0.15), number of branches per plant (0.37), number of peduncles per plant (0.28) and number of pods per plant (0.25) except plant heights at flowering (-1.4) and 100 seed weight (-0.3) as shown in Table 16.

Table 16: Correlations of agronomic and yield parameters

PH@21	PH@21											
PHF	0.27**	PHF										
DtF	0.03	0.03	DtF									
Dt50F	.002	0.05	0.86**	Dt50F								
nB	0.030	0.03	0.06	0.10**	nB							
nPed/Pl	0.15**	0.11**	0.05	0.07	0.10**	nPed/Pl						
nPo/Pe	-0.19**	-0.13**	0.02	0.00	0.05	-0.22**	nPo/Pe					
nPo/Pl	0.05	0.04	0.05	0.05	0.11**	0.87**	0.27**	nPo/Pl				
PL	0.15**	0.06	-0.10**	-0.09*	-0.01	-0.06	0.10**	-0.01	PL			
S/P	0.08*	0.06	0.02	-0.01	0.05	-0.03	0.02	-0.02	0.57**	S/P		
100SW	0.10**	-0.01	-0.33**	-0.32**	-0.15**	-0.16**	0.09*	-0.10**	0.35**	0.13**	100SW	
GY	0.18**	-0.01	0.25**	0.23**	0.32**	0.30**	-0.01	0.27**	0.11**	0.16**	-0.28**	GY

Values with * and ** implies that correlation is significant at P = 0.05 and P = 0.01 respectively
PH@21= Plant height @21DAP, **PHF** = Plant height at Flowering, **DtF** = Days to Flowering, **Dt50F** = Days to 50% flowering, **nB** = Number of branches, **nPed/Pl** = number of peduncles per plant, **nPo/Pe** = number of pods per peduncle, **nPo/Pl** = number of pods per plant, **PL** = pod length, **S/P** = seeds per pod, **100SW** = 100 seed weight, **GY** = grain yield (kg/ha)

4.8 Chi-square Test for Interdependence

The results for chi-square test of independence showed that germination capacity was dependent on germination index (χ^2 = 303.71, df = 8 and P < 0.001), decayed seeds (χ^2 = 426.05, df = 16 and P < 0.001) and hard seeds (χ^2 = 458.03, df = 16 and P < 0.001). Contrariwise, the test revealed that germination capacity does not depend on mycoflora infection (χ^2 = 23.25, df = 16 and P = 0.107) and yield (χ^2 = 24.81, df = 16 and P = 0.073) and hence an acceptance of the null hypotheses that germination capacity does not affect both mycoflora infection and yield (Table 17).

Table 17: Combined Chi-square test between germination capacity and five selected traits

Trait	χ^2	Degree of freedom (df)	P-value
Decayed seeds	426.05	16	<0.001
Hard Seeds	458.03	16	<0.001
Mycoflora infection	23.25	16	0.107
Germination Index	303.71	8	<0.001
Yield	24.81	16	0.073

Comparing mycoflora infection and four other measured parameters, the chi-square test revealed that mycoflora infection was not independent of germination index (χ^2 = 46.39, df = 8 and P < 0.001) and therefore a rejection of the null hypothesis that mycoflora infection does not depend on germination index. The test, however, showed that mycoflora infection does not depend on decayed seeds (χ^2 = 24.29, df = 16 and P = 0.083), hard seeds (χ^2 = 16.1, df = 16 and P = 0.446) and yield (χ^2 = 24.18, df = 16 and P = 0.086) hence triggering an acceptance of the null hypotheses that mycoflora

infection does not affect decayed seeds, hard seeds and yield of irradiated cowpea seeds (Table 18).

Table 18: Combined chi-square test between mycoflora infection and four measured traits

Trait	X^2	Degree of freedom	P-value
Decayed seeds	24.29	16	0.083
Hard seeds	16.1	16	0.446
Germination Index	46.39	8	<0.001
Yield	24.18	16	0.086

CHAPTER FIVE

5.0 DISCUSSIONS

The lack of significant difference in days to first germination among the genotypes could partly be attributed to the characteristic nature of cowpea i.e., the species unguiculata. Thus, cowpea seeds will show complete germination at about 3 days after sowing when growth conditions such as light, moisture and temperature are favourable. Notwithstanding, due to variations in individual seeds, the germination process can last up to a week within a seed lot (ISTA, 2010).

The lack of significant differences observed among the irradiation doses in parameters such as days to first germination and days to last germination influenced the time spread of germination; a parameter which measures how slow or fast the germination process takes between treatments (Kader, 2005). This could mean that the irradiation doses applied had a near similar effect on the seeds just like the control and hence, these measured germination parameters could not vary significantly. Also, the cowpea seeds used for the study can be said to be of high quality in terms of length of time in storage and the storage conditions before the study.

The significant differences observed among the genotypes in all the seed physiological parameters estimated could be attributed to the differences in varietal attributes which include the physical characteristics of the seed such as seed size and seed coat thickness. Seed size and seed coat thickness have been reported to influence imbibition in seeds (Zhang *et al.*, 2020) and subsequently the elongation of the embryonic axes (radicle or plumule) to

complete the germination process (Dunlap & Barnett, 1983; Liu *et al.*, 2013). Therefore, the significant differences among the genotypes on the germination parameters were expected since different varieties were used in the study.

Although there were non-significant differences among the doses of irradiation in percentage germination, the observed differences in days to 50% germination among the doses suggests that the range of irradiation applied was too low to induce lethality in the embryos of the seeds but could affect the rate and trend of germination in cowpea due to abnormal cell division and physiological mutation (Olasupo *et al.*, 2016; Dhanavel & Girija, 2019). The results of this study agree with the findings of Liu *et al.* (2017), who reported that low-dose gamma irradiation showed no significant difference in percentage germination. According to Horn and Shimelis (2013), gamma irradiation doses higher than 300 Gy significantly reduced percentage germination in cowpea. Similar results have been reported by Gnanamurthy, Dhanavel and Girija (2019) that 350 Gy irradiation dose significantly reduced percentage germination. High gamma irradiation is reported to significantly reduce percentage germination and doses that can cause lethality in seeds are dependent on the dose rate, range, species and type of seed (Aparna *et al.*, 2013).

Among the doses, there were no significant differences in the proportion of abnormal seedlings. This contradicts the results of Dhanavel and Girija (2019) and Gnanamurthy, Dhanavel and Girija (2019) who reported that increasing doses of irradiation influenced the proportion of deformed seedlings. The observed non-significant differences can be attributed to the relatively low dose range used for this study. The maximum dose of

irradiation applied in this study was 200 Gy (20k R) and is comparatively lower than the ranges applied by Dhanavel & Girija (2019) and Gnanamurthy, Dhanavel, & Girija, (2019). Hence, it is likely that the irradiation doses were not potent enough to induce chromosomal aberrations that affect seedling anatomy among the genotypes.

The significant differences observed among the doses in percentage hard seeds were expected. The increase in percentage hard seeds with increasing irradiation dose shows that irradiation doses have the tendency to kill seed embryo and also any mycoflora that the seed may harbour. However, the applied irradiation doses have been reported to be too low to kill seed embryos (Aparna *et al.*, 2013; Horn & Shimelis, 2013) or mycoflora (Bhat *et al.*, 2010; Jeong *et al.*, 2015). The results of ungerminated seeds in this study are comparable to ranges reported by Gnanamurthy *et al.*, (2019). Hence, the results of this study may be attributed to the fact that induced mutations are random events and that different genotypes respond differently to different irradiation doses (Horn & Shimelis, 2013).

The decline in percentage decayed seeds with increasing irradiation from 50 Gy to 200 Gy was expected since irradiation has been reported to have antifungal properties (Chu *et al.*, 2015; Jeong *et al.*, 2015; Jeong, Chu, Lee, Cho, & Park, 2016). Specifically, gamma-irradiation inhibits fungal spore germination and germ tube elongation. The results obtained in this study may suggest that dose ranges from 50 Gy to 200 Gy may have inhibitory effects on saprophytic fungi which cause seed decay. This is due to the fact that increasing doses of irradiation have detrimental effects on the growth and development of seed borne mycoflora. In effect, seeds that lose viability with

increasing irradiation doses will remain intact and show no mycelia growth; hence, the observed results of increase in percentage hard seeds and decline in percentage decayed seeds with an increase in irradiation dose.

The differences in mean germination rate observed among the doses of irradiation confirmed that irradiation had injurious effects on seeds. The mean germination of the seed samples exposed to the different doses of irradiation were significantly lower than the control, suggesting that although the irradiation doses did not show significant difference, the mean germination rate was negatively impacted. This is justifiable because mean germination rate is comparable only in seeds with similar germinabilities (Ranal & De Santana, 2006).

For mean germination time, the control (0 Gy) had a lower mean germination time compared to the irradiated seed samples, thus, suggesting that irradiation delayed the germination process. Similar results have been reported by Kusmiyati *et al.* (2018) on gamma-irradiated soybean. The lower mean germination time in the control (0 Gy) implies that the seeds germinated faster than the gamma-irradiated seed samples (Kader, 2005; Mendes-Rodrigues, Ranal, *et al.*, 2011). Since estimation of mean germination time is based on the weighted mean of seeds germinated per time, it may be deceptive when other measures of germination uniformity such as coefficient of variation of germination time is not measured (Ranal & De Santana, 2006).

The coefficient of variation of germination time is a good measure of variability as it relates to the relative dispersion observed in the germination cycles of the seed samples which otherwise were impossible to compare in mean germination time measurements (Ranal & De Santana, 2006). The

observed higher coefficient of variation of germination time in the control relative to the irradiated seeds suggests that less variation exists within the applied doses (50 Gy – 200 Gy) in terms of how the different doses affected germination trends and rate. Thus, higher coefficient of variation of germination time observed in the control suggests that the germination was more irregular (Mendes-Rodrigues *et al.*, 2011).

The non-significant differences in the effect of the doses on germination index were not expected among the ranges applied. This is in contrast with the findings of El-Bialee & Nawito (2020) who reported that germination index increased for irradiation doses up to 150 Gy and thereafter, declined. Since germination index is a measure of both germination capacity and the temporal aspects of germination (Al-Ansari & Ksiksi, 2016), the indifference in the effect of the irradiation doses on germination index can be attributed to the non-significant differences observed in the effect of the different doses on percentage germination.

The synchronization index was measured to assess the variation of the uncertainty that characterize the relative frequency of germination or its informational entropy as applied by Zpevak, De Andrade Perez, & Buckeridge (2012). This is because germination in general is assynchronized and that different environments affect seed germination differently (Ranal & De Santana, 2006). The observed difference between the control and the irradiated seeds with respect to synchronization demonstrates that the irradiated seeds were more synchronized and hence showed less variation in their germination trends, unlike the control. Thus, the seeds irradiated at doses (50 Gy – 200 Gy)

produced synchronization index closest to zero and therefore had better germination synchrony, unlike the control (0 Gy).

The uncertainty of germination was higher in the irradiated seeds than the control and the results obtained are consistent with synchronization index, mean germination time and coefficient of variation of germination time as reported by (Mendes-Rodrigues *et al*., 2011). The uncertainty of germination is used to measure the degree of spread of germination over time and that a single seed germinating over time will vary uncertainty of germination (Ranal & De Santana, 2006). The observed near similar uncertainty of germination measured among the irradiation doses suggests that they had close germination synchrony than with the control; which showed wider spread of germination over time as evident by the measured synchronization index (Ranal & De Santana, 2006).

The significant interactions between the cowpea genotypes and the radiation doses on germination parameters such as percentage hard seeds, percentage decayed seeds, days to 50% germination, mean germination rate, mean germination time, germination index, coefficient of velocity of germination, coefficient of variation of germination time, uncertainty of germination and synchronization index imply that there were differential responses to the irradiation doses among the genotypes (Gwata *et al*., 2016).

The six mycoflora species identified were all indigenous to Ghana. The only pathogenic fungi identified was *Fusarium* (Khare *et al*., 2014; Tsifodze, 2018). *Fusarium species* have been described as seed-borne and seed transmitted (Littke, 1990; Elmer, 2002) but the species *moniliforme* has not been proven to be pathogenic to cowpea. The other mycoflora were

saprophytic: *Aspergillus flavus, Aspergillus niger, Cladosporium sphaerospermum, Penicillium sp.* and *Rhizopus sp.* (Wain-Tassi *et al.*, 2012). The six species of fungi observed belonged to five genera.

Provenance effects could be responsible for the different genera of fungi observed (Afutu, 2012; Tsifodze, 2018). Thus, different agro-ecological locations tend to have distinct genera and species of fungi that affect plants as a result of the uniqueness of their prevailing elements of climate. This generally influences the degree of virulence of such fungi and other microbes on their hosts in their respective niches (Casadevall, 2009). The development of such niches is highly dependent on the cultural practices at play at such geographic locations. The dominance and prevalence of *Aspergillus flavus* on nearly all the tested seed samples is consistent with results of Khare, Loeto, Wale and Salani (2016) and it suggests that the environmental conditions at the different seed sources (Ghana, Nigeria and Uganda) promote the growth and development of the fungi.

The pervasiveness of saprophytic than pathogenic fungi in the treated samples suggest that the type of fungi have varying potencies to infect or infest their hosts (Afutu, 2012). Thus, the significant differences in mean percent mycoflora that infected the samples could be attributed to the different mycoflora types and their growth and development under favourable conditions. Saprophytic fungi are known to be opportunistic and hence proliferate under high moisture content of seeds due to poor seed processing and handling including transport/transit and storage (Cross, 1979; Jackson, 2009; Bhat *et al.*, 2010). The results of seed health testing is highly dependent on seed handling activities (De Tempe & Binnerts, 1979; Rao *et al.*, 2006).

The significant difference between the pre-treatment with NaOCl and the untreated samples were consistent with the findings of Afutu (2012) and Sobha & Dorcas (2017); where those seeds pre-treated before incubation had lower mean percent mycoflora infection than the untreated seed samples. This suggests that to a large extent, seed pre-treatment before incubation inhibits the growth and development of some seed-borne mycoflora, especially saprophytic fungi that reduce seed quality. Also, the fast growth associated with saprophytic fungi may tend to overshadow the slow growth and development of pathogenic seed-borne fungi when both types of mycoflora are present on the same seed sample (Neergaard, 1979). In *Rhizopus sp*., the near similar prevalence rate on both pre-treated and untreated seeds suggests that its growth and development was not affected by seed pre-treatment.

The observed significant differences among the doses of gamma irradiation for mean percent mycoflora recorded suggests that irradiation can interfere with the growth and development of seed-borne fungi just like any other microorganisms (Bhat *et al.*, 2010; Lima, Souza, Godoy, França, & Lima, 2011; Chu, Shin, Park, & Jeong, 2015; Jeong *et al.*, 2015). Among the doses, the 100 Gy irradiation recorded the highest percentage infection for *Aspergillus flavus, Aspergillus niger* and *Cladosporium sphaerospermum* suggesting that lower doses of irradiation have little or no lethal effect on the growth of seed-borne fungi. However, studies by Jeong, Shin, Chu, & Park (2015) showed that 1000 Gy of gamma irradiation could totally eradicate *Penicillium* but at 400 Gy plus 10 ppm sodium dichloro-*s*-triazinetrione (NaDCC), the same results can be replicated, implying that lower doses can effectively inhibit fungal growth only together with other chemical agents

such as NaDCC. It is reported that it takes not less than 3000 Gy of gamma irradiation dose to reduce the presence of *Aspergillus* and *Fusarium* in grains like wheat and malting barley (Bhat *et al.*, 2010; Kottapalli *et al.*, 2003; Calado, Venâncio, & Abrunhosa, 2014; Jeong *et al.*, 2015).

The field-grown irradiated cowpeas were assessed for their agronomic, yield and yield related traits. Variations in their growth and development were quantified to establish genotypic variations and also the specific dose effects under field conditions. The assessment of the M_1 and M_2 mutants showed similarities in various measured agronomic and/or yield related traits in their responses to gamma irradiation.

Among the irradiation doses, the general progressive decline in plant heights at 21DAP and anthesis in both M_1 and M_2 mutants was expected since the trend confirms similar findings in cowpea (Gnanamurthy *et al.*, 2013), pigeon pea (Ariraman *et al.*, 2014), soybean (Mudibu *et al.*, 2012; Kusmiyati *et al.*, 2018) and groundnut (Gunasekaran & Pavadai, 2015). This observation is suspected to be due to the injurious nature of ionising irradiations to some enzymes and growth hormones which consequently have inhibitory effects on plant vegetative traits such as height (Lagoda, 2012; Olasupo, Ilori, Forster, & Bado, 2016). The 100 Gy irradiation dose produced the tallest plants in both mutants, suggesting that a dose of 100 Gy promote shoot growth in cowpea. Similar results have been reported by (Olasupo *et al.*, 2016).

The number of branches per plant also showed a consistent general decline with increasing irradiation dose in both mutants (M_1 & M_2). Similar observations have been made in cowpea by Olasupo *et al.* (2016) and Dhanavel & Girija (2019); who both reported that gamma irradiation had

inhibitory effects on plant physiological and anatomical traits like branching which largely defines the plants' vegetative nature. Thus, the vegetative nature defines the plant's growth habit which in effect influences a farmers' cropping system: mono-cropping or mixed cropping.

At anthesis, the number of days to flowering showed significant differences in the M_1 but not in the M_2. The irradiated seeds flowered earlier than the control suggesting that irradiation at lower doses can be stimulative to plant flowering. Generally, it took less than 2 days from day of first flowering to attain 50% flowering when seeds were irradiated suggesting a near synchronous maturity of pods among determinate varieties can be achieved leading to synchronised harvesting. Although the days to 50% flowering were not significantly different among the irradiation doses, it has been reported to be positively affected with increasing doses of irradiation (Horn, Ghebrehiwot, & Shimelis, 2016). In soybean, irradiation dose was found to have little or no effect on the days to 50% flowering (Mudibu *et al.*, 2012) which is in tandem with the findings of this study.

Among the yield parameters of the M_1 mutants, there was a general decline in pod length with increasing irradiation dose from 0 Gy to 150 Gy. Similar trend was observed in seeds per pod from 0 Gy to 200 Gy. However, in the M_2 mutants, the effects of the irradiation were not visible in the pod length and seeds per pod suggesting that the M_2 mutants might have recovered from the possible chromosomal aberrations in the M_1 as a result of the exposure to ionising irradiation (Horn, Ghebrehiwot, & Shimelis, 2016). According to Mudibu *et al.* (2012), the indifference in the M_2 mutants in the

pod length and seeds per pod could also be attributed to environmental conditions.

The 100 seed weight in the M_1 and M_2 mutants were similar indicating that the dose effects in both generations were similar. The observation that the 200 Gy irradiation dose gave highest 100 seed weight did not reflect in the grain yield, since the 150 Gy irradiated samples recorded the highest yield (1778 kg/ha). Irradiation dose of 200 Gy has been reported to produce the highest yield in canola (Rahimi & Bahrani, 2011) and soybean (Mudibu *et al.*, 2012). This suggests that different species react to different doses differently and this is confirmed by the significant interaction effects between the genotypes and the irradiation doses.

The correlations of the germination parameters revealed the relationships that exist between the measured parameters and how well they inform about the nature of the germination process. The observed non-significant difference between percentage germination and days to last germination as well as time spread of germination was expected. Days to last germination only describes when the last germination was observed while time spread of germination quantifies the days between first and last germination and hence neither of the two influences percentage germination. Similar conclusions were made by Kader (2005).

Germination index measurement comprises percentage germination and speed of germination and hence, is a better rating for seed vigour measurements. Seed vigour measurement is complex and therefore, includes independent physiological potential such as germination speed and seedling growth (Marcos-Filho, 2015). The observed high significant positive

correlation between percentage germination and germination index suggests that an increase in percentage germination will result in an increase in germination index (Ranal & De Santana, 2006).

More so, the observed highly significant negative correlation between percentage germination and percentage hard seeds together with percentage decayed seeds reflect the fact that the latter parameters contribute largely to ungerminated seeds and so any increment in their magnitude will automatically negatively impact on percentage germination. Thus, the more seeds that germinate, the lesser the chance of encountering decayed or hard ungerminated seeds in a given sample. Similarly, the observed highly significant positive correlation of coefficient of variation of germination time with days to last germination and time spread of germination suggest that the latter two parameters both increase with an increase in coefficient of variation of germination time. Coefficient of variation of germination time is a measure of dispersion independent of mean germination time and hence, higher magnitude of days to last germination and time spread of germination will positively correlate with coefficient of variation of germination time (Ranal & De Santana, 2006).

The days to 50% germination was expected to negatively correlate with mean germination rate to suggest that with a finite number of seeds, the more seeds that germinate per day, the lesser the time to attain 50% germination in the lot. Similarly, mean germination time was expected to negatively correlate with mean germination rate because they are inversely proportional. Conversely, time to 50% germination was expected to positively correlate with mean germination time because seeds with similar

germinabilities, mean germination time and days to 50% germination will be directly proportional (Ranal & De Santana, 2006).

The observed positive correlation of grain yield with the number of branches per plant, days to flowering, days to 50% flowering, number of pods per peduncle, number of pods per plant, pod length and seeds per pod were expected as they were consistent with the results of (Manggoel, 2012; Afutu, Mohammed, Odong, Biruma, & Rubaihayo, 2016). This is because the pods that bear the seeds are borne on the branches, hence, at anthesis; the number of branches should positively correlate with the number of pods per plant. Thus, during the vegetative phase of development, the plant attains optimum canopy that can sustain its yield (Manggoel, 2012). The days to flowering allow for the development of vegetative organs such as branches that will ensure the successful completion of the plants' reproductive cycle. The pod characteristics of length and seed number have been reported to be major yield contributing factors (Uguru, 1996) and therefore, were expected to positively correlate with grain yield. Similar results have been reported by Peksen and Artik (2004) as well as Udensi, Ikpeme, Edu and Ekpe (2012).

The interdependence of selected parameters from all three experiments was performed using chi-square test. It was observed that germination capacity was dependent on the proportion of ungerminated seeds (decayed seeds and hard seeds) as well as germination index but not with mycoflora infection and grain yield. These observations were anticipated except for mycoflora infection because the proportions of both hard seeds and decayed seeds in a lot contribute to ungerminated seeds and will invariably reduce the germination capacity. Pathogens that colonise seeds reduce seed

germinabilities (Khare *et al.*, 2016). Also, the seed depends largely on energy stored in the cotyledons to germinate after which it develops organs to initiate its own photosynthesis with resources from its environment (Bhatla & Lal, 2018). The effects of germination capacity thus diminish after the primary organs of the plant are developed and hence germination capacity cannot influence grain yield. Albeit, seed vigour does influence plant yield under favourable environmental conditions (Roberts & Osei-Bonsu, 1988; Siddique & Wright, 2004).

The observation that mycoflora infection was independent of germination capacity implies that the pathogens that colonised the seeds were not invasive enough to prevent germination as saprophytic seed borne pathogens are known to reduce seed germination (Khare *et al.*, 2016; Olembo, 1985; Rao *et al.*, 2006). Also, germination index gives an indication of the proportion and speed of germinated seeds (Al-Ansari & Ksiksi, 2016) and hence, it is not out of place that it was found to be dependent on percent germination (Ranal & De Santana, 2006).

The mycoflora infection also showed dependence on germination index but not on decayed seeds, hard seeds and grain yield. Although hard seeds are ungerminated seeds, they remain intact and do not show any sign of rot or decay and hence, it was expected that percentage hard seeds would not show dependence on percentage infection. Similarly, heavily infected seeds, especially with saprophytic fungi, are not likely to establish well in the field (Rao *et al.*, 2006). The only surprising result is the independence of mycoflora infection on decayed seeds. However, this can be attributed to the general low infection rate and the high percentage germination recorded.

CHAPTER SIX

6.0 SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 Summary

The findings of this study are summarised as follows:

1. The genotypes showed significant differences in all measured physiological traits while the gamma irradiation doses showed significant effects in a few; especially, parameters related to ungerminated seeds, germination time, uniformity and synchronization of germination.
2. Highly significant positive/negative correlations were recorded among physiological quality parameters.
3. In the seed health test, six fungal species belonging to five genera were identified. These were mostly saprophytic except for one; *Fusarium* which is a seed-borne and seed transmitted pathogenic fungi.
4. There were significant differences among the genotypes, irradiation doses and the pre-treatments with NaOCl on percentage mycoflora infections.
5. The differences in mycoflora infection between pre-treated and untreated seeds was less than 10% in most cases.
6. Irradiation at a dose of 50 Gy recorded the lowest percentage infection for *Aspergillus flavus, Aspergillus niger* and *Penicillium sp.*
7. The 100 Gy irradiation dose recorded the highest percentage infection for *Aspergillus flavus, Aspergillus niger* and *Cladosporium sphaerospermum.*

8. The genotypes had significant differences in both mutants (M_1 & M_2) in all agronomic and yield-related parameters.
9. The irradiation doses had effects on both agronomic and yield related parameters in both M_1 & M_2 mutants.
10. Increasing irradiation up to 200 Gy led to decreased number of branches per plant, pod length and seeds per pod in both M_1 & M_2 mutants.
11. The 100 Gy irradiation dose produced the highest plant height in both mutant generations.
12. Though the 200 Gy irradiation dose gave the highest 100 seed weight, it did not reflect in the grain yield while the 150 Gy irradiated samples recorded the highest yield (1778 kg/ha)
13. Percentage mycoflora infection was not dependent on decayed and hard seeds as well as grain yield.
14. Percentage hard and decayed seeds were dependent on percentage germination.

6.2 Conclusions

1. Low doses of irradiation up to 200 Gy increased germination time (mean germination time and days to 50% germination) and germination synchrony but did not significantly affect percentage germination.
2. The irradiation doses up to 200 Gy had no lethal effects on seed borne mycoflora.
3. Although 100 Gy produced the tallest plants in both M_1 & M_2 mutants, the 200 Gy irradiation dose gave the highest 100 seed weight while the 150 Gy irradiated samples recorded the highest grain yield. Increasing

irradiation up to 200 Gy led to decreased number of branches per plant, pod length and seeds per pod in both M_1 & M_2 mutants.

6.3 Recommendations

1. Irradiated cowpea seeds can be assessed under controlled environments and assessed for shoot and root variability just before the peak of vegetative growth.
2. To investigate the effect of irradiation on seed borne mycoflora, isolates of individual mycoflora will have to be prepared and irradiated at different dose ranges to determine the effect of irradiation on the growth and development of seed-borne mycoflora.
3. The irradiation doses can be increased so as to see a clearer effect of the irradiation on the mycoflora identified.
4. The mutants can be advanced to higher generations so as to assess the impact of the irradiation/level of mutation.
5. Although the genotypes were either moderately or fully resistant to most common cowpea diseases in Ghana, disease incidence and severity data should be collected on the mutants because resistance can be broken with mutation.

REFERENCES

Afutu, E. (2012). *Seed-borne fungi of chilli (capsicum frutescens) and studies on the seed transmission of colletotrichum dematium in the coastal savannah zone of Central Region of Ghana*. MPhil. Thesis [University of Cape Coast Institutional Repository]. https://erl.ucc.edu.gh/jspui/handle/123456789/1111?mode=full

Afutu, E., Mohammed, K., Odong, T., Biruma, M., & Rubaihayo, P. (2016). Evaluation of Ugandan Cowpea Germplasm for Yield and Resistance to Scab Disease. *American Journal of Experimental Agriculture*, *12*(2), 1–18. https://doi.org/10.9734/ajea/2016/25138

Ahenkora, K., Adu Dapaah, H. K., & Agyemang, A. (1998). Selected nutritional components and sensory attributes of cowpea (*Vigna unguiculata* [L.] Walp) leaves. *Plant Foods for Human Nutrition*, *52*(3), 221–229. https://doi.org/10.1023/A:1008019113245

Akpan, A., & Mbah, E. U. (2016). Growth and yield of vegetable cowpea varieties (*Vigna unguiculata* (L) walp.) as influenced by potassium fertilizer rates in Umudike , Nigeria. *Nigerian Journal of Agriculture, Food and Environment*, *12*(1), 121–126.

Al-Ansari, F., & Ksiksi, T. (2016). A quantitative assessment of germination parameters: the case of and *Crotalaria Persica* and *Tephrosia Apollinea*. *The Open Ecology Journal*, *9*(1), 13–21. https://doi.org/10.2174/1874213001609010013

Alam, M. Z., Hamim, I., Ali, M. A., & Ashrafuzzaman, M. (2014). Effect of Seed Treatment on Seedling Health of Chili. *Journal of Environment,*

Science and Natural Resources, *7*(1), 177–181.

Amjad, M., & Anjum, M. A. (2002). Effect of gamma radiation on onion seed viability, germination potential, seedling growth and morphology. *Pakistan Journal of Agriculture Research*, *39*(3), 202–206.

Amjad, M., & Anjum, M. A. (2003). Effect of Post-irradiation Storage on the Radiation-induced Damage in Onion Seeds. *Asian Journal of Plant Sciences*, *2*(9), 702–707. https://doi.org/10.3923/ajps.2003.702.707

Aparna, M., Chaturvedi, A., Sreedhar, M., Kumar, P. D., Venu-Babu, P., & Singhal, R. K. (2013). Impact of Gamma Rays on the Seed Germination and Seedling Parameters of Groundnut (*Arachis hypogaea* L .). *Asian Journal of Experimental Biological Sciences*, *4*(1), 61–68.

Ariraman, M., Gnanamurthy, S., Dhanavel, D., Bharathi, T., & Murugan, S. (2014). Mutagenic effect on seed germination , seedling growth and seedling survival of Pigeon pea (*Cajanus cajan* (L.) Millsp). *International Letters of Natural Sciences*, *16*, 41–49.

Armah, F. A. (2011). Assessment of Pesticide Residues in Vegetables at the Farm Gate: Cabbage (*Brassica oleracea*) Cultivation in Cape Coast, Ghana. *Research Journal of Environmental Toxicology*, *5*(3), 180–202. https://doi.org/10.3923/rjet.2011.180.202

Asare-Bediako, E., Addo-Quaye, A., & Bi-Kusi, A. (2014). Comparative Efficacy of Plant Extracts in Managing Whitefly (*Bemisia tabaci* Gen) and Leaf curl Disease in Okra (*Abelmoschus esculentus* L). *American Journal of Agricultural Science and Technology*. https://doi.org/10.7726/ajast.2014.1004

Asare-Bediako, E., Wonkyi, D. M., van der Puije, G., Amenorpe, G., & Osei, M. K. (2017). Variation in the susceptibility of tomato (*'Lycopersicon solanum'* L.) genotypes to tomato yellow leaf curl virus (TYLCVD) infections at coastal savannah and forest zones of Ghana. *Australian Journal of Crop Science*, 11(4), 373–381. https://search.informit.org/doi/10.3316/INFORMIT.886573849196350

Asare, B. R., Afari-sefa, V., & Muilerman, S. (2016). Access to improved hybrid seeds in Ghana: implications for establishment and rehabilitation of cocoa farms. *Experimental Agriculture*, 54(2) 1–13. https://doi.org/10.1017/S0014479716000247

Atilaw, A., Alemu, D., Bishaw, Z., Kifle, T., & Kaske, K. (2011). Early Generation Seed Production and Supply in Ethiopia: Status, Challenges and Opportunities. *Ethiopian Journal of Agricultural Sciences*, *27*(1), 99–119. https://www.ajol.info/index.php/ejas/article/view/150369

Aveling, T. A. S. (2014). Global Standards in Seed Health Testing. In *Global Perspectives on the Health of Seeds and Plant Propagation Material* (pp. 17–29). Springer Dordrecht Heidelberg. https://doi.org/10.1007/978-94-017-9389-6

Aveling, T. A. S. (2016). Global Perspectives on the Health of Seeds and Plant Propagation Materials. In M. L. Gullino & G. Munkvold (Eds.), *Global Standards in Seed Health Testing* (Issue September 2014, pp. 18–29). Springer Dordrecht Heidelberg. https://doi.org/10.1007/978-94-017-9389-6

Belay, A., Claassens, A., & Wehner, F. (2002). Effect of direct nitrogen and

potassium and residual phosphorus fertilizers on soil chemical properties, microbial components and maize yield under long-term crop rotation. *Biology and Fertility of Soils*, *35*(6), 420–427. https://doi.org/10.1007/s00374-002-0489-x

Bhat, R., Sridhar, K. R., & Karim, A. A. (2010). Microbial quality evaluation and effective decontamination of nutraceutically valued lotus seeds by electron beams and gamma irradiation. *Radiation Physics and Chemistry*, *79*(9), 976–981. https://doi.org/10.1016/j.radphyschem.2010.04.002

Bhatla, S. C., & Lal, M. A. (2018). *Plant Physiology , Development and Metabolism*. Springer Nature Singapore. https://doi.org/10.1007/978-981-13-2023-1

Bhuiyan, M. R., Rashid, M. M., Khan, M. A. I., Hoque, M., Nessa, B., Rafii, M. Y., & Latif, M. A. (2013). Eco-friendly Management of Seed Borne fungi for Sustainable Crop Production. *Journal of Chemical Information and Modeling*, *53*(9), 1689–1699. https://doi.org/10.1017/CBO9781107415324.004

Bind, D., & Dwivedi, V. K. (2014). Effect of mutagenesis on germination , plant survival and pollen sterility in M1 generation of in cowpea [*Vigna unguiculata* (L .) Walp]. *Indian Journal of Agricultural Research*, *48*(5), 398–401. https://doi.org/10.5958/0976-058X.2014.01322.5

Boukar, O., Belko, N., Chamarthi, S., Togola, A., Batieno, J., Owusu, E., Haruna, M., Diallo, S., Lawan, M., Olusoji, U., & Christian, O. (2018). Cowpea (*Vigna unguiculata*): Genetics , genomics and breeding. *Plant Breeding*, *December 2017*, 1–10. https://doi.org/10.1111/pbr.12589

Boukar, O., Fatokun, C. A., Huynh, B., & Roberts, P. A. (2016). Genomic Tools in Cowpea Breeding Programs : Status and Perspectives. *Frontiers in Plant Science*, *7*, 1–13. https://doi.org/10.3389/fpls.2016.00757

Brodie, G., Ryan, C., & Lancaster, C. (2012). *The Effect of Microwave Radiation on Prickly Paddy Melon (Cucumis myriocarpus)*. *2012*. https://doi.org/10.1155/2012/287608

Calado, T., Venâncio, A., & Abrunhosa, L. (2014). Irradiation for Mold and Mycotoxin Control: A Review. *Comprehensive Reviews in Food Science and Food Safety*, *13*(5), 1049–1061. https://doi.org/10.1111/1541-4337.12095

Casadevall, A. (2009). Determinants of virulence in the pathogenic fungi. *Fungal Biology Review*, *21*(4), 130–132. https://doi.org/10.1016/j.fbr.2007.02.007.Determinants

Chu, E. H., Shin, E. J., Park, H. J., & Jeong, R. D. (2015). Effect of gamma irradiation and its convergent treatment for control of postharvest *Botrytis cinerea* of cut roses. *Radiation Physics and Chemistry*, *115*, 22–29. https://doi.org/10.1016/j.radphyschem.2015.05.042

Cross, J. E. (1979). Importance of Seed Pathology in Seed Trade Quality Control Programs. *Journal of Seed Technology*, *4*(2), 99–102.

De Tempe, J., & Binnerts, J. (1979). Introduction to methods of seed health testing. *Seed Science and Technology*, *7*, 601–636.

Department of Environment and Primary Industries. (2013). *Seed Health Testing in Pulse Crops* (ISSN 1329-8062; Issue June 2011). http://agriculture.vic.gov.au/agriculture/pests-diseases-and-weeds/plant-

diseases/grains-pulses-and-cereals/seed-health-testing-in-pulse-crops#.XwC8BPudCOE

Dube, E., & Fanadzo, M. (2013). Maximising yield benefits from dual-purpose cowpea. *Food Security*, *5*(6), 769–779. https://doi.org/10.1007/s12571-013-0307-3

Dugje, I. Y., Omoigui, L. O., Ekeleme, F., Kamara, a. Y., & Ajeigbe, H. (2009). Farmers' Guide to Cowpea Production in West Africa, IITA, Ibadan, Nigeria. *Ibadan, Nigeria: IITA*, *May*, 20. http://www.icrisat.org/tropicallegumesII/pdfs/Cowpea.pdf

Dunlap, J. R., & Barnett, J. P. (1983). Influence of seed size on germination and early development of loblolly pine (*Pinus taeda* L.) germinants . *Canadian Journal of Forest Research*, *13*(1), 40–44. https://doi.org/10.1139/x83-006

Egbadzor, K. F., Offei, S. K., Danquah, E. Y., Kotey, D. A., Gamedoagbao, D. K., Dadoza, M., Yeboah, M., & Ofori, K. (2015). Farmer participation in selection within segregating populations of cowpea in Volta Region , Ghana. *Agriculture & Food Security*, 1–7. https://doi.org/10.1186/s40066-015-0037-1

Egbadzor, K. F., Yeboah, M., Offei, S. K., Ofori, K., & Danquah, E. Y. (2013). Farmers ' key production constraints and traits desired in cowpea in Ghana. *Journal of Agricultural Extension and Rural Development* *5*(January), 14–20. https://doi.org/10.5897/JAERD12.118

El-Bialee, N. M., & Nawito, M. (2020). Germination scenario and growth analysis for irradiated cowpea. *Plant Archives*, *20*(1), 807–816.

Elmer, W. H. (2002). Seeds as vehicles for pathogen importation. *Biological Invasions*, *3*(1743), 263–271. https://doi.org/10.1023/A:1015217308477

Etwire, E., Ariyawardana, A., & Mortlock, M. Y. (2016). Seed Delivery Systems and Farm Characteristics Influencing the Improved Seed Uptake by Smallholders in Northern Ghana. *Sustainable Agriculture Research*, *5*(2), 27–40. https://doi.org/10.5539/sar.v5n2p27

Etwire, P. M., Atokple, I. D. K., Buah, S. S. J., Abdulai, A. L., Karikari, A. S., & Asungre, P. (2013). Analysis of the seed system in Ghana. *International Journal of Advance Agricultural Research*. 1, 7–13.

FAO. (2004). Seed multiplication by resource-limited farmers. In *Proceedings of the Latin American Workshop Goiania Brazil* (Issue April 2003).

FAO & AfricanSeeds. (2018). *Seeds toolkit (Seed quality assurance)* (H. Bahri & G. D. Méndez (eds.)). The Food and Agriculture Organization of the United Nations and AfricaSeeds.

FAOstat. (2017). *FAOSTAT*. http://www.fao.org/faostat/en/#data/QC

Girija, M., Dhanavel, D., & Gnanamurthy, S. (2013). Gamma rays and EMS induced flower color and seed mutants in cowpea. *Advances in Applied Science Research*, *4*(2), 134–139.

Gnanamurthy, S., & Dhanavel, D. (2014). Effect of EMS on induced morphological mutants and chromosomal variation in Cowpea (*Vigna unguiculata* (L.) Walp). *International Letters of Natural Sciences*, *22*, 33–43. https://doi.org/10.18052/www.scipress.com/ILNS.22.33

Gnanamurthy, S., Dhanavel, D., & Girija, M. (2013). Effect of Gamma irradiation on the morphological characters of Cowpea (*Vigna*

unguiculata (L.)Walp). *Int. J. Cur. Tr. Res*, *2*(1), 38–43.

Gnanamurthy, S., Dhanavel, D., & Girija, M. (2019). Effect of Gamma irradiation on the morphological characters of Cowpea (*Vigna unguiculata* (L .) Walp). *Int. J. Cur. Tr. Res*, *2*(1), 38–43.

Gnankambary, K., Batieno, T. B. J., Sawadogo, N., Sawadogo, M., Tignegre, J. B., Yonli, D., & Ouedraogo, T. J. (2019). Genetic Variability Induced by Gamma Radiation in Cowpea [(*Vigna unguiculata* L. (Walp)] in Burkina Faso. *European Scientific Journal ESJ*, *15*(15). https://doi.org/ 10.19044/esj.2019.v15n15p153

Gunasekaran, A., & Pavadai, P. (2015). Effect of Gamma Rays on Germination , Morphology , Yield and Biochemical Studies in Groundnut (*Arachis hypogaea* L .). *World Scientfic News*, *23*, 13–23.

Gupta, P. P., & Singh, J. V. (2010). Disease Management in Forage Legumes. In *Forage Legumes* (pp. 138–141). *Scientific Publishers*. https://books.google.com.gh/books?hl=en&lr=&id=r7s4DwAAQBAJ&oi=fnd&pg=PA138&dq=Gupta,+P.+P.,+%26+Singh,+J.+V.+(2010).+Disease+management+in+forage+legumes.+Forage+Legumes,+138.+&ots=OEGRnLCYUN&sig=cR9L8IzVHrJPf18ZRyHy9spJK2k&redir_esc=y#v=onepage&q=Gupta%25

Gwata, E. T., Shimels, H., & Motova, P. M. (2016). Potential of Improving Agronomic Attributes in Tropical Legumes Using Two Mutation Breeding Techniques in Southern Africa. In *Alternative Crops and Cropping Systems* (pp. 3–17). http://dx.doi.org/10.5772/62262

Hair, J. F. J., Black, W. C., Babin, B. J., & Anderson, R. E. (2010). Multivariate Data Analysis. In *Pearson Prentice Hall* (7th ed.). https://doi.org/10.2307/1266874

Harding, S. S., Johnson, S. D., Taylor, D. R., Dixon, C. A., & Turay, M. Y. (2012). Effect of Gamma Rays on Seed Germination, Seedling Height, Survival Percentage and Tiller Production in Some Rice Varieties Cultivated in Sierra Leone. *American Journal of Experimental Agriculture*, *2*(2), 247–255. https://doi.org/10.9734/AJEA/2012/820

Ho, R. (2006). Handbook of Univariate and Multivariate Data Analysis and Interpretation of SPSS. In *Taylor & Francis Group*. Taylor & Francis Group. https://doi.org/10.1198/000313008X332287

Horn, L. N., Ghebrehiwot, H. M., & Shimelis, H. A. (2016). Selection of Novel Cowpea Genotypes Derived through Gamma Irradiation. *Frontiers in Plant Science*, *7*(262), 1–13. https://doi.org/10.3389/fpls.2016.00262

Horn, L., & Shimelis, H. (2013). Radio-sensitivity of selected cowpea (*Vigna unguiculata*) genotypes to varying gamma irradiation doses. *Scientific Research and Essays*, *8*(40), 1991–1997. https://doi.org/10.5897/SRE 2013.5682

International Rice Rsearch Institute. (1994). A manual of rice seed health testing. In J. K. Misra & T. W. Mew (Eds.), *Manual of Rice Seed Health Testing*. International Rice Research Institute.

ISTA. (2010). *International Rules for Seed Testing* (1st ed.). The International Seed Testing Association (ISTA).

ISTA. (2011). *ISTA Annual Meeting Conclusion - Monday, 15 June* (Issue June).

ISTA. (2012). *Seed Testing International-ISTA News Bulletin No. 142* (Issue 142).

Jackson, T. (2009). *Corn Ear Rots & Grain Molds | CropWatch | University of Nebraska–Lincoln*. https://cropwatch.unl.edu/cw-09-11-06-corn-ear-rots-grain-molds-2

Jeong, R., Chu, E., Shin, E., Lee, E., Kwak, Y., & Park, H. (2015). Antifungal effect of gamma irradiation and sodium dichloroisocyanurate against *Penicillium expansum* on pears. *Advances in Applied Science Research*, *61*, 437–445. https://doi.org/10.1111/lam.12466

Jeong, R. D., Chu, E. H., Lee, G. W., Cho, C., & Park, H. J. (2016). Inhibitory effect of gamma irradiation and its application for control of postharvest green mold decay of *Satsuma mandarins*. *International Journal of Food Microbiology*, *234*, 1–8. https://doi.org/10.1016/j.ijfoodmicro.2016.06.026

Jeong, R. D., Shin, E. J., Chu, E. H., & Park, H. J. (2015). Effects of Ionizing Radiation on Postharvest Fungal Pathogens. *The Plant Pathology Journal*, *31*(2), 176–180. https://doi.org/10.5423/PPJ.NT.03.2015.0040

Kader, M. A. (2005). A Comparison of Seed Germination Calculation Formulae and the Associated Interpretation of Resulting Data. *Journal & Proceedings of the Royal Society of New South Wales*, *138*, 65–75.

Kameswara Rao, N., Hanson, J., Dullo, E. M., Ghosh, K., Nowell, D., & Larinde, M. (2006). Seed Quality Testing. In *Handbooks for Genebanks*

No. 8 Seed Handling in Genebanks (pp. 50–85). Food and Agriculture Organization.

Khare, K., Wale, K., & Ntshole, B. G. (2014). Fungi Associated With Seeds of Three Varieties of Sorghum Grown in Botswana and Its Control in Vitro Using Fungicide and Plant Extract Treatment. *International Jornal of Bioassays*, *3*(10), 3329–3331.

Khare, K. B., Loeto, D., Wale, K., & Salani, M. (2016). Seed-borne fungi of cowpea [*Vigna unguiculata* (L.) Walp] and their possible control in vitro using locally available fungicides in Botswana. *International Journal of Bioassays*, *5*(11), 5016. https://doi.org/10.21746/ijbio.2016.11.005

Kottapalli, B., Wolf-Hall, C. E., Schwarz, P., Schwarz, J., & Gillespie, J. (2003). Evaluation of hot water and electron beam irradiation for reducing Fusarium infection in malting barley. *Journal of Food Protection*, *66*(7), 1241–1246. https://doi.org/10.4315/0362-028X-66.7.1241

Kusmiyati, F., Sutarno, Sas, M. G. A., & Herwibawa, B. (2018). Mutagenic effects of gamma rays on soybean (*Glycine max* L.) germination and seedlings. *IOP Conference Series: Earth and Environmental Science*, *102*, 012059. https://doi.org/10.1088/1755-1315/102/1/012059

Lagoda, P. J. L. (2012). Effects of radiation on living cells and plants. In *Plant Mutation Breeding and Biotechnology* (pp. 123–134). CABI Publishing. https://doi.org/10.1079/9781780640853.0123

Langyintuo, A. S., Lowenberg-DeBoer, J., Faye, M., Lambert, D., Ibro, G., Moussa, B., Kergna, A., Kushwaha, S., Musa, S., & Ntoukam, G. (2003).

Cowpea supply and demand in West and Central Africa. *Field Crops Research*, *82*(2–3), 215–231. https://doi.org/10.1016/S0378-4290(03)00039-X

Lima, K. dos S. C., Souza, L. B. e., Godoy, R. L. de O., França, T. C. C., & Lima, A. L. dos S. (2011). Effect of gamma irradiation and cooking on cowpea bean grains. *Radiation Physics and Chemistry*, *80*, 983–989. https://doi.org/10.1016/j.radphyschem.2011.04.011

Littke, W. R. (1990). Seed Fungi. In *Growing Healthy Seedlings* (pp. 16–31).

Liu, B., Liu, X., Li, Y.-S., & Herbert, S. J. (2013). Effects of enhanced UV-B radiation on seed growth characteristics and yield components in soybean. *Field Crops Research*, *154*, 158–163. https://doi.org/10.1016/J.FCR.2013.08.006

Liu, H., Hu, D., Dong, C., Fu, Y., Liu, G., Qin, Y., Sun, Y., Liu, D., Li, L., & Liu, H. (2017). Low-dose ionizing radiation limitations to seed germination: Results from a model linking physiological characteristics and developmental-dynamics simulation strategy. *Journal of Theoretical Biology*, *427*, 10–16. https://doi.org/10.1016/j.jtbi.2017.05.024

Louwaars, N. P. (2002). The Importance of the Farmers ' Seed Systems in a Functional National Seed Sector. *Journal of New Seeds*, *9025*(January), 1–13. https://doi.org/10.1300/J153v04n01

Mabaya, E., Adzivor, S. Y., Wobil, J., & Muyoga, M. (2017). *Ghana Brief 2017 - The African Seed Access Index* (Issue December).

Manggoel, W. (2012). Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata*

(L.) Walp] accessions. *Journal of Plant Breeding and Crop Science*, *4*(5). https://doi.org/10.5897/jpbcs12.007

Marcos-Filho, J. (2015). Seed vigor testing: An overview of the past, present and future perspective. *Scientia Agricola*, *72*(4), 363–374. https://doi.org/10.1590/0103-9016-2015-0007

Mathur, S. B., Njala, M., & Kongsdal, O. (2003). *Handbook on Normal and Abnormal Seedlings for Tropical Crops* (First). Danish Government Institute of Seed Pathology for Developing Countries.

Mba, C., Afza, R., Bado, S., Vienna, L. S., & Jain, S. M. (2010). Induced Mutagenesis in Plants Using Physical and Chemical Agents. In *Plant Cell Culture: Essential Methods* (Issue March). John Wiley & Sons, Ltd. https://doi.org/10.1002/9780470686522.ch7

Mendes-Rodrigues, C., Oliveira, P. E., & Ranal, M. A. (2011). Seed germination and seedling growth of two Pseudobombax species (Malvaceae) with contrasting habitats from Brazilian Cerrado - PubMed. *International Journal of Tropical Biology and Conservation*, *59*(4), 1915–1925. https://pubmed.ncbi.nlm.nih.gov/22208102/

Mendes-Rodrigues, C., Ranal, M. A., & Oliveira, P. E. (2011). Does polyembryony reduce seed germination and seedling development in *Eriotheca pubescens* (Malvaceae: Bombacoideae)? *American Journal of Botany*, *98*(10), 1613–1622. https://doi.org/10.3732/ajb.1100022

MoFA; SRID. (2017). Agriculture in Ghana:Facts and Figures. In *Agriculture in Ghana:Facts and Figures* (Issue 911). https://doi.org/10.1126/science.35.911.927-a

Mshelmbula, B. P., Akomolafe, G. F., Thomas, T. L., & Ologundudu, F. A. (2019). Effect of varying UV radiation on germination and growthof cowpea (*Vigna unguiculata* (L.) Walp). *FuDMA Journal of Sciences*, *3*(2), 206–209.

Mudibu, J., Nkongolo, K. K. C., Kalonji-mbuyi, A., & Kizungu, R. V. (2012). Effect of Gamma Irradiation on Morpho-Agronomic Characteristics of Soybeans (*Glycine max* L.). *American Journal of Plant Sciences*, *3*, 331–337. https://doi.org/http://dx.doi.org/10.4236/ajps.2012.33039

Neergaard, P. (1979). *Seed Pathology*. Macmillan Press.

Nikolić, N., Squartini, A., Concheri, G., Stevanato, P., Zanin, G., & Masin, R. (2020). Weed seed decay in no-till field and planted riparian buffer zone. *Plants*, *9*(3). https://doi.org/10.3390/plants9030293

NVRRC. (2019). *Catalogue of crop varieties released & registered in Ghana*. www.mofa.gov.gh

OECD. (2016). Chapter 5 Cowpea (*Vigna unguiculata*). *Safety Assessment of Transgenic Organisms in the Environment*, *6*(December 2015), 211–242.

Olakunle, F., Olumuyiwa, C., & Abimbola, A. (2018). *Mutation induction for increasing genetic variability in cowpea (Vigna unguiculata [L.] Walp.). June*.

Olasupo, F. O., Ilori, C. O., Forster, B. P., & Bado, S. (2016). Mutagenic Effects of Gamma Radiation on Eight Accessions of Cowpea (*Vigna unguiculata* [L.] Walp.). *American Journal of Plant Sciences*, *7*, 339–351. https://doi.org/10.4236/ajps.2016.72034

Olembo, S. A. H. (1985). *Effect of fungal contaminants on laboratory germination tests*. PhD. Thesis: Iowa State University.

Peksen, E., & Artik, C. (2004). Comparison of Some Cowpea (*Vigna unguiculata* L. Walp). *Journal of Agronomy*, *3*(2), 137–140. https://doi.org/10.3923/ja.2004.137.140

Radomyski, T., Murano, E. A., Olson, D. G., & Murano, P. S. (1994). Elimination of pathogens of significance in food by low-dose irradiation: A review. *Journal of Food Protection*, *57*(1), 73–86. https://doi.org/10.4315/0362-028X-57.1.73

Rahimi, M. M., & Bahrani, A. (2011). Effect of gamma irradiation on qualitative and quantitative characteristics of canola (*Brassica napus* L.). *Middle-East Journal of Scientific Research*, *8*(2), 519–525.

Ranal, M. A., & De Santana, D. G. (2006). How and why to measure the germination process? In *Revista Brasileira de Botanica* (Vol. 29, Issue 1, pp. 1–11). Sociedade Botanica de Sao Paulo. https://doi.org/10.1590/S0100-84042006000100002

Ranal, M. A., Santana, D. G. de, Ferreira, W. R., & Mendes-Rodrigues, C. (2009). Calculating germination measurements and organizing spreadsheets. *Revista Brasileira de Botânica*, *32*(4), 849–855. https://doi.org/10.1590/S0100-84042009000400022

Rao, N. K., Hanson, J., Dulloo, M. E., Ghosh, K., Nowell, D., Larinde, M., No, G., Nowell, D., & Larinde, M. (2006). *Manual of Seed Handling in Genebanks* (Issue 8). Biodiversity International.

Roberts, E. H., & Osei-Bonsu, K. (1988). *Seed and seedling vigour* (pp. 897–910). Springer, Dordrecht. https://doi.org/10.1007/978-94-009-2764-3_71

Rozman, L. (2014). The effect of gamma radiation on seed germination of barley (Hordeum vulgare L.). *Acta Agriculturae Slovenica*, *103*(2), 307–311. https://doi.org/10.14720/aas.2014.103.2.15

Sanne, H., Vodouhe, R., Halewood, M., & De Jonge, B. (2017). *ISSD Africa Synthesis paper The support for farmer-led seed systems in African seed laws* (Issue 9).

Shahat, M. S., Sharaf, A. M., Mahmoud, K. A., & Abd EL-Naby, T. M. (2017). The Quality Evaluation of Cowpea Seeds as Affected by Gamma Irradiation 1- Evaluation of Cooking Aspects, Nutritional, Digestibility, Starch structure, Flatulent Effect and Sensory Improvement. *Current Science International*, *6*(1), 93–102.

Shathele, M. S. (2009). Effects of Gamma Irradiation on Fungal Growth and Associated Pathogens. *Research Journal of Environmental Toxicology*, *3*(2), 94–100. https://doi.org/10.3923/rjet.2009.94.100

Siddique, A. B., & Wright, D. (2004). Effects of date of sowing on seed yield, seed germination and vigour of peas and flax. *Seed Science and Technology*, *32*(2), 455–472. https://doi.org/10.15258/sst.2004.32.2.16

Singh, B. B., Raj, D. R. M., & Dashiell, K. E. (1997). *Advances in Cowpea Research*. Copublication of International Institute of Tropical Agriculture (UTA) and Japan International Research Center for Agricultural Sciences (JIRCAS). UTA, Ibadan, Nigeria

Singh, S. K., Surabhi, G., Gao, W., & Reddy, K. R. (2008). Journal of

Photochemistry and Photobiology B : Biology Assessing genotypic variability of cowpea (*Vigna unguiculata* [L .] Walp .) to current and projected ultraviolet-B radiation. *Journal of Photochemistry & Photobiology, B: Biology*, *93*(2), 71–81. https://doi.org/10.1016/j.jphotobiol.2008.07.002

Sobha, R. I., & Dorcas, M. (2017). Seed mycoflora associated with ragi (*Eleusine coracana* (L.) geartin. *Journal of Innovations in Pharmaceuticals and Biological Sciences*, *1*(1), 1–6. https://doi.org/10.23959/sfowj-1000006

Timko, M. P., Ehlers, J. D., & Roberts, P. A. (2007). Cowpea. In C. Kole (Ed.), *Genome Mapping and Molecular Breeding in Plant:Pulses, Sugar and Tuber Crops* (Vol. 3, pp. 51–67). Springer-Verlag. https://doi.org/https://doi.org/10.1007/978-3-540-34516-9_3

Timko, M. P., & Singh, B. B. (2008). Cowpea, a Multifunctional Legume. In *Genomics of Tropical Crop Plants* (pp. 227–258). Springer. https://doi.org/10.1007/978-0-387-71219-2_10

Tsifodze, S. (2018). *Seed quality and adaptability of some newly introduced cowpea lines in the coastal savannah zone of Ghana*. Mphil. Thesis. University of Cape Coast.

Udensi, O., Ikpeme, E. V., Edu, E. A., & Ekpe, D. E. (2012). Relationship studies in cowpea (*Vigna unguiculata* l. walp) landraces grown under humid lowland condition. *International Journal of Agricultural Research*, *7*(1), 33–45. https://doi.org/10.3923/ijar.2012.33.45

Uguru, M. (1996). Correlation and Path-Coefficient analysis of major yield components in vegetable Cowpea [*Vigna unguiculata* (L.) Walp.]. *Proc. 14th HORTSON Conference, Ago Iwoye*. https://scholar.google.com/scholar?hl=en&as_sdt=0%2C5&q=Uguru+MI+%281996%29.+Correlation+and+Path-Coefficient+analysis+of+major+yield+components+in+vegetable+Cowpea+%5BVigna+unguiculata+%28L.%29+Walp.%5D.+Proc.+14th+HORTSON+Conference%2C+Ago-Iwoye%2C+1-4+

Van Gastel, T. J. G., Gregg, B. R., & Asiedu, E. A. (2002). Seed Quality Control in Developing Countries. *Journal of New Seeds*, *4*(1–2), 117–130. https://doi.org/10.1300/J153v04n01_09

Van Gastel, A. J. G. V., Bishaw, Z., & Gregg, B. R. (2002). *Wheat seed production*. Wheat Seed Production. Bread Wheat–Improvement and Production. FAO, Rome. http://www.fao.org/3/y4011e0v.htm

Vijay, D., Kumar, A., Yadava, D, K., & Kumar, A. M. B. (2017). *Seed Law Enforcement* (Issue November). Division of Seed Science and Technology ICAR-Indian Agricultural Research Institute.

Wain-Tassi, A. L., dos Santos, J. F., de Cássia Panizzi, R., & Vieira, R. D. (2012). Seed-borne pathogens and electrical conductivity of soybean seeds. *Scientia Agricola*, *69*(1), 19–25. https://doi.org/10.1590/S0103-90162012000100004

Wekundah, J. M. (2012). *Why Informal Seed Sector is Important in Food Security. African Technology Policy Studies Network, Biotechnology trust Africa* (Issue 43).

Yin, H., Tsuzuki, T., Millington, K. R., & Casey, P. S. (2014). A comparative

interlaboratory study on photocatalytic activity of commercial ZnO and CeO2 nanoparticles. *Journal of Nanoparticle Research*, *16*(10). https://doi.org/10.1007/s11051-014-2641-6

Yirzagla, J., Atokple, I. D. K., Haruna, M., Kusi, F., & Muntari, A. (2016). *Scaling out Cowpea Production in Northern Ghana , Community Seed Production Scheme Cowpea Out-scaling Project* .

Zhang, J., Siemann, E., Tian, B., Huang, W., & Ding, J. (2020). Differences in seed properties and germination between native and introduced populations of *Triadica sebifera*. *Journal of Plant Ecology*, *13*(1), 70–77. https://doi.org/10.1093/jpe/rtz048

Zhou, Y. (2016). *Seed Policy Harmonization in ECOWAS : The Case of Ghana* (Issue January).

Zpevak, F. A., De Andrade Perez, S. R. J. G., & Buckeridge, M. S. (2012). Isothermal seed germination of *Adenanthera pavonina*. *Revista Brasileira de Botanica*, *35*(4), 401–408. https://doi.org/10.1590/s0100-84042012000400013

APPENDICES

Appendix1: Working Recording Sheet for Seed Health Testing

WORKING RECORDING SHEET NO. 1 FOR THE BLOTTER METHOD

Accession No. _____ Host_____
Date of plating _____ Date of recording _____
Analyst No. _____ Method _____
No. of seeds per dish 25 Total No. of seeds tested _____

Fungi \ Dish No.	1	2	3	4	5	6	7	8	Remarks*

*Use this space if extra space is needed for writing remarks.

_____
Signature of the analyst

Appendix 2: Mean rainfall and temperature during the field evaluation

Mutant	Date	Rainfall (mm)	Temperature (°C)
M_1 (2018)	August	31.1	23.7
	September	103.1	24.4
	October	194.5	25.2
	November	122.1	25.4
M_2 (2019	May	241.6	26.2
	June	83.6	25.1
	July	30.2	23.1
	August	24.7	24.2

Source: Ghana Meteorological Agency

Appendix 3: Results of soil analyses

Parameter	Value
Chemical properties	
Nitrogen (N) %	0.08
Phosphorus (P) cmol/kg	7.02
Potassium (K) cmol/kg	0.06
Calcium (Ca) cmol/kg	2.57
% Carbon	0.98
Physical properties	
pH	5.64
CEC (cmol/kg)	0.64
Bulk Density (g/ cm^3)	1.31
Particle Density (g/ cm^3)	2.69

Appendix4: Set ranges for measured traits used in Chi-square tests for interdependence

Trait						Rank	Remark
% Germination (%)	Germination Index	% Decayed seeds (%)	% Hard seeds (%)	% Infection (%)	Yield (kg/ha)		
90.0 – 100.0	> 12.0	< 1.0	<1.0	<1.0	>2499	1	Excellent
80.0 - 89.0	8.0 - 11.0	1.0 - 5.0	1.0 -5.0	1.0-5.0	>1999	2	V. good
70.0 - 79.0	4.0 - 7.0	6.0 – 10.0	6.0 – 10.0	6.0 – 10.0	>1499	3	Good
60.0 – 69.0	1.0 - 3.0	11.0 - 15.0	11.0 - 15.0	11.0 - 15.0	>999	4	Poor
< 60.0	< 1.0	>15.0	>15.0	>15.0	<1000	5	V. poor