UNIVERSITY FOR DEVELOPMENT STUDIES, TAMALE

EVALUATION OF MUTANT GENOTYPES OF GROUNDNUT (*Arachis hypogaea* L) FOR IMPROVED AGRONOMIC TRAITS AND STABILITY

BY

ADAZEBRA IRENE AYINSUHYA
(UDS/DCS/0001/17)

2019

UNIVERSITY FOR DEVELOPMENT STUDIES, TAMALE

EVALUATION OF MUTANT GENOTYPES OF GROUNDNUT (*Arachis hypogaea* L) FOR IMPROVED AGRONOMIC TRAITS AND STABILITY

BY

ADAZEBRA IRENE AYINSUHYA
(UDS/DCS/0001/17)

THESIS SUBMITTED TO THE DEPARTMENT OF AGRONOMY, FACULTY OF AGRICULTURE, UNIVERSITY FOR DEVELOPMENT STUDIES, IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF MASTER OF PHILOSOPHY (MPhil), DEGREE IN ANIMAL SCIENCE

AUGUST, 2019

DECLARATION

I, Adazebra Irene. Ayinsuhya, do hereby declare that this work is the result of my own original research towards degree in master of philosophy. Crop Science (Agronomy option) and that this thesis has neither in whole nor part been presented anywhere for a degree. All references cited in relation to other works, have been duly acknowledged.

Adazebra Irene Ayinsuhya ....

(Student) Signature Date

Supervisors'

We, hereby declare that the preparation and presentation of the thesis was supervised in accordance with the guidelines on supervision of thesis laid down by the University for Development Studies.

Dr. Isaac K. Addai ....

(Principal Supervisor) Signature Date

Dr. Fredrick Kankam ..... …….....

(Co-Supervisor) Signature Date

ABSTRACT

Groundnut productivity in Ghana is generally low when compared to other countries. The low yields can be partly attributed to unstable rainfall patterns, pest and disease infestation, and low yielding ability of varieties cultivated by farmers. The present study was undertaken to evaluate groundnut genotypes for yield and stability performances and early maturing genotypes with other superior agronomic traits. Four groundnut mutant genotypes (150 Gy, 200 Gy, 250 Gy and 300 Gy) and the unirradiated control (0 Gy) which served as standard check were evaluated at three locations namely Nyankpala, Bawku and Techiman, in the Guinea savannah, Sudan savannah and Transitional agroecological zones of Ghana respectively. This was done during the major cropping seasons of the years 2017 and 2018. Growth and yield parameters were collected for statistical analyses using GenStat (12 edition). The results revealed that earlier mutagenesis carried out on these genotypes had a great potential to improve upon the yield and some important traits in the genotypes such as; early flowering, maturity and yield. Genotype 200 Gy, recorded the highest results in terms of the above mentioned traits i.e (Days to 50% flowering 24.61; Days to maturity, 89 and Total grain yield, 1.68).

Plants from the 200 Gy genotypes should be subjected to proximate analysis to check the nutritional quality, disease and pest tolerance. Genotype 200 Gy, is recommended for release to farmers in the Guinea Savannah agroecological zone.

DEDICATION

This work is dedicated to my beloved and caring parents; Mr. Adazebra Clement Ayimbire and Mrs. Adazebra Rose Nma for their care and struggle in bringing me up to this level. I also dedicate this thesis to my children Mehetabel and Medad Ayamga for all the struggles that they have gone through during my studies and research

ACKNOWLEDGEMENTS

I am very grateful to the Almighty God for his loving kindness and blessings for the successful completion of this program. I would like to extend special thanks and appreciation to my supervisor Dr. Isaac K. Addai for his support and guidance throughout my thesis. For all his advice and resources, I say God bless him. I would also like to extend heartfelt thanks and appreciation to my Co-Supervisor, Dr. Frederick Kamkam. I want to also express my sincere gratitude to my younger Ms. sister Gloria Adazebra, Mr. Baba Kasim of SARI and also Mr. Maganoba Charles for their assistance in analyzing my data generated during the course of this study.

I am very grateful and wish to express my wholehearted indebtedness to Rev. brother John Dorgbadzi Yaw for his advice, encouragement in difficult times, kept me going and also helped me to gain admission to pursue this course, l say God richly bless him. I am also grateful to the lecturers of the University for Development studies especially those in Agronomy Department of the Faculty of Agriculture for their immense efforts in making me what I am today.

My heartfelt gratitude goes to my mother Mrs. Adazebra Rose Nma for her care and support given to me throughout my education and all my siblings for their prayers and support given to me, I could not have reached this far without them. May God bless them and enrich them with long life and good health. Finally, I would like to express my immeasurable gratitude to all my course mates and friends for their advice, kindness and co-operation.

TABLE OF CONTENTS

CONTENT **PAGE**

LIST OF TABLES

TABLES **PAGE**

LIST OF FIGURES

FIGURES **PAGE**

LIST OF APPENDICES

APPENDICES **PAGE**

ABBREVIATIONS AND ACRONYMS

CRI:	Crop Research Institute
CSIR:	Council for Scientific and Industrial Research
FAO:	Food and Agriculture Organization
GY:	Gray
ICRISAT:	International Crop Research Institute for the Semi-Arid Tropics
MoFA:	Ministry of Food and Agriculture
RCBD:	Randomized Complete Block Design
SARI:	Savannah Agricultural Research Institute
WAP:	Weeks after Planting
ANOVA:	Analysis of Variance
GEI:	Genotype by Environment Interaction
GGE:	Genotype main effects and Genotype by Environment
G x E:	Genotype by Environment interaction
G x L:	Genotype by Location Interaction
G x Y:	Genotype by Year Interaction
G x L x Y:	Genotype by Location by Year Interactions
LSD:	Least Significant Difference
NPK:	Nitrogen, Phosphorus and Potassium
SAS:	Statistical Analysis System
SSA:	Sub-Sahara African
AMMI:	Additive main effects and multiplicative Interaction
WHO:	World Health Organization
YSI:	Yield Stability index
ASV:	Additive Stability Value

USDA:	United States Department of Agriculture
USA:	United State of America
SVD:	Singular Value Decomposition
IPCAS:	Iterative Protein Crystal structure Automatic Solution

CHAPTER ONE

INTRODUCTION

1.1 Background

Groundnut (*Arachis hypogea* L.) originated from Latin America and was introduced to Africa from Brazil in the 16th century by the Portuguese (Gibbon and Pain, 1985; Abalu and Etuk, 1986). It is the most prominent oil seed crop ranked second worldwide after soybean (Mensah and Obadoni, 2007). Groundnut is a self-pollinated, tropical annual legume which is fairly drought resistant and mainly cultivated in dry tropical areas (Ntare *et al.*, 2008). It is produced in over 100 countries both tropical and sub-tropical countries. China is the world's largest groundnut producer, with 40% of world's production, followed by India (23%), a group of Sub-Saharan African (SSA) countries (8.4%) and the United States (5.6%). It is the 13th most important food crop in the world and contributes 20-50% vegetable protein, 40-50% fat and 10-20% carbohydrates (Vijaya *et al.*, 1997; Waliyar, 2006).

Groundnut was grown on nearly 23.95 million ha of land worldwide with the total production of 36.45 million tons and an average yield of 1520 kg/ha in 2009. It was reported that between 2000 and 2009, the annual global production increased marginally by 0.4%, the area by 0.3% and yield by 0.1% (FAOSTAT, 2011). The total production in sub-Saharan Africa was 8.2million tons per year from 9.5 million hectares of land (Ntare, 2007). According to USDA (2010), groundnut production levels in 2008/09 in Nigeria, Sudan and Senegal respectively, were 1.55, 0.85, 0.75 million metric tons respectively with Ghana producing 0.44 million metric tons.

In Ghana groundnut is grown in all agroecological zones. About 85% of the area under groundnut production is in the Guinea savanna zones (Atuahenen-Amankwa *et al.*, 1988). Groundnut is often grown as an intercrop in West Africa but there are parts of Mali where they are mostly grown as a sole crop (Ndjeunga *et al.*, 2008). However, smaller quantities are produced in all parts of the country (Tweneboah, 2000). Groundnut contains on average 12% to 15% carbohydrates, 25% to 30% protein and 4 % to 50% oil (Kwarteng and Towler, 1994). The nuts can be boiled, fried, or crushed into groundnut butter or for oil (Porler, 1997; Owens, 1999). Groundnut butter is extensively used in the preparation of soup and as bread spread (Tsigbey *et al.*, 2004). Groundnut hay is used as animal fodder, and shells as sources of fuel and fertilizer (De Waele and Swanevelder, 2001). Groundnut is grown throughout Ghana, but it is mostly produced in the north where about 92% of the national production is obtained. (Wumbei *et al.*, 2000). The majority of groundnuts production in Ghana is from small-scale farmers of less than 2 hectares of arable land (MoFA, 1997).

Groundnuts provide a valuable source of protein, fats, energy, and minerals, and generate cash income to many poor farmers in the developing world, especially in USA and Asia (Diop *et al*., 2004). According to Awuah (2000), the national per capital groundnut consumption was estimated at 0.61 kg per week and 80 percent of Ghanaians consume groundnuts or its products at least once a week. Groundnut production in Ghana nearly tripled from 168,200 ton in 1995 to 420,000 ton in 2005 and this was primarily due to increase in the area under cultivation from 180,400 ha in 1995 to

450,000 ha in 2005 (FAO, 2006). Average yields, however, continued to remain below 1.0 ton/ ha which is far below the potential yields of 2.0-3.0 ton/ha.

In Ghana, the major constraint to groundnut production is disease incidence, particularly, early leaf spot caused by *Cercospora arachidicola* and late leaf spot by *Phaeoisariopsis personata* (Frimpong *et al.,* 2006). Both early and late leaf spots diseases are widely distributed and occur in epidemic proportions in northern Ghana (Nutsugah *et al.*, 2007). Epidemics of early and late leaf spots on susceptible groundnut genotypes can cause complete defoliation, which can drastically reduce yields (Shew *et al.*, 1995). Losses due to diseases can be attributed to the high defoliation caused by leaf spot diseases, which thus affect pod filling and subsequent grain yield. Defoliation affects hay quality of vines that are fed to animals (Tsigbey *et al.,* 2004). In addition, fallen leaves from infected plants provide organic matter as a food source for other fungi particularly, *Sclerotium rolfsii,* and this can contribute to inoculums build-up on farms (Lucas *et al.,* 1992) Diseases of groundnut reduce yield and quality of grains and increase cost of production wherever the crop is grown (Wynne *et al.*, 1992).

Field pests are one of the major problems affecting groundnut production. There are many varieties of groundnut field insect pests which are accountable for significant yield losses (Biswas, 2014). Among these pests are aphids that are vectors of the rosette virus which is the most damaging viral disease of groundnut (Waliyar *et al*., 2007). In addition to pre-harvest constraints, there are several challenges associated with groundnut postharvest management practices. These challenges are related to poor drying and storage resulting in microbial contamination, and pest (insect, rodent) attacks.

Postharvest losses resulting from pests and poor management practices can rise up to 70% after six months of storage (Oaya *et al*., 2012). Losses of stored seeds, caused by infestation from *Caryedon serratus*, Bruchids and Pyralids are the most common storage pests, (Purseglove, J.W. 1998). On the other hand, groundnut is among the major food commodities that can be affected by mycotoxins such as aflatoxins, which are the toxic chemical substances produced by toxigenic strains of fungi such as *Aspergillus flavus* (Smith and Ross, 2002), under specific conditions. Aflatoxins and insect infestations are the most important quality problems in groundnut worldwide having serious health and economic implications (IARC, 1993). Gamma irradiation is a physical technique of food preservation that seems to have a potential to protect such commodity from insect's infestation and microbial contamination during storage. Therefore, it has been proposed as a good alternative to methyl bromide and other fumigants for pest control (Gupta, 2001). However, development of this technique involves consideration that gamma rays might change the nutritive value of stored seeds. The absolute relationship of radiation application dose and possible changes must be known in order to comprehensively assess the acceptability of radiation – treated food seeds.

1.2 Problem statement and justification

The yield of several crops has been increased by creating variation of the parental crops. Most of these crops studied are cereals. Legumes are also important in Ghana. Plant breeding requires genetic variation of useful traits for crop improvement. Often, however, desired variation is lacking (Novak and Brunner, 1995). Consequently, the

extent to which cultivars may be improved through conventional breeding methods is limited. Mutation breeding supplements conventional plant breeding as a source of increasing variability and could confer specific improvement without significantly altering the phenotype (Ojomo *et al*., 1979).

Genetic engineering and hybridization have also been used in the generation of genotypic variation. Genetic engineering however, has a number of challenges concerning the release of transgenic plants into the environment in terms of religion, health, environment and ethical interest. Hybridization though may be useful, the various problems often encountered in effecting crosses and the non-availability of parents with desirable genes have resulted in a limitation on the use of hybridization (Shanthala, *et al*., 2012). It has been demonstrated that, genetic variability for several desired characters can be induced successfully through mutations, and the practical value of mutagenesis in plant improvement programme has been well established (Chopra, 2005).

The successful utilization of gamma rays to generate genetic variability through mutagenesis in plant breeding has been reported (Takagi and Anai, 2006). The main advantage of induced mutation breeding is the possibility of improving one or two characters without changing the rest of the genotype. More than 2252 mutant varieties of different crops have been officially released in the world. (Maluszynski, *et al*., 2000). Ahloowalia *et al*. (2004) also reported the fruitful application of gamma rays for the development of new varieties. Micke (2004) also reported beneficial use of mutation in legumes. Induced mutations provide beneficial genetic variations for the development

of improved cultivars. The present study used genotypes which had been developed through induced mutation studies of the parental groundnut variety, Chinese.

1.3 Main objective

Evaluate mutant genotypes of groundnuts through multilocational trials for improved agronomic traits.

1.3.1 Specific Objectives

1. To determine earliness in flowering and maturation of genotype 0 Gy, 150 Gy, 200 Gy, 250 Gy and 300 Gy in three locations i.e (Nyankpala, Bawku and Techiman).
2. To determine which of the mutant genotype are high yielding in the study areas
3. To determine the stability of cultivating the mutant genotypes in the study areas.

CHAPTER TWO

LITERATURE REVIEW

2.1 Origin and distribution

Groundnut (*Arachis hypogaea* L.) belongs to the family Leguminosae and the subfamily Papilionoideae (Tweneboah, 2000). There are several schools of thought about the origin of the crop. It is a leguminous oil and seed crop believed to have originated in the southern Bolivia extending to North West region of Argentina in South America. It was introduced into West Africa in the 16th century by the Portuguese and has since become an important food and cash crop (Gregory *et al.,* 1980 and Isleib *et al.,* 1994). Important producing countries are India, China and the USA. However, the leading exporters are the Nigeria, Gambia, Senegal and Niger. In Ghana some people claim it is the number one legume, others say it is the number two next to cowpea. The cultivated groundnut (*Arachis hypogaea* L.*)* is an ancient crop of the New World, which originated in South America (Southern Bolivia/North West Argentina region) where it was cultivated as early as 1000 B.C. (Weiss *et al.,* 2000). Groundnut originated from Latin America and was introduced to the African continent from Brazil by the Portuguese in the 1600's (Adinya *et al.,* 2010).

Globally, groundnut is grown on approximately 42 million hectares with a total production of over 35 million tons (Rao *et al.,* 2013). More than half of the production area is in arid and semi-arid regions (Reddy *et al.,* 2003). Tanzania accounts for 2.9% of the global area for groundnut cultivation and 1.7% of global production (FAOSTAT, 2013). Today, it is grown in areas between 40°S and 40°N of the equator, where average rainfall is 500 to 1200 mm, and mean daily temperatures are higher than 20°C. The

groundnut crop is cultivated in 108 countries on about 22.2 million hectares, of which 13.69 million ha are in Asia (India 8 million ha; China 3.84 million ha), 7.39 million ha in Sub Saharan Africa, and 0.7 million ha in Central and South America. Average pod yields on a global scale increased slightly from 1.08 Mt ha^{-1} in the 1980's to 1.15 Mt ha^{-1} in the 1990's (Carley and Fletcher, 1995), and the global production was 29 million ha of pods. India, China, and the United States are the leading producers and grow about 70% of the world's groundnuts (FAOSTAT. (2010).

2.2 Botany and Morphology

Domesticated groundnut (*Arachis hypogaea* L.) is described as *Arachis* (from the Greek word arachus), meaning weed and *hypogaea* meaning underground chamber, referring to the formation of pods in the soil. Like the bambara groundnut of West Africa, all species of *Arachis* are geocarpic, forming their fruits underground (Tweneboah, 2000). Groundnut is a self-pollinated legume with a central, upright stem and many lateral branches. According to Krapovickas and Gregory (1994), groundnut is divided into two large botanical groups. The two major types or botanical groups of cultivated groundnuts are the bunch or erect types and the runner or trailing types.

The bunch or erect type is designated as Valencia or Spanish groundnut; while the runner or trailing type is called the Virginia groundnut. The Virginia type consists of both the bunch and runner types (Chapman and Carter, 2000). The most important criteria used by Krapovickas and Gregory (1994) were the presence or absence of reproductive axes (inflorescence) on the main stem and the arrangement of reproductive and vegetative axes on the primary laterals. The Virginia type is characterized by the

absence of reproductive axes on the main stem. It has an alternate branching pattern. The first two branches on the primary lateral are always vegetative (Dumor, 2015). The Spanish or Valencia group is characterized by the presence of reproductive axes in a continuous series on successive nodes of lateral branches, on which the first branch is always reproductive. It has a sequential branching pattern. In addition, the Valencia or Spanish type is early maturing and the plant is generally erect and has pods clustered about the base of the plant while the seeds possess little fresh dormancy. The Virginia type, on the other hand, is late maturing and has pods dispersed along the secondary and tertiary branches and the seeds possess appreciable fresh dormancy (Bansal *et al.*, 1993).

The leaves are pinnate normally with two pairs of leaflets and are green or dark green in color. Darker leaves are found in Virginia groundnut, while Spanish and Valencia groundnut tend to have lighter leaves (Schilling and Gibbon, 2002). The flowers are sometimes white, but more often yellow to orange and are borne on inflorescence in the leaf axils. According to Chapman and Carter (2000), the flowers are sessile and are borne in leaf axils either singly or in groups up to three and are self-pollinated. Natural cross pollination occurs at the rates of less than 1% to greater than 6% (< 1% > 6%) due to action of bees (Knauft *et al.*, 1987; Coffelt, 1989). After fertilization, the aerial flower grows downwards and enters the soil in a positive geotropic manner where the ovary at the tip of the peg grows into a pod containing the seeds (Tweneboah, 2000). Chapman and Carter (2000) indicated that the gynophore (a stalk-like structure) is commonly referred to as peg and the stage of the plant development at which the gynophore is activated and elongated is referred to as pegging. Tweneboah (2000) further described

groundnut as an annual herb with a remarkable characteristic of producing fruits underground.

Groundnut plant has taproots with abundantly branched lateral roots on which globular, often dark brown nodules are usually present (Gregory and Gregory, 1986). Nodulation in groundnut is very essential in symbiotic N_2 fixation which can make N available to crops that succeed the groundnut. The ability to nodulate and fix N_2 is a genetic factor affected by environmental conditions (Dakora *et al*., 1987; Giller and Wilson, 1991). The leaves are pinnate normally with two pairs of leaflets and are green or dark green in colour. Darker leaves are found in Virginia groundnut, while Spanish and Valencia groundnut tend to have lighter leaves (Schilling and Gibbon, 2002).

Flowering begins 17–35 days after seedling emergence depending on the cultivar and environmental conditions. Low temperatures generally delay flowering. The flowering pattern varies among and within botanical varieties. One or more flowers may be present at a node. Flower opening is normally at sunrise, but may be delayed by low temperatures (Prasad *et al*., 1999). The stigma becomes receptive to pollen about 24 hours before anthesis and remains so for about 12 hours after anthesis (Boote, 1982) and the dehiscence of anthers takes place 7 - 8 hours prior to opening of the flower in some varieties whereas in others they may not do so even at flower opening in the morning (Boote, 1982). Fertilization occurs about 6 hours after pollination. Fertilization of the egg activates the growth and elongation of the intercalary meristem which is located at the base of the ovary. As a result, a stalk-like structure or 'peg' becomes visible

within 4-6 days after fertilization under normal environmental conditions. Depending upon the prevailing temperatures, the peg or gynophore carrying the ovary and fertilized ovule on its tip appears in 6-10 days and grows to enter the soil (positively geotropic) where it develops into pods. The tip orients itself horizontally away from tap root (Nigam *et al*., 1990).

2.3 Soil and climatic requirements

Groundnut (*Arachis hypogea* L.) is essentially a tropical plant. It requires a long and warm growing season. The most favorable climatic conditions for groundnuts are well-distributed rainfall of at least 500 mm during the growing season, abundance of sunshine and relatively warm temperature. Mean temperatures of 21.0°C - 26.5°C are favourable. Lower temperatures are not suitable for its proper development. During the ripening period, it requires about a month of warm, dry weather. It is best suited to sandy loams but require calcium in the soil for successful pod fill (Mulei *et al*., 2011). Groundnut is not suited to growing in very dry areas or at altitudes higher than 1500 metres above sea level. Generally higher altitudes with cooler climates are not suitable for groundnut production (Reddy *et al*., 2003).

Optimum mean daily temperature ideal for groundnut is 27^{o}C – 30^{o}C and growth ceases at less than 15^{o}C. According to Schilling and Gibbon (2002), the optimum temperatures for growth of groundnut are from 25^{o}C to 33^{o}C and that germination is inhibited if temperature falls below 15^{o}C or rises above 45^{o}C. According to Prasad *et al*. (1998) groundnut plants are sensitive to hot days from six days before flowering until fifteen (15) days after coming into flower, with maximum effects occurring in nine days after

flowering. Tweneboah (2000) reported temperature ranges of 24°C – 30°C but minimum of 12°C – 15°C for germination and at least 24°C for flowering and seed setting. Mohammad (1984) reported cardinal temperature for groundnut seed germination as 29 to 36.5°C. Higher temperatures above 38°C from 21 to 90 days after planting reduced total dry weight by 20 to 35%, harvest index by 10 to 65%. Genotypic differences in response to temperature were noticed and reduction in total dry matter, pod and seed dry weight and harvest index at high temperatures were noticed only in susceptible genotypes (Craufurd *et al*., 2002).

Rainfall has been reported by researchers to be the most significant climatic factor affecting groundnut production in the semi-arid tropics where there are low and erratic rainfalls. Low rainfall and prolong dry spells during the growth periods have been reported to be the main reason for low average yields in most of the regions of Asia and Africa (Reddy *et al*., 2003; Camberlin and Diop, 1999). Between 500 and 1000 mm of rainfall reasonably distributed during the growing season allows good production. Kochhar (1986) indicated that enough rainfall of 500 to 1000 mm per year ensures high respiratory exchange during pod formation and vegetative period of growth.

Challinor *et al.* (2003), analyzing 25 years of historical groundnut yield of India in relation to rainfall, concluded that rainfall accounts for about 50 percent of variance in yield. Analysis of the relationship between simulated groundnut yield and climate in Ghana showed that yield was influenced by rainfall from flowering to maturity (Christensen *et al*., 2004). Factors such as drought, mild water stress and nutrient deficiencies are known to adversely affect groundnut growth rate and dry matter accumulated at the close of the season (Ali and Malik, 1992; Abdullah *et al.*, 2007).

Moisture stress and adverse temperature have been observed to significantly reduce number of pods per plant (Sivakumar *et al*., 1993). Although groundnut is generally tolerant to drought, its sensitivity varies at different growth stages.

The seed needs large amounts of water, close to the soil water retention capacity, in order to germinate. In contrast, as soon as germination begins, the embryo has a high requirement for oxygen. During the period up to flowering (0-30 days) the crop has good resistance to drought, but this is followed by a period of maximum sensitivity, during which there is considerable physiologically active flowering and pod formation. Relatively dry conditions are again favourable in the period to maturity. Rain at this stage can have a highly negative effect on yields especially in non-dormant types, which tend to germinate in wet soils or even while drying after harvest (Boote and Ketring, 1990; ICRISAT, 1992).

Studies in controlled environment showed that phenology of groundnut is not affected by day length (Bell and Wright, 1998). However, Lanier *et al*. (2014) indicated that pod yield is significantly influenced by day length. Further works have established that long days promote vegetative growth at the expense of reproductive growth, increase dry matter accumulation, decrease partitioning of photosynthate to pods and decrease duration of effective pod filling phase (Ketring, 1979); (Nigam *et al*., 1994 and 1998). Bagnal and King (1991) observed that flower, peg and pod numbers were consistently enhanced by short day treatment for several groundnut varieties. Flower and peg number at 60 – 70 days from emergence were approximately doubled by 12 hours/day exposure to light compared with plants receiving 16 hours light per day.

Groundnut is adapted to well-drained, loose, friable medium textured soils. Heavy textures cause problems in lifting the crop at harvest (Nautiyal, 2002). According to Schilling and Gibbon (2002), the soil for groundnut cultivation should be soft enough to allow pegging and the lifting of matured pods. They added that groundnut needs well-drained and aerated soils, owing to high respiratory exchange during pod formation and that sandy or fine textured friable soil with good infiltration are most suitable. Groundnut usually grows well in light sandy to sandy-loam, well-drained aerated soils. Heavy soils or soils with the tendency to form crust are unsuitable because they hamper penetration of pegs and impact negatively on harvesting (De Waele and Swanevelder, 2001). Groundnut is highly sensitive to salinity. However, it tolerates a wide range of pH and prefers neutral to slightly acidic soil (Schilling and Gibbon, 2002). Chong *et al.* (1987) found that while maximum root growth of groundnuts occurred at pH 7.3, shoot growth, nodulation and N_2 fixation were best at pH 5.9 – 6.3.

2.4 Economic importance

Groundnut seed contain 44-56% oil and 22-30% protein on a dry seed basis and is a rich source of minerals (phosphorus, calcium, magnesium and potassium) and vitamins (Savage and Keenan, 1994). Studies show that peanut butter, and peanut oil significantly reduce the risk of heart disease when consumed daily. More than 300 different varieties of peanuts are grown worldwide, they are usually consumed after roasting or boiling, and also processed into different forms such as peanut butter, candy, chocolates, cakes, and others. Peanut butter and jelly sandwiches are popular in the American culture (Settaluri *et al*., 2012), with raw, roasted, shelled or unshelled forms of peanuts being available in United States throughout the year. The nutritional importance of peanuts is

due to the energy and growth supplementing constituents present in them. These include carbohydrates, lipids, proteins, vitamins, minerals, some organic acids and purine.

The uses of groundnut are diverse; all parts of the plant can be used. About two thirds of world production is crushed for oil, which makes it an important oil seed crop (Dwivedi *et al*., 1993). The oil is used primarily for cooking, manufacture of margarine, shortening and soaps. Seeds are consumed directly either raw or roasted, chopped in confectioneries, or ground into peanut butter. Young pods may be consumed as a vegetable, while young leaves and tips are utilized as a cooked green vegetable (Dwivedi *et al.,* 1996; Yav *et al*., 2008; Ingale and Shrivastava, 2011)

Scorched seeds may serve as a coffee substitute (Duke, 1981). Non-food products such as soaps, medicines, cosmetics, pharmaceuticals, emulsions for insect control, lubricants and fuel for diesel engines can be made from groundnut. The oil cake, a high protein livestock feed, may be used for human consumption. Groundnut shells may be used for fuel (fireplace "logs"), as a soil conditioner, for sweeping compounds, as a filler in cattle feed, as a raw source of organic chemicals, as an extender of resin, as a cork substitute, and in the building trade as blocks or hardboard (Gibbons, 1980). In folk medicine, groundnut is used for aphrodisiac purposes, inflammation, cholecystosis, and nephritis and decoagulant. In China, the oil is taken with milk for treating gonorrhea, and used externally for rheumatism, while in Zimbabwe the groundnut is used in folk remedies for plantar warts (Duke and Wain, 1981).

According to Kochhar (1986), green haulm of groundnut makes excellent high protein hay for horses and ruminant livestock. Lower grade oil from the feed is also used in the manufacture of soap, lubricant and illuminants. Groundnut is used as food boiled and salted to improve flavour and taste, used as butter, eaten alone and in sandwiches or mixed into candies, cookies, pies and other bakery products (World Book of Encyclopedia, 1990). In Africa, they are eaten fresh, boiled or grilled and also in the preparation of soup (De Waele and Swanevelder, 2001). The paste obtained after the oil has been extracted is also moulded into different shapes and fried as groundnuts cake. It is used to make a synthetic textile fibre, 'ardil' from groundnut protein as the fibres have wool-like texture (Kochhar, 1986). Oils of groundnuts are used as ingredient in face powders, shaving creams, shampoos and paints. They are also used in making nitroglycerin (an explosive). The residue after oil extraction is a high-protein livestock feed. Groundnuts can also be used as flour, peanut protein, and peanut milk for human consumption. Medicinally, the oil of groundnut is used as a laxative and emollient (Abbiw, 1990)

2.5 Cultivars grown in Ghana

Several improved groundnut varieties have been developed by the Savannah Agricultural Research Institute (Nyankpala Ghana). An example of such cultivars is Kpanielli which matures in 120 days and has a potential yield of 2.4 tons/ha. It is resistant to cercospora leaf spot disease and has high oil content (51%). Mani Pinta is also a cultivar of groundnut and has high oil content (about 53%) and is high yielding. It resists common diseases, particularly leaf spot. It is late-maturing (120-130 days) and

has a kennel yield potential of approximately 2.2 tons/ha. Edorpo-Munikpa has higher oil content than earlier varieties such as Mani Pintar. It is high yielding (Rahman *et al*., 2019) with (kernel yield of 1.2 tons/ha), early-maturing (100 days), and moderately resistant to early and late leaf spot. Jusie Balin is another cultivar of groundnut that has a high level of resistance to leaf spot disease; is early-maturing (approximately 104 days), and the kernel yield potential is approximately 2.0 tons/ha.

The most commonly adopted (about 50%) variety in Northern Ghana is the Chinese groundnut. It has been known by most local farmers as "Simbaligu" meaning small kernel (Ibrahim *et al*., 2012). This variety among others were tested for three years at different locations to have yield potentials of 0.969, 0.547, 1.077, and 0.885 tons/ha respectively at Damango, Manga, Nyankpala and Wa with mean maturity period ranging between 85 and 95 days. The Council for Scientific and Industrial Research (CSIR)-Crops Research Institute (CRI) in Kumasi and the Savanna Agricultural Research Institute (SARI) in Nyankpala, have conducted a number of researches on groundnut improvement over the past decades and have subsequently released some improved groundnut varieties in the country.

Mani-Pintar, Shitaochi (Chinese), F-mix and Sinkarzei were released in 1960, 1970, 1985, and 1988, respectively (Atuahene-Amankwa *et al*., 1990; Ibrahim *et al*., 2012). Following the devastating effects of the rosette virus in 1993, forty groundnut accessions were received from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and evaluated at the CSIR-Crops Research Institute for resistance to the rosette virus. The study eventually led to the release of four improved

varieties of groundnut in 2006 which were both high yielding and rosette virus resistant. The released varieties included Adepa, Nkosour, Jenkaah, and Azivivi. In addition, two Confectionery varieties (Oboshie and Obolo) were released in 2012 by CSIR-Crops Research Institute (CRI).

With an ever-increasing consumer preference for high quality edible oils in Ghana and the desire to increase groundnut export on the world market, a study was carried out to investigate the nutritional quality of twenty groundnut varieties grown in Ghana (Asibuo *et al*., 2008*a*). Other studies carried out over the past years by the Crop Research Institute (CRI) include the study of the inheritance of fresh seed dormancy in groundnut (Asibuo *et al*., 2008*b*), chemical composition of groundnut (Asibuo *et al*., 2008*c*), among others.

2.6 Induced mutation

Mutation induction has become a proven way of creating variation within a crop variety especially for pulse crops which generally lack genetic variation (Micke, 1988; Novak and Brunner, 1992). Mutation is hence considered as a valuable tool in crop improvement, a source to increase genetic variability resources from which useful variants could be obtained either directly or after recombination (Shanthala, *et al*., 2013). Gamma irradiation and X-rays are the most commonly used physical mutagenes. The use of gamma radiation to induce mutation has for long been applied in plant breeding to increase genetic variations (Brunner, 1995). Different doses of gamma irradiation have successfully been used to induce mutation in several crop species including black grain, cowpea mungbean (Ashraf *et al*., 1975; Thirugnanakumar, 1986; Ignacimuthu and Babu 1990).

Ahmed (1991) studied the effect of gamma irradiation on seeds of blackgram which led to the release of a mutant variety of blackgram. Sigh *et al* (1997) stated that mutation breeding is useful to select the mutant lines with desirable characters. In any mutation breeding programme, selection of an effective and efficient mutagen is very essential to produce high frequency of desirable mutations (Singh and Singh, 2001). The role of mutation breeding is to increase the genetic variability for desired traits in various crop plants and has been proved beyond doubt by a number of scientists.

Hermelin *et al.* (1987) and also Ahmed and Goud (1979) reported a reduction in germination in the M_1 generation of sunflower and attributed the observations to the effects of irradiation. Similar observations were made by Chowdry and Singh (1980) in pigeon pea; Sree Rengasamy (1988) in sesamum and also Morie *et al* (1981) and Jayaraj (2004) in soybean. Packiaraj (1988) and Raveendran (1998) observed a similar reduction in parents and hybrid of cowpea. Inhibition of seed germination and elongation of roots and shoots from germinating seeds have been reported as methods for the detection of irradiated seeds of crop species by Vadivelu and Rathinam (1980). Ashraf *et al.* (1975) reported a reduction in plant height in the M_1 generation.

Mishra and Kumar (1999) recorded reduced plant height in all mutagenic treatments in green gram. Mohanty *et al* (1998) on the contrary observed that plant height was increased in M_1 generation with gamma rays. Jayaraj (2004) also reported an increased plant height in soybean due to gamma rays. Similarly, Ignacimuthu and Babu (1988)

recorded increased plant height when seeds were treated with 20kR gamma rays in blackgram. Thirugnanakumar (1986) observed that the reduction in seedling height was dose dependent with gamma rays. Quantitative characters of *Vigna unguiculata* such as number of branches, clusters, pods and yield were also stimulated by treatment with the gamma rays. Ahmed (1991) also found that a differential inhibitory effect of radiation was observed in shoot length, root length, and number of rootlets and size of cotyledonous leaf. Toker *et al*. (2005) attributed those reductions to the fact that the irradiation of seeds with high doses of gamma rays disturbs the synthesis of protein, hormonal balance, leaf gas exchange, and water exchange and enzyme activity. Rajendiran (1993) observed several morphological variations induced by gamma irradiation in sunflower. The gamma rays at higher dose had gross retarding effect on the overall growth and yield, whereas the lower dose had beneficial effect on plant growth.

Verma and Singh (1984) reported a high number of pods per cluser in greengram treated with gamma rays. Khan (1987; 1988) also reported a greater number of pods per plant in mungbean treated with gamma rays. Packiaraj (1988) observed that the number of clusters, number of pods per plant, and pod length declined in cowpea with an increased dosage of gamma rays. Gunasekaran *et al.* (1998) noticed an increase in number of clusters per plant in cowpea with 20kR gamma ray's treatment. Ignacimuthu and Babu (1990) reported a high number of clusters per plant in blackgram due to gamma rays. Ahmed (1991) recorded a decrease in number of pods per plant following an increase dose of irradiation. It has been documented that gamma radiation can be useful for the

alteration of physiological characters (Kiong *et al*., 2008). The biological effect of gamma rays is based on the interaction with atoms or molecules in the cell. These radicals can damage or modify the important components of plant cells and have been reported to affect differentially the morphology, anatomy, biochemistry and physiology of plants depending on the radiation dose (Ashraf *et al*., 2003).

From the year 1930 to 2014 more than 3200 mutagenic plant varieties have been released either as direct mutants or from their progeny (FAO, 2014). Some of the notable mutagen varieties include Colorado irradiado groundnut, Puita INTA-CL rice, Amaroo rice, Binamoog-5 mung bean, Maybel tomato, Henong series soybean, Balder J barley, and Tek bankye cassava (Kharkwal *et al*., 2008). Mutation breeding in crop plants offers an improvement in crops with low genetic base. It is an essential supplementary strategy in improving crops (Mudibu *et al.,* 2010). Gamma irradiation and x rays are the most commonly used physical mutagens. Rajendiran (1993) observed several morphological variations induced by gamma irradiation in sunflower. The gamma rays at higher dose had gross retarding effect on the overall growth and yield, whereas the lower dose had beneficial effects on plant growth. Mutation has far long been applied in plant breeding to increase genetic variations (Brunner, 1995). Sarka *et al,* (1996) reported that the plant height of seeds subjected to 15KR gamma rays was reduced in the M_1 generation.

Mishra and Kumar (1999) also recorded reduced plant height in all mutagenic treatments in green gram. Mutation induction has become a proven way of creating variation with a crop variety especially for pulse crops which generally lack genetic

variation due to their highly autogenous nature (Micke, 1988; Novak and Brunner, 1992).

2.7 Genotype by Environment Interaction (GEI)

Genotype by environment (G x E) interaction refers to the changes in the relative performance of genotypes across different environments; or simply the differential ranking of genotypes among locations or years (Yau, 1995). Genotype describes the complete set of genes that is inherited by an individual and is important for the expression of specific traits (Suzuki *et al*., 1981). The observable uniqueness ensuing from the interaction between the genetic make-up and the environment are known as the phenotype. Phenotypes can therefore be observed, assessed, estimated, and arranged in groups according to features that they have in common. Environmental features such as locations, growing seasons, years, rainfall pattern, temperatures, soil pH, and biotic stresses such as diseases, insect pests and weeds could have positive or negative effects on genotypes (Falconer and Mackay, 1996). Genotype x environment interaction (GEI) makes it difficult to select the best performing and most stable genotypes.

G x E interactions are therefore of leading importance in expansion of improved genotypes by plant breeders since they cause technical hitches in selecting genotypes evaluated in diverse environments (Kang and Gorman, 1989). Very often breeders encounter situations where the relative rankings of varieties change from location to location and or from year to year. When varieties are grown at several locations for testing, their performance or their relative rankings usually do not remain the same. This causes difficulty in demonstrating significant superiority of any variety (Smith *et al.*,

2005). The stability of genotype for yield and agronomic performance is an urgent breeding objective. Therefore, an understanding of the environmental stability of genotypes helps in determination of their stability for the fluctuations in growing conditions that are likely to be encountered. Plant breeders evaluate germplasm in multi-environment to study the performance and adaptation for specific or general environment (Yan and Hunt, 1998). It is therefore important to identify or develop cultivars for specific purposes through the understanding of the interaction of genotypes with predictable environmental factors. In addition, an understanding of environmental and genotypic causes of G x E is important at all stages of plant breeding, including parent selection based on specific traits, and selection based on yield. Knowledge of G x E can also be used to establish breeding objectives and to formulate recommendations for areas of optimal cultivar adaptation (Kang, 1996; Jackson et al., 1998).

Every factor that is part of the environment of a plant has the potential to cause differential performance that is associated with genotype x environment interaction (Peipho and Mohring, 2005). Environmental variables can be classified as either predictable or unpredictable factors. Predictable factors are those that occur in a systematic manner or are under human control, such as soil type, planting date, row spacing, plant population and rates of nutrient application. Unpredictable factors, on the other hand, are those that fluctuate inconsistently, including rainfall, temperature and relative humidity (Kang *et al*., 2004).

Predictable factors can be evaluated individually and collectively for their interactions with genotypes. For example, genotype x soil type; genotype x row spacing; genotype x planting date; and genotype x plant population interactions can be evaluated individually and collectively (Crossa, 2012). Unpredictable factors contribute to the interactions of genotypes with locations and years. Some interactions of unpredictable factors include genotype x location (G x L), genotype x year (G x Y), and genotype x location x year (G x L x Y) interactions (Ramagosa et al., 1993). The relative performance of genotypes across environments determines the importance of an interaction. The most important G x E interaction which is of interest to a plant breeder is one caused by changes in rank among genotypes. Genotype by environment interaction (GEI) can also be classified according to the behaviour of the genotypes that is either stable or adapted to a particular environment in terms of their yield or in some other interesting agronomic features. Generally, the term stability refers to the ability of the genotypes to be consistent, both with high or low yield levels in various environments (Vargas et al., 1999). Adaptability, on the other hand, refers to the adjustment of an organism to its environment, example, a genotype that produces high yields in specific environmental conditions and poor yields in another environment (Balzarini et al., 2005). The response of genotypes to variable productivity levels among environments provides an understanding of their stability of performance.

Genotype by environment interaction (GEI) is a phenomenon that is of significance to plant breeders, agronomists and farmers. Breeding materials can be selected and assessed on the basis of their different responses to the environments. Deitos *et al*. (2006) indicated that genotype by environment interaction is important for plant

breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability. On the other hand, different genotypes may have different performance in each region that can be exploited to maximize productivity (Souza *et al*., 2008). Grain yield is one of the most important traits to consider when the performance of cultivars is compared across environments (Vargas *et al*., 1999). However, selection based on yield only may not always be adequate when genotype by environment interaction is significant (Kang *et al*., 1991). Linnemann *et al.* (1995) reported that it is important to understand crop development in relation to biophysical conditions and changes in season when selecting well-adapted genotypes and correct planting date. Varieties that show low genotype by environment interaction but have high and stable yields are desirable for plant breeders and farmers because it indicates that the environment has less effect on them and their higher yields are largely due to their genetic composition. Knauft and Wynne (1995) reported significant genotype by environment interactions on yield and other agronomic traits in groundnut cultivars.

2.7.1 Stability and adaptability

The term stability refers to the ability of a cultivar to perform consistently across a broad range of locations (Zivanovic *et al.*, 2004; Kandus *et al*., 2010). Stability measurements give an indication of the ability of a genotype to maintain a relatively constant yield independent of changing environmental conditions (Odewale *et al*., 2012). According to Becker and Leon (1988), stable genotypes will not change in performance in spite of differences in the prevailing environmental conditions. It allows researchers to identify broadly adapted cultivars for use in breeding programs and have assisted in advancing

suggestions to farmers (Yayeh and Bosland, 2000). A genotype is considered stable if its environment variance is small. Stability analysis provides a general solution for the response of the genotypes to environmental change.

Issa (2009) described two basic concepts of phenotypic stability namely, the biological concept and dynamic concept. He related the biological concept of stability to the constant performance of a genotype over a wide range of environments and the dynamic stability, also known as agronomical concept of stability, implies that a stable genotype should always give high yield at the level of productivity of the respective environments. In biological stability, the performance of a genotype will not change regardless of changes in environmental conditions, thus implying that differences among environments is zero and that stable genotype should show minimal variance in different environments (Becker and Leon, 1988; Dabholkar, 1999).

Adaptability of a given cultivar or genotype is defined as the inherent genetic ability of a cultivar to be stable or high yielding in various environments (Zivanovic *et al*., 2004). Almost all living organisms are capable of adjusting to the normal functions of their environment, which enable them to cope with conditions within their surroundings. Moreover, adaptability refers to the manner in which an organism adjusts to its environment. For example, certain g enotypes may produce high yields under certain environmental conditions but poor or low yields in other conditions.

Genotype main effect and genotype by environment interaction (GGE) bi-plot is a data visualization instrument that uses diagrams or graphs to illustrate G x E interaction in a two-way chart (Yan *et al*., 2000). It is a valuable instrument used for the evaluation of mega-environment for instance “which won- where” pattern, through which particular

genotypes can be proposed for particular mega-environments (Yan and Kang, 2003). The GGE bi-plot can also be used for the evaluation of genotype mean performance and stability as well as for the evaluation of environment to differentiate between genotypes in target environments. The GGE bi-plot analysis is more frequently used in G x E interaction studies in plant breeding research (Yan, 2001; Yan and Kang, 2003).

2.7.2 Additive main effects and multiplicative interaction (AMMI) model

The additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992) is one of the most widely used statistical methods. It can be used to understand and structure interactions between genotypes and environments. In its essence, the AMMI model applies the singular value decomposition (SVD) to the residuals of an additive two-way analysis of variance (ANOVA) model as applied to the GEI table of means (Gauch, 2013; Rodrigues *et al.*, 2014). The two main purposes of AMMI analysis of a yield trial's treatment design are, understanding complex GEI, which includes delineating mega-environments and selecting genotypes to exploit narrow adaptations and increasing accuracy to improve recommendations, repeatability, selections, and genetic gains.

The main purposes of an experimental design are assigning experimental units to treatments, quantifying errors, and gaining accuracy (Gauch, 2013). In breeding, the researcher is interested in choosing the genotypes with superior performance in different environments. Poor efficiency in the genotype-by-environment interaction analysis of variance can represent a problem for breeders, who can take advantage of the interaction effect to choose genotypes with high productivity. The choice of an appropriate statistical method depends on the experimental data, the number of available

environments, and the accuracy of the information. Applications of the AMMI model to yield trials have appeared frequently during the last two decades, and there have been several recent review articles (Dias and Krzanowski, 2006; Gauch, 2006; Yan *et al.*, 2007; Gauch *et al.*, 2008; Yan *et al.*, 2009; Gauch, 2013; Rodrigues *et al.*, 2014). This analysis can help in the identification of genotypes which have high productivity and are well adapted to an agronomic zone, and having the aim of regionalised recommendation and selection of test sites (Gauch and Zobel, 1996; Gauch *et al.*, 2011; Gauch, 2013). By using the AMMI model, it assesses the adaptability and stability of productivity of genotypes in different environments.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Experimental site

The research was conducted at three locations namely Nyankpala, Bawku and Techiman in two different season i.e 2017 and 2018. The First location was sited in Nyankpala in 2017 and 2018 cropping seasons at the experimental field of the Faculty of Agriculture, University for Development Studies (UDS), Nyankpala located in the Northern Region of Ghana. This experimental site is located between longitude 0°58` W and latitude 9°5`N with an altitude of 183m above sea level. The area lies within the Guinea savanna agroecological zone and therefore experiences a unimodal rainfall pattern ranging from 1000 mm to 1200 mm (MoFA, 2013). Rainfall starts from late April and reaches a peak in July - September with a sharp decline and absolutely no rain in November (Lawson *et al*., 2013). There is a dominant grassland vegetation with few interspersed woody perennials such as Neem tree (*Azadiracta indica*), shea tree (*Vitlleria paradoxa*), Mahogany (*Khaya sesnegalensis*), dawadawa tree (*Parkia biglobosa*) and teak (*Tectonia grandis*). Common weeds in the area include broom weed (*Sida acuta*), spear grass (*Imperata cylindrica*) pig weed (*Boehevia difusa*), goat weed (*Andropogon gayanus*) (Blench, 1999; SARI 2004) described the soil in the area as Nyankpala series and is mainly sandy loam.

Second location was sited at Techiman in the Brong Ahafo Region which is located in the transitional agroecological zone of Ghana, during the cropping seasons of 2017 and 2018. The area has a bimodal rainfall with an average annual total rainfall of 1,100 mm - 1,401 mm. (43-55 inches) (MoFA, 2019). The experimental site is located between

longitude 01°55’45”W and latitude 07°34’38”N and is characterized by trees and grasses such as spear grass *(Imperata cylindrica*), shea tree (*Vetileria paradoxa*) and brown mahogany (*Khaya senegalensis*). The soil type is described as Akumadan-Bekwae/Oda Complex Association (MoFA, 2019)

Third location was also sited in 2017 and 2018 rainy season in Bawku, located in the Sudan savannah agroecological zone of Ghana. The area receives a unimodal rainfall and the average rainfall per annum is 500 mm-700 mm and with a temperature range of 18-30°C (Whitty et al., 2008). The area is characterized by an alternate and distinct hot, rainy season (from May to September) and cool, dry season (October to April). Prevailing winds of the zone are the trade winds. The experimental site is also located between longitude 0°14’W and latitude 11°3’N.

The experimental site is characterized by shrubs and also trees such as baobab (*Adansonia digitata*), mahogany (*Khaya senegalensis)* and grasses such as the spear grass (*Imperata cylindrical)* and Bermuda (*Cynodon dactylon*). Soils are coarse texture, weak with low organic matter content. Soil in the area ranges from sandy loam, clay loam to slit loam.

3.2 Experimental design and cultural practices

The study used five genotypes of groundnut (four mutant genotypes and one control serving as standard check) in each location. The study used three factor (genotypes, locations, and seasons) replicated three times in randomized complete block design. Genotypes used were 0 Gy, (control) standard check, 150 Gy, 200 Gy, 250 Gy and 300

Gy. Three locations were Nyankpala (Guinea Savnnah agroecology), Bawku (Sudan savannah agroecology) and Techiamen (Forest-transitional zone). The experiment were conducted in the 2017 and 2018 cropping seasons. The mutant genotypes were obtained from plants selected after induced mutation studies of parental groundnut variety, Chinese, using gamma irradiation in 2013 by the Department of Agronomy, University for Development Studies. Selections over the years had resulted in these promising mutant genotypes with improved agronomic traits. A plot size of 4 m x 6 m (24 m^2) was used with spacing of 0.8 m between plots and 1m between blocks. A planting distance of 50 cm x 20 cm was used. Weed control was carried out on the 3rd week after planting by hoeing and on the 6th week by hand picking. No insect pest control measures was carried out.

3.3 Data Collection

Data were collected on parameters such as plant height, number of leaves, number of branches, days to 50% flowering, number of days to maturity, number of pods per plant, number of seeds per pod, 100 seed weight, pod length, total grain yield.

3.3.1 Plant height

The heights of ten tagged plants in each plot were measured every two weeks by the use of a meter rule. The average plant height for each plot was established by dividing the sum of the ten plant heights by ten. This average height of the sample unit was used as a representative value of the treatment. In order to avoid border effect, the ten plants were selected at the middle of each plot.

3.3.2 Number of leaves

The leaves for the tagged plants in each experimental unit were counted and recorded and used to represent each treatment. This was done at two weeks intervals.

3.3.3 Number of branches

The total number of branches for each tagged plant in every plot were counted and recorded every two weeks.

3.3.4 Number of days to 50% flowering

Days to flowering was collected on the number of days taken for half of the total plant population in each plot to flower. This was done by counting the number of days from sowing to the day on which 50% of population from each experimental unit flowered.

3.3.5 Number of days to maturity

This was measured as the number of days it took for plants of each experimental unit to mature and was done by counting the number of days from sowing to the day physiological maturity was observed.

3.3.6 Number of seeds per pod

Twenty pods were randomly selected from each plot after harvest and seeds in each of the sampled pods were counted and average was taken for each plot and used to represent each particular treatment.

3.3.7 Pod length

After the plants were harvested, twenty pods were randomly selected from each plot and their lengths measured using a meter rule. The average pod length for each genotype

was obtained by adding each of the measured pod lengths in their respective lines and dividing by twenty.

3.3.8 Hundred seeds weight

Hundred seeds were collected from each plot and weighed in grams by the use of an electronic balance.

3.3.9 Total grain yield

The weights of seeds obtained from each experimental unit were recorded in grams and expressed in tons per hectare. This was done after the seeds were dried to 12% moisture content.

3.4 Data analysis

Data collected in 2017 and 2018 seasons were subjected to combine analysis. The combined data was subjected to analyses of variance (ANOVA) using GENSTAT statistical package 4th edition. Means were separated using Least Significance Difference (LSD) at 5% and results were presented in tables and graphs. The stability data was analyzed using the R statistical software (version 3.5.3) (R Core Team, 2019). Additive main effect and multiplicative interaction (AMMI) model was fitted to the data using the agricolae package. Significance of the model components including the multiplicative terms (IPCAs) were determined using F-test.

Depending on the number of IPCAs that were significant, AMMI1 or AMMI2 was fitted for each trait in each year. Stability of the genotypes for each trait was determined using AMMI stability value (ASV) and yield stability index (YSI), respectively. Biplots were generated using means across locations and IPCA1 and, IPCA1 and IPCA2 for AMMI1

and AMMI2, respectively. Where genotype-by-environment interaction was not significant, a general linear model without interactive terms was fitted using R base functions. Significance of main effects were determined using Tukey's HSD test at 5% probability.

CHAPTER FOUR

RESULTS

4.1. Plant height

All the genotypes recorded increases in plant height at 4WAP and 10WAP. The highest mean plant height recorded at 4WAP was 300 Gy and 150 Gy with mean values of 15.8 cm and 15.64 cm respectively. Genotype 200 Gy recorded the least plant height at 4 WAP with mean value of 13.82 cm. At 10WAP, values were significant (P<0.05) planting from 0 Gy and 150 Gy recorded the highest height with average values of 36.27 cm and 35.57 cm, respectively while 250 Gy recorded the least height of 31.32 cm (Figure 1).

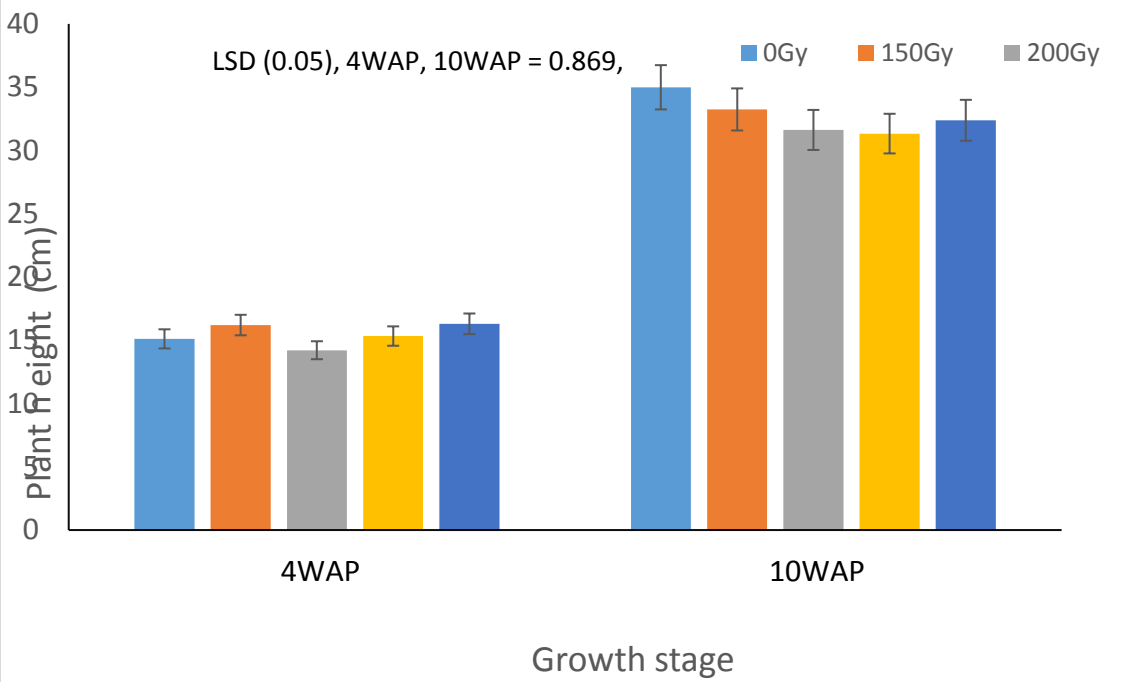

Figure 1: Effect of mutagenesis on plant height at 4WAP and 10WAP of groundnuts genotypes evaluated in 2017and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Significant differences (P<0.05) in plant height occurred at the various locations. The genotypes at Nyankpala recorded the highest plant height at 4WAP. Similar trend was observed in genotypes at 10WAP. However, Techiman recorded the least plant height at 4WAP and 10WAP (Figure 2).

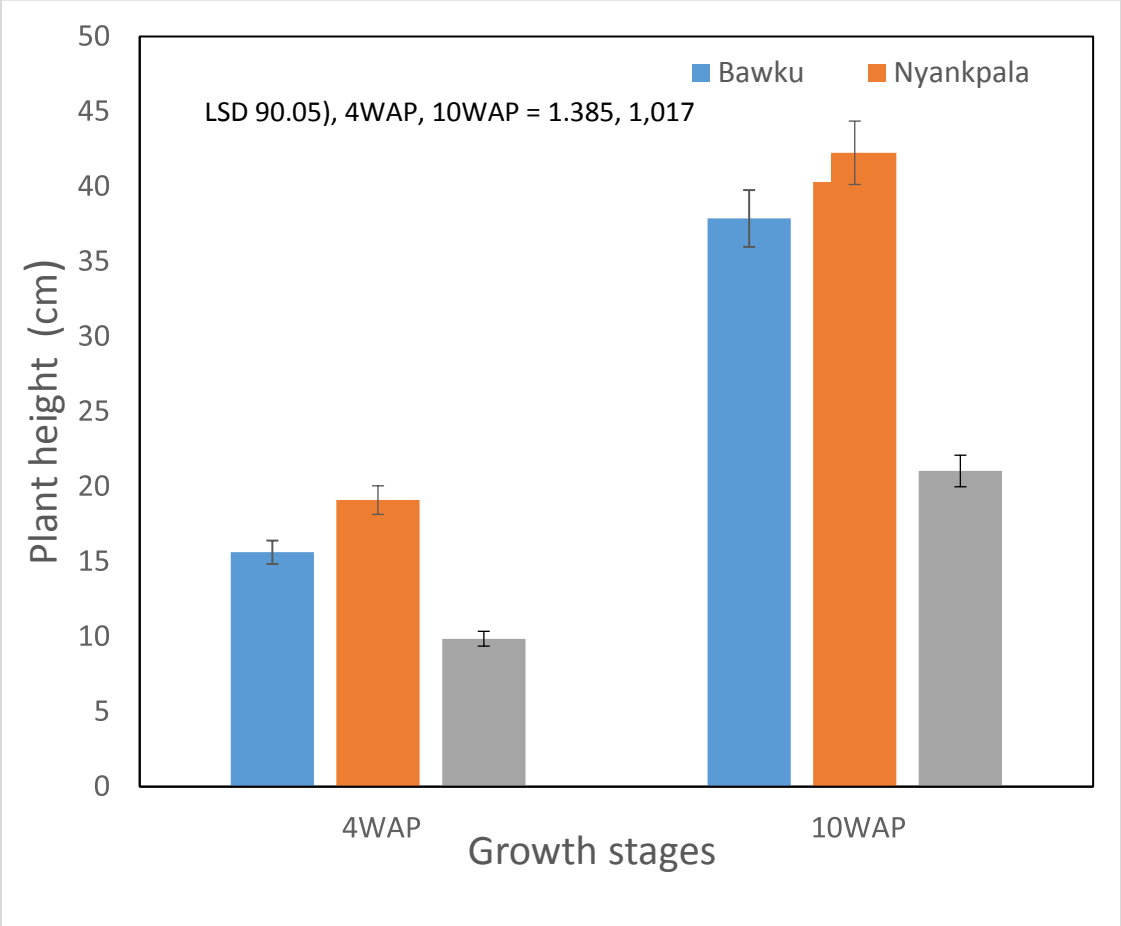

Figure 2: Effect of mutagenesis on plant height at 4WAP and 10WAP of groundnuts genotypes at various locations evaluated in 2017and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

4.2 Number of leaves

The 150 Gy plants recorded the highest number of leaves of average value of 60 leaves and 250 Gy plants also recorded the least with a mean value of 54.11 leaves at week 4. Similar trends in results was observed at 10WAP where 150 Gy plants recorded the highest number of leaves and the 250 Gy recorded the least number of leaves (Figure 3).

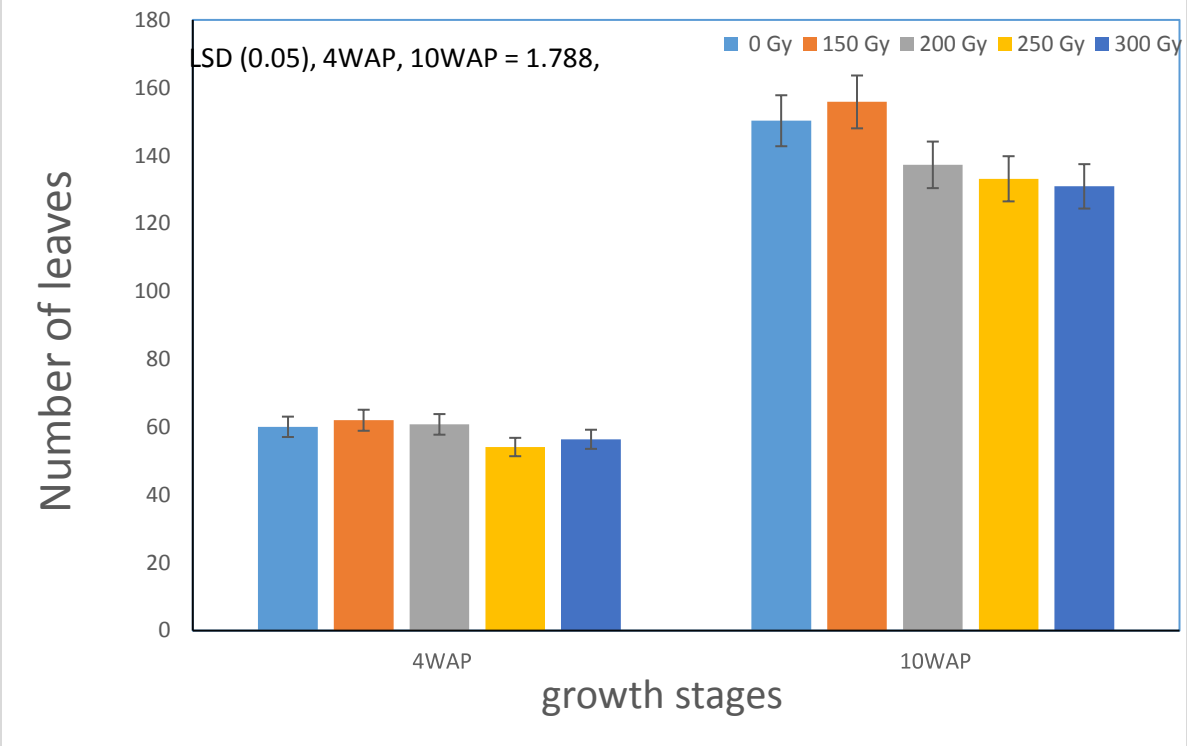

Figure 3: Effect of mutagenesis on number of leaves at 4WAP and 10WAP of groundnuts genotypes evaluated in 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

Significant differences ($p < 0.05$) were observed in the main effect of locations (figure 4) in leaf numbers formed. At week 10, Techiman recorded the highest number of leaves of 211.67 followed by Bawku. But at week 4, genotypes at Bawku and Techiman recorded the highest number of leaves of 63.23. Genotypes at Nyankpala had 50.13 leaves being the least (Figure 4).

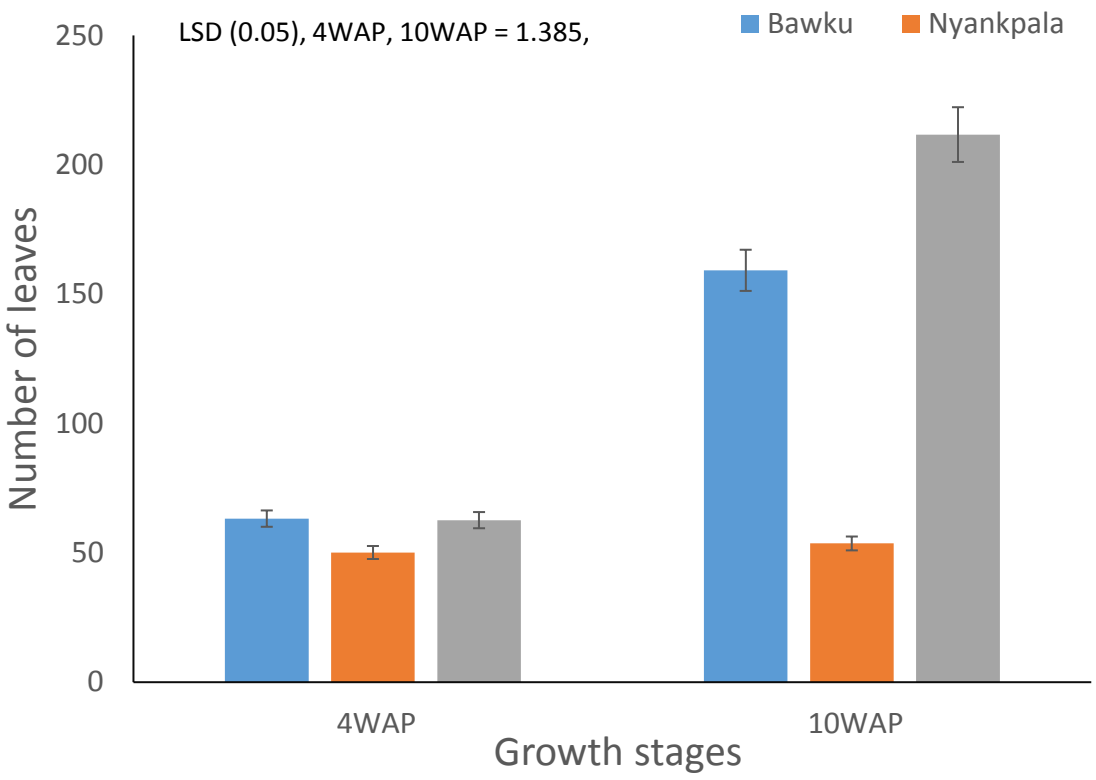

Figure 4: Effect of mutagenesis on number of leaves at 4WAP and 10WAP of groundnuts genotypes evaluated at three locations in 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

4.3 Number of Branches

The data presented in Figure 5 showed significant differences ($P < 0.05$) in number of branches among genotypes. The highest number of branches of average value was 8.83 which was genotype 200 Gy followed by genotype 150 Gy with an average value of 8.56. The lowest was recorded in both genotypes 250 Gy and 300 Gy with a value of 7.67.

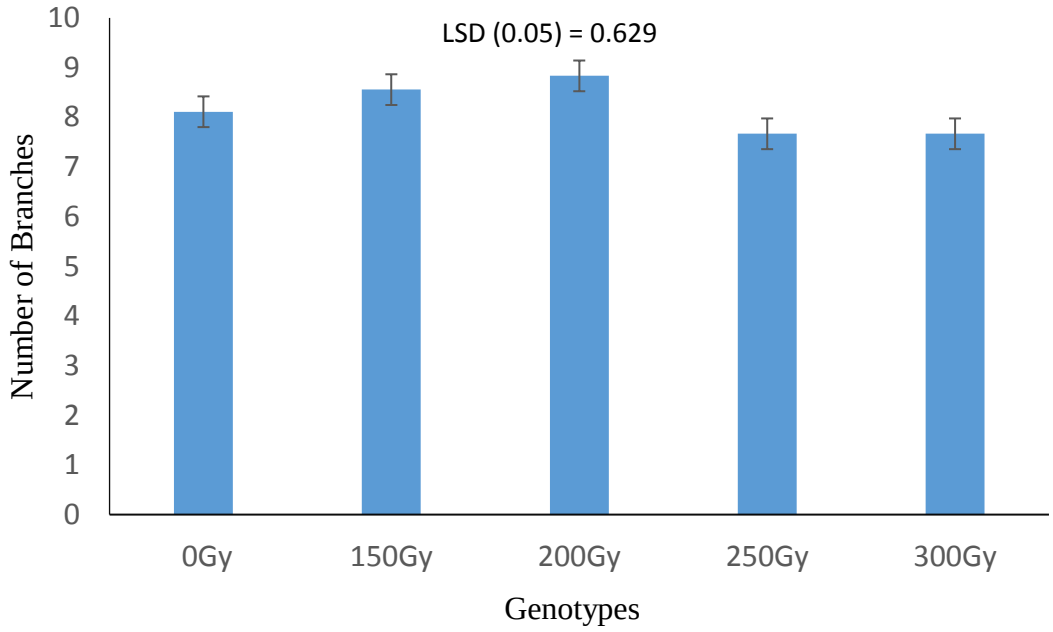

Figure 5: Effect of mutagenesis on number of branches of groundnuts genotypes evaluated. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Variations among locations was also significant (P<0.05) for branching. The genotypes at Bawku recorded the highest number of branches with an average value of 9.21 followed by genotypes at Techiman recording a mean of 9.10 while plants at Nyankpala recorded the lowest with a mean value of 6.17 (Figure 6).

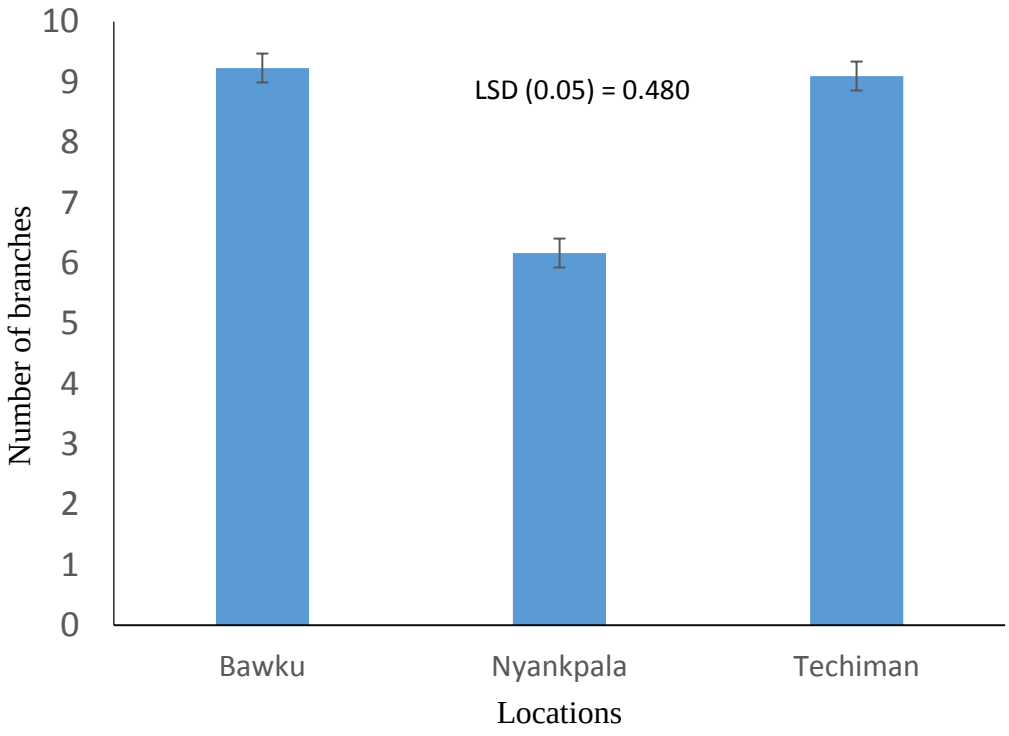

Figure 6: Effect of mutagenesis on number of branches of groundnuts genotypes evaluated at three locations in the 2017 and 2018 cropping season. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was season difference. The genotypes in 2018 cropping season recorded higher number of branches with an average value of 10.87 while plants from the 2017 cropping season recorded the lower number of branches with a mean of 5.47 (Figure 7) .

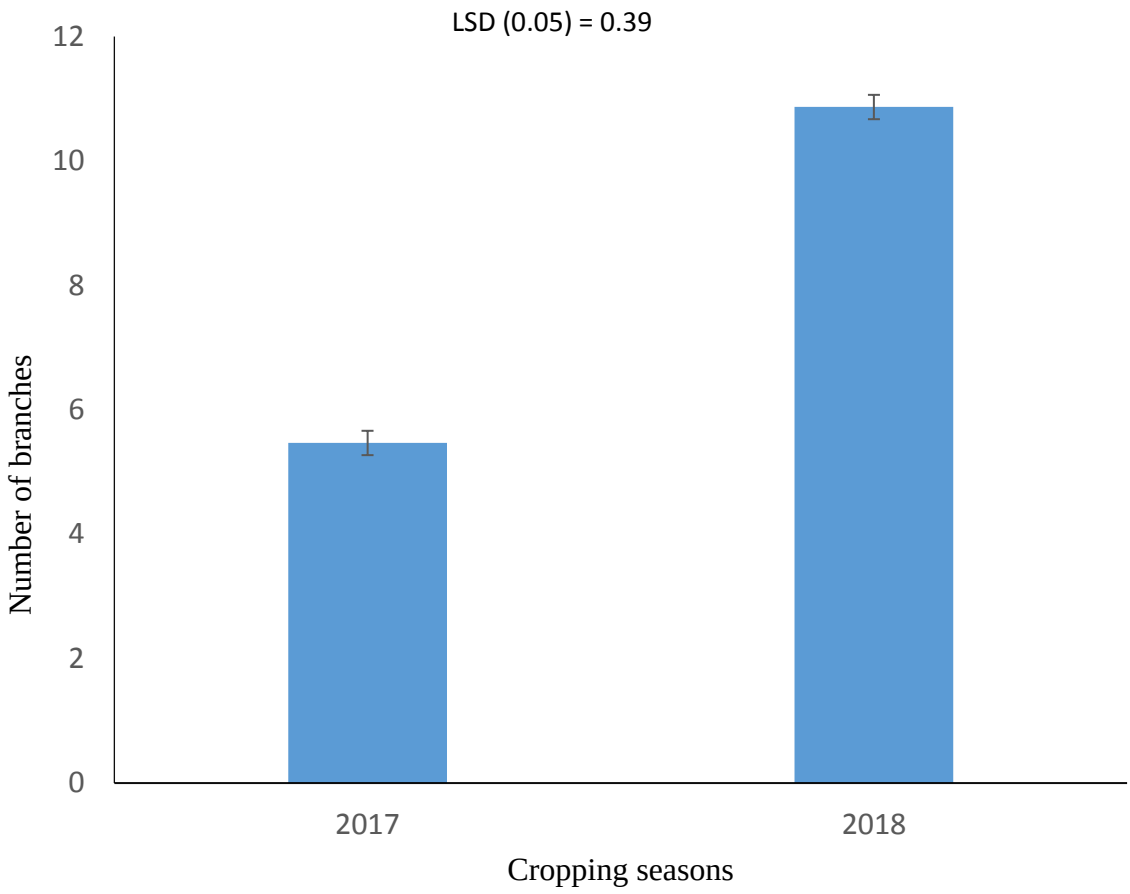

Figure 7: Effect of mutagenesis on number of branches of groundnuts genotypes evaluated in 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

Genotype × location interaction also varied significantly (P<0.05) for number of branches of the genotypes. Plants from 200 Gy at Bawku recorded the highest number of branches followed by those from 150 Gy at Techiman (9.83) whilst those from 300 Gy at Nyankpala recorded the lowest number of branches (5.33) (Table 1).

Table 1: Genotypes × locations interactions for number of branches during evaluation in the 2017 and 2018 cropping seasons

Genotype	Location		
	Bawku	Nyankpala	Techiman
0 Gy	8.833	6.000	9.500
150 Gy	9.333	6.500	9.833
200 Gy	10.000	7.333	9.167
250 Gy	8.333	5.667	9.000
300 Gy	9.667	5.333	8.000

LSD (0.05): Genotypes × locations =1.07; Genotype 0 Gy = Chinese (Standard check)

Also, there was significant differences (P<0.05) in the interaction between locations and the seasons in terms number of branches counted. The genotypes at Techiman evaluated during the 2018 cropping season recorded highest value (13.27) followed by those from Bawku in the same season (13.06). The genotypes from Techiman for 2017 season recorded the lowest for number of branches (4.93) (Table 2).

Table 2: Locations × season interactions for number of branches during evaluation in the 2017 and 2018 cropping seasons

Location	Season	
	2017	2018
Bawku	5.400	13.067
Nyankpala	6.067	6.267
Techiman	4.933	13.267

LSD (0.05); Locations × season = 0.68: Genotype 0 Gy = Chinese (Standard check)

The three-way interactions (genotypes × locations × seasons) also differed significantly ($P<0.05$) for number of branches. The 0 Gy (standard check) from Techiman during the 2018 cropping season and 200 Gy plants from Bawku recorded the highest number of branches (14.33) followed by 250 Gy from Techiman and 300 Gy plants from Bawku. The lowest number of branches was recorded by 300 Gy plants at Techiman (4.33) during evaluation in the 2017 season (Table 3).

Table 3: Three-way interactions (genotypes × location × season) for number of branches during evaluation of plants in the 2017 and 2018 cropping seasons

Genotype	Location	Season	
		2017	2018
0 Gy	Bawku	5.333	12.333
	Nyankpala	5.667	6.333
	Techiman	4.667	14.333
150 Gy	Bawku	5.333	13.333
	Nyankpala	6.000	7.000
	Techiman	6.333	13.333
200 Gy	Bawku	5.667	14.333
	Nyankpala	8.333	6.333
	Techiman	5.000	13.333
250 Gy	Bawku	5.000	11.667
	Nyankpala	5.333	6.000
	Techiman	4.333	13.667
300 Gy	Bawku	5.667	13.667
	Nyankpala	5.000	5.667
	Techiman	4.333	11.667

LSD (0.05); genotype × location × season = 1.5165; Genotype 0 Gy = Chinese (Standard check)

4.4 Days to 50% flowering

There was significant variation (P<0.05) in the days to 50% flowering of the groundnut genotypes. The 0 Gy plants took highest number of days to record 50% of flowering with average value of 27.22 days followed by the 250 Gy and the 300 Gy with mean values of 25.77 and 25.56 days respectively. The 200 Gy plants took least number of days to reach flowering at 24.61 days (Figure 8).

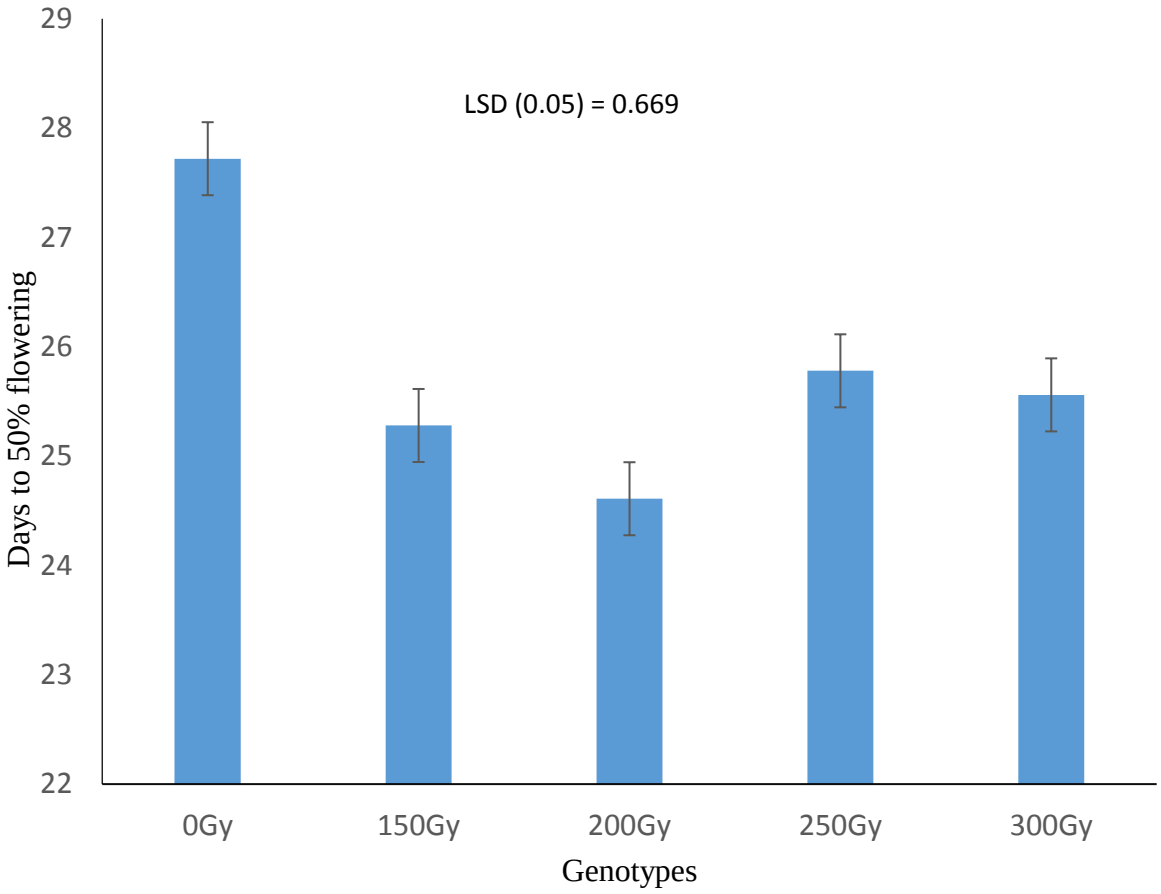

Figure 8: Effect of mutagenesis on days to 50% flowering of groundnuts genotypes evaluated in 2017and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was significant differences (P<0.05) also in the days to 50% flowering across the locations. At Techiman, the genotypes took highest number of days to record 50% flowering with an average value of 26.13 days while Bawku and Nyankpala, took less number of days with mean values of 25.7 and 25.53 days, respectively (Figure 8).

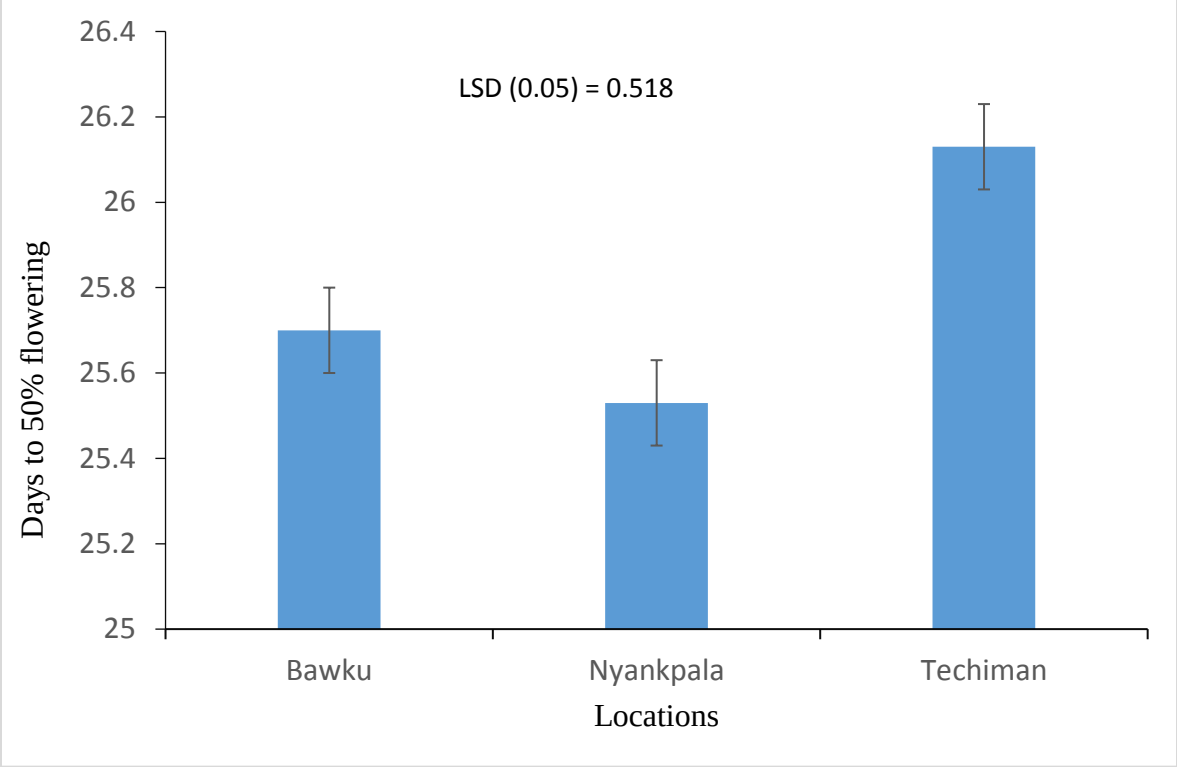

Figure 9: Effect of mutagenesis on days to 50% flowering of groundnuts genotypes evaluated in three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Significant difference (P<0.05) was also observed for genotype × locations interaction for number of days to 50% flowering evaluated during the field work. The 200 Gy plants at Nyankpala (23.83) took the least number of days to reach 50% flowering. The 0 Gy at Techiman (28.33) took the highest number of days for 50% flowering of the groundnut genotypes (Table 4).

Table 4: Genotypes × locations interactions for days to 50% flowering during evaluation in the 2017 and 2018 cropping seasons

Genotype	Location		
	Bawku	Nyankpala	Techiman
0 Gy	26.67	28.17	28.33
150 Gy	25.17	26.17	24.50
200 Gy	25.33	23.83	24.67
250 Gy	26.00	25.33	26.00
300 Gy	25.33	24.17	27.17

LSD (0.05) : Genotypes × locations =1.158; Genotype 0 Gy = Chinese (Standard check)

Among the two growing seasons, the genotypes varied significantly (P<0.05) among locations for number of days to 50% flowering. The genotypes at Techiman recorded the least number of days for 50% flowering in the 2017 whist genotypes at Techiman in the 2018 cropping took the highest number of days to reach 50% flowering (Table 5).

Table 5: Location × season interactions for days to 50% flowering during evaluation in the 2017 and 2018 cropping season

Location	Season	
	2017	2018
Bawku	25.93	25.47
Nyankpala	25.47	25.60
Techiman	25.07	27.20
LSD (0.05) : Location ×season = 0.732; Genotype 0 Gy = Chinese (Standard check)		

4.5. Days to maturity

The data presented in Figure 5 showed significant difference ($P < 0.05$) among genotypes. The least number of days to reach maturity was 89 days which was recorded in genotype 200 Gy followed by genotype 250 Gy with a value of 90.28 days. The highest number of days to reach maturity was recorded in genotype 0 Gy with a value of 96.56 days (Figure 10).

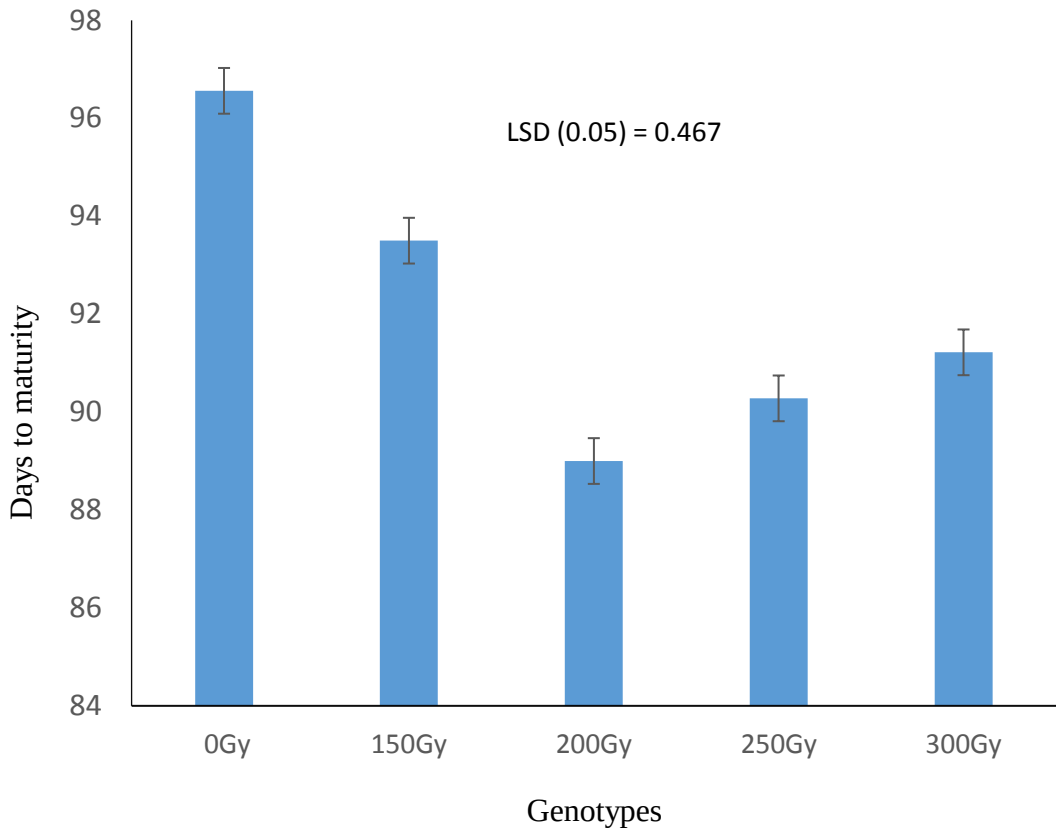

Figure 10: Effect of mutagenesis on days to maturity of groundnuts genotypes evaluated in 2017and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

Across the locations, the groundnut genotypes varied significantly (P<0.05) in the days to maturity. The genotypes evaluated at Bawku took highest number of days to mature (98.57) followed by those from Techiman with mean value of 89.5 days. Plants from Nyankpala took the least number of days to mature at 88.27 days (Figure 11).

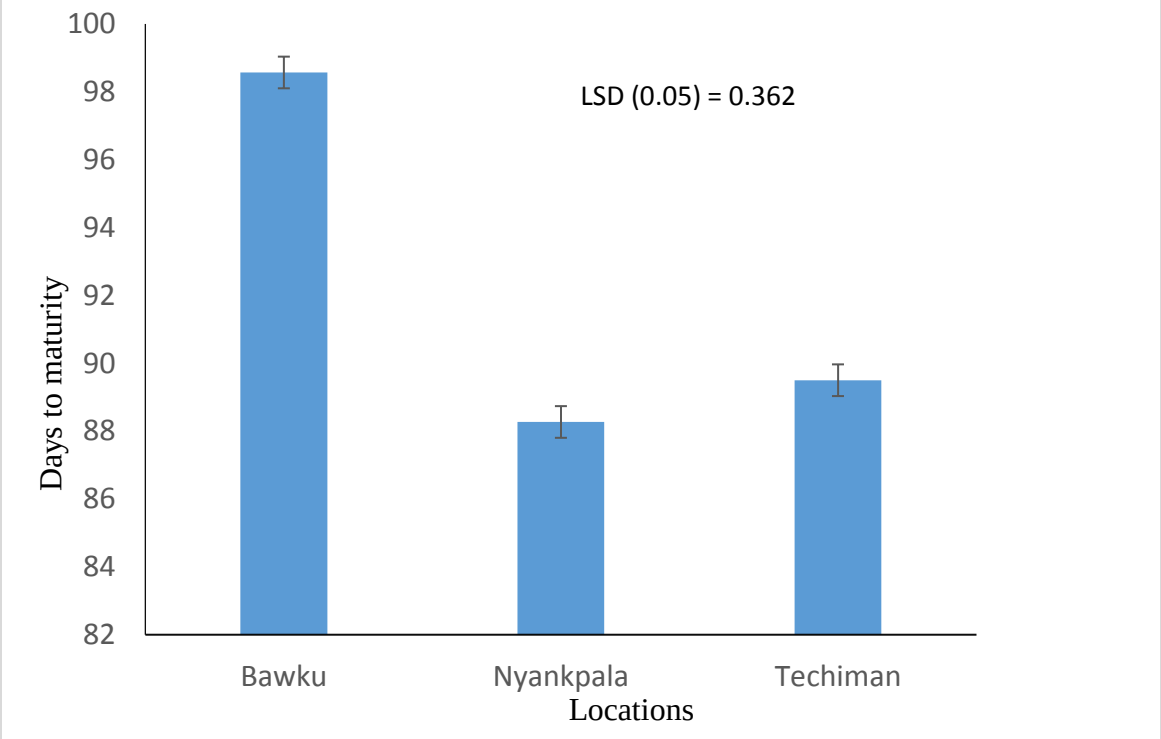

Figure 11: Effect of mutagenesis on days to maturity of groundnuts genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was significant (P< 0.05) differences in the days to maturity of groundnut genotypes evaluated in 2017 and 2018 cropping seasons. The genotypes evaluated in 2017 cropping took higher number of days to mature with the (95.98) as compared to genotypes evaluated in 2018 cropping season which took (88.24) to mature (Figure 12).

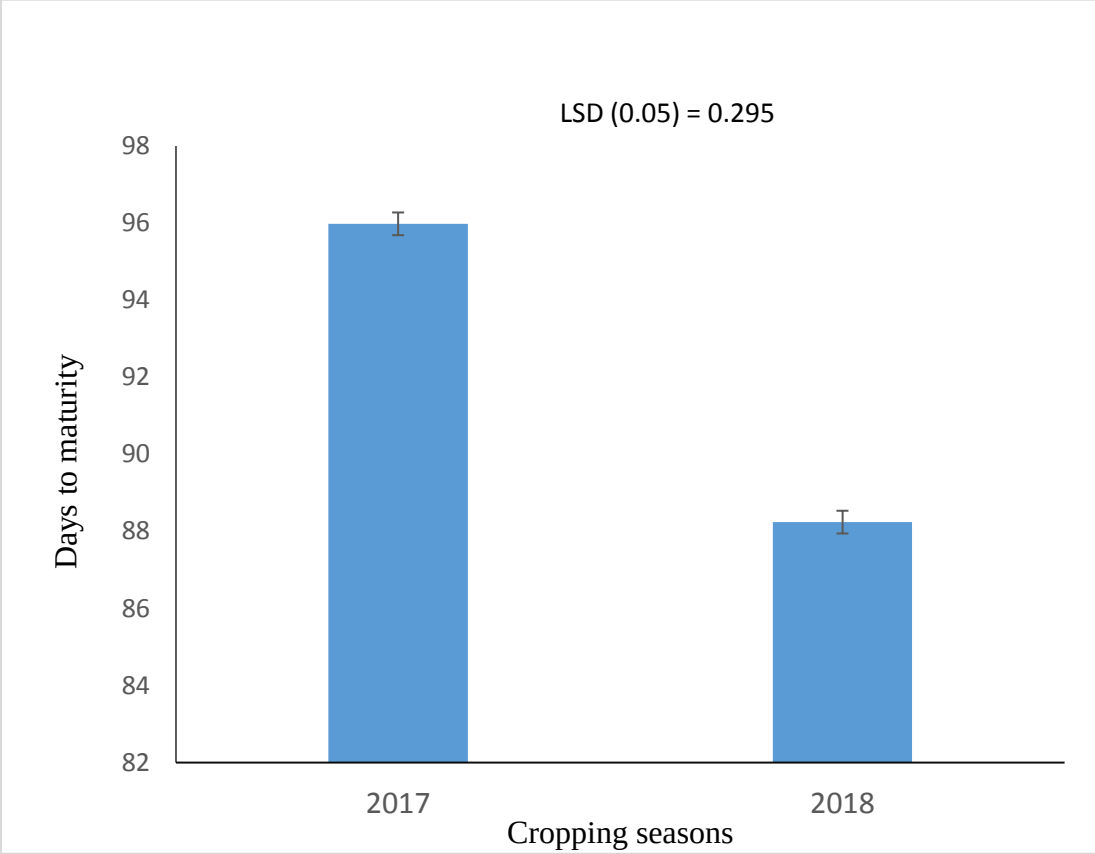

Figure 12: Effect of mutagenesis on days to maturity of groundnuts genotypes evaluated in the 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was also significant (P< 0.05) difference for genotype × location interaction for number of days to maturity. The 200 Gy plants at Nyankpala took the least number of days to reach maturity (83.17) followed by the 250 Gy plants at Nyankpala (84.67). The 0 Gy plants at Bawku took the highest number of days to mature (102.67) (Table 6).

Table 6: Genotype × locations Interactions for number days to maturity during evaluation in the 2017and 2018 cropping season

Genotype	location		
	Bawku	Nyankpala	Techiman
0 Gy	102.67	96.33	90.67
150 Gy	99.50	91.00	90.00
200 Gy	95.83	83.17	88.00
250 Gy	96.50	84.67	89.67
300 Gy	98.33	86.17	89.17

LSD (0.05): Genotype × location = 0.809; Genotype 0 Gy = Chinese (Standard check)

The genotype × season interactions also were significant (P<0.05) for days to maturity. The 200 Gy and 250 Gy evaluated during the 2018 season matured early at 85.22 and 85.78 days respectively, but the 0 Gy evaluated during the 2017 season matured the latest at 99.89 days (Table 7).

Table 7: Genotype × season interaction for number of days to maturity during evaluation in the 2017and 2018 cropping season

Genotype	Season	
	2017	2018
0 Gy	99.89	93.22
150 Gy	96.89	90.11
200 Gy	92.78	85.22
250 Gy	94.78	85.78
300 Gy	95.56	86.89
LSD (0.05); Genotype ×season = 0.661; Genotype 0 Gy = Chinese (Standard check)		

The results from Table 8 revealed that location × season was significant (P<0.05) for number of days to maturity. The plants at Bawku during the 2018 cropping season recorded the least number of days for maturity (88.00). The genotypes at Bawku during the 2017 cropping season took the highest number of days to mature (109.13).

Table 8: Locations × seasons interaction for number days to maturity of plants during evaluation in the 2017and 2018 cropping season.

Location	Season	
	2017	2018
Bawku	109.13	88.00
Nyankpala	88.27	88.27
Techiman	90.53	88.47
LSD (0.05) : Location × season = 0.512 ; Genotype 0 Gy = Chinese (Standard check)		

The three-way interactions (genotypes × locations ×seasons) for number of days to maturity of plants also differed significantly (P<0.05). The 200 Gy plants at Bawku during the 2018 cropping season matured earliest at 82.33days followed by 200 Gy evaluated at Nyankpala at 83.00 days during the 2017 cropping season. The genotype that recorded highest number of days to mature was 0 Gy at Bawku at 109.67 days during evaluation in the 2017 cropping season (Table 9).

Table 9: Three-way interactions (genotype × location × season) for number days to maturity during evaluation in the 2017and 2018 cropping seasons

Genotype	Location	Season	
		2017	2018
0 Gy	Bawku	109.67	95.67
	Nyankpala	96.33	96.33
	Techiman	93.67	87.67
150 Gy	Bawku	108.67	90.33
	Nyankpala	91.00	91.00
	Techiman	91.00	89.00
200 Gy	Bawku	109.33	82.33
	Nyankpala	83.00	83.33
	Techiman	86.00	90.00
250 Gy	Bawku	109.00	84.00
	Nyankpala	84.33	85.00
	Techiman	91.00	88.33
300 Gy	Bawku	109.00	87.67
	Nyankpala	86.67	85.67
	Techiman	91.00	87.33

LSD (0.05) **:** Genotypes × Locations × Seasons = 2.290 ; Genotype 0 Gy = Chinese (Standard check)

4.6 Number of pods per plant

Significant variations (P<0.05) were observed for genotype main effect in number of pods per plant. The 200 Gy plants recorded the highest number of pods per plant of 34.22 followed by plants of 300 Gy with 26.06 pods. The 250 Gy recorded the lowest number of pods per plant of 21.06. (Figure 13).

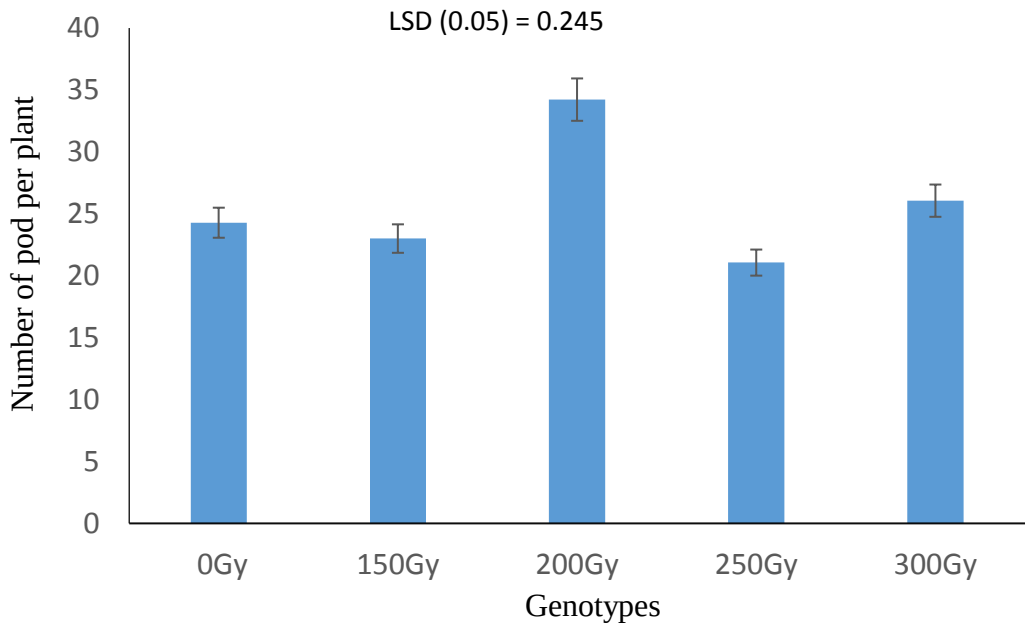

Figure 13: Effect of mutagenesis on number of pods per plant of groundnuts genotypes evaluated in the 2017 and 2018 cropping season. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

As seen in Figure 14, significant differences (P < 0.05) were observed in main effects of locations for number of pods per plant of the genotypes. Nyankpala recorded the highest number of pods per plant of 36.63 pods followed by Techiman while Bawku recorded the least number of pods in both season with 17.77 pods (Figure 14).

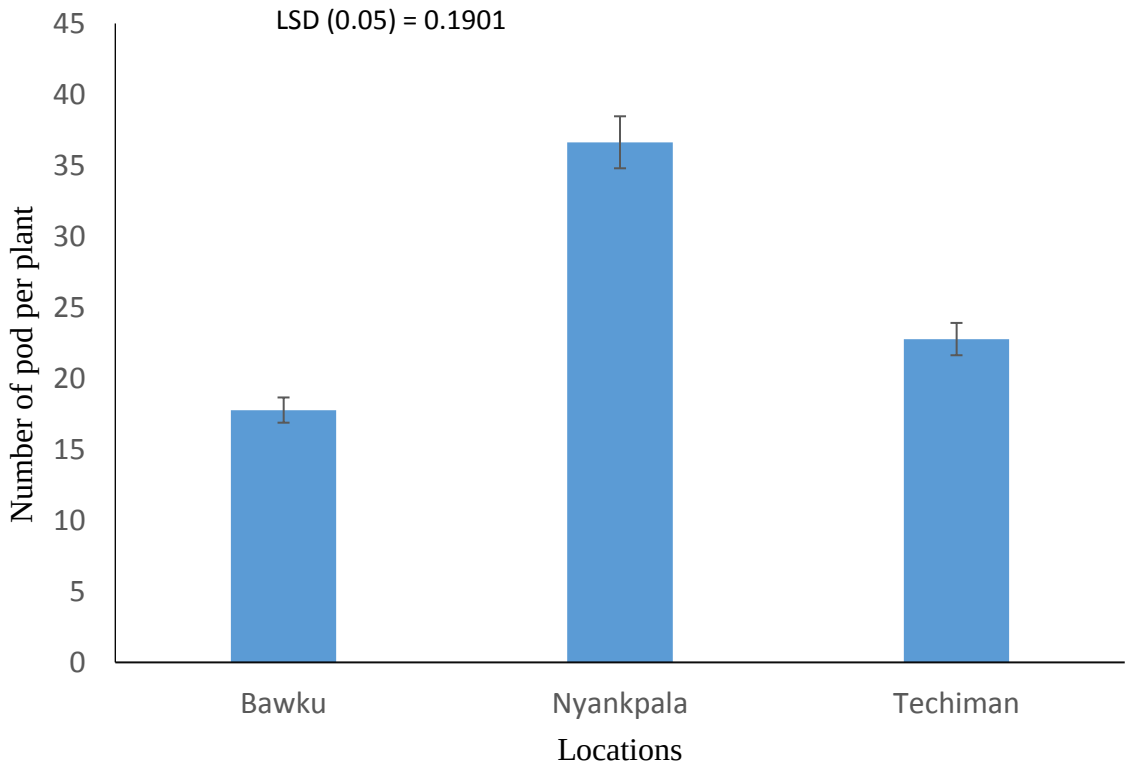

Figure 14: Effect of mutagenesis on number of pods per plant of groundnuts genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

There were also significant differences (P< 0.05) for genotype × location interaction for number of pod per plant. The 200 Gy plant at Nyankpala recorded the highest number of pods per plant (55.83) and 0 Gy plants at Bawku recorded the lowest in terms of number of pods per plant of the groundnut genotypes (14.83) (Table 10).

Table 10: Interaction of genotype and locations for number of pod per plant during evaluation in the field of groundnut genotypes

Genotype	Location		
	Bawku	Nyankpala	Techiman
0 Gy	14.83	34.33	23.6
150 Gy	15.67	32.17	21.17
200 Gy	24.67	55.83	22.17
250 Gy	15.50	23.00	24.67
300 Gy	18.17	37.83	22.17

LSD (0.05) Genotype × Locations =0.15; Genotype 0 Gy = Chinese (Standard check)

The genotype × season interactions was also significant (P<0.05) for number of pods per plant. The 200 Gy plants in 2018 season recorded the highest number of pods per plant (36.00) while the 150 Gy plants from same season had the least number of pods per plant (Table 11).

Table 11: Interaction of genotypes and seasons for number of pods per plant during evaluation in the field of groundnut genotype

Genotype	Season	
	2017	2018
0 Gy	24.78	23.78
150 Gy	23.33	22.67
200 Gy	32.44	36.00
250 Gy	24.11	18.00
300 Gy	25.67	26.44

LSD (0.05) :Genotype × season = 0.1226 ; Genotype 0 Gy = Chinese (Standard check)

The interaction between locations and seasons for number of pods per plant differed significantly (P<0.05). The genotypes at Nyankpala recorded highest number of pods per plant in both 2017 and 2018 cropping season whilst the genotypes at Bawku recorded least number of pods per plant (Table 12)

Table 12: Interaction between location and season for number of pod per plant during evaluation in the 2017and 2018 cropping seasons

Location	Season	
	2017	2018
Bawku	17.00	18.53
Nyankpala	36.00	37.27
Techiman	25.20	20.33

LSD (0.05) :Locations × Season = 0.10; Genotype 0 Gy = Chinese (Standard check)

The three-way interactions among genotypes, locations and seasons for number of pods per plant also differed significantly (P<0.05). The 200 Gy plants at Nyankpala during the 2017 cropping season had the highest number of pods per plant (56.33) followed by plant from 200 Gy at Nyankpala in the 2018 cropping season. The genotype that recorded the least number of pods per plant was the 0 Gy at Bawku (13.33) during the 2017 season (Table 13).

Table 13: Three-way interactions (genotypes × location × season) for number of pod per plant during evaluation in the 2017and 2018 cropping season

Genotype	Location	Seasons	
		2017	2018
0 Gy	Bawku	13.33	16.33
	Nyankpala	33.67	35.00
	Techiman	27.33	20.00
150 Gy	Bawku	16.33	15.00
	Nyankpala	31.67	32.67
	Techiman	22.00	20.33
200 Gy	Bawku	18.67	30.67
	Nyankpala	56.33	55.33
	Techiman	22.33	22.00
250 Gy	Bawku	19.67	11.33
	Nyankpala	23.00	23.00
	Techiman	29.67	19.67
300 Gy	Bawku	17.00	19.33
	Nyankpala	35.33	40.33
	Techiman	24.67	19.67

LSD (0.05) : Genotype × location × season = 0.21; Genotype 0 Gy = Chinese (Standard check)

4.7 Number seeds per pod

There was no significant difference (P>0.05) in number of seeds per pod for the main effect of genotypes. The 150 Gy plants were observed to record highest average number of seed per pods of 2.38 followed by those of 200 Gy and 300 Gy, while the 250 Gy recorded the least number of seeds per pod with an average value of 2.17 (Figure 15).

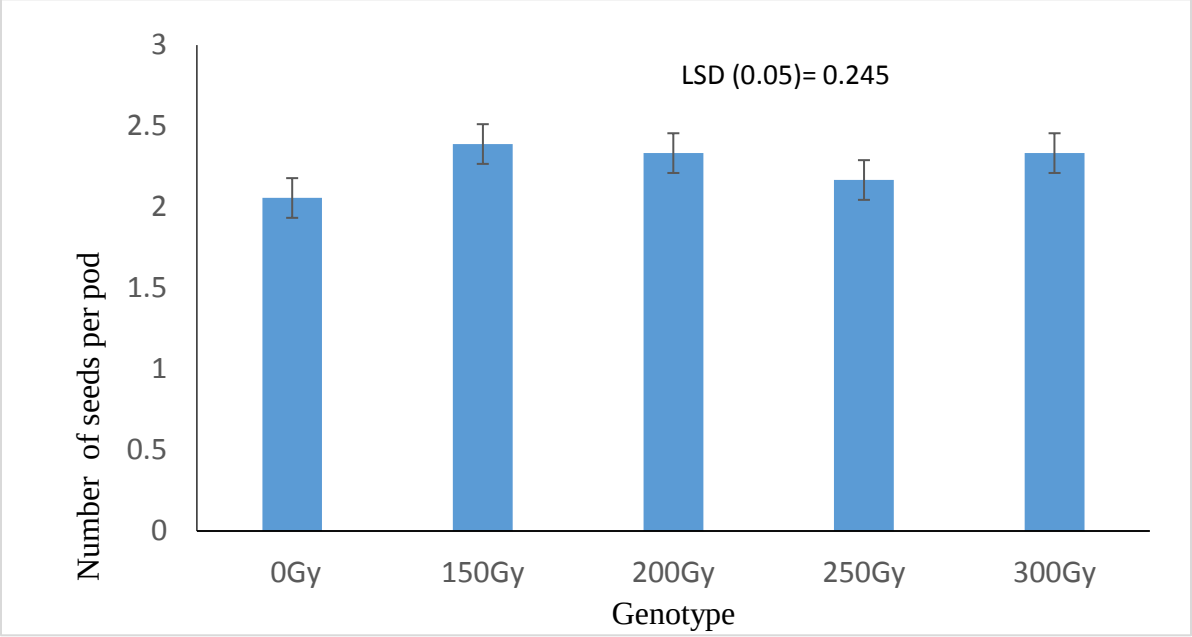

Figure 15: Effect of mutagenesis on number of seed per pod of groundnuts genotypes evaluated in the 2017 and 2018 cropping season. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

The data presented in figure 16 showed significant difference (P < 0.05) in number of seeds per pod for the three locations. The genotypes at Techiman recorded the highest average number of 2.43 seeds per pod, followed by genotypes at Bawku with average of 2.33 seeds whereas Nyankpala had 2 seeds per pod.

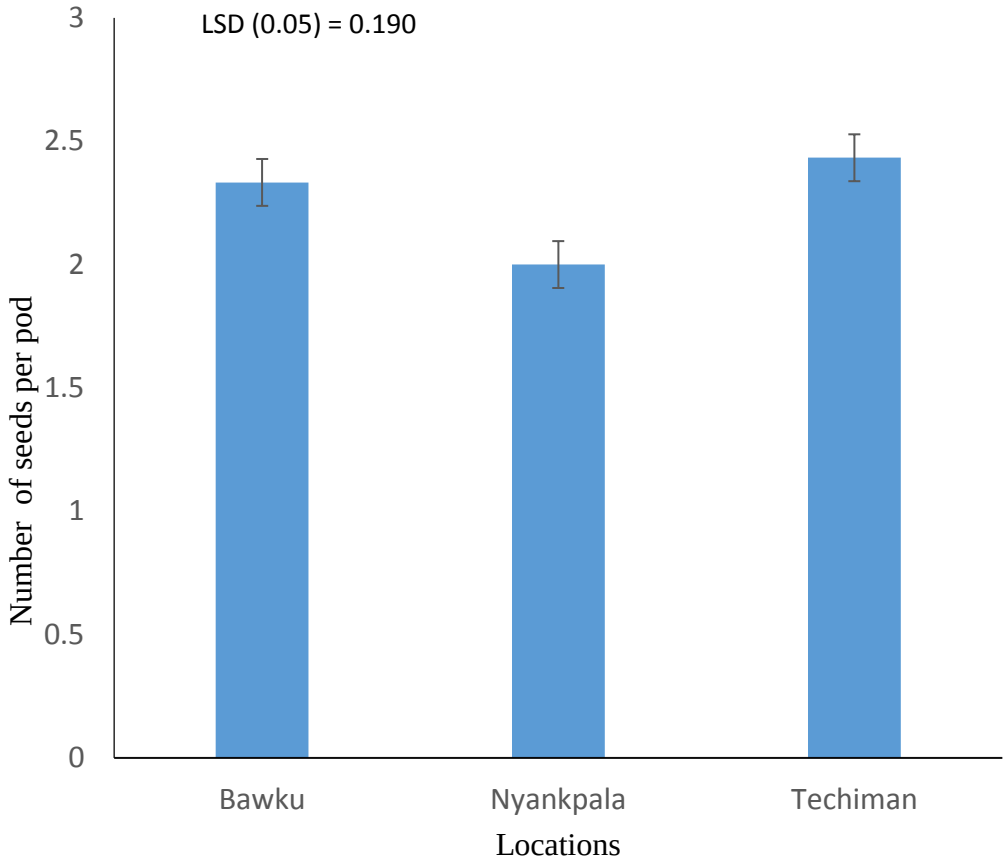

Figure 16: Effect of mutagenesis on number of seeds per pod of groundnuts genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was significant difference (P<0.05) in number of seeds per pod of plants across the season. The genotypes in 2017 cropping season were observed to have higher number of seeds per pods (2.33) seed while the genotypes in 2018 cropping season recorded lower number of seed per pod (2.17) (Figure 17).

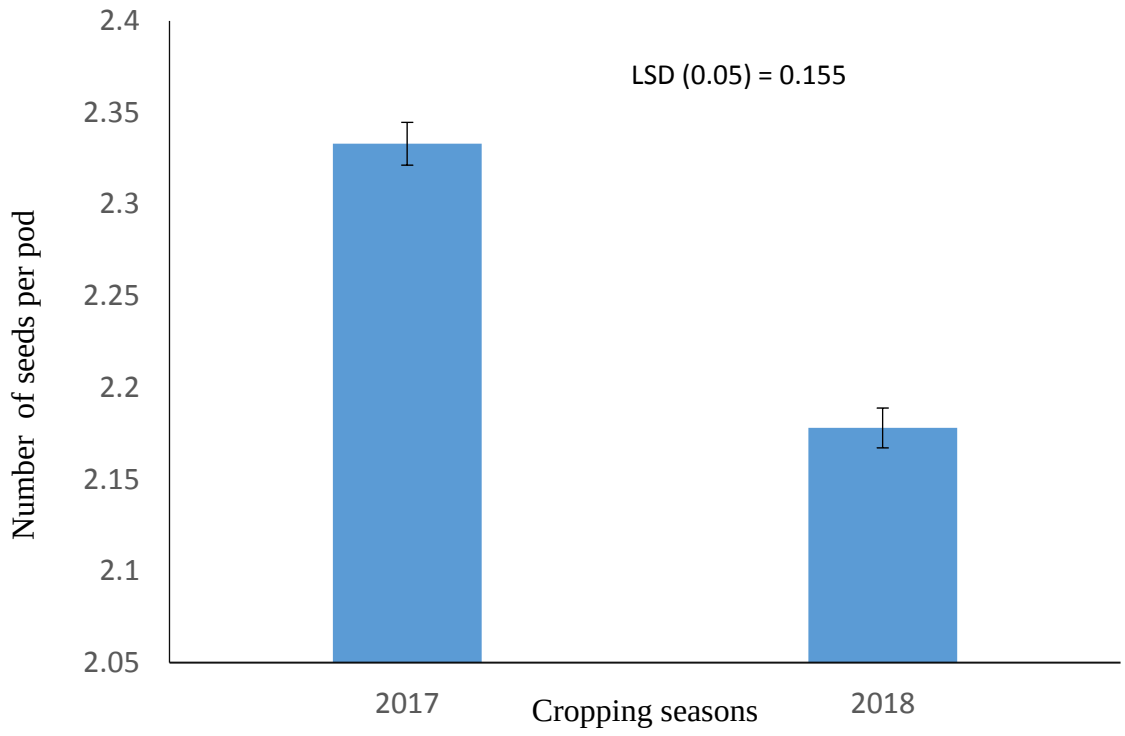

Figure 17: Effect of mutagenesis on number of seeds per pod of groundnuts genotypes evaluated in the 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

Significant difference (P<0.05) existed for genotype × location interaction for number of seed per pod. The 150 Gy and 250 Gy plants at Techiman recorded the highest number of seeds per pod with an average value of 2.67. The 300 Gy plants at Nyankpala recorded least number of seeds per pods (Table 14).

Table 14: Genotypes × locations interaction for number of seeds per pod during evaluation in the 2017 and 2018 cropping seasons

Genotype	Location		
	Bawku	Nyankpala	Techiman
0 Gy	2.167	2.000	2.000
150 Gy	2.500	2.000	2.667
200 Gy	2.500	2.000	2.500
250 Gy	1.833	2.000	2.667
300 Gy	2.667	2.000	2.333

LSD (0.05): Genotype × Locations =0.15; Genotype 0 Gy = Chinese (Standard check)

The genotype × season interactions for number of seeds per pod were also significant ($P<0.05$). The 150 genotypes in the 2017 cropping season recorded the highest number of seeds per pods followed by plants of 200 Gy in the 2018 cropping season while the 0 Gy and 250 Gy in 2018 recorded least number of seeds pods (Table 15).

Table 15: Genotypes × season interactions for number of seeds per pod during evaluation in the 2017 and 2018 cropping seasons

Genotype	Season	
	2017	2018
0 Gy	2.111	2.000
150 Gy	2.667	2.111
200 Gy	2.111	2.556
250 Gy	2.333	2.000
300 Gy	2.444	2.222

LSD (0.05) :Genotype × season = 0.1226 ; Genotype 0 Gy = Chinese (Standard check)

4.8. Pod length

Pod length for main effect of genotypes varied significantly ($P<0.05$). The 250 Gy recorded highest pod length of 2.71 cm as compared to those of 150 Gy, 300 Gy and 250 Gy. The 0 Gy recorded the lowest pod length of 2.39 cm (Figure 18).

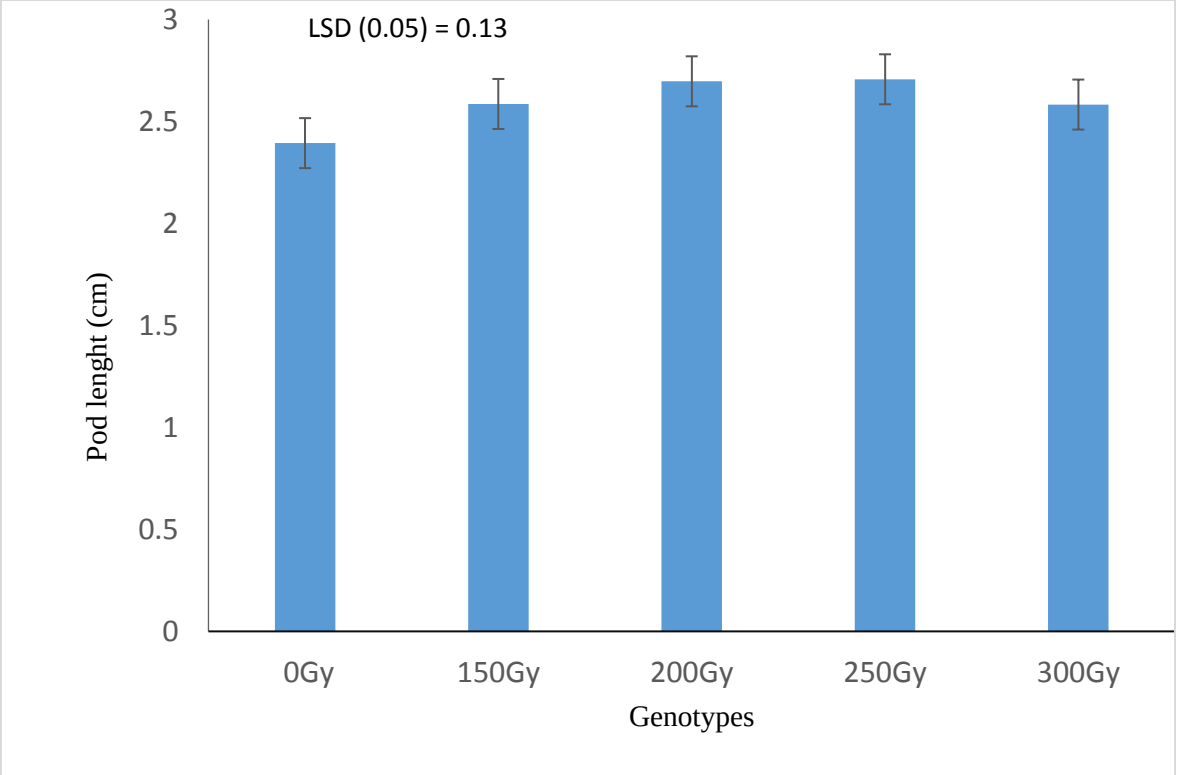

Figure 18: Effect of mutagenesis on pod length of groundnuts genotypes. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

Pod lengths from the three locations (location main effect) also varied significantly different ($P<0.05$). Genotypes at Nyankpala recorded the highest pod length with a value of 2.79. Genotypes at Techiman and Bawku recorded the lowest pod length of 2.49 (Figure 19).

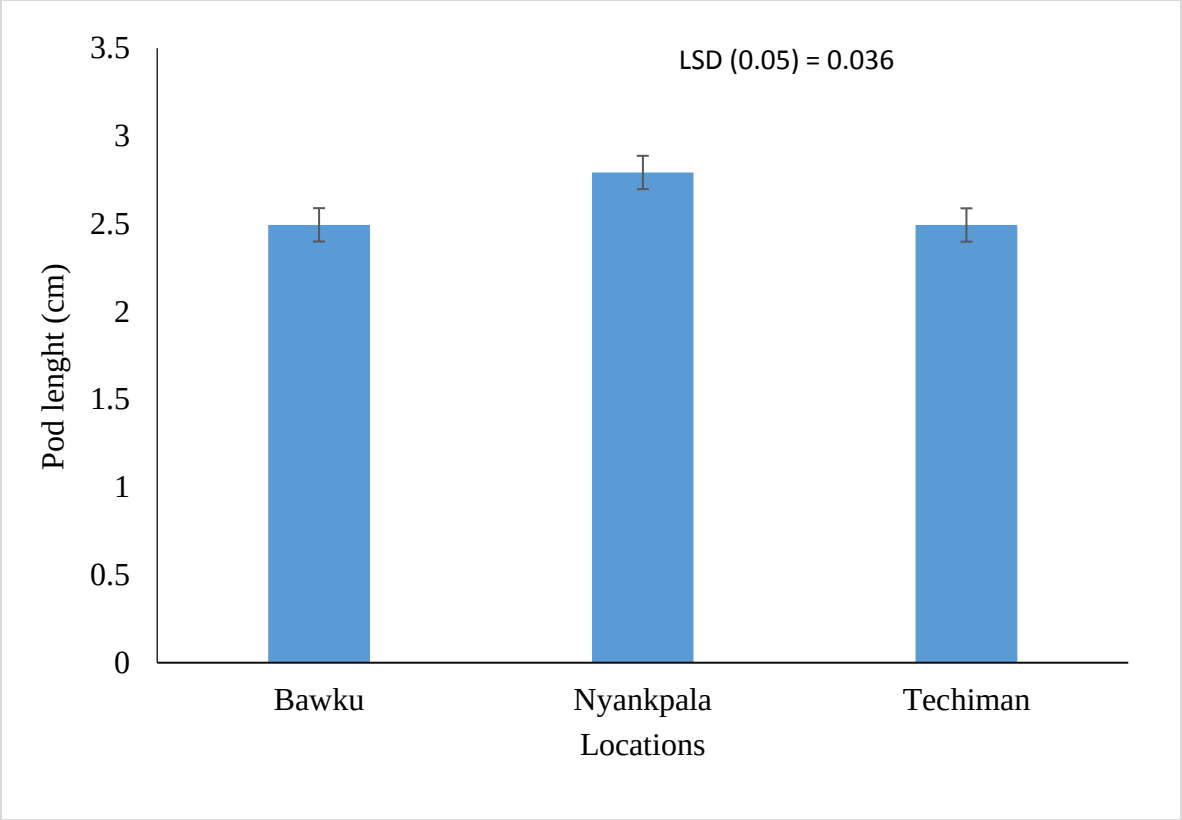

Figure 19: Effect of mutagenesis on pod length of groundnuts genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Variation in seasons (main effect of season) was also significantly different ($P<0.05$) for pod length. The genotypes in 2018 cropping season recorded highest pod length of 2.73 cm while the genotypes in 2017 cropping season recorded the lower pod length of 2.45 cm (Figure 20).

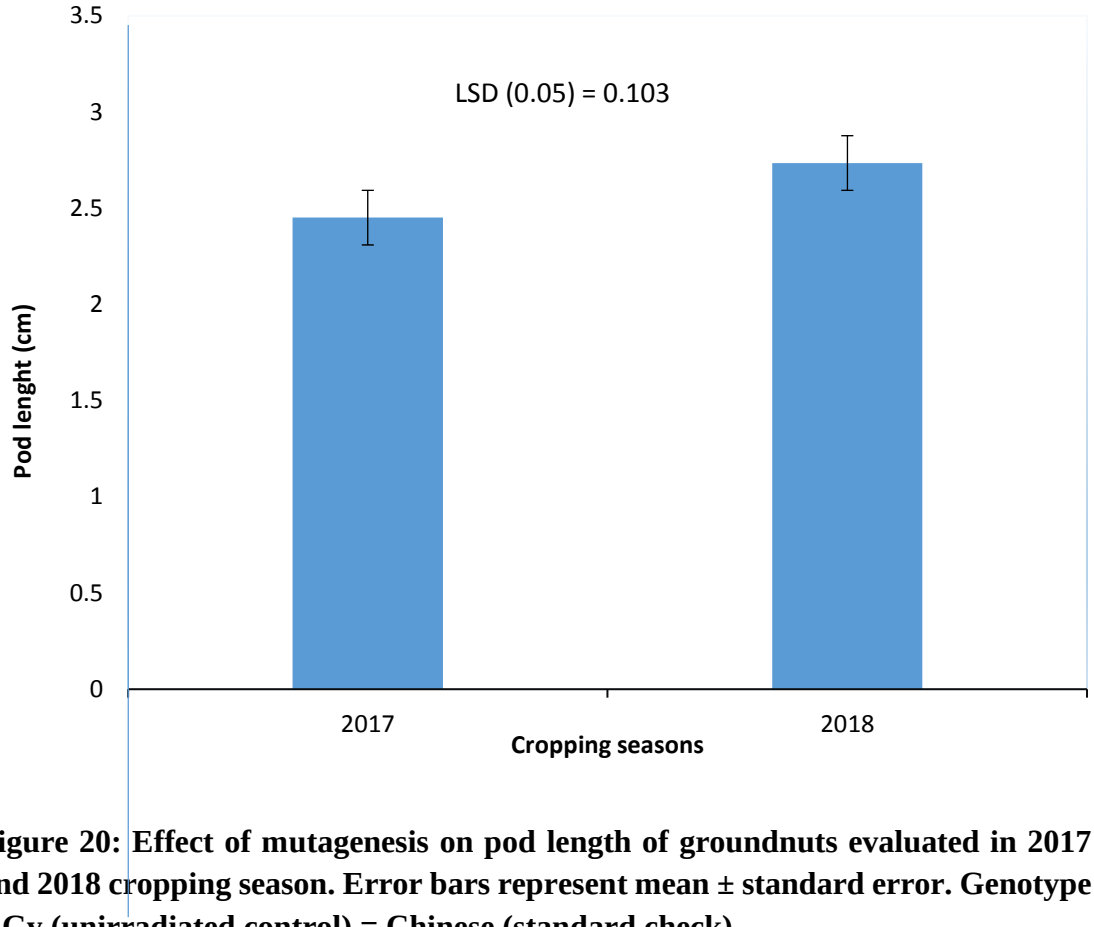

Figure 20: Effect of mutagenesis on pod length of groundnuts evaluated in 2017 and 2018 cropping season. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

The results from Table 16 revealed that, the interaction between locations and seasons (Locations × season) for pod length differed significantly ($P<0.05$). The genotypes at Nyankpala recorded highest pod length in both 2017 and 2018 cropping seasons, while the genotypes at Techiman in 2017 recorded the least pod length (Table 16).

Table 16: Location × season interaction for pod length during evaluation in the 2017 and 2018 cropping seasons

Location	Season	
	2017	**2018**
Bawku	2.360	2.629
Nyankpala	2.787	2.798
Techiman	2.207	2.779
LSD (0.05) : Locations × Seasons = 0.15; Genotype 0 Gy = Chinese (Standard check)		

4.9 Hundred Seeds weight

Hundred seed weight of the genotypes (genotype main effect) varied significantly (P< 0.05). The 200 Gy plants recorded the highest in term of hundred seed weight (41.67 g), and the 0 Gy plants recorded the least hundred seeds weight (34.30 g) (Figure 21).

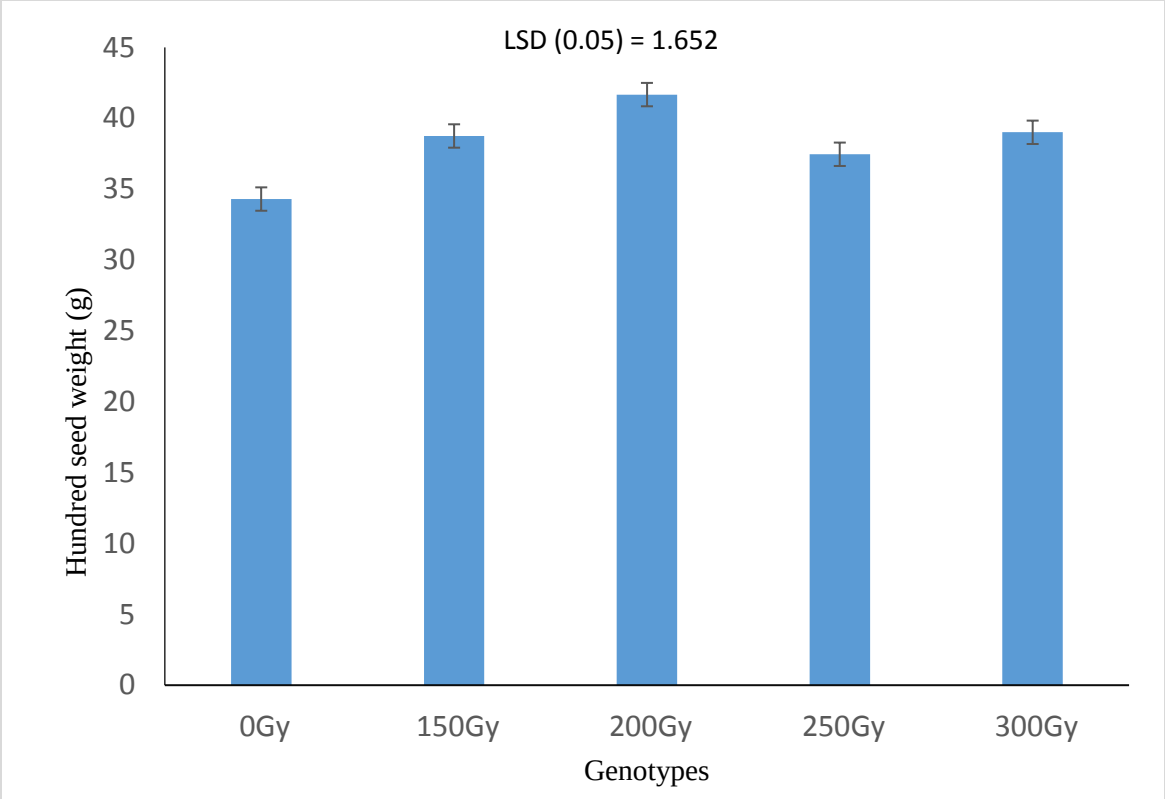

Figure 21: Effect of mutagenesis on hundred seeds weight of groundnuts genotypes evaluated. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chines (standard check).

Among the locations, the variation was significantly different ($p<0.05$) for hundred seeds weight. At Techiman, the genotypes recorded the highest hundred seeds weight in both season (49.23 g) followed by Nyankpala (37.83 g) whereas Bawku recorded the least hundred seeds weight (27.66 g) of groundnut genotypes in both growing season (Figure 22).

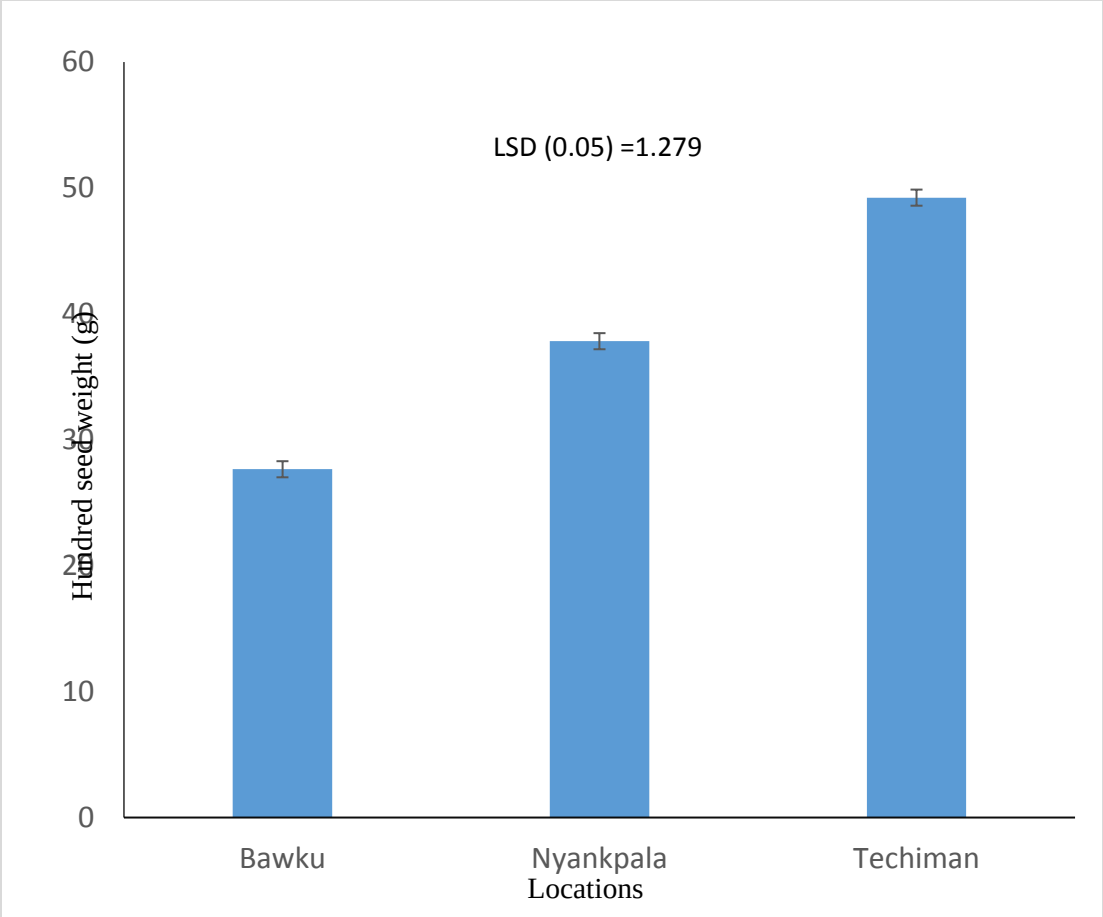

Figure 22: Effect of mutagenesis on hundred seeds weight of groundnut genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Variation in season were significantly (P<0.05) different for 100 seed weight. The genotypes in 2018 cropping season recorded highest seed weight of 41.97 g while the genotypes in 2017 cropping season recorded the least of 34.50 g (Figure 23).

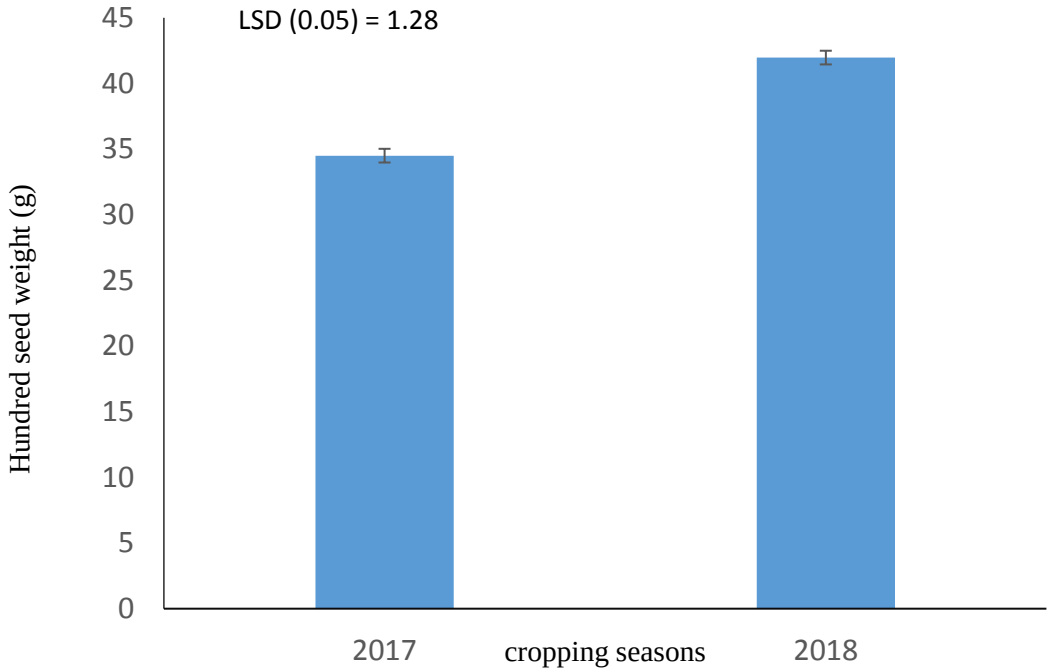

Figure 23: Effect of mutagenesis on hundred seeds weight of groundnut genotypes evaluated in the 2017 and 2018 cropping season. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check).

There was significant difference ($P < 0.05$) for genotype × location for seed weight. The 150 Gy plants at Techiman recorded the highest 100 seed weight (52.66 g) followed by 200 Gy at same location whilst 0 Gy plant at Bawku recorded the least (24.82) (Table 17).

Table 17: Genotype × location interactions for hundred seeds weight during evaluation in the 2017 and 2018 cropping seasons

Genotype	Locations		
	Bawku	Nyankpala	Techiman
0 Gy	24.82	32.42	45.66
150 Gy	26.70	36.58	52.98
200 Gy	31.31	42.47	51.22
250 Gy	26.70	37.71	47.98
300 Gy	28.77	39.98	48.30
LSD (0.05) : Genotypes × locations = 4.06 ; Genotype 0 Gy = Chinese (Standard check)			

The interaction between the location and season for hundred seed weight also varied significantly ($P<0.05$). The genotypes at Techiman in 2018 recorded the highest hundred seeds weight (51.10 g) but the genotype in 2017 cropping season at Bawku recorded the lowest in terms of hundred seeds weight (18.39g) (Table 18).

Table 18: Location × season interactions for hundred seeds weight during evaluation in the 2017 and 2018 cropping seasons

Location	Season	
	2017	2018
Bawku	18.39	36.92
Nyankpala	37.76	37.90
Techiman	47.36	51.10
LSD (0.05) Locations × season = 1.809 Genotype 0 Gy = Chinese (Standard check)		

The interactions among genotype, location and season (three –way interactions) for hundred seeds weight also differed significantly ($P<0.05$). The 150 Gy plants at Techiman in 2018 cropping season recorded highest hundred seeds weight (59.79 g) followed by 200 Gy plants at Techiman in the 2018 cropping season. The genotype that recorded least hundred seeds weight was 0 Gy at Bawku (17.33 g) during evaluation in the 2017 season (Table 18).

Table 19: Three-way interactions (genotype × location × season) for hundred seeds weight during evaluation in the 2017and 2018 cropping season

Genotype	Location	Seasons	
		2017	2018
0 Gy	Bawku	17.13	32.51
	Nyankpala	32.13	32.70
	Techiman	44.97	46.36
150 Gy	Bawku	18.37	35.03
	Nyankpala	36.27	36.90
	Techiman	46.17	59.79
200 Gy	Bawku	19.80	42.81
	Nyankpala	43.77	41.18
	Techiman	49.90	52.54
250 Gy	Bawku	17.90	35.49
	Nyankpala	36.87	38.55
	Techiman	46.30	49.66
300 Gy	Bawku	18.77	38.77
	Nyankpala	39.77	40.18
	Techiman	49.47	47.12

LSD (0.05) Genotype × location × season = 4.05; Genotype 0 Gy = Chinese (Standard check)

4.10 Total grain yield

Generally, total grain yield of the genotypes (genotypes main effect) was significant ($P<0.05$). The 200 Gy plants recorded the highest total grain yield average value of 1.7 ton/ha followed by 250 Gy with 1.53 ton/ha and 0Gy recorded the lowest total grain yield of 1.199 ton/ha (Figure 24).

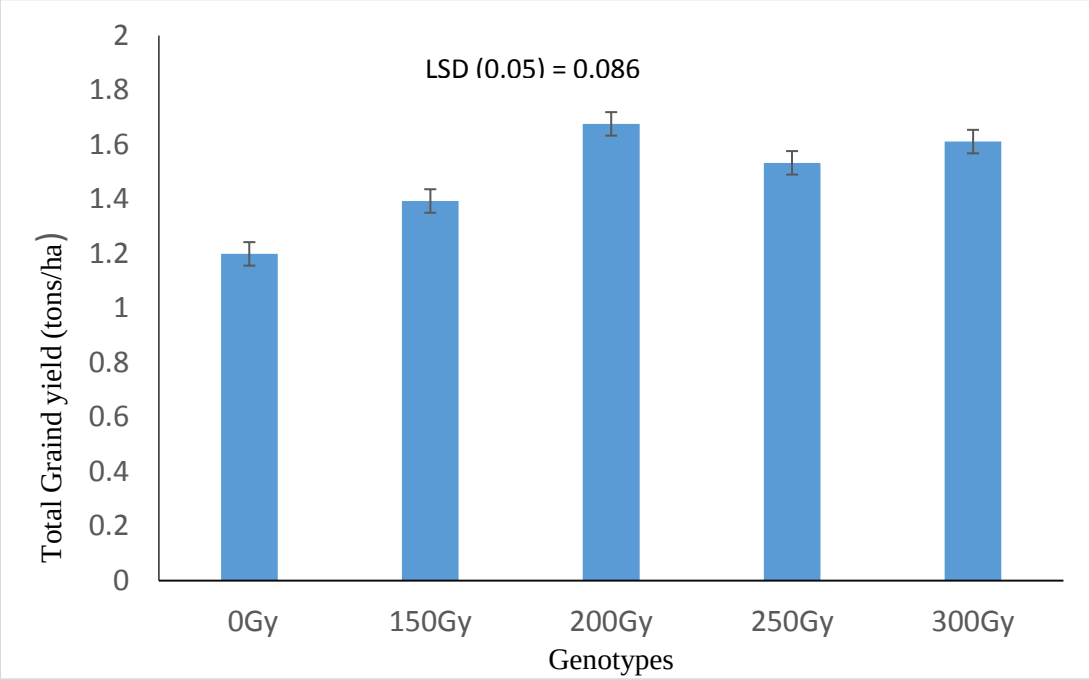

Figure 24: Effect of mutagenesis on total grain yield of groundnuts genotypes evaluated. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

From Figure 25, the total grain yield was significant ($P<0.05$) in both seasons. The genotypes at Nyankpala recorded the highest total grain yield average value of 1.64 t/ha, followed by genotypes at Bawku with 1.47 ton/ha.

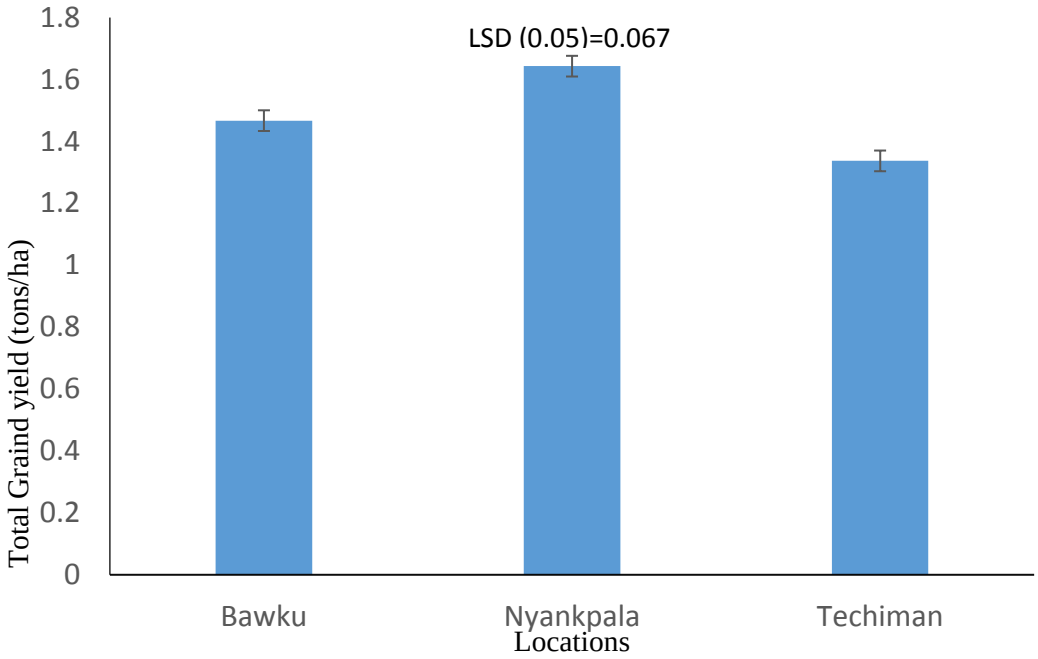

Figure 25: Effect of mutagenesis on total grain yield of groundnut genotypes evaluated at three locations. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Total grain yield was also significantly different (P<0.05) for the two seasons. The genotypes in 2017 cropping season recorded the higher total grain yield mean value of 1.57 t/ha while the genotypes in 2018 cropping season recorded the lower total grain yield average value of 1.39 t/ha (Figure 26).

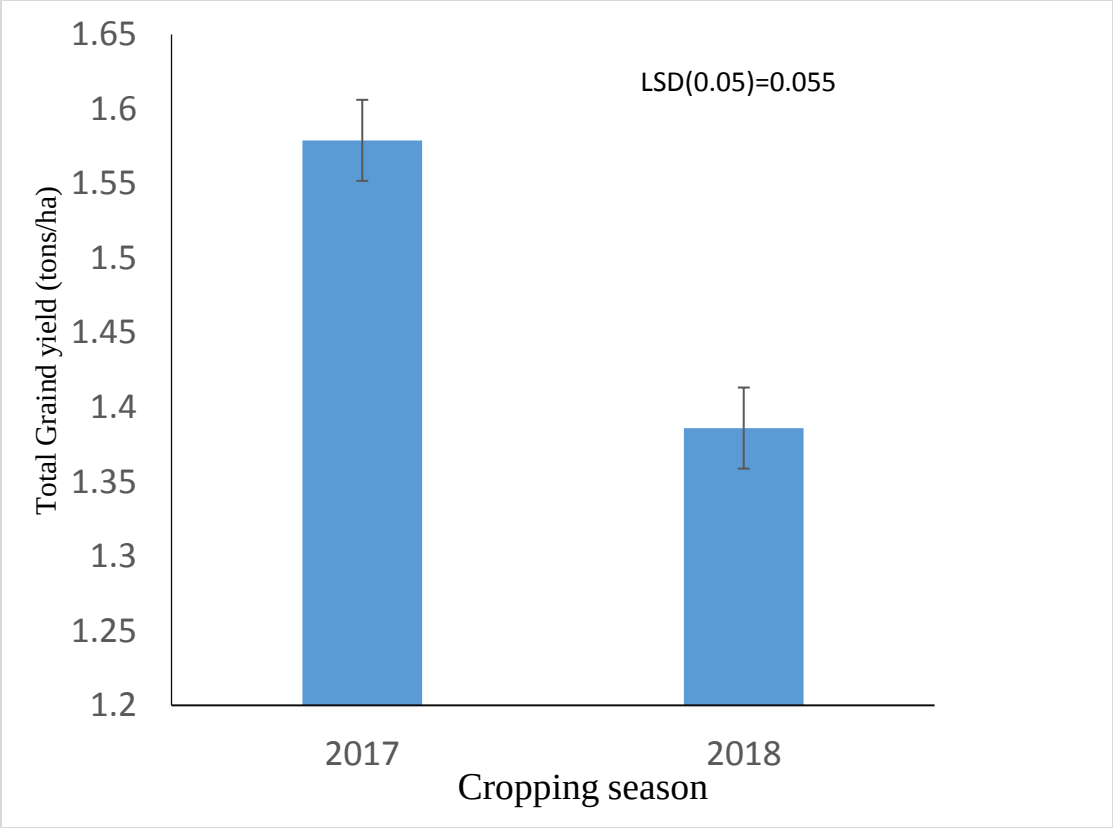

Figure 26: Effect of mutagenesis on total grain yield of groundnut genotypes evaluated in the 2017 and 2018 cropping seasons. Error bars represent mean ± standard error. Genotype 0 Gy (unirradiated control) = Chinese (standard check)

Genotype × location ×season (three-way) interaction was significant ($P<0.05$) for total grain yield. The 200 Gy plants at Nyankpala in 2017 cropping season recorded the highest total grain yield (2.29 tons/ha) followed by the 300 Gy plants at Nyankpala in 2017 (2.11 tons/ha). The 0 Gy evaluated at Techiman in the 2017 cropping season recorded the least yield (1.10 tons/ha) (Table 19).

Table 20: Three-way interactions (genotype × location × season) for total grain yield during evaluation in the 2017and 2018 cropping season

Genotype	Location	Seasons	
		Season 2017	Season 2018
0 Gy	Bawku	1.273	1.110
	Nyankpala	1.427	1.283
	Techiman	1.050	1.053
150 Gy	Bawku	1.520	1.263
	Nyankpala	1.650	1.410
	Techiman	1.180	1.333
200 Gy	Bawku	1.833	1.550
	Nyankpala	2.293	1.513
	Techiman	1.370	1.493
250 Gy	Bawku	1.657	1.317
	Nyankpala	1.750	1.497
	Techiman	1.563	1.417
300 Gy	Bawku	1.703	1.443
	Nyankpala	2.107	1.503
	Techiman	1.307	1.600

LSD(0.05) Genotype × Location × Season = 0.211; Genotype 0 Gy = Chinese (Standard check)

4.11 Stability analysis

AMMI1 model was used in figure 27 the genotype main effect and the genotype-by-environment interaction were significant ($p < 0.05$) in 2017. From the AMMI1 biplot, genotype 200Gy had the highest mean in 2017. Techiman and Bawku fell within the same sector in 2017.

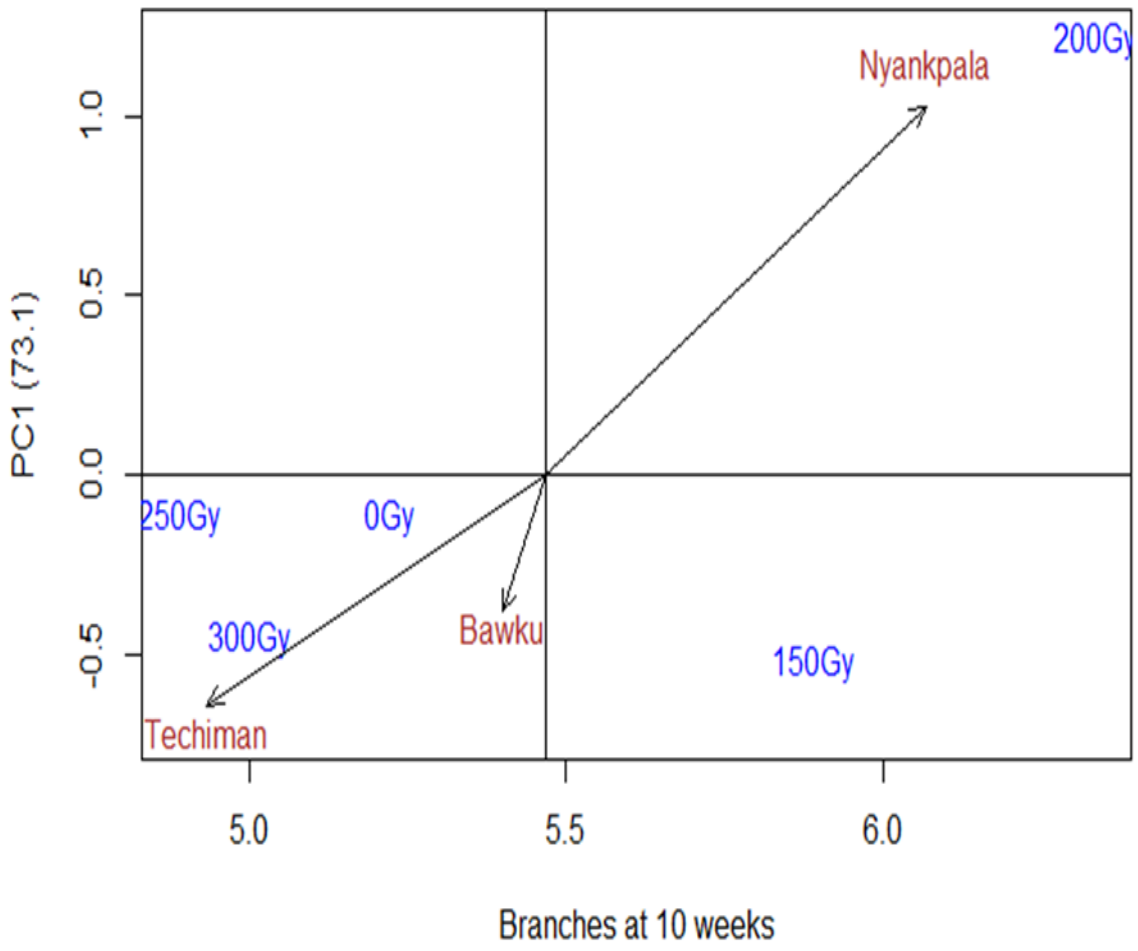

Figure 27: AMMI biplot for number of branches at 10 weeks in 2017

In 2018, the environment main effect and the genotype-by-environment interaction were significant ($p < 0.05$). In 2018, 200Gy and 150Gy had the highest mean.

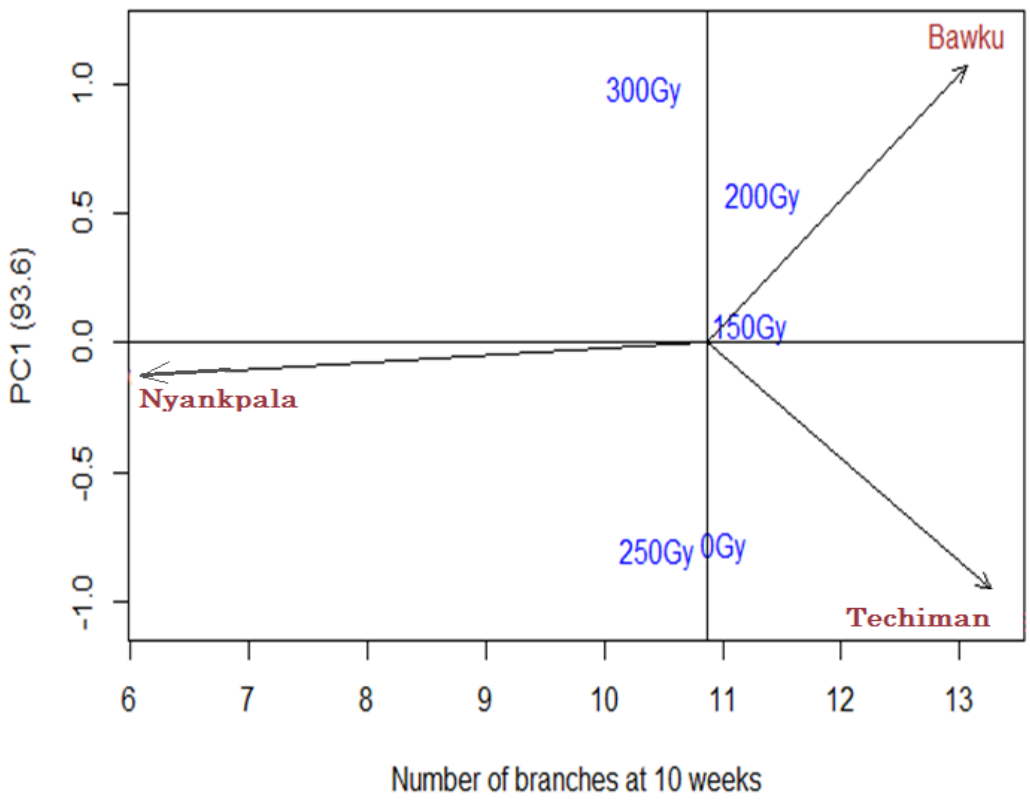

Figure 28: AMMI1 biplot for number of branches at 10 weeks in 2018

4.11.2 Days to 50% flowering

All the main effects as well as the interactive effects were significant in both 2017 and 2018 ($p < 0.05$). AMMI2 model was used in 2017 while AMMI1 model was used in 2018. Genotype 250Gy was closed to the origin of the biplots for both years and hence, most stable for both years.

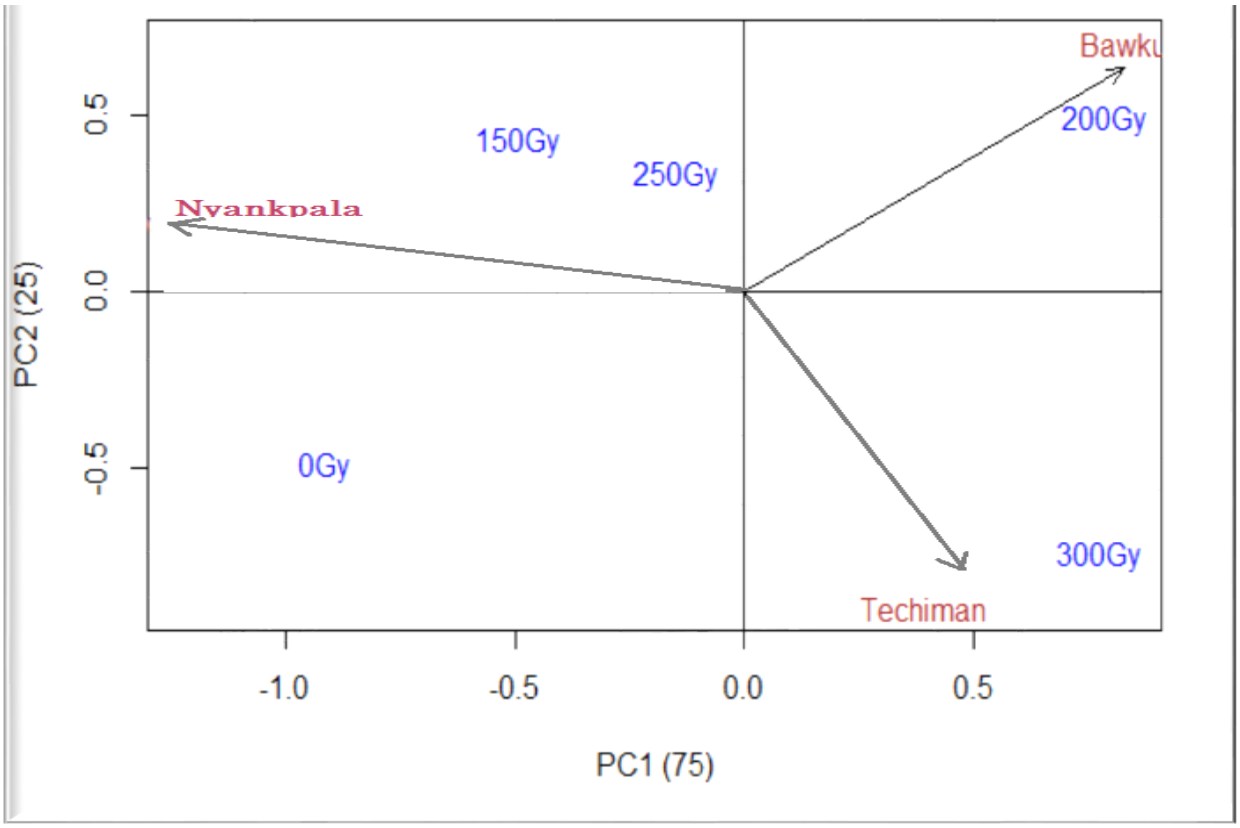

Figure 29: AMMI2 biplot for days to 50% in 2017

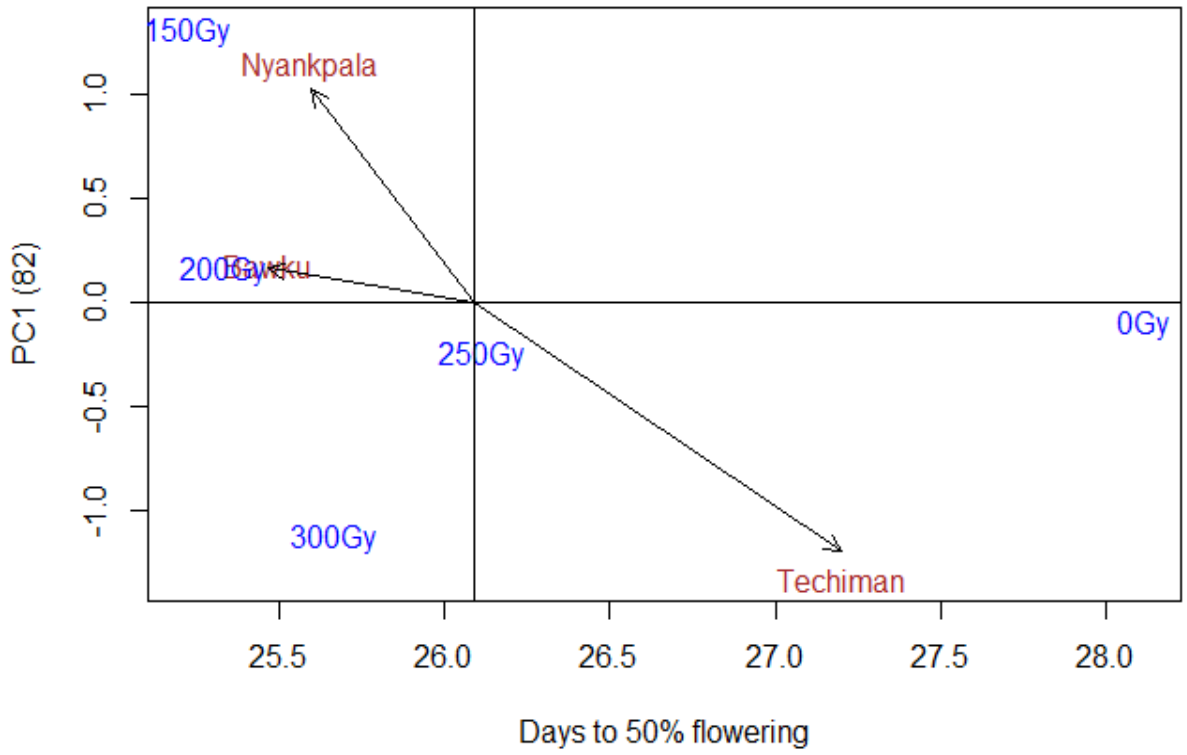

Figure 30: AMMI1 biplot for days to 50% flowering in 2018

4.11.3 Days to maturity

All the main effects as well as the interactive effects were significant ($p < 0.05$) in 2017, however in 2018 ($p < 0.05$), the genotype main effect and the genotype-by-environment interaction were the only components that were significant, ($p < 0.05$). Both AMMI2 in 2017 and AMMI1 in 2018 identified genotypes 150Gy and 300Gy as closest to the origin of the biplots.

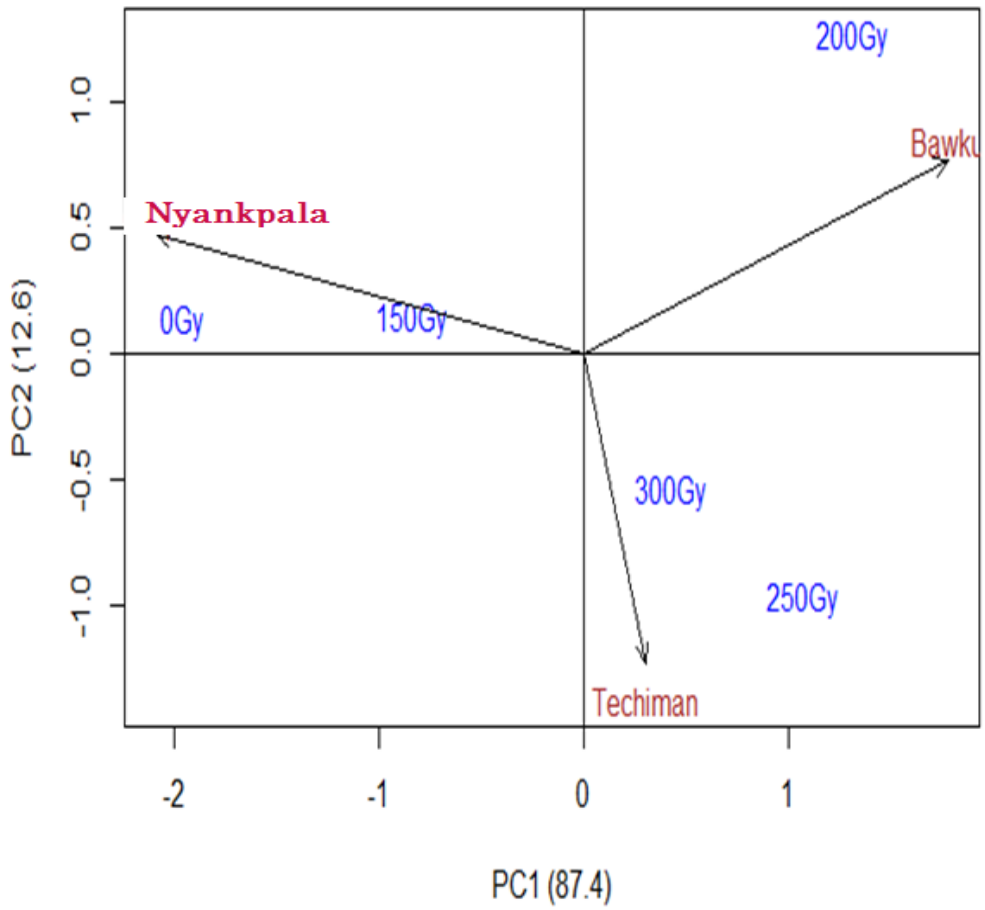

Figure 31: AMMI2 biplot for days to maturity in 2017.

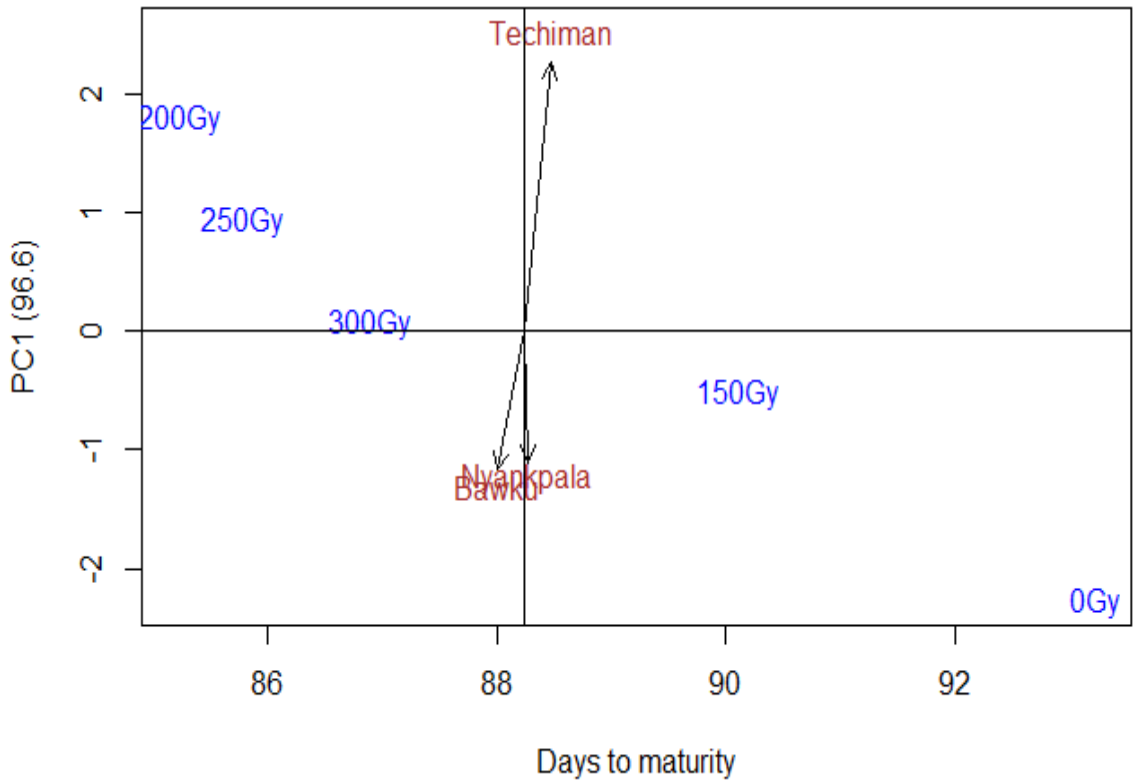

Figure 32: AMMI1 biplot for days to maturity in 2018

4.11.4 Hundred weight

The main effects were significant (P< 0.001) in 2017, however in 2018, all the components were significant (P< 0.001). Genotype 200Gy had the highest hundred seed weight in 2018.

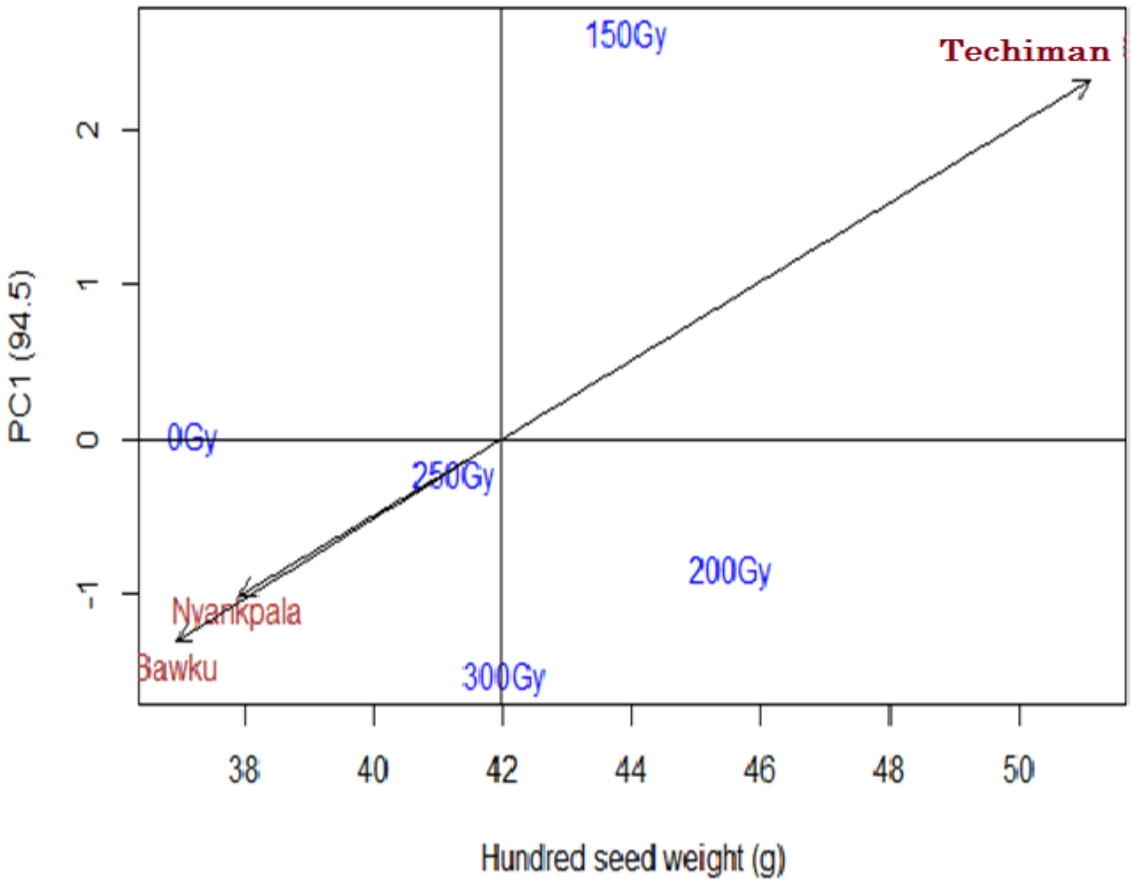

Figure 33: AMMI1 biplot for hundred seed weight in 2018

4.11.5 Number of pod per plant

All components were statistically significant (P< 0.05) in 2017 and 2018. AMMI2 was used in 2017 while AMMI1 was used in 2018. In both cases, genotype 300Gy was the most stable as it was the closest to the biplot origin.

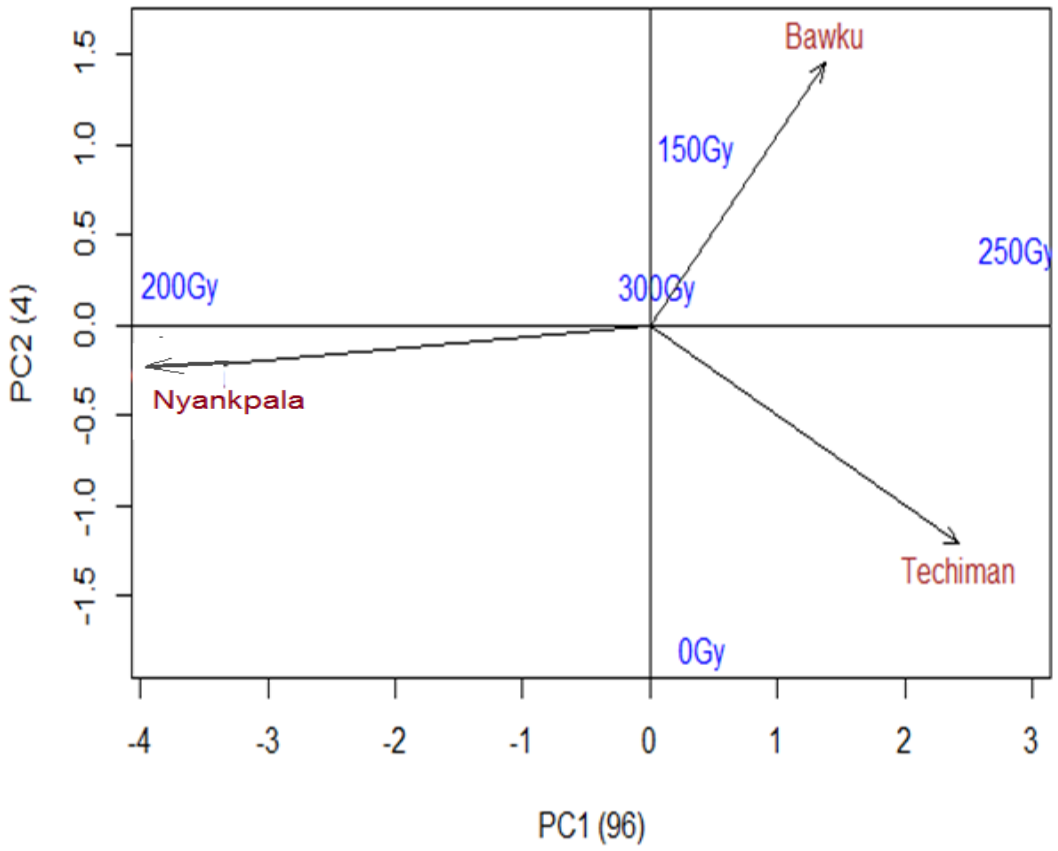

Figure 34: AMMI2 biplot for number of pods per plant in 2017

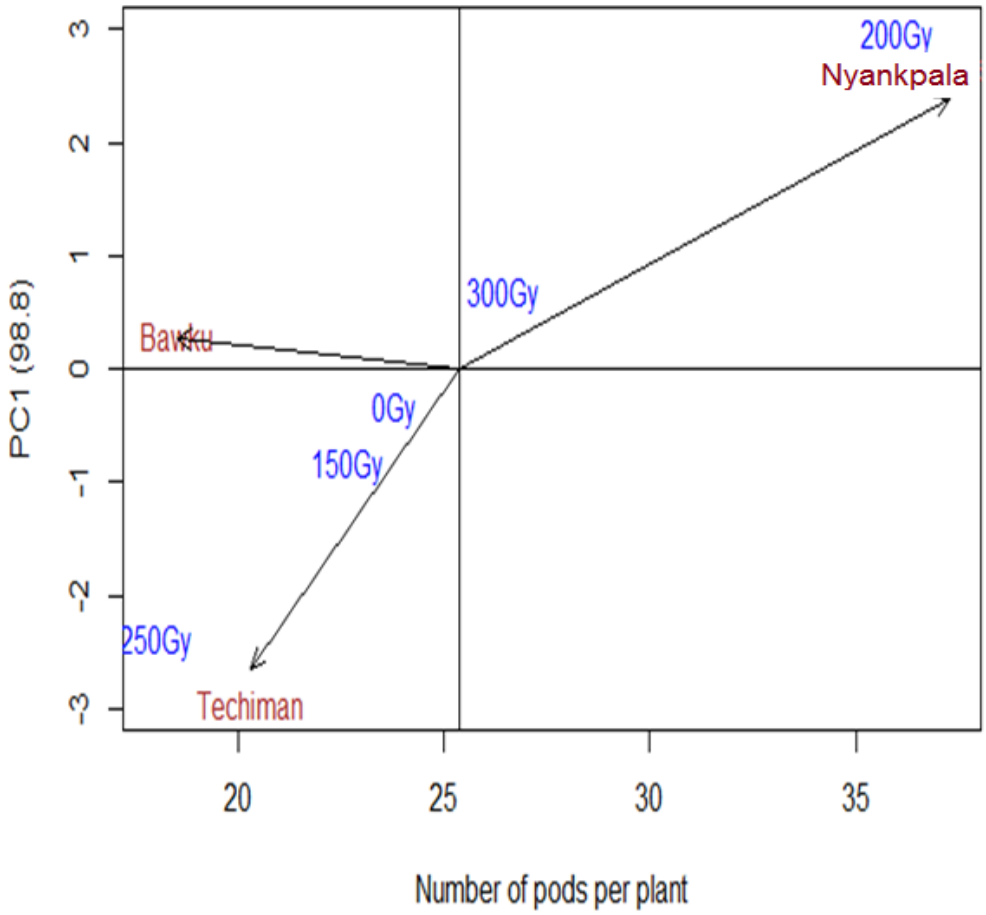

Figure 35: AMMI1 biplot for number of pods per plant in 2018

4.11.6 Total grain yield

All model components were significant in 2017 ($P < 0.05$), however in 2018, only the main effects were different. Genotype 200Gy had the highest grain yield in 2017.

AMMI1 biplot for grain yield in 2017

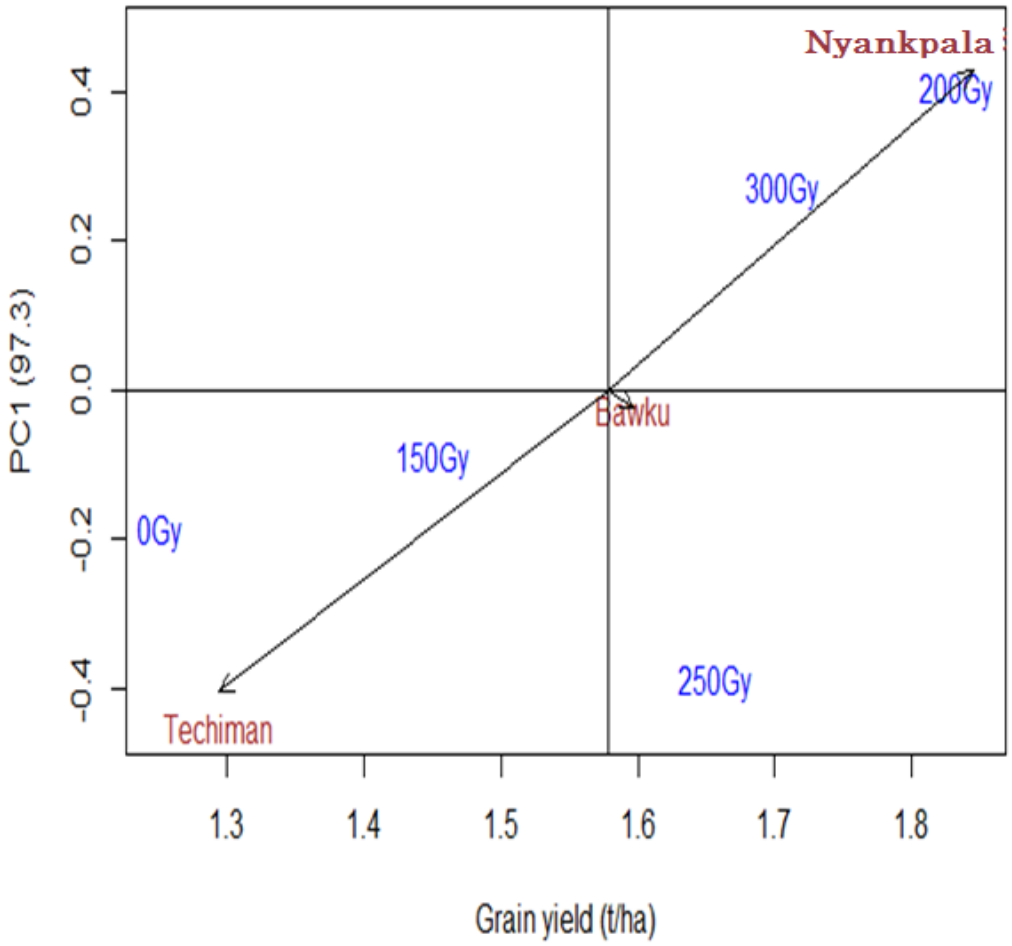

Figure 36 : AMMI1 biplot for grain yield in 2017

CHAPTER FIVE

DISCUSSIONS

5.1. Variation in Growth parameters

Exposure of plant materials to gamma radiation has been reported to give rise to morphological, physiological and biochemical mutants (Songsri *et al*., 2011). Sumira *et al*. (2011) reported that irradiation with lower doses of gamma rays significantly increased vegetative traits while higher doses had inhibitory effects on vegetative parameters. In the present study number of branches increased exponentially for genotype with 200 Gy plants recording the highest number of branches in Bawku whereas 300 Gy and 250 Gy recorded reduction in branching. These results agree with that of Ramachandran and Goud (2014) who reported that higher doses of gamma irradiation reduced plant height, number of leaves and branching capacity of safflower. The variation observed among genotypes and/or plants from different location is probably as a result of genetic makeup of the groundnut genotypes or soil and climatic differences. The observation made with the interactions between locations and the season, of vegetative or growth parameters in this study could be due to G×E interactions. In general the 2018 plants recorded higher number of branches and other vegetative parameters as compared to 2017 season and this might be as a result of yearly changes in climatic factors or differences in conditions prevailing in soils and seasons where the experiments were carried out.

Variation in dosages or concentration of mutagens in earlier studies during mutagenesis might have resulted in changes in photosynthetic rate of plants especially from 200 Gy

that recorded the highest parameters. Pungulani *et al*. (2012) indicated that parameters associated with photosynthesis are good characteristics for selection for yield.

Number of days to flowering is one of the early indicators of maturity of genotype. Zaka *et al*. (2004) had earlier reported a reduction in the number of days to flowering in pea (*Pisum sativum*) following irradiation and this result has been confirmed in the present study. Mutagenesis also decreased the number of days to maturity significantly as compared to the control 0 Gy. The variation in maturity period and earliness to flower were possibly due to induced genotypic modifications in the mutant genotypes and their reactions with the environment. The variation observed with respect to the number of branches and earliness indicate greater sensitivity of the mutant genotypes due to occurrence of more genic chromosomal and physiological disturbances. The most early flowering and matured genotype was 200 Gy followed by 250 Gy evaluated at Nyankpala. The results on locations and seasons interactions revealed that, genotypes took varying days to mature depending on the season and also location. In general, however, genotypes evaluated in 2018 cropping season matured earlier as compared to genotypes evaluated in 2017 cropping season and this could be due to variation not only in genotypes but also climatic and edaphic factors during field experiment.

5.2 Components of yield and total grain yield

Variations in yield performance among genotypes at the test locations and seasons could also be attributed to differences in soil conditions, rainfall patterns, temperatures and relative humidity. These observations are consistent with the findings of Badu-Apraku *et al*. (2003) and Mohammadi *et al*. (2009) who reported that the largest proportion of

total variation in multi-environment trials is attributed to locations, whereas G and G × L sources of variation are relatively smaller. The observed significant G x E (genotype × location; genotype × seasons) interaction for pod yield suggested that the locations in which the genotypes were tested consist of a number of special environments. This highlights the need to identify best performing genotypes for each test sites.

The significant differences observed among locations for traits such as days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, grain yield per plant, 100 seed weight and number of seeds per pod revealed that the genetic expressions of these parameters were influenced by the prevailing environmental conditions at the test locations during the two cropping seasons of 2017 and 2018. Also the significant differences due to genotypes that were observed among the genotypes used points to the fact that the genotypes used in the study were developed from diverse genetic backgrounds. The effects of mutagenesis on genotypes of groundnut as observed in this study could have arisen from changes in genetic material which promoted growth and yield of the plants.

It has been documented that induced mutations can be useful for the alteration of physiological characters (Kiong *et al.*, 2008). This was possibly as a result of genetic improvement of the mutant genotype by gamma irradiation. The result is consistent with the report by Khan *et al.* (2005) which indicated a decrease in number of pods during induced mutation. Similar results have been reported by Ramani and Jadon (2002) in groundnut.

Uguru (2005) reported similar results stating that diverse agronomic characteristics are controlled by diverse genetic factors and so genotypes perform differently in a given

location or a number of locations. Differences in pod yields among test locations studied in the present work may be attributed to the varying genetic composition of the genotypes used in the study. The diverse genetic backgrounds of the genotypes may help explain the observed genotypic variations. The 200 Gy in both cropping seasons recorded the highest total grain yield followed by 250 Gy; and 0 Gy recording the lowest total grain yield. The genotypes at Nyankpala recorded the highest total grain yield followed by genotypes at Bawku and 0Gy recoding the lowest total grain yield for 2017 and 1.27 for 2018 cropping season. The genotypes in 2017 cropping season were observed to record the highest total grain yield while the genotypes evaluated in 2018 cropping season recorded the least total grain yield. Results obtained in this study are consistent with the work of Mensah *et al*. (2005) and Warghat *et al*. (2011). Increases in yield and components of yield as a result of gamma irradiation have been recorded by many authors (Dubey *et al*., 2007; Sharma and Mishra, 2007). Increased number of pods per plant reflected positively on seed yield. Enhancement of seed yield was recorded by Sundaravadivelu *et al*. (2006) in cotton. These results have been confirmed by the findings of this study and agrees with the results obtained by Singh and Singh (2003) in okra.

Generally, higher yields were realized in Nyankpala and Bawku in 2017 than in 2018 cropping seasons, while yields from Techiman in 2018 was higher than that in 2017 cropping season. This clearly indicates that the year with a higher yield provides fairly optimum environmental conditions for the cultivation of groundnuts. The low yields recorded during the 2018 cropping season also confirmed the results of Camberlin and Diop (1999) and Reddy *et al*. (2003). Brink and Belay (2006) also stated that although

groundnut is a drought tolerant crop and can withstand severe lack of water, yields can be adversely reduced. Similar findings were reported by Prathima *et al*. (2011).

Earlier investigations preceding this work used gamma irradiations as mutagen to induce mutation in the seedlot. This created genetic variation which served as the bases of selection of desirable groundnut mutant as reported by Edmeades *et al*. (1997). The biological effect of gamma rays is based on the interaction with atoms or molecules in the cell. These radicals can damage or modify the important components of plant cells and have been reported to affect differentially the morphology, anatomy, biochemistry and physiology of plants depending on the radiation dose (Ashraf *et al*., 2003). The primary trait, pod yield is a complex character governed by a large number of cumulative duplicate, non-dominant genes and is quantitatively inherited (Dorairaj, 1992). The use of secondary traits in breeding significantly improves breeding progress as compared to selection for yield alone (Edmeades *et al*., 1997).

The selection of superior genotypes in earlier studies which preceded this work was based on yield performance and earliness. Based on this, plants from 200 Gy emerged as the best performing genotype across all the test locations in the two seasons, except Techiman. From the results, genotypes 200 Gy exhibited superior yield performances at Nyankpala and Bawku in both seasons. The 200 Gy produces higher total grain yield and also matures earlier compared to the findings of Marfo and Padi (1999), hence recommended to farmers for cultivation at specific locations in the Guinea savannah agroecological zone of Ghana.

5.3 The GGE biplot analysis

In plant breeding, multilocation testing of genotypes is associated with relative performance of genotypes which almost invariably changes from one environment to another. Genotype x environment interaction has over the years, continued to cause setback for plant breeders which necessitate the need to carry out multilocation yield trials to identify and select high yielding genotypes with specific or wide adaptation to diverse agroecological zones. When genotype by environment interaction (GEI) is highly significant for a specific trait such as yield, no valid comparison could be made regarding the relative performance of genotypes over all environments.

In this study, significance of all sources of variation indicated differential behaviour of the tested genotypes, which was not consistent with different environments. Genotypes indicated diversity of tested genotypes, with large difference among genotypic means causing variation in the plant seed yields. However, the pronounced difference in yield and other attributes over locations is an indication that these characters are under both genetic and environmental effects Nath (2002). The higher genotypic variation relative to environmental counterparts is consistent with the autogamous nature of groundnut which shows homozygosity at various locations. The additive main effect and multiplicative interaction (AMMI) model demonstrated the presence of GEI showing that certain genotypes performed better than others and their yield potential differed from location to another.

The consistency of a genotype across several locations is a very important concern for plant breeders. It highlights the ability of a genotype to perform better and determines its stability and ability to adapt to a wide range of locations (Fehr, 1987). The

adaptability parameter showed that genotypes 150 Gy, 250 Gy and 300 Gy were relatively stable whereas 200 Gy far from the origin indicated higher yield environment.

In addition, the observed differences in yield at the different test locations and seasons could be attributed to differences in soil conditions, rainfall patterns, temperatures and relative humidity. This was evident by the higher grain yield performance of genotypes at Nyankpala during the two cropping seasons; a location characterized by sandy loam soils as compared to coarse texture which are weak with low organic matter at Bawku (MoFA, 2019). This is in agreement with De Waele and Swanevelder (2001) who reported that groundnut grows best in well-drained sandy loam soils, as light soil promotes easy pegs penetration and development. The 250 Gy and 150 Gy genotypes showed the highest plant height in Techiman 2018 and 2017 respectively. This is in line with the findings of Jayaraj (2004) who reported an increase plant height in soybean due to gamma rays. Sakin (2002) also observed that, gamma irradiation treatment increased plant height compared with unirradiated seeds. Plants from 0 Gy recorded the highest plant height in two locations and seasons (Nyankpala and Bawku) whilst the 250 Gy and 200 Gy recorded the shortest plant height in both seasons. Reduced height in plants help to prevent lodging and this may led to reduction in yield loss.

There have been reports by several authors on the reduction in sprouting, plant height, leaf number floral abnormalities, branch number, morphological and floral changes in size following irradiation (Dwivedi *et al*., 2009). Ramesh and Reddi (2002) also reported of dose dependent reduction in plant height in irradiated crops of three cultivars of *O. sativa*. The negative effect of increase in dosage of gamma irradiation on plant growth may be due to the inhibition of cell division or elongation, or the alteration of

metabolic processes that affect the synthesis of phytohormones or nucleic acid. The differences in plant height led to a significant difference in the number of leaves produced among the various mutant genotypes.

In general, data obtained on stability showed that none of the tested genotypes could be considered as completely stable. The ideal genotype should have the higher mean performance and be absolutely stable with zero GEI. The stability analysis showed among top yielding genotype 300 Gy appearing as a widely adapted genotype. Genotype 150 Gy and 250 Gy were identified as being averagely stable but very poor in yield. However genotype 200 Gy which was high yielding coupled with its low GEI could be recommended for specific environment which showed good performance. In a biplot display, any genotypes or environments that fall almost on a horizontal line had similar interactions. The closer the point is to the biplot origin, the more stable is the genotype; the more distant, the greater the contribution to the interaction, Yan and Hunt (2002).This was seen in Nyankpala and Bawku on days to maturity.

Based on the biplot analysis 200 Gy, was the highest yielding genotype at Nyankpala and Bawku (best genotype across two test environments); followed by 300 Gy and 150 Gy at Techiman, also emerging as the 2nd and 3rd best genotype across all test environments.

CHAPTER SIX

CONCLUSION AND RECOMMENDATIONS

6.1 Conclusion

Groundnut genotypes were evaluated across three locations during the major seasons of 2017 and 2018 to investigate the genotypes with desirable traits and the influence of G x E interaction on growth and yield performance and stability prior to release as varieties. Most of the genotypes exhibited differential ranking in performance across the test locations, which suggests that evaluation of the genotypes according to their interactions with the studied environments is indeed necessary. The observed variations due to location effects revealed that the genetic expressions of these parameters were influenced by the prevailing environmental conditions. This indicates that environmental factors significantly influenced the performance of genotypes. Generally, higher yields were realized in Nyankpala and Bawku in 2017 than in 2018 cropping season as confirmed by results from both ANOVA and the AMMI biplot analysis. Based on the overall yield performance, 200 Gy emerged as the best performing genotype.

Genotype 200 Gy, which emerged as the highest performer across all test locations, was also identified as an ideal genotype in terms of high yielding ability and stability through the use of the ANOVA and AMMI biplot analysis. Other stable and high yielding genotypes included 150Gy. The ANOVA and AMMI biplot analysis used in this study could assist breeders to make better decisions in variety selection and recommendation for release.

6.2 Recommendations

In the development and release of groundnut genotypes for cultivation, analysis of GEI is necessary to determine the stability of performance of the variety across environments. From this study, genotype 200 Gy is recommended for specific environment across the Guinea Savannah agro ecological zone.

Based on the above results, it is recommended that supplementary test on diseases and pest resistance should be carried out on the high yielding genotype (200 Gy) that was identified from the study in order to generate data to support on-farm testing for possible release in Ghana. Again, genotype from 200 Gy should be subjected to proximate analysis to check the nutritional quality. Genotypes selected from 200 Gy are recommended for farmers in the Guinea Savannah agroecological zone.

REFERENCES

Abalu, G.O.I & Etuk, E.G. (1986). Traditional versus improved groundnut production Practices, Some further evidence from Northern Nigeria. Experimental Agriculture, 22, pp. 33-38.

Abbiw, D. K. (1990). Useful plants of Ghana. Intermediate Technology Publication Ltd. pp. 337.

Abdullah, T., Rahmianna, A. A., Hardaningsih, S. & Rozi, F. (2007). Increasing groundnut yield on dry land Alfisols inIndonesia. *Journal of SAT Agricultural Research* 5(1). pp. 45-47.

Adinya, I. B., Enun, E. E. & Ijoma, J. U. (2010). Exploring profitability potentials in groundnut production through agroforestry practices: a case study in Nigeria. *Journal of Animal and Plant Sciences* 20(2): 123 – 131.

Ahloowalia, B. S., Aaluszynski, M. & Nichterlein, K. (2004). Global impact of mutation -derived varieties. *Euphytica* 135; 187-204

Ahmed, M. I. & Goud. J.V. (1979). Mutagenesis in sunflower: Studies on M1 generation. *Journal of Genetics and Agriculture* 33: 25-36.

Ahmed, S. (1991). Mutation Studies in blackgram (*Vigna mungo* (L.) Hepper). Ph.D. Thesis. Bharathidasan University, Tiruchirappalli, India.

Ali, N. & Malik, N.S. (1992). Performance of short duration groundnut lines suitable to increase cropping intensity in rainfed areas of Pakistan. International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Indian, p. 433.

Ashraf, M., Cheema, A. A., Rashid, M. & Qamar, Z. (2003). Effect of gamma rays on M1 generation in Basmati rice. *Pakistan Journal of Botany* 35(5): 791-795.

Ashraf, Y., Khurshid, A. & Mohamed, Y. (1975). The effect of Ionizing radiation in mung bean (Phaseolus aureus Rokb.). *Pakistan Journal of Genetics* 23: 50-57.

Asibuo, J. Y., Akromah, R., Adu-Dapaah, H. & Safo-Katanka, O. (2008a). Evaluation of nutritional quality of groundnut (Arachis hypogaea L.) from Ghana. *African Journal of Food, Agriculture, Nutrition and Development,* 8(2): 133-150.

Asibuo, J. Y., Akromah, R., Safo Kantanka, O., Adu-Dapaah, H. K., Ohemeng-Dapaah & Agyeman A. (2008b). Inheritance of Fresh Seed Dormancy in Groundnut. *African Journal of Biotechnology*, 7:421-424.

Asibuo, J. Y., Akromah, R., Safo Kantanka, O., Adu-Dapaah, H. K., Ohemeng-Dapaah & Agyeman A. (2008c). Chemical Composition of groundnut (*Arachis hypogaea* L.) Landraces. *African Journal of Biotechnology*, 7(13):2203-2208.

Atuahene-Amankwa, G. & Hossain, M. A. (1988). Groundnut Production and Improvement in Ghana. First ICRISAT Regional Groundnut Meeting for West Africa; 13-16 Sept 1988; Niamey, Niger: ICRISAT.

Atuahene-Amankwah, G. Hossain, M.A. and Assibi, M.A. (1990). Groundnut Production and Improvement in Ghana. First ICRISAT Regional Groundnut Meeting for West Africa, 13-16 Sept. 1988. Niamey, Niger, pp. 45-47.

Awuah, R. T. (2000). Aflatoxigenic fungi and aflatoxin contamination of groundnut based products in Ghana: Implications and concerns. In: R T Awuah and W O Ellis (eds): Proceedings of the National Workshop on Groundnut and Groundnut Aflatoxins. 19-21 September, 1999, Santasi-Kumasi, Ghana. pp 17-26.

Badu-Apraku, B., Abamu, F. J., Menkir, A., Fakorede, M. A. B., Obeng-Antwi, K. & the, C. (2003). Genotype by environment interactions in the regional early variety trials in West and Central Africa. *Maydica,* 48, 93-104.

Bagnal, D. J. & King, R. W. (1991). Response of peanut (*Arachis hypogaea* L.) to temperature, photoperiod and irradiance effect on peg and pod development. *Field crop research* 26: 279 – 293.

Balzarini, M, Setim ela, P. S., Hodson, D. and Vivek, B. (2005). Breeding for improved drought tolerance in maize adapted to southern Africa. Proceedings of the 4th International Crop Science Congress, pp. 630-641.

Bansal u. k., Satija D. R. & Ahuja K. L. (1993). Oil composition of diverse groundnut (*Arachis hypogaea* L) genotypes in relation to different environments. Woodbury, MN. pp. 147-171..

Bäuerl, C., Pérez-Martínez, G., Yan, F., Polk, D. B., & Monedero, V. (2010). Functional analysis of the p40 and p75 proteins from Lactobacillus casei BL23. *Journal of molecular microbiology and biotechnology*, *19*(4), 231-241.

Becker, H. C. & Leon, J. (1988). Stability analysis in plant breeding. *Plant Breeding,* 101:1-23.

Bell, M.J. and G.C. Wright, 1998. Groundnut growth and development in contrasting environments. 2. Heat unit accumulation and photo-thermal effects on harvest index. *Experimental Agriculture.*, 34: 113-124

Beyene, Y., Mugo, S., Mutinda, C., Tefera, T., Karaya, H., Ajanga, S., Shuma, J., Tende, R. & Kega, V. (2011). Genotype by environment interactions and yield stability of

stem borer resistant maize hybrids in Kenya. *African Journal of Biotechnology*, 10(23): 4752-4758.

Biswas, G. C. (2014). Insect pests of groundnut (*Arachis hypogaea* L.), nature of damage and succession with the crop stages. *Bangladesh Journal of Agricultural Research*, 39(2), 273-282.

Bolhuis, G. G., Frinking, H. D., Leeuwaugh, I., Reno, R. G. & Staritsky, G. (1965). Observations on the opening of flowers, dehiscence of anthers and growth of pollen tubes in *Arachis hypogaea*. Netherlands Journal of Agricultural Sciences, 7:138-140.

Booste, K.J. (1982). Growth Stages of Peanut (*Arachis hypogaea* L.). *Peanut Science*, 9: 34-40.

Boote, K. J. & Ketring, D. L. (1990). Peanut. In: Irrigation of agricultural crops; Steward, B. A. and Nielson, D. R. (eds). ASA – CSSA – SSSA, Madison.

Brink, M. & Belay, G. (2006). Cereals and Pulses – PROTA. Foundation and Buckhuys publishers/ CTA. Wageningen, Netherlands. Pp. 20-25.

Brunner, H. (1995). Radiation induced mutation for plant selection, Radiations, 589-594.

Camberlin, P. & Diop, M. (1999). Inter-Relationship between groundnut yield in Senegal, Inter-Annual rainfall variability and sea surface temperatures. *Theoretical and Applied Climatology*, 63 (3 & 4): 163-181.

Carley DH, Fletcher SM. 1995. An overview of world peanut market, In: (ed.) Pattee H.E. and H.T. Stalker, Advances in peanut science, *Amazon Peanut Research and Education Soc. Inc*., Stillwater, Ok, 554–557.

Challinor, A. J., Salingo, J. M., Wheeler, T. R., Craufurd, P. Q. & Grime, D. I. F. (2003). Towards a combined seasonal weather and crop productivity forecasting system: Determination of the spatial correlation scale. *Journal of applied meteorology* 42: 175 – 192.

Chapman, R. S. & Carter, P. L. (2000). Crop Production: Principles and Practices. Surjeet Publications, Delhi, India. 62 (4):16-18

Chin Choy, E.W., J.F. Stone, R.S. Matlock & G.N. McCauley, 1982. Plant population and irrigation effects on Spanish peanuts (*Arachis hypogaea* L.). Peanut Sci., 9: 73-76.

Chong, K., Wynne J.C., Elkan, G.H., & Schneeweis, T.J. (1987). Effects of soil acidity and aluminium content on Rhizobium inoculation, growth, and Nitrogen fixation of peanuts and other grain legumes. *Topical Agriculture*. 64:97-104.

Chopra, V. L. (2005). "Mutagenesis: Investigating the Process and Processing the Outcome for Crop Improvement," *Current Science*, Vol. 89, No. 2, pp. 353-359.

Chowdry, R.K. & Singh, B.P. (1980). Effect of gamma irradiation on germination in pulse crops. Tropical Grain Legume Bulletin, 21: 1-5.

Christensen, J.H., Olesen, J.E., Feddersen, O.H., Andersen, U.J., Heckrath, G., Harpoth, R.& Andersen, L.W. (2004). Application of seasonal climate forecasts for improved management of crops in western Africa. Danish CLIMATE Centre, Report 03-02, pp: 17.

Coffelt, T. A. (1989). Peanut. In: Oil Crops of the World: Their Breeding and Utilization. Robbelen, G., Downey, R. K. and Ashri, A. (eds). *New York: McGraw-Hill Publishing company.* Pp. 319-338.

Craufurd, P.Q., Prasad, P.V.V. & Summerfield, R.J. (2002). Dry matter production and rate of change of harvest index at high temperature in peanut. *Crop Science* 42: 146 – 151.

Crossa, J. (2012). From genotype × environment interaction to gene × environment interaction. Current Genomics, 13: 225-244.

Dabholkar, A. R. (1999). Elements of Bio Metrical Genetics (revised And Enlarged Edition). Concept publishing company.

Dakora, F. D., Abotinga, R. A., Mahama, Y. & Apaseku, J. (1987). Assessment of N_2-fixation in groundnut (*Arachis hypogaea*) and cowpea (*Vigna unguiculata*) and their relative contribution to a succeeding maize crop in Northern Ghana. *MIREEN Journal*, 3:389-399.

Das, S., Maji, A., Singha, P., & Sarkar, K. K. (2007). Selection of some Useful Mutants of Mungbean Vigna radiata (L.) Wilczek in M~ 3 Generation. *environment and ecology*, *25*(2), 258.

David, D.K. (2015). Selection of M3 generation of groundnut and soybean in Guinea savanna zone of Ghana. BSc. Dissertation University for Development Studies

De Waele, D. & Swanevelder, C. J. (2001). Crop production in Tropical Africa. Goikink Graphic nv. Belgium. Pp. 747-753.

Deitos, A., Arnhold, E. & Miranda, G. V. (2006). Yield and combining ability of maize cultivars under different eco-geographic conditions. *Crop Breeding and Applied Biotechnology*, 6: 222-227.

Dias C.T.S., Krzanowski W.J. (2006): Choosing components in the additive main effect and multiplicative interaction (AMMI) models. Scientia Agricola 63: 169–175.

Diop, J. B. & Mirvat, S. (2004). Groundnut Policies, Global Trade Dynamics and Impact of Trade Liberalization. World Bank Policy Research Working Paper 3226.

Dorairaj, M.S., (1992). Preliminary steps for the formulation of selection index for yield in groundnut. *Mandras Agriculture. Journal*., 49: 12-27.

Dubey A.K., Yadav, J.R. & Singh, B. (2007). Studies on induced mutations by gamma ray. *Madras Agricultural Journal,* 56(5):239-243. M

Duke, J. A (1981). Handbook of legumes of world economic importance. New York: Plenum Press. Pp. 134-144.

Dumor, D. (2015). Selection for yield and other agronomic traits in M_3 populations of groundnut (*Arachis hypogaeal*.), cowpea [*Vigna unguiculata* (L.)Walp.] and soybean [*Glycine max* (l.) Merill] in the guinea savannah zone of Ghana. BSc. Dissertation, *University for development studies, Tamale,* 44pp.

Dwivedi S. L., Upadhyaya H. D., Blair W. M., Bartioli D. J., Nielen S., Ortiz R. O. (2009). Enhancing crop gene pools with beneficial traits using wild relatives. *Plant Breed Review.* 30 179–230.

Dwivedi S.L., Nigam SN., Jambunathan R.., Sahrawat KL., Nagabhushanam GVS , & Raghunath K (1996) Effect of Genotypes and Environments on oil and oil quality parameters and their cprrelation in peanut (Arachis hypogeal L.). *Peanut Science* 20:84-89.

Dwivedi SL, Reddy DVR., Nigam SN., Ranga Rao GV., Wightman JA., Amin PW., Nagabhushanam GVS., Reddy AS., Scholberg E, & Ramraj VM (1993) Registration of ICGV 86031 peanut germplasm. *Crop Science* 33:220.

Edmeades, M. Bänziger, H. R. Mickelson, & C. B. Peña-Valdivia (1997). Developing Drought and Low N Tolerant Maize. Proceedings of a Symposium, March 25-29, 1996, CIMMYT, ElBatán, Mexico, 222-234.

Falconer, D. S. & Mackay, T. F. C. (1996). Introduction to quantitative genetics. 4th edition, Longman, New York, P.132-133.

FAO (2006). Plant breeding and genetics Food and Agricultural Organization Production year Book. Vol. 60.

FAO (2014). Plant breeding and Genetics. Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, www-naweb.iea.org. Retrieved 31 July 2014. FAO. Rome, Italy.

FAOSTAT (2010). Available at: http://faostat.fao.org/ (accessed on October 15, 2012).

FAOSTAT (2011). Screening of groundnuts. Available at http://faostat.fao.org. Accessed 17 May 2018.

FAOSTAT (2013). Screening of groundnuts. Available At http://faostat.fao.org. Accessed 22 October 2014.

Fehr, W. R. (1987). Principles of cultivar development. Macmillan publishing company. A Division of Macmillan Inc. New York, 1: 1-465.

Follkerstma, R., Nalini, M. (2009). Opportunities for improving crop water productivity through genetic enhancement of dryland crops. Rainfed Agriculture: Unlocking the Potential. CAB International, 2009.

Frimpong, A., Padi, F. K. & Kombiok, J. (2006). Registration of foliar disease resistant and high-yielding groundnut varieties ICGV 92099 and ICGV 90084. International Arachis Newsletter. no.26.

Gauch H.G., Rodrigues P.C., Munkvold J.D., Heffner E.L., Sorrells M. (2011): Two New Strategies for Detecting and Understanding QTL × Environment Interactions. In Crop Science 51: 96–113.

Gauch, H. G. (2006). Statistical analysis of yield trials by AMMI and GGE. *Crop science*, *46*(4), 1488-1500.

Gauch, H. G. (2013). A simple protocol for AMMI analysis of yield trials. *Crop Science*, *53*(5), 1860-1869.

Gauch, H. G., Piepho, H. P., & Annicchiarico, P. (2008). Statistical analysis of yield trials by AMMI and GGE: Further considerations. *Crop science*, *48*(3), 866-889.

Gauch, H.G. 1992. Statistical analysis of regional yield trials; AMMI analysis of factorial designs. Elsevier Science, New York.

Gauch, H.G., and R.W. Zobel. 1996. AMMI analysis of yield trials. In M.S. Kang and H.G. Gauch (ed.) Genotype by environment interaction. *CRC Press, Boca Raton*, FL. 21:807–832. p. 85–122.

Gibbon, D. & Pain, A. (1985). Crops of the drier regions of the tropics. Longman group, UK limited. pp. 120-127.

Gibbons, R. W. & Martins, J. V. (1980). Proceedings of an international workshop on groundnuts, 13-17 October.ICRISAT, Hyderabad, India.

Giller, K. E. & Wilson, K. J. (1991). Nitrogen fixation in tropical cropping systems. CAB International. Pp. 305.

Gregory W. C., Krapovickas A., Gregory M. P. (1980). "Structure, variation, evolution, and classification in *Arachis*," in *Advances in Legume Science*, Volume 1 edition 2 Summerfield R. J., Bunting A. H., editors. (Kew: Royal Botanic Gardens) 469–481

Gregory, W. C. & Gregory, M. P. (1986). Groundnut (*Arachis hypogaea)* in evolution of crop plants – (ed.) Simmonds. Longman, London. pp. 154 -155.

Gunasekaran, M., Selvaraj, U. & Raveendran, T.S. (1998). Induced polygenic mutation in cowpea. *South Indian Journal of Horticulture*, 46:13-17.

Gupta, P.K. & Yashvir. (2001). Induced mutations in Foxtail millet (Setaria italica Beauv.) available at http://greenplanet.eolss.net/EolssLogn/mss/C10/E1.

Hermelin, T., Daskalov, S., Micke, A., Stonescu, F. & Iuoras, M. (1987). Chimerism in M1 plants of sunflower and its significance of mutation breeding. *Helia.*, 10: 29-30.

Ibrahim, M., Florkowski, W. & Kolavalli, S. (2012). The determinants of farmer adoption of improved peanut varieties and their impact on farm income: Evidence from Northern Ghana. Presented at the Agricultural and Applied Economics Association Annual Meeting, Seattle, WA.

Ibrahim, M., Wojciech J. F. & Kolavalli, S. (2012). The Determinants of Farmer Adoption of Improved Peanut Varieties and Their Impact on Farm Income: Evidence from Northern Ghana. Agricultural and Applied Economics Association Annual Meeting, Seattle, WA, August 12-14, 2012.

ICRISAT. (1992). ICRISAT Groundnut: a global perspective. Available at http://www.icrisat.org. Accessed 3 November 2018.

Ignacimuthu, S. & C. R. Babu. (1988). Radio sensitivity of the wild and cultivated urd and mungbeans. *Indian Journal of Genetics*, 48: 331-342.

Ignacimuthu, S. & Babu, C. R. (1990). Induced variation in yield traits of wild and cultivated beans. *Journal. Nuclear Agriculture*, 19, 119-123.

Ingale S and Shrivastava S. K. (2011). "Nutritional study of new variety of groundnut (*Arachis hypogaea* L.) JL-24 seeds" *African Journal of Food Science* Volume 5(8), pp. 490 - 498

International Agency for Research on Cancer. (1993) some naturally occurring and mycotoxins. IARC monographs on the evaluation of carcinogenic risk of chemicals to humans, vol 56. *International Agency for Research on Cancer, Lyon*, p 571

Issa, A. B. (2009). Genotype by Environment Interaction and yield stability of maize hybrids evaluated in Ethiopia. Thesis pdf. Accessed 6 November 2018.

Jackson, P., Robertson, M., Cooper, M. & Hammer, G. L. (1998). The role of physiological understanding in Plant Breeding: From a breeding perspective. *Field Crops Research*, 49: 11-37.

Jayaraj, M. (2004). Genetic improvement in soybean (Glycine max (L). Merrill) following gamma irradiation. Ph.D. Thesis, Bharathidasan University, Tiruchirappalli. India.

Kandus, M. D., Almorza, R., Boggio, R. and Salerno, J. C. (2010). Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays* L.).

Kang, M. S. & Gorman, D. P. (1989). Genotype by environment interaction in maize. *Agronomy Journal*, 81(4): 662-664.

Kang, M. S. (1996). Using genotype-by-environment interaction for crop cultivar development. *Advances in Agronomy*. 62: 199-252.

Kang, M. S., Balzarini, M. G. & Guerra, J. L. L. (2004). Genotype-by-environment interaction. In (A.M. Saxton Ed.) Genetic Analysis of Complex Traits Using SAS. Cary, NC, USA.

Kang, M. S., Gorman, D. P. & Pham, H. N. (1991). Application of stability statistic to international maize yield trial. Baton Rouge LA, 70803-2110, USA. *Theory of Apply Genetics*, 81:161-165.

Ketring, D. L. (1979). Light effects on development of an indeterminate plant. Plant Physiology 64: 665 – 667.

Ketring, D. L. (1979). Light effects on development of an indeterminate plant. *Plant Physiology* 64: 665 – 667.

Khan M. R., Qureshi A.S., Hussain S.A. & Ibrahim, M. (2005). Genetic Variability Induced by gamma irradiation and Its Modulation with Gibberellic Acid in M2 Generation of Chickpea (*Cicer arietinum* L.), *Pakistan Journal of Botany*, Volume 37, No. 2, Pp. 285-292.

Khan, A. (1987). Effect of selection for improvement of quantitative characters in irradiation population of mungbean. *Journal of Nuclear Agriculture and Biology*, 16: 5-8.

Khan, A. (1988). Mutation studies in Mungbean IX estimates of genetic variability. *Legume Research*, 11: 89-93.

Kharkwal, M. C. & Shu, Q. Y. (2008). "The role of induced mutations in world food security" (PDF). Induced plant mutations in the gemomics era. Proceedings of an international joint FAO/IAEA Symposium, 2008 2009. Vienna, Austria: Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency: 33-38.ISBN 9789251063248.

Kiong, A., Ling Pick, A., Grace Lai, S.H. &Harun, A.R. (2008).Physiological responses of orthosiphon stamineus plantlets to gamma irradiation. *Am-Eurasian Journal of Sustainable Agriculture*, 2(2): 135-149.

Knauft, D. A. & Wynne, J. C. (1995). Peanut breeding and genetics. *Advances in Agronomy*, 55:393-445.

Knauft, D. A., Norden, A. J. & Gorbet, D. W. (1987). Peanut. In: Principles of cultivar development (Fehr, W. R., Fehr, E. L., and Jessen, H. J. (Eds.). Vol. 2. New York, USA: Macmillan. Pp. 346-384.

Kochhar, S. L. (1986) Tropical crops a textbook of economic botany. Macmillan Publishers Ltd pp. 157.

Krapovickas, A & Gregory, WC (1994). Correlation Studies of 21 Traits in F2 Generation of Groundnut (*Arachis hypogaea* L.). *Pakistan Journal of Biological Sciences*, 9: 929-934

Kwarteng, J. A & Towler, M. J. (1994). Agriculture for West African Schools and Colleges. The Macmillan press Limited. pp.321.

Lanier, J.E., D.L. Jordan, J.F. Spears, R. Wells and P.D. Johnson. (2014). Peanut response to planting pattern, row spacing and irrigation. *Agronomy Journal*. 96: 1066-1072.

Lanier, J.E., Jordan, D.L Spears, J.F. Wells R. & P.D. Johnson et al., (2004). Peanut response to planting pattern, row spacing and irrigation. *Agronomy Journal*. 96: 1066-1072.

Lawson, I.Y.D., Issahaku, A., Acheampong, S.K., Adams, B. & Tuffour, V. (2013). Time of planting and weed suppression abilities of some legumes intercropped

with maize in the Guinea Savannah zone of Ghana. *Agriculture Journal. North America,* 4:358-363.

Linnemann, A. R., Westphal, E. & Wessel, M. (1995). Photoperiod regulation of development and growth in bambara groundnut (*Vigna subterranea*). *Field Crops Research,* 40(1):39-47.

Lucas, A., Morley, R., Cole, T. J., Lister, G., & Leeson-Payne, C. (1992). Breast milk and subsequent intelligence quotient in children born preterm. *The Lancet*, *339*(8788), 261-264.

Maluszynski, K. N., Zanten, L.Van Zzanten, & Ahlowalia, B. S. (2000). Officially released mutant varieties. The FAO/LAEA Database. *Mutation Breeding*. 12: 1-84.

Marfo, K. O., & Padi, F. K. (1999). Yield stability of some groundnut accessions in Northern Region, Ghana. *Journal of Developments in Sustainable Agriculture*, 6(2), 199-214.

Mensah, J. K. & Obadoni, B. (2007). Effects of sodium azide on yield parameters of groundnut (*Arachis hypogaea* L.). *African Journal of Biotechnology*. Volume 6. No. 6. pp. 668-671.

Mensah, J. K., Akomeah, P. A. & Ekpekurede, E. O. (2005). Gamma irradiation induced variation of yield parameters in cowpea (*Vigna uguiculata* (L.) Walp). *Global Journal of Pure and Applied Science,* 11(3):327-330.

Micke, A. (1988). Genetic improvement of grain legumes using induced mutations. An overview In: Improvement of Grain Legume Production Using Induced Mutations. IAEA, Vienna, pp. 1-51.

Micke, A. (2004). Mutation breeding of grain legumes. *Journal of Plant and Soil*, 152 (1): 81-85.

Mishra, V. K. & Kumar, Y. (2007). Effect of gamma rays and diethyl sulphate on germination, growth, fertility and yield in green gram. Annual Agricultural Research, 20: 144-147.

Mishra, V. K. and Kumar, Y. (1999). Effect of gamma rays and diethyl sulphate on germination, growth, fertility and yield in green gram. *Annual Agricultural Research*, 20: 144-147.

MoFA (2019). Agriculture in Ghana: Facts and Figures. Accra: Ministry of Food and Agriculture, Statistics, Research and Information Directorate, 2019.

MOFA, (1997), Agriculture in Ghana. Fact and figures. Policy planning, monitoring and evaluation. Ministry of food and agriculture. Accra, Ghana 63-67

Mohamed, H.A. (1984). Varietal differences in the temperature responses of germination and crop establishment. Ph.D.Thesis, University of Nottingham, Nottingham, U.K. University of Nottingham, U.K.

Mohammadi, R., Amri, A., Haghparast, R., Sadeghzadeh, D., Armion, M. & Ahmadi, M. M. (2009). Pattern analysis of genotype-by-environment interaction for grain yield in durum wheat. *Journal of Agricultural Science*, 147, 537-545.

Mohanty, S. K., Baisak, B. & Dikshit. W. N. (1998). Improvement of genetic archietecture of a local cultivar kalamung of green mung by mutation. *Legume*. Registered. 21: 125-127.

Morie, M.J., Klobe, D. & Skold, L.N. (1981). Differential and combined effect of beta, gamma and fast neutron irradiation on soybean seedling. *Journal of Heredity*, 10: 4 29-435.

Mudibu J., K. K. Nkongolo, A. Kalonji-Mbuyi & Kizungu, R. (2010). "Effect of Gamma Irradiation on Morphological Agronomic Characteristics of Soybeans (Glycine max L.)," *American journal of plant science* vol.3 no.3 pp. 331-337.

Mulei, W. M., Ibumi, M. & Woomer, P.L. (2011). Grain Legume Processing Handbook: Value Addition to Bean, Cowpea, Groundnut and Soybean by Small-Scale African Farmers. Tropical Soil Biology and Fertility Institute of the International Centre for Tropical Agriculture. Nairobi. Pp 42.

Nath U. K., Alam M. S. (2002). Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea* L.). *Journal of Biology and Science.* 2 762–764

Nautiyal, P.C. (2002). Groundnut: Post-harvest Operations. Mejia, D. (Ed) ICAR (National Research Center for Groundnut). Pp 16.

Ndjeunga, J., Ntare, B., Waliyar, F., Echekwu, C., Kodio, O., Kapran, I. & Diallo, A. (2008). Breeding beans for smallholder farmers in Eastern, Central and Southern Africa: 24, Patancheru: ICRISAT.

Nigam, S. N., Vasudeva Rao, M. J. & Gibbons, R. W. (1990). Artificial hybridization in groundnut. Information Bulletin no. 29. Patancheru, A.P. 502 324, India: International Crops Research Institute for the Semi-Arid Tropics.

Nigam, S.N., Rao, R.C.N., & Wynne J.C. (1998). Effects of temperature and photoperiod on vegetative and reproductive growth of groundnut (*Arachis hypogaea* L.). *Journal of Agronomy and Crop Science* 181:117-124.

Nigam, S.N., Rao, R.C.N., Wynne, J.C., Williams, J.H., Fitzner, M. & Nagabhushanam, G.V.S. (1994). Effect and interaction of temperature and photoperiod on growth and partitioning in three groundnut (*Arachis hypogaea* L.) genotypes. *Annals of Applied Biology* 125: 541-552.

Novak F. J. & Brunner, H. (1992). 'Plant breeding: Induced mutation technology for improvement in crop'. IAEA bulletin 4/, pp. 25-33.

Novak, F. J. & Brunner, H. (1995). Plant breeding: Induced mutation technology for improvement in crop'. IAEA bulletin 4/, pp. 25-33.

Ntare, B. R. (2007). *Arachis hypogaea* L. Invan der Vossen, H.A.M. & Mkamilo, G.S. (eds.), PROTA14: Vegetable oils/Oleagineux.[CD-ROM] .PROTA, Wageningen, Netherlands.

Ntare, B. R., Diallo, A. T., Ndejenga R. & Waliyar, F. (2008). Groundnut seeeds production manual. Patancheru 502 324, Andhra Pradesh, India; international crops Reseach institute for Semi-Arid Tropics (ICRISAT).P.20. The FAO/IAEA Databse. Mutation Breed. Revised. 12: 1-12.

Nutsugah, S. K., Oti-Boateng, C., Tsigbey, F. K. & Brandenburg, R. L. (2007). Assessment of yield losses due to early and late leaf spots of groundnut (*Arachis hypogaea* L.) *Ghana Journal of Agriculture Science,* 40(1): 21-26.

Oaya, C. S., Malgwi, A. M., & Samaila, A. E. (2012). Damage Potential and Loss Caused By the Groundnut Bruchid Caryedon Serratus Olivier (*Coleoptera:*

Bruchidae) on Stored Groundnut and Tamarind in Yola. *IOSR Journal of Agriculture and Veterinary Science*, 1(6), 58-62.

Odewale, J. O., Collins, A., Ataga, C. D., Odiowaya, G., Ahanor, M. J., Edokpayi, A. A., Okoye, M. N. & Uwadiae, E. O. (2012). Comparison of yield and stability assessment of five coconut (*Cocos nucifera* L.) varieties in a lethal yellow disease (LYD) endemic field over nine different environments. *World Journal of Agricultural Sciences*, 8 (3): 229-233: 1817-2047.

Ojomo, A. O., Omueti, O., Raji, J. A. &Omueti, O. (1979). "Studies in Induced Mutation in Cowpea, 5. The Variation in Protein Content Following Ionizing Radiation," *Journal of Applied Science*, Vol. 21, pp. 61-64.

Owens, B. (1999). Virginia-Carolina Peanut Promotions: A short peanut history. Available at: http://aboutpeanuts.com/every.html#anchor241393. Accessed 14/05/2018

Packiaraj, D. (1988). Studies on induced mutagenesis of parents and hybrid in cowpea (*Vigna unguiculata* (L.)Walp.). M.Sc. (Ag.) Thesis, Tamil Nadu Agriculture University, Coimbatore.

Packiaraj, D. (1998). Studies on induced mutagenesis of parents and hybrid in cowpea [*Vigna unguiculata* (L.)Walp.]. M.Sc. (Ag.) Thesis, Tamil Nadu Agriculture University, Coimbatore.

Peipho, H. P. & Mohring, J. (2005). Best Linear unbiased prediction of cultivar effects for subdivided target regions. *Crop Science*, 45: 1151-1159.

Porter, D. M. (1997). The peanut plant. In: Compendium of peanut diseases. 2nd Edition, APS Press, USA. pp. 1-2.

Prasad, P. V. V., Craufurd, P. Q., Summerfield, R. J. & Wheeler, T. R. (1998). Sensitivity of fruit set to heat stress in groundnut. *Journal of Experimental Botany*, 40: 30.

Prasad, P. V. V., Craufurd, P. Q., Summerfield, R. J. and Wheeler, T. R. (1999). Sensitivity of fruit set to heat stress in groundnut. *Journal of Experimental Botany, 40: 30*.

Prathima, T., Yellamanda Reddy, T., Murali Krishna, T., Devaki, K., Sudhakar, P., Sarala, N. V., Muneendra Babu, A., & Naga Madhuri, K. V. (2011). Validation of peanut growth model for moisture stress effects on rainfed groundnut in major crop growing areas of Andhra Pradesh, India - A critical review. *International Journal of Applied Biology and Pharmaceutical Technology*, 2(4) 482-509.

Pungulani, L., Kadyampakeni, D., Nsapato, L. & Kachapila, M. (2012). Selection of high yielding and farmers' preferred genotypes of bambara nut (*Vigna subterranean* (L.) Verdc) in Malawi. *American Journal of Plant Sciences*, 3, 1802-1808.

Purseglove, J.W. (1998). Tropical crops-Dicotyledon. Longman pp. 225-235.

Rahman, N. A., Terry, A. Alimatu, S., Frimpong, S. & Arnold, A. (2019). Improved *Arachis hypogeae* variety effect on grain yield, fodder quality and livestock growth. *Agriculture and Natural Resources*, [S.l.], No. 3. Vo. 53, Pp. 244–250.

Rajendiran, K. (1993). Morphological and cytological variations induced in *Helianthus annus* L. By gamma irradiation. *Indian Journal of Botany*. Contactor, 10: 89-96.

Ramachandran, M. & Goud, J. V. (2014). Mutagenesis in sunflower (*Carthamus tinctorius*). Differential Radiation. 63 (3 & 4): 163-181

Ramagosa, I., Fox, P. N., Garcia Del Moral, L. F., Ramos, J. M., Roca De Togores, F. and Molina Cano, J. L. (1993). Integration of statistical and physiological analyses of adaptation of near-isogenic barley lines. Theory of Applied Genetics, 86, 822-826.

Ramani, G. M. and Jadon, B. S. (1991). Induced Variability in Groundnut in M2 Generation, *Gujarat Agricultural University Research Journal*, Vol. 16, No. 2, 1991, pp. 23-26.

Ramesh, D.V. & Seetharam, I. R. T. (2002). Induced morphological variability among three genotypes of rice, *J. Cyto. Genet.* 3 (NS) pp.115-120.

Rao, H. S. B., Venkatesh, B., Rao, T. V. & Reddy, K. H. C. (2013). Experimental investigation on engine performance of diesel engine operating on peanut seed oil biodiesel blends. International Journal of Current Engineering and Technology 3(4): 1429 – 1435.

Raveendran, P., (1998). Induced mutation studies in cowpea (*Vigna unguiculata* (L.) walp for crop improvement Ph.D. Thesis, Bharathidasan University.

Reddy, E. Y., Reddy, V. R. & Anbumozhi, V. (2003). Physiological responses of groundnut (*Arachis hypogaea* L.) to drought stress and its amelioration: a critical review. *Plant Growth Regulation*, 41: 75-88.

Ribaut, J. M., Bänziger, M., Setter, T., Edmeades, G., & Hoisington, D. (2004). Genetic dissection of drought tolerance in maize: a case study. *Physiology and biotechnology integration for plant breeding*, *15*, 571-609.

Rodriques, P., Dasgupta, A., Patwardhan, A., Nagpal, S., Karunakaran, T. and Saxena, N. (2014). Report of the Working Group on Science and Technology for Small and

Medium Scale Enterprises for the Eleventh Five Year Plan 2007 - 2012. *The Working Group, New Delhi, India*. 28pp.

Sakin, M. A. (2002). The use of induced micro mutation for quantitative characters after EMS and gamma ray treatments in durum wheat breeding. *Pakistan Journal of Applied Sciences* 2(12): 1102-1107.

SARI (2004). Annual report for the year (2004), Savannah Agricultural Research Institute, Nyankpala, Ghana, Pp. 22.

Sarkar, K.K., Sharma S. & Hussain M. (1996). Induced genetic variability in mungbean in M1 generation. *Environmental Ecology*. 14: 815-817.

Savage, G. P. & Keenan, J. I. (1994). The composition and nutritive value of groundnut kernel. The groundnut crop. A scientific basis for improvement. J. Smart (ed). Chapman and Hall, London. Pages 173-213

Schilling, R. & Gibbon, R. (2002). Groundnut. Macmillan Education Limited, London and Oxford. pp. 1-93.

Settaluri, V.S., Kandala, C. V. K., Puppala, N. & Sundaram,J. (2012).Peanut and their nutritive aspects- review. vol 3, No 12.

Shanthala, J., Gururaja Rao, M. R., Gangappa, E. & Venkataravana, P. (2012). Enhanced variability due to shifts in mean created through induced mutation, hybridization and its combination in groundnut (*Arachis hypogaea* L.). International Journal of Plant Science, 8 (1): 1-9.

Shanthala, J., Gururaja Rao, M. R., Gangappa, E. & Venkataravana, P. (2013). Enhanced variability due to shifts in mean created through induced mutation,

hybridization and its combination in groundnut (*Arachis hypogaea* L.*). International Journal of Plant Science*, 8 (1): 1-9.

Sharma BK & Mishra MN (2007). Micro-mutations for fruit number, fruit length and fruit yield characters in gamma-irradiated generation of ANKUR-40 variety of okra [*Abelmoschus esculentus* (L.) Monech]. *International Journal. Plant Science*. Muzaffarnagar 2(2): 208-211.

Shew, B. B., Beute, M. K. & Stalker, H. T. (1995). Towards sustainable peanut production: Progression in breeding for resistance to foliar and soil borne pathogens of peanut. Plant Distance. 79: 1259-1261.

Singh A. K., Mehan V. K., & Nigam S. N. (1997). Sources of Resistance to Groundnut Fungal and Bacterial Diseases: An Update and Appraisal. Information Bulletin no. 50. Patancheru: ICRISAT

Singh, J. & Singh, S. (2001). Induced mutations in basmati rice (*Oryza sativa* L.). Diamond Jubilee Symposium, New Delhi, pp. 212.

Singh, V. & Singh, F. (2003) Stability of yield and yield component characters in chickpea. *Indian Journal of Genetics and Plant Breeding* 51, 183–189

Sivakumar, M. V. K., Maidouka, A. & Stern, R. D. (1993). Agro-climatology of West Africa: Niger. Information Bulleting No. 5. Patancheru, ICRISAT.

Smith, A. B., Cullis, B. R. and Thompson, R. (2005). The analysis of crop cultivar breeding and evaluation trials: an overview of current mixed model approaches. *Journal of Agricultural Science*, 143: 449-462.

Smith, A. B., Cullis, B. R., & Thompson, R. (2005). The analysis of crop cultivar breeding and evaluation trials: an overview of current mixed model approaches. *The Journal of Agricultural Science*, *143*(6), 449-462.

Songsri, P., Suriharn, B., Sanitchon, J., Srisawangwong, S., & Kesmala, T. (2011). Effects of gamma radiation on germination and growth characteristics of physic nut (*Jatropha curcas* L.). *Journal of Biological Sciences*, *11*(3), 268-274.

Souza, L. V. D., Miranda, G. V., Galvão, J. C. C., Eckert, F. R., Mantovani, É. E., Lima, R. O., & Guimarães, L. J. M. (2008). Genetic control of grain yield and nitrogen use efficiency in tropical maize. *Pesquisa Agropecuária Brasileira*, *43*(11), 1517-1523.

Sree Rengasamy, S.R. (1988). In vitro culture studies in sesame (*Seasmum indicum*) oil crops Newsletter. 9: 34-37.

Sumira, J., Talat, P., & Siddiqi, T. O. (2011). Gamma radiation effects on growth and yield attributes of Psoralea corylifolia L. with reference to enhanced production of psoralen. *Plant Growth Regulation*, *64*(2), 163-171.

Sundaravadivelu, K., Ranjithselvi, P., & Reddy, V. R. K. (2006). Induced genetic variability in cotton (*Gossypium hirsutum* L.) for yield and its components. *CROP RESEARCH-HISAR-*, *32*(3), 442.

Suzuki, D., Griffiths, A. & Lewontin, R. (1981). An introduction to genetic analysis. W. H. Freeman and Company. San Francisco, USA. Pp. 220-242

Takagi, Y. and Anai, T. (2006). Development of Novel Fatty Acid Composition in Soybean Oil by Induced Mutation," Oleoscience, Vol. 6, No. 4, pp. 195-203.

Takagi, Y., Rahman, S. M., & Anai, T. (1998). Construction of novel fatty acid composition in soybean oil by induced mutation. In *Gamma Field Symposia* (Vol. 37, pp. 17-28).

Thakur, S. B., Ghimire, S. K., Shrestha, S. M., Chaudhary, N. K., & Mishra, B. (2013). Variability in groundnut genotypes for tolerance to drought. *Nepal Journal of Science and Technology*, *14*(1), 41-50.

Thirugnanakumar, S. (1986). Studies on induced mutagenesis in cowpea, (*Vigna unguiculata* (L.) walp.) M.Sc., (Agric.) Thesis, Tamil Nadu Agriculture University of Coimbatore.

Toker, C., Uzun, B., Canci, H., & Ceylan, F. O. (2005). Effects of gamma irradiation on the shoot length of Cicer seeds. *Radiation Physics and Chemistry*, *73*(6), 365-367.

Tsigbey, F. K., Brandenburg, R. L. & Clottey, V. A. (2004). Peanut production methods in Northern Ghana and some disease perspectives. World Geography of the Peanut. pp. 1-10.

Tweneboah, C. K. (2000). Modern Agriculture in the Tropics with special reference to Ghana. Co-Wood Publishers, Accra, Ghana. pp. 189-190.

Uguru, M. I. (2005). Crop Genetics and Breeding (Revised). Epharata Press, Nsukka, Enugu State, Nigeria. P. 113.

USDA (2010). Top ten producers of peanut in 2008/2009. Foreign Agricultural Services. In: Wikipedia encyclopedia. en.wikipedia.org/wiki/peanut.

Vadivelu, K. K., & Rathinam, M. (1980). Mutagenicity of gamma rays and EMS and their combination in Bengalgram (Cicer arietinum L.). *Madras agricultural journal*. Pp. 33-62

Vargas, M., Crossa, J., Van Eeuwijk, F. A., Ramirez, M. E. and Sayre, K. (1999). Using AMMI, factorial regression and partial least squares regression models for interpreting genotype by environment interaction. Crop Science, 39: 955-967. V

Vargas, M., Crossa, J., Van Eeuwijk, F. A., Ramirez, M. E., & Sayre, K. (1999). Using AMMI, factorial regression and partial least squares regression models for interpreting genotype x environment interaction. *Crop Science*, *39*(4), 955-967.

Verma, R. K., & Singh, D. P. (1984). Gamma-ray induced variability in greengram. *Indian Journal of Agricultural Science*, *54*(4), 277-279.

Vijaya Kumar, P., Ramakrishna, Y. S., Krishna-Murty, K., & Ashok-Kumar, B. (1997). Identifying the climatic constraints for optimum production of groundnut and delineating the areas with highest production potential on climatic basis. In *Proc. of the symposium on Tropical crop Research and Development India International, Trissur, India*.

Waele, D., & Swanevelder, C. J. (2001). Crop production in tropical Africa. *Goikink Graphic nv. Belgium*, 747-753.

Waliyar, F., Kumar, P. L., Ntare, B. R., Monyo, E., Nigam, S. N., Reddy, A. S., Osiru, M., & Diallo, A. T. (2006). A Century of Research on Groundnut Rosette Disease and its Management (Information Bulletin, 75).

Waliyar, F., Kumar, P. L., Ntare, B. R., Monyo, E., Nigam, S. N., Reddy, A. S., & Diallo, A. T. (2007). A century of research on groundnut rosette disease and its management. *Information Bulletin no*. 75.

Warghat, A.R., Rampure, N.H. and Wagh, P. (2011). Effect of Sodium azide and Gamma rays treatments on percentage germination, survival, morphological variation and chlorophyll mutation in Musk okra, (*Abelmoschus moschatus* L.). *International Journal of pharmacy and pharmaceutical science*. Pp. 66-93

Weiss, E. A. (2000). Oilseed crops. Blackwell Science. London

Whitty, J. M., Phillips, N. M., Morgan, D. L., Chaplin, J. A., Thorburn, D. C., & Peverell, S. C. (2008). Habitat associations of Freshwater Sawfish (*Pristis microdon*) and Northern River Sharks (*Glyphis sp*. C): including genetic analysis of P. microdon across northern Australia.

Wright, D. L., Tillman, B., Jowers, E., Marios, J., Ferell, J. A., Katsvairo, T. & Whitty, E. B. (2009). Management and Cultural Practices for Peanuts. Publication SS–AGR–74 (www.edis.ifas.ufl.edu. Accessed 29 May 2014).

Wumbei, A. K., Koyiri, G., Ayariga, S. K., Anglarere, J., & Paul, F. (2000). Report on Women Income Generating Activities. *A Study for IFAD/MoFA, Northern Region, Ghana*.

Wynne, J. C., Beute, M. K. and Nigam, S. M. (1992). Breeding for disease resistance in peanut (*Arachis hypogaea* L.) *Annual Review of phytopathology*. 48: 160-165.

Wynne, J. C., Beute, M. K., & Nigam, S. N. (1991). Breeding for disease resistance in peanut (Arachis hypogaea L.). *Annual Review of Phytopathology*, *29*(1), 279-303.

Yan R. C., Crossa J., Cornelius P.L., Burgue˜no J. (2009): Biplot analysis of genotype × environment interaction: Proceed with caution. Crop Science. 49: 1564–1576.

Yan W., Kang M.S., Ma B., Woods S., Cornelius P.L. (2007): GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Science. 47: 643–655.

Yan, W. & Kang, M. S. (2003). GGE bi-plot analysis: A graphical tool for breeders, geneticists, and agronomists. 1st Edition, CRC Press, LLC. Boca Raton, Florida, USA. Pp. 271.

Yan, W. (2001). GGE Biplot - A windows application for graphical analysis of multienvironment trial data and other types of two-way data. *Agronomy Journal*, 93:1111-1118.

Yan, W., & Hunt, L. A. (1998). Genotype by environment interaction and crop yield. *Plant Breeding Reviews*, *16*, 135-178.

Yan, W., & Hunt, L. A. (2002). Biplot analysis of diallel data. *Crop Science*, *42*(1), 21-30.

Yan, W., Cornelius, P. L., Crossa, J., & Hunt, L. A. (2001). Two types of GGE biplots for analyzing multi-environment trial data. *Crop Science*, *41*(3), 656-663.

Yan, W., Hunt, L. A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, *40*(3), 597-605.

Yau, S. K. (1995). Regression and AMMI analyses of genotype× environment interactions: An empirical comparison. *Agronomy Journal*, *87*(1), 121-126.

Yav, A. S., Richard, A., Osei, A. K., Kofi, A. D. H., Seth, O. D. and Adelaide, A. (2008). Chemical composition of groundnut, (*Arachis hypogeal* (L) landraces. *African Journal of Biotechnology* 7: 2203 – 2208.

Yayeh, Z. and Bosland, P. W. (2000). Evaluation of genotype, environment and genotype-by-environment interaction for capsaicinoids in *Capsicum annum* L. *Euphytical*, 111: 185-190.

Zaka, R., Chenal, C., & Misset, M. T. (2004). Effects of low doses of short-term gamma irradiation on growth and development through two generations of Pisum sativum. *Science of the total environment*, *320*(2-3), 121-129.

Zaman, M. A., Tuhina-Khatun, M., Ullah, M. Z., Moniruzzamn, M., & Alam, K. H. (2011). Genetic variability and path analysis of groundnut (Arachis hypogaea L.). *The Agriculturists*, *9*(1-2), 29-36.

Zewdie, Y., & Bosland, P. W. (2000). Evaluation of genotype, environment, and genotype-by-environment interaction for capsaicinoids in Capsicum annuum L. *Euphytica*, *111*(3), 185-190.

Živanović, T., Vračarević, M., Krstanović, S., & Šurlan-Momirović, G. (2004). Selection on uniformity and yield stability in maize. *Journal of Agricultural Sciences*, *49*(1), 117-130.

APPENDICES

Appendix 1: Analysis of variance for plant height of groundnut *(Arachis hypogaea* L.*)* 4WAP

Variate: Ht_at_4WAP

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	51.817	12.954	7.64	<.001
Location	2	1306.250	653.125	385.16	<.001
Season	1	28.866	28.866	17.02	<.001
Genotype. Location	8	35.107	4.388	2.59	0.017
Genotype. Season	4	1.463	0.366	0.22	0.929
Location. Season	2	853.325	426.662	251.61	<.001
Genotype.Location.season	8	3.813	0.477	0.28	0.970
Residual	58	98.352	1.696		
Total	89	2383.492			

Appendix 2: Analysis of variance for plant height of groundnut *(Arachis hypogaea* L.*)* 10WAP

Variate: Ht_at_10_WAP

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	320.864	80.216	20.72	<.001
Location	2	7529.740	3764.870	972.70	<.001
Season	1	91.748	91.748	23.70	<.001
Genotype. Location	8	297.194	37.149	9.60	<.001
Genotype. Season	4	55.397	13.849	3.58	0.011
Location. Season	2	410.558	205.279	53.04	<.001
Genotype.Location.season	8	81.062	10.133	2.62	0.016
Residual	58	224.492	3.871		
Total	89	9026.896			

Appendix 3: Analysis of variance for number of leafs of groundnut (*Arachishypogaea L.)* 4WAP

Variate: Leaf_No_4WAP

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	781.889	195.472	27.19	<.001
Location	2	3282.200	1641.100	228.28	<.001
season	1	8448.711	8448.711	1175.25	<.001
Genotype. Location	8	149.244	18.656	2.60	0.017
Genotype. Season	4	234.733	58.683	8.16	<.001
Location. Season	2	4846.689	2423.344	337.10	<.001
Genotype.Location.season	8	633.200	79.150	11.01	<.001
Residual	60	431.333	7.189		
Total	89	18808.000			

Appendix 4: Analysis of variance for number of leafs of groundnut (*Arachis hypogaea L.)* 10WAP

Variate: Leaf No. 10WAP

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	8661.333	2165.333	242.29	<.001
Location	2	388716.067	194358.033	21748.10	<.001
Season	1	191084.544	191084.544	21381.81	<.001
Genotype. Location	8	14137.933	1767.242	197.75	<.001
Genotype. Season	4	5625.956	1406.489	157.38	<.001
Location. Season	2	231833.889	115916.944	12970.77	<.001
Genotype.Location.season	8	19091.444	2386.431	267.03	<.001
Residual	58	518.333	8.937		
Total	89	859674.500			

Appendix 5*:* Analysis of variance for branches of groundnut (*Arachis hypogaea L.)* 10WAP

Variate: BRANCHES_10WAP					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	19.7778	4.9444	5.74	<.001
Location	2	180.2667	90.1333	104.69	<.001
Season	1	656.1000	656.1000	762.09	<.001
Genotype. Location	8	16.9556	2.1194	2.46	0.023
Genotype. Season	4	1.5111	0.3778	0.44	0.780
Location. Season	2	305.8667	152.9333	177.64	<.001
Genotype.Location.season	8	20.0222	2.5028	2.91	0.009
Residual	58	49.9333	0.8609		
Total	89	1252.5000			

Appendix 6*:* Analysis of variance for days to 50% flowering of groundnut (*Arachis hypogaea L.)*

Variate: Days_to_50%_flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	97.933	24.483	24.38	<.001
Location	2	5.756	2.878	2.87	0.065
Season	1	8.100	8.100	8.07	0.006
Genotype. Location	8	48.800	6.100	6.07	<.001
Genotype. Season	4	6.289	1.572	1.57	0.196
Location. Season	2	27.800	13.900	13.84	<.001
Genotype.Location.season	8	7.644	0.956	0.95	0.482
Residual	58	58.244	1.004		
Total	89	262.989			

Appendix 7: Analysis of variance for days to maturity of groundnut (*Arachis hypogaea L.*)

Variate: Days to maturity					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	639.222	159.806	81.37	<.001
Location	2	1898.156	949.078	483.24	<.001
Season	1	1345.600	1345.600	685.14	<.001
Genotype. Location	8	257.178	32.147	16.37	<.001
Genotype. Season	4	20.511	5.128	2.61	0.045
Location. Season	2	2036.067	1018.033	518.35	<.001
Genotype.Location.season	8	226.822	28.353	14.44	<.001
Residual	58	113.911	1.964		
Total	89	6538.889			

Appendix 8: Analysis of variance for number of pods per plant of groundnut (*Arachis hypogaea L.)*

Variate: No of pods per plt					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr
Genotype	4	1865.444	466.361	75.42	<.001
Location	2	5732.356	2866.178	463.52	<.001
Season	1	10.678	10.678	1.73	0.194
Genotype. Location	8	2063.422	257.928	41.71	<.001
Genotype. Season	4	223.489	55.872	9.04	<.001
Location. Season	2	196.622	98.311	15.90	<.001
Genotype.Location.season	8	229.378	28.672	4.64	<.001
Residual	58	358.644	6.184		
Total	89	10692.056			

Appendix 9: Analysis of variance for pod length of groundnut (*Arachis hypogaea L.)*

Variate: Pod length					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	1.14250	0.28562	7.15	<.001
Location	2	1.78607	0.89303	22.36	<.001
Season	1	1.81476	1.81476	45.43	<.001
Genotype. Location	8	0.57636	0.07205	1.80	0.095
Genotype. Season	4	0.08287	0.02072	0.52	0.722
Location. Season	2	1.18145	0.59072	14.79	<.001
Genotype.Location.season	8	0.15032	0.01879	0.47	0.872
Residual	58	2.31696	0.03995		
Total	89	9.15573			

Appendix 10: Analysis of variance for number of seeds per pods of groundnut (*Arachis hypogaea L.)*

Variate: No. of seeds per pod					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	1.4000	0.3500	2.59	0.046
Location	2	3.0889	1.5444	11.42	<.001
Season	1	0.5444	0.5444	4.03	0.049
Genotype. Location	8	3.1333	0.3917	2.90	0.009
Genotype. Season	4	2.5111	0.6278	4.64	0.003
Location. Season	2	0.6889	0.3444	2.55	0.087
Genotype.Location.season	8	1.7556	0.2194	1.62	0.138
Residual	58	7.8444	0.1352		
Total	89	21.1222			

Appendix 11: Analysis of variance for hundred seed weight (g) of groundnut (*Arachis hypogaea L.*).

Variate: %100_Seed_weight_g					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	516.973	129.243	21.09	<.001
Location	2	6986.668	3493.334	570.11	<.001
Season	1	1254.997	1254.997	204.82	<.001
Genotype. Location	8	170.793	21.349	3.48	0.002
Genotype. Season	4	58.747	14.687	2.40	0.061
Location. Season	2	1424.450	712.225	116.24	<.001
Genotype.Location.season	8	223.958	27.995	4.57	<.001
Residual	58	355.391	6.127		
Total	89	10995.033			

Appendix 12: Analysis of variance for total grain yield (t/ha) of groundnut (*Arachis hypogaea L.*)

Variate: grain yield ton/ha					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	4	2.59962	0.64990	38.95	<.001
Location	2	1.42125	0.71062	42.59	<.001
Season	1	0.83907	0.83907	50.29	<.001
Genotype. Location	8	0.20563	0.02570	1.54	0.163
Genotype. Season	4	0.14393	0.03598	2.16	0.085
Location. Season	2	0.94927	0.47463	28.45	<.001
Genotype.Location.season	8	0.49332	0.06166	3.70	0.002
Residual	58	0.96775	0.01669		
Total	89	7.69921			