GENERATION OF SALT TOLERANT AND HIGH YIELDING GENOTYPES OF GROUNDNUT (*Arachis hypogaea* L.) THROUGH INTERVARIETAL CROSSES

MD. AKRAM HOSSAIN CHOWDHURY

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY DHAKA-1207

December, 2014

GENERATION OF SALT TOLERANT AND HIGH YIELDING GENOTYPES OF GROUNDNUT (*Arachis hypogaea* L.) THROUGH INTERVARIETAL CROSSES

BY

MD. AKRAM HOSSAIN CHOWDHURY

REGISTRATION NO.: 10-04205

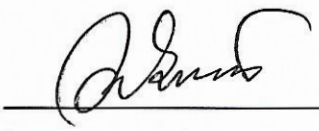
A Thesis
submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka,
in partial fulfillment of the requirements
for the degree of

DOCTOR OF PHILOSOPHY
IN
GENETICS AND PLANT BREEDING

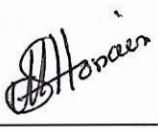
SEMESTER: JULY - DECEMBER, 2014

Approved by:

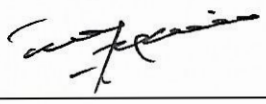
(Prof. Dr. Md. Shahidur Rashid Bhuiyan)
Chairman
Advisory Committee



(Prof. Dr. Md. Shah-E-Alam)
Member
Advisory Committee



(Prof. Dr. Md. Sarowar Hossain)
Member
Advisory Committee



(Prof. Dr. Md. Fazlul Karim)
Member
Advisory Committee

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mob: +8801552467945
E-mail: ipbscfc2009@gmail.com

CERTIFICATE

This is to certify that thesis entitled, **"Generation of salt tolerant and high yielding genotypes of groundnut (*Arachis hypogaea* L.) through intervarietal crosses"** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* **DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING,** *embodies the result of a piece of bona fide research work carried out by* **MD. AKRAM HOSSAIN CHOWDHURY,** *Registration No.* **10-04205** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: December,2014
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Shahidur Rashid Bhuiyan)
Chairman
Advisory Committee

DEDICATED
TO

MY BELOVED PARENTS,

WIFE AND DAUGHTER

ACKNOWLEDGEMENT

All praise be to Almighty Allah, all-knowing, all-wise, Whose endless blessing and kindness enable the author to carry out this doctoral programme and present the dissertation.

The author deem it a proud privilege to express his deepest appreciation and heartfelt gratitude to his supervisor and Chairman, Advisory Committee, Dr. Md. Shahidur Rashid Bhuiyan, Professor, Dept. of Genetics and Plant Breeding, the Pro-Vice Chancellor of Sher-e- Bangle Agricultural University for continuous guidance and endless support throughout the entire period of the research work as well as in preparing the dissertation.

Author's sincere appreciation and gratitude is also to all the members of the advisory committee, Prof. Dr. Md. Shah-E-Alam, Ex- Vice chancellor, SAU; Prof. Dr. Md. Sarowar Hossain, Chairman, Dept. of Genetics and Plant Breeding and Prof. Dr. Md. Fazlul Karim, Dept. of Agronomy, Sher-e- Bangle Agricultural University, Dhaka for their valuable suggestions, constant encouragement and useful criticism throughout the whole period of this study. The author is also grateful to all his honorable teachers of the Department of Genetics and Plant Breeding, Sher-e- Bangle Agricultural University, Dhaka.

The author is grateful to National Agriculture Technology Project (NATP), Project Implementation Unit (PIU), Department of Agricultural Extension (DAE), Khamarbari, Dhaka for an award which enabled him to pursue higher studies leading to Ph.D. The author is also grateful to the Sub-Committee, National Training Council (NTC), Ministry of Public Administration and Ministry of Agriculture for granting deputation to carry out the Ph.D. studies.

Author's heartiest thanks are also to Dr. M.A. Hamid, Ex-Director General, BINA, Dr. Abul Kalam Azad, CSO, Mrs Fahmina Yasmin, SSO, Plant Breeding Division, BINA, Mymensingh, Dr. Monjurul Kadir, PSO, RARS, Jamalpur, BARI, Dr. Motiar Rahman, SSO, Mr. Md. Abdul Muktadir-Himu, SO, Mr. Md. Mahbub Alam, SO, BARI, Gazipur; Mr. Md. Atikur Rahman, SO, Mr. Md. Rafikul Islam, SA, ARS, BARI, Benarpota, Satkhira; Mrs. Salma Jannat, Mr. Sarkar Md. Russel, SO, SRDI, Dhaka for their inspiration, moral support and all-out help.

Author's special thanks are to the staff of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

The author is forever indebted to his beloved wife Fatema Shahanaz, Piya and daughter Labiba Tasnim Chowdhury, Alif for encouragement and sacrificing a lot for the successful completion of the study.

The Author

GENERATION OF SALT TOLERANT AND HIGH YIELDING GENOTYPES OF GROUNDNUT (*Arachis hypogaea* L.) THROUGH INTERVARIETAL CROSSES

by

Md. Akram Hossain Chowdhury

ABSTRACT

In order to develop salt tolerant and high yielding groundnut genotypes four separate experiments were carried out during the period from August 2010 to January 2014. Of which experiment 1 and 2 were conducted at the net house premises of Sher-e-Bangla Agricultural University (SAU), Dhaka; and experiment 3 and 4 were conducted in the field experimental plot of SAU campus, Dhaka and Agricultural Research Station, Bangladesh Agricultural Research Institute, Benarpota, Satkhira, respectively. To screening the salt tolerant and sensitive genotypes the study was conducted based on sixteen characters of 25 genotypes of groundnut at different salinity levels of 10dS/m, 8dS/m and control tap water 0.38dS/m. From the study it was found that shoot-root characters were reduced with the increase of salinity levels. The yield and yield attributing characters were reduced with the increase of salinity levels. In shoot tissues up take of Na^+ and K^+ content (%)/plant increased with the increase of salinity, but Ca^{++} up take increased with the increase of salinity up to 8 dS/m and reduced again with the increase of salinity at 10dS/m level. On the basis of % reduction of shoot biomass, total biomass, pod number, pod yield and kernel yield under salinity six genotypes were selected viz. Binachinabadam-5 as tolerant; Binachinabadam-2 and Binachinabadam-6 as moderately tolerant, BARI Chinabadam-6 and BARI Chinabadam-5 as moderately sensitive and Dhaka-1 as sensitive. To study the combining ability and the nature of gene action the selected seven diverse genotypes were crossed in half diallel fashion and their 21 F_1 progenies along with their parents were evaluated in pot culture with saline soil. The significant variation in general and specific combining ability estimated for all the characters were observed which indicated the importance of both additive and non-additive gene actions in inheritance of these characters. The characters are controlled either by additive x dominant or by dominant x dominant type gene interaction and thus non-fixable. Wr-Vr analysis showed absence of non-allelic interaction for the expression of total biomass, pod number, pod yield and kernel weight. The genetic studies of all traits is appeared to be controlled by poly genes (two to five groups) with preponderance of dominance effect and the genes with positive and negative effects followed asymmetrically distribution amongst the parents. Pod yield, kernel weight and pod number had highest, higher and moderate narrow sense heritability respectively. This means simple progeny selection could be effectively followed in the segregating generations for these traits under salinity. The genotypic effects and comparative performance of F_2 7x7 diallel population in experiment 3and 4 showed the presence of wide range of variation among the genotypes for all characters in non-saline and saline field condition, respectively. In non-saline field condition cross P2xP5 showed the highest pod yield per plant followed by cross P4xP6, P5xP7, P5xP6, P1xP7, P4xP7 and P3xP7. In both field conditions, moderate to high estimates of heritability along with high genetic advance in percentage of mean for pod yield and yield contributing traits suggests that improvement of these would be further progressed through selection. The F_2 crosses P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 as the most salt tolerant genotypes could serve as a source of genetic material for the improvement of high yielding salt tolerant varieties in saline field condition.

CONTENTS

CONTENTS (Continued)

CONTENTS (Continued)

LIST OF TABLES

LIST OF TABLES (Continued)

LIST OF TABLES (Continued)

LIST OF FIGURES

LIST OF FIGURES (Continued)

LIST OF THE PLATES

LIST OF THE PLATES (Continued)

LIST OF APPENDICES

Acronyms and symbol used

ABA	= Abscisic acid	ICRISAT	= International Crops Research Institute for the Semi-Arid Tropics
APX	= Ascorbate peroxidase		
ANOVA	= Analysis of variance		
ATP	= Adenosene tri phosphate	K^+	= Ionic Potassium
BARI	= Banglaseh Agricultural Research Institute	ml	= Mili litre
		MSS	= Mean sum of square
BARC	= Bangladesh Agricultural Research Council	mg	= Mili gram
		MS	= Moderately sensitive
BAU	= Bangladesh Agricultural University	MT	= Moderately tolerant
Ca^{2+}	= Ionic calcium	NaCl	= Sodium chloride
CAT	= Catalase	Na_2SO_4	= Sodium sulphate
CGIAR	= Consultative Group on International Agricultural Research	$NaHCO_3$	= Sodium bicarbonate
		no.	= Number
		Na^+	= Ionic sodium
CRD	= Completely randomized design	NRS	= Non reducing sugar
cc	= Cubic centimeter	O^-	= Super oxide
cm	= Centimeter	OH	= Hydroxyl radical
$CaCl_2$	= Calcium chloride	PAW	= Plant available water
Chl-a	= Chlorophyll-a	ppm	= parts per million
Chl-b	= Chlorophyll-b	p and q	= Dominant and recessive allele frequencies
CO_2	= Carbon dioxide		
Cl^-	= Ionic chloride	ROS	= Reactive oxygen species
°C	= Degree centigrade	SAU	=Sher-e-Bangla Agricultural University
dS/m	= Desi siemen per meter		
DMRT	= Duncan's multiple range test	SRDI	= Soil Resources Development Institute
dwt	= Dry weight		
ECe	= Electrical conductivity of soil extract	SOS1	= salt overly mutant 1
		SOS2	= salt overly mutant 2
ESP	= Exchangeable sodium percent	SOS3	= salt overly mutant 3
FAO	= Food and Agriculture Organization	SOD	= Super oxide dismutase
		SAIC	= SAARC Agricultural Center
Fig.	= Figure	sca	= Specific combining ability
F_1	= First filial generation	SE	= standard error
F_2	= Second filial generation	SL_{50}	= Salinity level that reduce any parameter by 50%
FAA	= Free amino acid		
fwt	= Fresh weight	S	= Sensitive
GR	= Glutathione reductage	SS	= Sum of square
g	= gram	T	= Tolerant
gca	= General combining ability	Vr	= Varience
h^2b	= Broad sense heritability	Wr	= Covarience
h^2n	= Narrow sense heritability		
$HClO_4$	= Perchloric acid		
HNO_3	= Nitric acid		

CHAPTER I

INTRODUCTION

World wide soil salinity is one of the major abiotic stress factor affecting production and quality of food crops by limiting growth and development as well as yield potential of crop plants (Bray *et al*. 2000; Tester and Davenport 2003). According to FAO Land and Nutrition Management Service (FAO, 2008), over 6% of the world's land is affected by either salinity or sodicity which accounts for more than 800 million hactre of land. These soils are technically suited for crop production but left uncultivated or cultivated with low yields due to salinity problems. Saline soils are defined by Ponnamperuma (1980) as those contain sufficient salt in the root zone to impose the growth of crop plants. However, since salt injury depends on species, variety, growth stage, environmental factors, and nature of the salts, it is difficult to define saline soils precisely. The USDA Salinity Laboratory defines a saline soil as having an electrical conductivity of the saturation extract (EC) of 4 dS m^{-1} or more. EC is the electrical conductivity of the 'saturated paste extract', that is, of the solution extracted from a soil sample after being mixed with sufficient water to produce a saturated paste. The most widely accepted definition of a saline soil has been adopted from FAO (FAO, 1996) as one that has an EC of 4 dS m^{-1} or more and soils with EC's exceeding 15 dS m^{-1} are considered strongly saline.

Food security has become a major and fast growing concern worldwide. It is proposed that there is a need to double the world food production in order to feed the ever increasing population which is set to reach nine billion mark by 2050 (UN 2009). In

the current scenario, improving yields in both normal and less productive farm lands including salt affected lands is the only way to address food security concerns, as the amount of unused land available to bring into cultivation is limiting. Among various factors affecting agricultural production, abiotic stress factors are considered to be the main source of yield reduction. Potential yield losses due to individual abiotic stresses are estimated at 17% by drought, 20% by salinity, 40% by high temperature, 15% by low temperature and 8% by other factors (Ashraf and Harris 2005).

The climate in Bangladesh is changing and it is becoming more unpredictable every year due to global warming. The impacts of higher temperatures, more variable precipitation, more extreme weather events, and sea level rise are already felt in Bangladesh and will continue to intensify. Climate change poses now-a-days severe threat mostly in agricultural sector and food security among all other affected sectors. Crop yields are predicted to fall by up to 30 per cent, creating a very high risk of hunger and only sustainable climate-resilient agriculture is the key to enabling farmers to adapt and increase food security (Climate change cell, 2007).

Bangladesh is a deltaic country with the total area of 147, 570 km^2. The coastal area covers about 20% of the country and over thirty percent of the net cultivable area. It extends inside up to 150 km from the coast. Out of 2.85 million hectares of the coastal and offshore areas about 0.83 millions hectares are arable lands, which cover over 30% of the total cultivable lands of Bangladesh. A part of the coastal area, the Sundarbans, is a reserve natural mangrove forest covering about 4,500 km^2. The remaining part of the coastal area is used in agriculture. The cultivable areas in coastal districts are affected with varying degrees of soil salinity (Appendix II). The coastal and offshore area of Bangladesh includes tidal, estuaries and river floodplains in the

south along the Bay of Bengal. Agricultural land use in these areas is very poor, which is roughly 50% of the country's average (Petersen and Shireen 2001).

Extent of salinity occurring in different land sites in Bangladesh. Coastal saline soils occur in the river deltas along the sea coast, a few kilometers to 180 kilometers. The landscapes are low-lying land, estuaries and inland along the seacoast of Bangladesh. According to salinity survey (Appendix II) findings and salinity monitoring information, about 1.02 million ha (about 70%) of the cultivated lands are affected by varying degrees of soil salinity. About 0.282, 0.297, 0.191, 0.450 and 0.087 million hectares of lands are affected by very slight, slight, moderate strong and very strong salinity respectively. Cropping intensity may be increased in very slight and slightly alkaline areas by adopting proper soil and water management practices with introduction of salt tolerant varieties of different crops.

Salinity causes unfavorable environment and hydrological situation that restrict normal crop production throughout the year. The freshly deposited alluviums from upstream in the coastal areas of Bangladesh become saline as it comes in contact with the sea water and continues to be inundated during high tides and ingress of sea water through creeks. The factors which contribute significantly to the development of saline soils are, tidal flooding during wet season (June-October), direct inundation by saline or brackish water and upward or lateral movement of saline ground water during dry season (November-May). Observations in the recent past indicated that due to increasing degree of salinity of some areas and expansion of salt affected area as a cause of further intrusion of saline water, normal crop production becomes more restricted. In general, soil salinity is believed to be mainly responsible for low land use as well as cropping intensity in the area (Rahman & Ahsan, 2001). Salinity in the country received very little attention in the past. Increased pressure of growing

population demand more food. Thus it has become increasingly important to explore the possibilities of increasing the potential of these (saline) lands for increased production of crops.

Groundnut (*Arachis hypogaea* L.) is one of the most economically important food legume crops of the world. The groundnut is known as peanut and sometimes called monkeynut or earthnut. Groundnut, family Fabaceae, sub-family, Papilionoidae under the genus *Arachis* is native to South America. Its probable center of origin is Central Brazil, in a region extending from the southwest of Mato Grosso do Sul State and the adjacent border of Paraguay to the South of Goias (Valls, 2000). The genus contains 80 described species, assembled into nine taxonomic sections (Krapovickas and Gregory, 1994; Valls and Simpson, 2005).

The cultivated groundnut (*Arachis hypogaea* L.) is an allotetraploid (2n= 4x =40 chromosomes) with an AABB genome formula. It is believed that peanut originated through the crossing of two distinct diploid species (2n =20 chromosomes), one with an A genome and the other with a B genome. This cross must have been followed by spontaneous duplication of chromosomes, at least in some tissues of the sterile diploid hybrid, which restored hybrid (Halward *et al*., 1991; Young *et al*., 1996). The resulting tetraploid plant has been selected and grown in diverse regions of South America for more than 5000 years, and spread worldwide by the time of the European discovery of the New World, or even before that, following pre-Columbian navigation routes in the Pacific Ocean (Krapovickas, 1998). But in Bangladesh, it was introduced in the later 1930s from China (Kaul and Das, 1986).

Arachis hypogaea L., the only cultivated species, is classified, based on the presence or absence of flower on the main axis, into two subspecies, *hypogaea* and *fastigiata* Waldron. The subspecies *hypogaea* was divided into two botanical varieties,

hypogaea and *hirsuta* Köhler, while *fastitigiata* was divided into the varieties *fastigiata* and *vulgaris* Harz, (Krapovickas and Gregory, 1994). Though having possibility of cross pollination up to 2-3.9%, it is highly self pollinated crop (Hammons, 1963).

Groundnut is currently grown on 25.02 million hectare of land worldwide with the production of 35.9 million metric tons (FAO, 2006). Globally, it is the third major oilseed crop next to soybean and cotton (FAO Food outlook, 1990). Major groundnut producing countries are China, India, Nigeria, the United States of America and Indonesia. In Bangladesh, it ranks third among the oilseed crops after rapeseed-mustard and sesame based on both acreage and production with the highest per hectare yield (BBS, 2012). Groundnut cultivation in Bangladesh is on decline. During 2009 the area under groundnut was nearly 0.034 million hectare, but it came down to 0.029 million hectare by 2012 (SAIC, 2012).

The groundnut, being a multipurpose crop, can help to reduce edible oil, food and fodder shortage of Bangladesh. The nut (kernel) contains 40 to 58% edible oil (Boshou *et al*., 2003), 22 to 30% high quality protein (Bunting and Elston, 1980), 20 to 25 % carbohydrate (Pattee *et al*., 1974) and E and B vitamins (Ahmed and Young, 1982). Groundnut oil provides 900 K.cal. Whereas butter and fish oil provides 729 and 273 K.cal. energy, respectively. Because of its high digestibility, it is an excellent component of children's food. It can play a vital role to meet up the daily per capita consumption of protein of Bangladeshi people who are suffering from acute protein-caloric malnutrition. The daily per capita consumption of protein in Bangladesh is only 10gm but it is as high in the neighboring country like India (FAO, 1984). After extraction of oil, cake and haulms are cheap sources of high quality animal feed (Alam *et al*., 1985). On the other hand, groundnut being a legume crop, fixes 40-80 kg

nitrogen/hectare/year (Islam and Noor,1982) in soil through its nodule bacteria and keeps environment most friendly (Lee *et al.*,1998).

The soil and climate of Bangladesh are suitable for the production of groundnut. Among the three botanical types, Virginia, Valencia and Spanish, the later one is mostly grown in Bangladesh as a rainfed crop and is locally known as "China badam". Groundnut can be grown both in Rabi and Kharif season in Bangladesh for its photoinsensibity. It is cultivated in sandy, sandy loam soil and rever beds of Noakhali, kisorganj, Rangpur, Dhaka, Sylhet, Barisal, Patuakhali, Chittagong, Comilla, Rajshahi, Jamalpur, Pabna, Tangail, Faridpur and Kustia.

Bangladesh is seriously deficit in edible oil production. Annually Bangladesh is producing 0.16 mt. of edible oil as against the requirement of 0.50 mt. (Wahhab *et al*., 2002). More than 50% of its requirement is being imported every year by spending near about 160 million US dollar every year (Bangladesh Economic Survey, 1998). Under such critical condition of edible oil and protein supply in Bangladesh, groundnut being a prospective crop with annual production of 53654 mt. (BBS, 2012), can contribute significantly. The productivity of groundnut can be raised manifold in Bangladesh if cultivation expanded in new areas like coastal belts with suitable salt tolerant high yielding varieties. Coastal belts of Bangladesh comprised of about 0.83 million hectares of arable land, affected by various degrees of salinity, ranging from 2 to >16dS/m (Karim and Iqbal, 2001). Of this 4, 26, 430 ha falls in the category of 4 -8dS/m salinity where no crop can be grown in the rabi season (October- March). The soil salinity in that area remains lower in monsoon upto November, thereafter it starts increasing and accentuates in May. Groundnut is moderately sensitive to soil salinity and can tolerate up to 3.2 dS/m without affecting

yield (Shalhevet *et al*., 1969). It can be grown throughout the year with higher yield advantage in rabi season.

In the southern part of Bangladesh soil salinity increasing day by day due to the effect of climate change. It is very important to develop salt tolerant high yielding variety for this area. High water demanding crop cultivation is not possible in the saline areas of Bangladesh because of unavailability of suitable irrigation water. Groundnut requires only 150mm water for completing life cycle (Field, 1995) and thus mostly grown under rainfed condition during November to May. Groundnut being a leguminous crop, its root nodule fixes nitrogen with biological symbiotic process. Many leaves dropping occur at the growing and harvesting time. In this sense it adds organic matter to the soil which can help to increase soil health. In Bangladesh, there is no mentionable high yielding variety tolerant to salinity and widely adaptable to different ecological areas. In this context we need to screen the existing varieties tolerant to salinity and to generate variety(s) of groundnut that will be able to tolerate certain level of salinity. If it does so, area under groundnut could be expanded over those saline areas and this will help in the reduction of import of edible oil with our hard-earned foreign currency. We can address the effect of climatic changes with improving soil health that will help to ensure our food security.

With these facts in mind, the present study was undertaken with the following objectives:

i) To screen the groundnut genotypes against salinity and discriminate salt tolerant and sensitive groups.

ii) To assess combining ability and genetic behavior of salinity tolerance in groundnut.

iii) To identify the salt tolerant and high yielding genotype(s) in saline and non-saline field conditions, respectively.

CHAPTER II

REVIEW OF LITERATURE

2.1 Saline Soils:

It is difficult to define saline soil precisely. However, a common definition to define saline soil is one that has enough salt in root zone to give an electrical conductivity (EC) in the saturation extract exceeding 4 ds/m at 25°C, an exchangeable sodium percentage (ESP) less than 15 and usually P^H below 8.5 (Rahman, 1992. Appendix II) Strongly saline soils have also been defined as soils with EC'S more than 15 ds/m (FAO-UNESCO, 1974). Saline soils are common in interflow and irrigation, so that influx of salt into the soil profile is greater than efflux (Ponnamperuma and Bandyopadhya, 1980) Soil profiles in the costal areas of Bangladesh have an excess of Magnesium, Calcium and Sulphate and are generally growing areas is caused mainly by sodium and chloride ions, (Flowers and Yeo, 1995). Salinity possesses the greatest threat to increase food production in the Asian continent (Abrol, 1986).

2.2 Units expressing salinity:

Several units are commonly used to express salinity like ds/m, mmhos/m, mM, meq/1, g/1, perecent, ppm, mpa, osmotic pressure, etc. The moral concentration of the solution is used in physiological studies. It is from 20 to 300 mm in the root medium (Flowers *et al*., 1977)

2.3 Impact of salinity on Agriculture:

According to Yeo (1998) and Grattan and Grieve (1999) that the direct effect of salts on plant growth may be divided into three broad categories: (i) a reduction in the osmotic potential of the soil solution that reduces plant available water, (ii) a

deterioration in the physical structure of the soil such that water permeability and soil aeration are diminished, and (iii) increase in the concentration of certain ions that have an inhibitory effect on plant metabolism (specific in toxicity and mineral nutrient deficiencies). The relative contribution of osmotic effects and specific in toxicities on yield is difficult to quantify. However, with most crops, Dasberg *et al.* (1991) reported that yield losses from osmotic stress could be significant before foliar injury is apparent.

The impact of salinity on agricultural production is hard to quantify as water stress, high temperature, poor irrigation practice and over exploitation of land, especially in over populated areas of the developing would, all inter-act to reduce food production. The more serious long term consequence of this continuation of events is desertification, which to varying degree now affects over 100 countries and is perceived as a major threat to the food security in the developing would (Szabolcs, 1987). Soil salinity is one of the most serious problems for irrigated agriculture, which drastically affect crop productivity throughout the world. This is mainly due to low precipitation and high transpiration causing disturbance in salt balance in the soil, this also renders ground water brackish and affects plant growth adversely (Rhoades and Loveday, 1990; Evans, 1998). Plants are classified as glycophytes or halophytes according to their capacity to grow on high salt medium. Most plants are glycophytes and cannot tolerate salt-stress. Adverse effects of soil salinity on plants can be observed wilted foliage and necrosis of tips, margins and lamina of leaves. Ultimately, many nutrient deficiency symptoms will occur as a result of acutely impaired nutrient uptake by the injured root system (Nelson, 1991). Overall, salinity reduces growth rate and causes poor and spotty growth of crops, uneven or stunted growth and poor yields (Abrol *et al*. 1986).

For the development of saline tolerant lines of groundnut, it is necessary to identify the molecular mechanisms involved in the tolerance/sensitivity of crop plants. Salt stress is a complex trait, involves osmotic, water deficit stresses and finally excessive accumulation of CI^- and Na^+ ions. The latter one leads to direct toxicity apart from indirect toxicity in uptake of essential nutrient elements. All these constraints are perceived by the genome, which activates appropriate mechanisms to re-establish water transport, limit Na^+ and CI^- uptake or lowers concentration in cytoplasm allowing the absorption of ions indispensable for growth. Tolerance depends on arange of physiological, biochemical and molecular adaptations activated by the genome to survive in saline medium.

2.4 Regulation of osmotic potential

Synthesis of compatible solutes

Osmotic adjustment is the central cellular response to water deficit generated by drought, salinity or freezing temperature in halophytes and glycophytes (Chinnusamy *et al.* 2005). This adjustment helps maintain turgor despite low water potentials and proceed to the uptake of K, compartmentalization of Na Into the vacuole or synthesis of compatible solutes such as praline (Khatkar and Kuhad, 2000; Singh *et al*, 2000) glycinebetaine (Rhodes and Hanson, 1993; Khan *et al*., 2000; Wang and Nil, 2000) polyol (Ford, 1984, Popp *et al.,* 1985; Orthen *et al*., 1994 Bohnert *et al.,* 1995) and sugar (Kerepesi and Galiba, 2000; Bohnet and Jensen, 1996, Pilon Smits *et al*., 1995) these are highly soluble and low molecular-mass compounds, termed compatible as they do not interfere normal biochemical reaction (Ford, 1984, Ashihara *et al*., 1997; Hasegawa *et al*, 2000; Zhifang and Loescher, 2003). They protect plants from stress by turgor maintenance, detoxification of reactive oxygen species (ROS) and by

stabilization of quaternary protein structure (Yancey *et al.,* 1982; Bohnert and Jensen, 1996, Hasegawa *et al.,* 2000).

2.5 Reduction of transpiration

The most important criteria for identifying stress tolerance is to ascertain positive correlation with stress. The first developmental interference of salt stress is linked to growth inhibition induced by water deficit. Water stress signals could be detected by ABA accumulation. In *Phaseolus vulgaris*, ABA mediates both short-and long-term responses to Na toxicity in addition to salt-induced water deficit (Montero *et al*., 1998; Sibole *et al.,* 1998, 2000) signal perception induces mechanisms of adaptation or tolerance to salt stress. For example certain species living in an environment rich in salt, survive by limiting the transpiration through closure of stomata (Sibole *et al*., 2003) carbon assimilation is central to leaf growth and productivity. Under saline conditions, photosynthetic carbon assimilation is severely restricted by reduced leaf expansion and plant growth.

In addition to the ABA effect K^+ plays determinant role in stomata closure. Thus the presence of Na^+ in the apoplastic space of guard cells could disturb the K^+ channels that participate in stomata movement (Schroeder *et al.,* 2001) Recent results indicated that most of the conductance of water is realized by aquaporins which are membrane proteins forming water channels (Tyeman and Skerrett, 1998; Maurel and Chrispeels, 2001). Expression of aquaporin genes in certain cellular and environmental conditions such as physiological processes, drought and salinity (Sakurai *et al.,* 2005, and Suga *et al*., 2002) suggest their role in the control of water use and water loss under conditions of drought, salinity and heat stresses. cDNA-arrays of *Populus eupphratica* Oil., a salt-tolerant species that can cope with up to 450 mM NaCI, showed certain transcripts significantly up-regulated by salt stress and related to the control of water

(Gu *et al*., 2004). Among these transcripts, the authors identified a seed germination-related protein, a plasma membrane intrinsic protein (aquaporin), The photosynthesis-activating enzyme Rubisco activase and photorespiration related glycolate oxidase. Considering such results, the regulation of aquaporin expression appeared to be important for adequate tissue and cellular water transport under salt stress.

2.6 Regulation of ionic constraint

Ion regulation and compartmentalization

Ion uptake and compartmentalization are crucial not only for normal growth but also for growth under saline conditions (Adams *et al,* 1992) since stress disturbs ion homeostasis. Plants, whether glycophyte or halophyte, cannot tolerate large amounts of with in the cytoplasm and therefore under saline conditions they either restrict the excess salts in the vacuole or compartmentalize the ions in different tissues to facilitate their metabolic functions (Reddy *et al,* 1992, lyengar and Reddy, 1996, Zhu, 2003) Glycophytes limit sodium uptake or partition it in older tissues that serve as storage compartments and are eventually sacrificed (Cheeseman, 1988).

Removal of sodium from the cytoplasm or compartmentalization in the vacuoles is done by a salt-inducible enzyme Na^+/H^+ antiporter (Apse *et al,* 1999) when under salt stress, plants maintain high concentration of K^+ and low concentrations of Na^+ in the cytosol. They do this by regulating the expression and activity of K^+ and Na^+ transporters and of H^+ pumps that generate the driving force for transport (Zhu *et al*, 1993). Although salt-strees sensors remain elusive, some of the intermediary signaling components have been identified. Evidence suggests that a protein kinase complex consisting of the cryristoylated calcium-binding protein SOS3 and the serine/threonine protein kinase SOS2 is activated by a salt- stress elicited calcium

signal. The protein kinase complex been phosphorylaes and activated various ion transporters, such as the plasma membrane Na^+/H^+ antiporter SOS1(Zhu*et al,* 1993). Experimental evidence implicates Ca^{2+} function in salt adaptation. Externally supplied Ca^{2+} reduces the toxic effects of NaCI, presumably by facilitating higher K^+/Na^+ selectivity (Liu and Zhu, 1997; Lauchli and Schubert, 1989). High salinity also results in increased cytosolic Ca^{2+} that is transported from the apoplast and intracellular compartments (Knight *et al.,* 1997) The resultant transient Ca^{2+} increase potentiates press signal transduction and leads to salt adaptation (Mendoza *et al.,* 1994; Knight *et al*., 1997). Variety, salinity level and growth stage showed highly significant differences for most of the yield attributes and uptake of nutrient elements except shelling percentage for variety and Na^+, K^+ and Na^+/K^+ for growth stage. Of the stages, tolerance could be classified in order of vegetative>pod filling>flowering stage. The tolerance of a variety based on economic yield was conferred by its low $Ca^{2+/}Na^+$ ratio in the shoot tissues. Moreover, the variety that could mobilize Ca^{2+} more at flowering stage from shoot tissues to reproductive organs particularly kernel under salinity stress attained more tolerance. The excess Na^+ in shoot tissues of salinity stressed groundnut does not move to flower rather a portion to the kernel. In contrast, K^+ and Ca^+ move from shoot tissues to all reproductive organs including flower with being the highest to the kernel Azad *et al*., 2013).

2.7 Oxidative stress tolerance

Salt stress, in addition to water and ionic stresses, imposes secondary stress called oxidative stress (Greenway and Munns, 1980; Chyeeseman, 1988) through dysfunction of photosynthetic machinery or other metabolic disorder. This oxidative stress leads to the formation of reactive oxygen species (ROS) which is in excess to that produced unavoidably by normal cellular activity in the chloroplast (Mehler, 1951; Krause, 1994) and in organs that lack of chloroplast (Hossain *et al*., 2006). The

ROS includes super oxide (O^-), hydrogen peroxide (H_2O_2) and hydroxyl redical (OH^-) and singlet oxygen O_2 (Asada 2006). These cytotoxic activated oxygen species can seriously disrupt normal metabolism through oxidative damage to lipids (Fridovich, 1986; Wise and Naylor, 1987), protein and nucleic acids (Fridovich, 1986; Imlay and Linn, 1988). The capacity of plants to scavenge ROS and to reduce their damaging effects appears to represent and important stress tolerant trait. Plants with high levels of antioxidants, either constitutive or induced, have been reported to have greater resistance to this oxidative damage (Harper and Harvey, 1978; Dhindsa and Matowe, 1981; Wise and Naylor, 1987; Spychalla and Desborough, 1990). The activities of the antioxidative enzymes such as catalase (CAT), ascorbate peroxidase (APX) guaicol peroxidase (POD), Glutathione reductase (GR), and superoxide dismutase increase under salt stress in plants, and a correlation of these enzyme levels and salt tolerance exists (Gosset *et al,* 1994; Hernandez *et al*., 1995 and Hernandez *et al.,* 2000; Sehmer *et al*., 1995; Kennedy and De Fllippis, 1999; Sreenivasulu *et al*., 2000; Benbavides *et al.,* 2000; Lee *et al*., 2001; Mittova *et al.,* 2002 and Mittova *et al.,* 2003).

2.8 Effect of salinity on different phenological stages of groundnut

Effect of salinity differs significantly with changes in growth stage (Haque, 2006, Heenan *et al.,* 1988; Garg *et al*., 1997).

Effect on Germination:

The salt tolerance of groundnut during germination was quite high (Shalhevet*et al.,* 1969, Joshi *et al.* 1990). Contrary to this, increased reduction in germination with increased salinity was also reported (Patel*et al.,* 1992, Janila *et al*., 1999, Nautiyal *et al.,* 1989), in groundnut and other legumes (Esechie *et al*., 2002; Sekhar, 1994; Sharma and Saran, 1994; Manzoor *et al.*1986). Germination of groundnut increased at lower salinity levels (Nautiyal*et al*., 1989). Salinity significantly delayed germination and also reduced the final percentages at electrical conductivities greater than 2.60

mS/cm (Mensah *et al.,* 2006). Sodium carbonate has been reported as the most toxic salt for germination while sodium sulphate the least. Calcium chloride, sodium chloride and magnesium sulphate were reported to be the intermediates.

Effect on seedling development stage:

Salt stress reduced seedling development of groundnut (Shalhevet *et al,* 1969) and also caused reduction in length, fresh weight of seedlings and dry weight of roots (Nautiyal *et al.,* 1989; Srivastava *et al.,* 1998), it reduced dry matter production in other legumes also (Patil *et al*., 1996; Yupsanis *et al.,* 2001; Manzoor *et al*., 1986; Ayoub, 1976; Yasin *et al.,* 2002). Seedling emergence, radical elongation tended to decrease with increasing salinity (Mensah *et al.,* 2006).

Effect on vegetative and flowering stages:

Plant height, specific leaf weight (SLW), Number of immature and mature pods, total pods and pod and kernel yields gradually decreased with increasing salinity levels, respective of stage of imposition and varieties (Haque, 2006; Joshi *et al*., 1990; Vadez *et al.,* 2005). Exposure of salinity increased stem/ leaf ration and that tolerant plants were able to maintain leaf size to that of control even at high salinity (Vadez *et al.,* 2005). Plant height, dry matter weight, number of leaves per plant and number of branches per plant were significantly reduced with salinities higher than 2.60 mS/cm (Mensah *et al.,* 2006).

Effect of nutritional balance:

Imposition of relatively low concentrations of NaCl at the vegetative stage of groundnut (*Arachis hypogaea*), disrupted the nutritional balance of plants, mainly by Na^+/K^+ competition in uptake, and to a smaller degree by Cl^-/NO^-_3 interaction (Silberbush and Ben, 1989). Salt exposure leads to accumulation of Na^+ and Cl^- ions more in roots than shoot and leaves (Srivastava *et al*., 1998)

Effect at Biochemical level:

Upon exposer to salinity stress, groundnut produced osmoticants; proline and glycinebetaine (Girija *et al.,* 2002; Satakopan and Rajendran, 1989) During germination, proline and gylcinebetaine concentrations in the embryonic axis increased continuously, Sodium and calcium had additive role in the accumulation of gylcinebetaine. The addition of calcium chloride to NaCl stressed seedings lowered the praline concentration by increasing the level of praline oxidase and decreasing gamma glutamyl kinase activities. Salinity stress, in the absence of calcium, increased proline due to redused proline oxidase activity and increased gamma-glutamyl kinase (Gllutamate 5-kinase) activity both in the cotyledons and embryonic axis of groundnut seedlings. This means that calcium ions increase gylcinebetaine production but decrease praline level in NaCl stressed groundnut seedlings.

Increased salt stress decreased water and solute potentials in the cell lines of groundnut (*A. hypogaea* L) and maintained cellular turgo indicating active osmotic adjustments (Jain *et al*., 2001) in addition to the extrusion of Na^+ in the NaCl selected cell lines, a significant accumulation of praline took place, probably associated with osmotic adjustments and the protection of membrane integrity.

Salt exposure decreased plasma membrane and tonoplast ATPase activity in groundnut seedling (Srivastava *et al.,* 1998). These result5s were correlated with seedlings growth reduction under saline conditions.

Effect on yield and yield attributes:

Groundnut is moderately sensitive as it can tolerate soil salinity up to 3.2 dS/m without affecting yield (Shalhevet *et al.,* 1969). Above this level it causes yield reduction (Shalhevet *et at.,* 1969; Hunshal *et al.,* 1991; Sharma *et al.,* 2003).

However, below this level there is some increase in yield. Hunshal *et al.,* (1991) reported a 2.8% increase in yield at 2 dS/m.

Salinity stress reduced pod and seed weight of groundnut and caused seed injury (Silberbush and Lips, 1988; Lauter *et al*., 1988). Seed injury was associated with Accumulation of Na+ and Cl- and depletion of Ca^{2+} in pods and seeds. Accumulation of Na+ decreased Ca^{2+} absorption by the developing peg (Arjunan and Gopalakrishnan, 1987). Change in K^{+} content depends on applied Ca^{2+} and/or Na^{+} rates. The ultimate target of any breeding program under stress or unstressed environments is economic yield. This means, for assessing salinity tolerance in groundnut economic yield should be considered rather than biological yield (Azad *et al*., 2012; Azad *et al*., 2013). Based on reduction in shoot biomass the mutants or varieties could be classified into four groups: the mutants or varieties with (a) <20% reduction = tolerant (b) 20% to 40% reduction = moderately tolerant (c) 41 to 60% reduction = moderately sensitive and finally (d) >60% reduction = sensitive to salinity. It was revealed that the tolerant mutant or variety accumulated increased total sugar contents to that of unstressed control treatment when exposed to salinity stresses during flowering and pod filling stages and free amino acid during pod filling stage, helped maintaining turgor of guard cell and intake of CO_2 through opened stomata. This CO_2 in presence of undamaged chloroplast helped maintaining photosynthesis and mobilization of assimilates to reproductive organs, particularly kernel.

6.14 Genetics for salt tolerance in groundnut

In any varietal development program, it is crucial that there should be sufficient intra-specific variability for the trait of importance in the existing germplasm/cultivars. Large genotypic variation exists in groundnut for salt tolerance. Some of them could survive and produce acceptable pod yield at salinity 6-12 dS/m (Joshi *et al.,* 1990;

Hunshal *et al.,* 1991; Patel *et al.,* 1992, Hebbara *et al*., 1992, Janila *et al*., 1999; Nautiyal *et al.,* 2000). A study was performed using 6x6 F_1 diallel population without reciprocals to assess the mode of inheritance of pod yield and related traits in groundnut with imposed salinity stress. Data on general and specific combining ability (gca and sca) indicated additive and non-additive gene actions. The gca:sca ratios were much less than unity suggesting predominant role of non-additive gene effects. Cross combinations showing high sca effects aristing from parents with high and low gca values for any trait indicate the influence of non-additive genes on their expression. Parents of these crosses can be used for biparental mating of reciprocal recurrent selection for developing high yielding varieties. Crosses with high sca effects having both parents with good gca effects could be exploited by pedigree breeding to get transgressive segregants (Azad *et al.,* 2014). A 10x10 half diallel experiment was conducted on groundnut (*Arachis hypogaea* L.) to ascertain the gene action and getic parameters of ten traits. The estimates of gene effects indicated that significance of both additive and non-additive variance for pod size, 100 pod weight and diseases infection among the traits and presence of over dominance satisfying assumptions of diallel except dormancy. However, both additive and non-additive gene affects together importance to control of most quantitative traits in the groundnut (Alam*et al*., 2013).

6.15 Genetics of salt tolerance in various crops

Without knowledge of genetics, breeding program for development of salt tolerant variety will not be fruitful. Perhaps the first attempt to evaluate the inheritance of salt tolerance was made by Lyon (1941) in tomato. Since then only 34 salt tolerant cultivars have registered (Flowers and Yeo, 1995; Flowers, 2004; Owen *et al,* 1994; Al-Doss and Smith, 1998; Dierig *et al*., 2001; Dobrenz, 1999). The slow progress in

breeding for salinity tolerance is because of (i) limited knowledge in the genetics of tolerance, (ii) involvement of several complex tolerance mechanisms (Yea and flowers, 1886), (iii) inadequate *en masse* screening techniques, (iv) low selection efficiency (Gregorio and Senadhira, 1993), and (v) poor understanding of salinity and environmental interactions (Akbar, 1986) and finally , (vi) lack of understanding the molecular basis of salt tolerance and lack of availability of genes that confer salt tolerance (Chinnusamy *et al*., 2005). A plants response to salt stress is modulated by many physiological and agronomical characteristics, controlled by the actions of several to many genes whose expressions are influenced by various environmental factors (Foolad, 2004). In rice, sterility under saline conditions determined by at least three genes (Akbar *et al*., 1972; Akbar and Yabuno, 1977) with both additive and dominance effects (Moeljopawiro and Ikehashi, 1981; Akbar *et al*., 1986). In pigenopea *(Cajanus cajan)* dry weight production under satinity stress was determined by a dominant genetic factor (Subbarao *et al.*, 1990). However, there is evidence of dominance in the salt tolerance of sorghum and tomato. In sorghum relative root length was controlled by dominant genetic factor (Azhar and McNeilly, 1988) while in tomato, stem elongation and dry weight were controlled by dominant genetic factors (Saranga *et al*., 1991; Tal and Shannon, 1983). Accumulation of sodium and potassium under saline conditions was mostly controlled by additive genes (Foolad, 1997) and was heritable (Garcia*et al*., 1997). In contrast, Gregorio and Senadhira (1993) reported a high degree of heterosis and large environmental effects on Na+/K+ ratios, which indicated that this was a quantitative trait.

Variability

Variations for pod yield and its contributing characters in groundnut were studied extensively. Some of these reviewed here:

Uddin*et al.* (1995) studied variabilityfor 7 yieldcomponentsin23 divergentgroundnut genotypes. High genotypic coefficients of variation were obtained for plantheight, number of branches per plant, seed yield per plant, seeds per pod and 100 seed weight.

Kumar *et al*. (1998) observed high genotypic and phenotypic coefficient of variation for length of main axis, number of kernel per pod, kernel yield per plant and oil yield per plant.

Naaz *et al.* (2000) derived information on genetic variability from data on pod yield, pod length, seed weight, shelling percentage and oil content in 16 groundnut varieties and found high genotypic and phenotypic variances for seed weight and pod length and also observed genotypic and phenotypic coefficient of variability for pod yield.

Prakash *et al.*,(2000) conducted an experiment and found that genotypic coefficient of variations ranged from 3.68 (oil content) to 29.2% (pod yield per plant), while the phenotypic coefficient of variation ranged from 2.95 (days to 50% flowering) to 31.13% (pod yield per plant)

Azad and Hamid (2000) studied genetic variability in nine breeding lines of groundnut and observed that the differences between genotypic and phenotypic coefficient of variations were very for all the characters except primary branches per plant. They also estimated high genotypic and phenotypic coefficients of variation for plant height, pod number, kernel and pod yields.

Nath (2001) conducted an experiment to estimate variability and observed little ifferences between genotypic and phenotypic variances for days to maturity, plant

height, immature pods per plant, number of kernels per pod, 100 pod weight and yieldper plant. He also found highgenotypic and phenotypic coefficient of variations forplant height, number pods per plant and pod yield per plant.

Sarker (2001) reported that genotypic and phenotypic variations were relatively high for plant height, 100 pod weight and yield per plant when she studied variability of 17 characters in 15 groundnut genotypes.

Venkataramana (2001) evaluated thirty genotypes for genetic variability and observed high genotypic coefficient of variation for oil yield, 100 kernel weight and kernel yield.

Yogendra *et al*. (2002) conducted an experiment to estimate the genetic variability for ten characters of 30 Spanish groundnut genotypes and revealed highly significant differences among the genotypes for all characters except the number of branches. The range was highest for plant height (23.50-43.23) cm and lowest for the number of primary branches (3.10-6.40) cm. The phenotypic coefficient of variation and genotypic coefficient of variation were highest for harvest index and lowest for percentage of sound mature kernel, shelling percentage, days to first flowering and days to 50% flowering.

Badigannavar *et al*. (2002) conducted an experiment with 61 distinct groundnutgenotypes and observed considerable variability for vegetative, reproductive and agronomic traits.

Islam (2003) observed highest genotypic and phenotypic variances for 100 pod weight followed by plant height and also observed relatively higher genotypic and phenotypic coefficient of variation with considerable differences for shelling percentage, number of immature pod per plant, number of mature pod per plant and

number of primary branches per plant when he conducted a similar type of experiment.

Makhan *et al*. (2003) conducted an experiment and observed genetic variation and selection response for 12 traits (number of days to germination, number of days to first flower, leaf length, leaf width, plant height, number of days to maturity, number of mature pod per plant, root length, root weight, number root nodules per plant, 100 pod weight and yield per plant in 67 groundnut lines and cultivars. They found higher phenotypic co-efficient of variation than genotypic co-efficient variation for all the characters except root length, plant height, number of mature pods per plant, number of nodules per plant, 100 pod weight and yield per plant showed high phenotypic and genotypic variation.

Singh and Chaubey (2003) conducted an experiment with forty genotypes of groundnut and recorded wide range variation for all the characters except days to flowering and days to maturity under study. Phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the characters. Great variability were observed among 23 accessions by Frimpong in 2004 for the quantitative traits such pod yield, haulm yield, crop growth rate, pod growth rate, partition coefficient and harvest index.

Khan (2004) observed highest genotypic and phenotypic variances for plant height followed by shelling percentage when he studied variability for yiel and yield contributing characters of 50 groundnut genotypes.

Kumar and Rajamani (2004), in an experiment with 12 groundnut genotypes, found highly significant differences among the genotypes for seed yield and other characters. High phenotypic co-efficient of variation and genotypic co-efficient of

variation were exhibited for yield, plant height and percentage of sound mature kernels.

Golakia *et al*. (2005) in an experiment recorded observations for 11 characters, i.e., main stem height, number of aerial pegs per plant, number of developed pods per plant, kernel weight per palnt, shelling percentage, 100 kernel weight, harvest index, oil content, recovery percentage (ratio of mature pods to total pod number of aerial pegs), biomass yield per plant and pod yield per plant. They found that the values of the phenotypic co-efficient of variation (PCV) were close to that of the genotypic co-efficient of variation and the magnitude of PCV and GCV was high for all the characters except for shelling percentage and oil content.

John *et al.* (2006) conducted an experiment with 3 high-yielding Spanish bunch cultivars. The estimates of phenotypic co-efficient of variation were higher than those of the genotypic co-efficient variation for all characters such as plant height, number branches per plant, number of pods per plant, pod weight and kernel weight.

Krishna *et al.* (2006) evaluated one hundred groundnut accessions for plant height and podyield, and observed high genotypic and phenotypic co-efficient of variation for pod yield per plant.

Kadam *et al*. (2007) evaluated forty genotypes of different botanical groups to assess the amount of genetic variation and found high genetic co-efficient of variation for kernel yield, pod yield, number of pods, number of branches, plant height and harvest index.

Heritability and Genetic Advance

Heritability coupled with genetic advance had widely used in determining the degree to which a character may be transmitted from parents to offspring. For this reason, heritability coupled with genetic advance for pod yield and its different contributing

characters in groundnut were studied by many authors. Some of those are reviewed below:

In 1998, Islam and Rasul studied heritability and genetic advance in 90 groundnut genotypes and recorded high heritability values for days to 50% flowering (96.25) and days to maturity (91.67). Highest genetic advance as a percentage of the mean was also recorded for number of developed pods per plant and seed yield per plant (49.66 and 43.36, respectively).

Kumar *et al*. (1998) showed high genotypic and phenotypic coefficient of variation along with heritability and genetic advance in percentage of mean for number of kernels per pod, kernel yield and pod yield.

Singh and Singh (1999) shown high heritability for days to maturity, plant height, branches per plant, pods per plant, pod weight per plant, shelling percentage and 100 kernel weight.

Prakash *et al*. (2000) in experiment observed high heritability with high genetic advance for pod yield per plant, pod per plant and 100 kernel weight.

Azad and Hamid (2000) obtained higher heritability and genetic advance in percentage of mean for plant height, pod number, kernel and pod yields.

Naazar *et al*.,(2000) estimated fairly high heritability for pod yield, pod length, seed weight, shelling percentage and oil content which ranged from 0.55 to 0.92.

Nath (2001) conducted an experiment with 17 characters of groundnut and observed high heritability coupled with high genetic advance for plant height, number of total pods per plant, 100 pod weight, 100 kernel weight, shelling percentage and yield per plant.

Sarkar (2001) showed wide variations in heritability coupled with genetic advance of different characters when conducted an experiment on 15 groundnut genotypes. In

broad sense, she observed high heritability coupled with high genetic advance for plant height, number of total pods per plant, 100 pod weight, 100 kernel weight and yield per plant.

Yogendra *et al.* (2002) conducted an experiment of 30 Spanish groundnut genotypes to estimate the heritability and genetic advance for ten characters and found low genetic advance for the number of primary branches, days to first flowering and days to 50% flowering. High heritability (in broad sense) accompanied with high genetic advance (as percent of mean) was observed for H_1, pod yield per plant, plant height and number of pods per plant.

Adhay and Nagada (2002) evaluated twenty-two germplasm lines to study heritability and genetic advance and estimated high heritability, genetic advance and genetic gain for dry pod yield, 100 kernel weight and kernel yield. High heritability was accompanied with low genetic advance for days to 50% flowering, days to maturity, shelling percentage, 100 kernel weight and oil content.

Islam (2003) reported high heritability along with high genetic advance in percentage of mean in plant height, number of mature pod per plant, 100 pod weight, number of total pods per plant, number of primary branches per plant and yield per plant when he conducted an experiment with 29 groundnut genotypes. He also observed intermediate heritability with low genetic advance for number of immature pods per plant.

In an experiment Makhan *et al.* (2003) estimate high heritability for leaf length, leaf width, plant height, number of days to maturity, number of nodules per plant and 100 pod weight and recorded greatest genetic advance for number of nodules per plant.

Singh *et al*. (2003) experimented with forty genotypes of groundnut and recorded high heritability along with high magnitude of genetic advance in percentage of mean

for plant height, number of primary branches per plant, pods per plant, pod weight per plant and 100 kernels weight. Days to 50% flowering, days to maturity and shelling percentage exhibited high heritability and low genetic advance.

Kumar and Rajamani (2004) in an experiment with 12 groundnut genotypes, found highly significant differences among the genotypes for seed yield and other characters. High phenotypic coefficient of variation and genotypic coefficient of variation were exhibited for yield, plant height and percentage of sound mature kernels.

Arifuzzaman (2005) studied an experiment on groundnut and found high heritability and genetic advance for the characters 100 pod weight, 100 kernel weight and plant height and also observed low genetic advance for days to maturity, number of primary branches per plant, number of kernels per plant, shelling percentage and yield per plant.

Golakia *et al.* (2005) conducted an experiment with 25 Virginia runner and 24 Spanish bunch groundnut genotypes and recorded high heritability coupled with high genetic advance for most of characters studied except for shelling percentage and oil content.

John *et al.* (2006) in an experiment estimated heritability ranging from 21.39 (shelling out turn) to 76.03% (number of secondary branches per plant). High heritability values were found for plant height, number of primary branches per plant, number of pods per plant, pod weight and kernel weight. Genetic advance was high for number of primary branches per plant, number of pods per plant and pod weight.

Krishna *et al*. (2006) in an experiment recorded high heritability for plant height and pod yield ranging from 66.89 to 96.11%.

Mensah *et al.* (2006) revealed that treated plants maintained high heritability and genetic advance values in characters such as 100 seed weight, pod number per plant and seed number per plant, indicating that the characters under were controlled by additive genes and could be improved by selection.

Kadam *et al*. (2007) conducted an experiment with forty groundnut genotypes of different botanical groups to assess heritability and genetic advance. High heritability coupled with high genetic advance was observed for pod yield and kernel yield.

CHAPTER III

MATERIALS AND METHODS

In pursuance of the stated objectives of the present thesis works, four separate experiments were conducted with the following material and methods.

3.1 Experimental plan

Four separate experiments were carried out during the period from September 2011 to February 2014. These were:

Experiment 1 : Screening of salt tolerant and sensitive genotypes of groundnut based on shoot biomass and pod yield at different salinity levels

Experiment 2 : Combining ability and genetic analysis of salinity tolerance in 7x7 F_1 diallel population

Experiment 3 : Genetic variability of yield and yield attributing characters of 7x7 F_2 diallel population of groundnut in non-saline field condition

Experiment 4 : Genetic variability of yield and yield attributing characters of 7x7 F_2 diallel population of groundnut in saline field condition

3.2 Experimental location and duration

The first and second experiments were conducted in polyethylene lined earthen pots under rain out shelter in net house and its premises at Sher-e-Bangla Agricultural University, Dhaka (Plate1) during September 2011 to January 2012 and January to May 2013, respectively. Experiments-3 was conducted at research field of Sher -e-Bangla Agricultural University, Dhaka during August to December 2013 and

Plate 1. Pot culture under rain out shelter in net house

Experiment-4 was conducted at research field of Agriculture Research Station (ARS), BARI, Benarpota, Shatkhira during September 2013 to February 2014. Average temperature during the experimental period was 18-34ºC and relative humidity was 55%-82% in Dhaka (Appendix V, VI and VII) and at Satkhira average temperature during the experimental period was 15-32ºC and relative humidity was 72%-85% (Appendix VIII).

3.3 Materials and experimental design

Experiment 1: Tweny five genotypes of groundnut were used in this experiment for screening under salinity levels: 0.40 (control, using tap water), 8.0 and 10.0 dS/m, imposed at the flowering stage following a two factor experiment in CRD design with three replications. Of the genotypes 20 were representatives of Spanish botanical group, 3 were in Virginia and 2 were in Valencia botanical group. The sources of these genotypes are shown in Table 1.

Experiment 2: In the experiment-1, the genotypes were discriminated based on shoot biomass and their pod yield. Thereafter, salt tolerant and sensitive genotypes were selected for crossing in diallel mating system without reciprocals for genetic studies (Table 2). After that, a 7x7 F_1 diallel population was used under 8dS/m salinity stress imposed during flowering till harvest stage following a two factor experiment in CRD design with three replications in earthen pots under rain out shelter in net house.

Experiments 3 and 4: The experiments 3 and 4 were designed to study the genetic variability and performance of yield and yield attributing characters of F_2 7x7 diallel population with parents of groundnut in the non-saline field condition at experimental field of Sher-e-Bangla Agricultural University, Dhaka and in the saline field conditionat Agriculture Research Station, BARI, Benarpota, Shatkhira respectively. A factorial

Table 1. The list and sources of the genotypes used in the experiments

Serial No.	Code used in Expt. 1	Name of Genotypes	Sources	Botanical group
1	V1	Binachinabadam-1	BINA	Spanish
2	V2	Binachinabadam-2	BINA	Spanish
3	V3	Binachinabadam-3	BINA	Spanish
4	V4	Binachinabadam-4	BINA	Spanish
5	V5	Binachinabadam-5	BINA	Spanish
6	V6	Binachinabadam-6	BINA	Spanish
7	V7	Dhaka-1(Maizchar)	BARI	Spanish
8	V8	Pk-1 (Pakshi local)	BARI	Spanish
9	V9	Basantibadam (DG-2)	BARI	Virginia
10	V10	Tridanabadam (DM-1)	BARI	Valencia
11	V11	Jhingabadam	BARI	Valencia
12	V12	Barichinabadam-5	BARI	Spanish
13	V13	BARI Chinabadam-6	BARI	Spanish
14	V14	BARI Chinabadam -7	BARI	Spanish
15	V15	BARI Chinabadam -8	BARI	Spanish
16	V16	BARI Chinabadam -9	BARI	Spanish
17	V17	ICGV-96175	ICRISAT	Spanish
18	V18	ICGV-01249	ICRISAT	Virginia
19	V19	ICGV-00203	ICRISAT	Spanish
20	V20	ICGV-91068	ICRISAT	Spanish
21	V21	ICGV-97119	ICRISAT	Virginia
22	V22	ICGV-96178	ICRISAT	Spanish
23	V23	J-2001-14	ICRISAT	Spanish
24	V24	J-2001-6	ICRISAT	Spanish
25	V25	J-2001-22	ICRISAT	Spanish
26	-	ICGV-00309*	ICRISAT	Spanish

*ICGV-00309, was included in diallel crossing as a tolerant (Srivastava, 2006) parent, but not used in experiment-1 as becauseof the non-availability of the genotype at the starting of experiment1.

Table 2. Selected parents that were used in 7x7 diallel crossing system.

Sl. No.	Code used in Expt. 1	Symbol used in Expt. 2, 3 &4	Selected Parents name	Selected as
1	V6	P1	Binachinabadam-6	Moderately Tolerant
2	V5	P2	Binachinabadam-5	Tolerant
3	V2	P3	Binachinabadam-2	Moderately Tolerant
4	V12	P4	BARI Chinabadam-5	Moderately Sensitive
5	V13	P5	BARI Chinabadam-6	Moderately Tolerant
6	V7	P6	Dhaka-1	Sensitive
7	-	P7	ICGV-00309*	Tolerant

*the genotype was used in diallel crossing as a tolerant (Srivastava, 2006) genotype.

experiment with a randomized complete block design (RCBD) was used for both of the experiments with three replicates. Seeds were hand sown at 15 cm distances in a row and row to row distances were 40 cm. A unit plot size comprised of one row of 4.2 m long.

3.4 Methods

Preparation of pot, sowing of seeds, determination of plant available water, initial moisture content, bulk density, initial salinity and preparation of saline stock solution were done. The methods for the above steps were:

3.4.1 Preparation of pot, field and sowing of seed:

Sun dried earthen pots, 30.50 x 25 cm size were weighed and lined with polyethylene sheet so that water could not leakout. Thereafter, it was filled with 9 kg soil mixture, prepared with sandy loam soil and rotten cow dung in a 1:1 ratio. Five pre germinated seeds of each genotype were sown in each pot. When the plants were established, only two healthy plants were kept in each pot. For field experiments, land preparation was done with a tractor. Later, cross ploughings and final preparation were followed with a power tiller. Finally, clods were broken with hammer, and weeds and stubbles were removed manually. The fertilization was determined following the fertilizer recommendation guide-2005 (BARC, 2005) for both pot culture and field experiment. The total amount nitrogen, phosphorus, potash, sulphur and zinc were applied in the form of Urea, TSP, MP, Gypsum and Zinc sulphate. These were mixed thoroughly with the soil before sowing in the field and seeds were hand sown at 15 cm distances in rows of 40 cm apart. Land preparation, sowing of seeds and testing of salinity in field condition at Agriculture Research Station, BARI, Benarpota, Shatkhira were presented in Plate 2 to Plate 4.

Plate 2. Land preparation to grow F_2 7x7 diallel population of groundnut in saline field condition at Agriculture Research Station (ARS), Benarpota, Satkhira, BARI.

Plate 3. Testing of soil salinity by EC meter of experimental field at Agriculture Research Station (ARS), Benarpota, Satkhira, BARI. (Salinity level was moderate 4.5 dS/m at September 2013).

Plate 4. Sowing seeds of $F_2$7x7 diallel population of groundnut in saline fieldcondition at Agriculture Research Station (ARS), Benarpota, Satkhira, BARI.

3.4.2 Estimates of plant available water (PAW) of soil:

For determination of plant available water analogous to field capacity, three such empty pots were weighed and filled with same amount of soil, as above. Then these were watered until leaked through the hole at the bottom. Thereafter, these were covered with black polyethylene sheet and weighed after cessation of water leaking through the perforated hole. Finally, plant available water was determined using the following formula-

$$\%PAW = \frac{\text{Final weight (pot+ soil + water)} - \text{Initial weight (pot + soil)}}{\text{Soil weight}} \times 100$$

3.4.3 Estimation of initial moisture content and bulk density of soil:

Three brass cores with 8.5 cm height and 5 cm diameter were properly filled with the soil mixture and weighed. These were then oven dried at 105 ºC for 24 hours. After cooling, these were again weighed and the dry soil removed. Weight of the blank cores was also recorded. Initial moisture content of the soil was calculated by the following formula-

% Initial moisture content

$$= \frac{\text{Initial weight (brass core + soil} - \text{oven dry weight (brass core + soil)}}{\text{Oven dry weight of soil}} \times 100$$

While, bulk density was calculated using the formula-

$$\textbf{Bulk density (g/cc)} = \frac{\text{Oven dry weight of soil mixture (g)}}{\text{Volume of soil mixture (cc)}}$$

Here, volume of soil mixture = $\pi r^2 l$

Where, r = radius of brass core (cm)

l = height of brass core (cm)

3.4.4 Estimation of initial salinity of the soil:

Three random samples of mixed soil were taken each with 50g sun dried, pulverized and sieved. Twenty ml distilled water was added with 8g of such sieved mixed soil and was stirred for 30 minutes at 250 rpm. The following day, it was stirred again and electrical conductivity was recorded in dS/m using an EC meter (HI98304, by HANNA, Philippines).

3.4.5 Intercultural operations:

When the plants were established, only two healthy plants were kept in each pot. The pots were kept free from weeds. The plants were protected from insect pest and diseases by spraying appropriate insecticides, fungicides and acaricides as and when necessaryfor both pot and field experiments. Pot culture under rain out shelter with saline solution and tap water in net house is presented in Plate 5.

3.4.6 Preparation of saline stock solution:

The saline water was synthesized by using mixture of different salts: 50% NaCl, 15% Na_2SO_4, 10% $NaHCO_3$, $CaCl_2$ and $MgCl_2$ together with 5% $MgSO_4$ so that that their compositions were almost alike their average compositions in the ground water of saline areas of Bangladesh (SRDI, 2003). Fifty grams of such salt was dissolved per liter tap water to prepare the stock solution. The salinity of the stock solution was 80 dS/m.

3.4.7 Salinity imposition:

The total amount of stock solution needed to raise the desired salinity of the soil mixture was estimated with the following equation-

$V_1S_1 = V_2S_2$

Plate 5. Pot culture under rain out shelter with saline solutions and tapwater in net house

Where,

V_1 = Volume of soil mixture in a pot

S_1 = Desired salinity – Initial salinity of the soil

V_2 = Volume of water at 70-80% PAW

S_2 = Salinity of stock solution

Again, volume of soil mixture (V_1) was determined using the following formula-

$$V_1 = \frac{\text{Weight of oven dried soil}}{\text{Bulk density of soil}}$$

Volume of water (V_2) was determined by dividing the weight of water with its density (0.98g/cc).The estimated amount of stock solution was then diluted to the desired salinity levels by adding tap water and then imposed during the flowering stage till harvest. The total amount of saline water for the respective doses was applied at different installments. At such installment, 0.5 to 1.0 liter saline water was applied so that the moisture content of the pots remained 70-80% of plant available water (PAW). For the control, same amount of only fresh tap water was applied.

3.4.8 Diallel crossing

Crossing was done following the technique of Kumar and Patel (1996) with some modifications. Early formed buds close to the soil surface were used for hybridization so that the pegs could easily penetrate into the soil (Plate 6). The well developed buds close to the soil, of the recipient parents were emasculated (removal of anthers from bud flowers before their dehiscence to avoid self pollination) during 4:30- 6:30 PM. By that time of day, the hypanthium was sufficiently elongated and the bud was big enoughto be handled easily during emasculation, and the anthers did not dehisce. Once a well-developed bud selected, all other buds at that node (axil of the leaf) were removed with forceps. Removal of these buds ensured that only one flower was allowed to set a peg at each node and that facilitated the identification of hybrid pods.

A. Selection of right-sized bud

B. Emasculated bud covered with pink colored straw tube

C. Just above the internode the emasculated bud marked with 2 mmplastic white cable tie

D**. Pollen mass squeezed out from male flower, ready to be used for pollination**

Plate 6. Different stages ofhybridization techniques

E. Pollination the female flower with pollen sticking to the stigma

F. Covered with green colored straw tube after pollination

G. Pegs entering the soil after successful fertilization

H. A female plant at harvest showing identification white cable ties and the hybrid pods

Plate 6. Continued.

The leaf was pulled down gently to expose these buds. The bud was held gently between the thumb and index finger of the left hand. Using forceps held in the right hand, the single sepal opposite the standard petal was pulled down. The fused sepal was also folded down and held back. The standard was then gently and carefully opened with forceps and was held back by the thumb and index finger. The wing petals were pulled down locking them with standard. The keel was pulled outwards by its ridge with forceps to expose the anthers. All the anthers were removed with the filaments from their bases. This left only the stigma and style, which were now well exposed. The emasculated buds were covered with pink colored straw tube sealed on one side to avoid fertilization with undesirable foreign pollen and just above the internode the emasculated bud was then marked with 2 mm plastic white cable tie. Before pollination, healthy flowers from male parents were collected early in the morning by 6:00-7:00 AM to ensure steady supply of male flowers. During 6:00-8:30 AM, pollination was performed by collecting pollen from male parents. The standards and wings (petals) were removed and the keel petal was gently pressed between the thumb and index finger to squeeze the sticky pollen mass out from the anthers. The sticky lump of pollen was deposited on the tip of the stigma of the emasculated flower. Finally, the stigma was further covered with green colored straw tube. After completion of crossing, the newly formed flowers were removed daily from the recipient parents. For getting the F_1 diallel population, the crossing was carried out during July to November 2012. At maturity the crossed pods were harvested carefully by checking the marked internode with white cable tie on 12 November 2012.

The number of F_1 hybrid pods obtained from 21 cross combinations under the half-diallel method involving 7 selected parents are presented in Table 3. The obtained F_1 hybrid seeds were used in experiment 2 for combining ability and genetic studies. After using in experiment 2, the rest of F_1 hybrid seeds were sown in non-saline pots seperately to get adequet number of F_2 seeds. The F_2 seeds obtained from experiment-2 and non-saline pots were used in experiment 3 and 4. The scientists of different organizations were visited experimental site (Plate 7 and Plate 8). Experimental procedures were presented in Plate 9 to Plate 14.

Table 3. The numbers of F_1 hybrid pods obtained from 21 cross combinations under the half-diallel involving 7 selected parents of groundnut genotypes

Sl. No.	Cross combinations	Flower emasculated/ pollinated	No. of F_1 hybrid pods	% of success
1	P1xP2	268	125	46.57
2	P1xP3	233	114	48.95
3	P1xP4	250	93	37.14
4	P1xP5	220	119	54.31
5	P1xP6	440	114	25.80
6	P1xP7	323	148	45.80
7	P2xP3	285	143	50.02
8	P2xP4	256	122	47.84
9	P2xP5	396	120	30.23
10	P2xP6	407	111	27.20
11	P2xP7	433	193	44.56
12	P3xP4	307	116	37.85
13	P3xP5	241	82	33.83
14	P3xP6	386	170	43.92
15	P3xP7	376	146	38.82
16	P4xP5	321	145	45.17
17	P4xP6	311	111	35.82
18	P4xP7	313	110	35.18
19	P5xP6	272	109	40.09
20	P5xP7	213	87	40.82
21	P6xP7	188	67	35.47
Range		**440-188**	**193-67**	**54.31-25.80**
Average		**306**	**121**	**40.26**

Plate 7. The experiment site visited by national- international scientists and professors of different institutions

Plate 8. Professors and scientists of different national institutions were visited the experimental site

Plate 9. Effect of salinity imposed during flowering to harvest stages at 8 dS/m level

Plate 10. Crossing plot of groundnut at net house premises

Plate 11. Crossing plot of groundnut at net house

Plate12. Crossing activity in the net house

Plate 13. Harvesting of the hybrid pods

Plate 14. Drying of harvested pods in the sunlight

3.4.9 Harvesting

All plants were uprooted at full maturity and washed with running tap water. After sun drying, plant height, number of branches and pegs per plants were recorded. Thereafter, leaves, stems, roots and pods were separated. The additional roots and pods left in the soil mixture were also collected. Finally, the leaves, stems and roots were oven dried at 70^0C for 72 hours and weighed after cooling. Pods were sun dried separately.

3.4.10 Data recording

Data on different parameters mentioned below were recorded:

3.4.10.1 Shoot-root characters*:* All the shoot-root characters and yield attributes gathered from all the plants grown in pots were averaged.

Plant height(cm): It was measured after harvest from the junction between stem and root to the base of the apex to the main stem.

Branch per plant (no.): Number of primary and secondary branches from all the plants in pots were counted and averaged.

Shoot biomass (g): Oven dry weight of leaves and stems were gathered from all the plants in pots and then averaged.

Root biomass (g): Oven dry weight of roots were gathered from all plants in pots and then averaged.

Root and shoot ratio: Root biomass was divided by its corresponding shoot biomass yield.

Total biomass yield per plant (g): The total biomass yield was estimated from the summation of shoot biomass and root biomass yields.

3.4.10.2 Yield and yield attributes

Pod per plant (no.): Number of pods in all plants were counted from all plants in pots and averaged.

Pod weight per plant (g): Sun dried pods from all plants were weighed and then averaged.

Pod and peg ratio: Total number of pods in a plant was divided by the total number of pegs.

Kernel weight per plant (g): Kernels in all plants was weighed and then averaged.

Shelling percent: Kernel weight was divided by its corresponding pod weight and multiplied by 100.

Relative performance of a characteristic was calculated following the formula:

Relative performance (% of control) =

$$\frac{\text{Performance of a trait under saline condition}}{\text{Performance under control condition}} \times 100$$

3.4.10.3 Chemical parameters

Determination of Na^+, K^+ and Ca^{2+} contents

Digestion: One gram finely grinded shoot tissues (50% leaf + 50% stem) were digested following the procedure of Johnson and Ulrich (1959) with a mixture of HNO_3 and $HClO_4$ acids at the ratio of 5:3. One gram oven dried ground tissue was taken into a clean and dry 100 ml volumetric flask and 5 ml concentrated HNO_3 added , kept overnight at room temperature for pre-digestion. The pre-digested material was then heated with agitation at 100-120ºC for one hour on a hot plate within a fume hood to evolve the brown nitrous oxide fumes. Thereafter, 2.5 ml

HNO_3 was added and further heated with agitation at 100-120ºC for one hour. This steps was repeated two times. Then it was cooled at room temperature and 3 ml $HClO_4$ added, heated at 120-150ºC and again cooled at room temperature. This step was also repeated two times and heating at this temperature was continued till it became colorless. This step completes oxidation of all soluble inorganic form. The digested sample was then made 50 ml by adding de-ionised water. To prepare working solution, 5 ml of the above solution was taken and further diluted to 50 ml by adding distilled water.

Estimation:

Na^+: Estimated directly from the working solution with a flame photometer together with standard solutions of 10, 20, 40 and 80 ppm Na^+.

K^+: 5 ml of the working solution was taken and further diluted to 50 ml and readings were taken with a flame photometer along with standard solutions of 1, 2 and 4 ppm K^+.

Ca^{2+}: Two ml lanthanum oxide wasadded with 20 ml working solution and then reading was taken with a flame photometer along with standard solutions of 0, 20, and 30 ppm Ca^{2+}.

3.4.11 Discrimination of genotypes into salinity tolerant and sensitive classes

Reduction in performance (% of control) =

$$\frac{\text{Performance of a trait under saline condition}}{\text{Performance under control condition}} \times 100$$

% Reduction under salinity stress = 100 - reduction in performance

Then, it was classified into four groups : (a) <20% reduction (b) 20% to 40% reduction (c) 41 to 60% reduction and finally (d) >60% reduction to discriminate (i)

tolerant, (ii) moderately tolerant (iii) moderately sensitive and (iv) sensitive genotypes to salinity, respectively (Azad *et al.*, 2013). The flowering stage was the most sensitive stage for both biomass growth and yield. Salinity level between 7-9 dS/m was appropriate for screening program in groundnut as maximum dispersion amongst genotypes appeared in that salinity range (Azad, 2008). In this study, screening of salt tolerant and sensitive genotypes find out by imposing salinity stress during flowering till harvest stages at 8dS/m level both biomass growth and yield.

3.4.12 Analysis of data

The recorded data were analyzed statistically as per the design used by using MSTAT-C software. The treatment means were compared by using DMRT/LSD at 5% level of probability (Gomez and Gomez, 1984).

3.4.12.1 Estimation of Genetic parameters

Estimation of phenotypic (δ^2p), genotypic (δ^2g) and environmental (δ^2e) variance were calculated by the following formula (Johnson *et al*., 1955).

$$\textbf{Genotypic variance } (\delta^2 g) = \frac{\text{MSG-MSE}}{r}$$

Where,

MSG = Mean square due to genotypes

MSE = Mean square error

r = Number of replication

Phenotypic variance (δ^2p) = $\delta^2g + \delta^2e$

Where,

δ^2g = Genotypic variance

δ^2e = Environmental variance

Environmental variance ($\delta^2 e$) = MSE

Where,

MSE = Mean Square Error

3.4.12.2 Estimation of Genotypic Co-efficient of variation (GCV%) and Phenotypic Co-efficient of Variation (PCV%):

Genotypic and phenotypic co-efficient of variation were estimated according to the formula given by Burton (1952) and Singh and Chudhury (1985).

$$\textbf{Genotypic Co-efficient of Variation (GCV\%)} = \frac{\sqrt{\delta^2 g}}{\overline{X}}$$

Where,

$\delta^2 g$ = Genotypic variance

$\overline{X}$= Population mean

$$\textbf{Phenotypic Co-efficient of Variation (PCV\%)} = \frac{\sqrt{\delta^2 p}}{\overline{X}}$$

Where,

$\delta^2 p$ = Genotypic variance

$\overline{X}$= Population mean

3.4.12.2 Estimation of heritability

Heritability in broad sense was estimated using the given formula suggested by Johnson et al., (1955) and Hanson et al., (1956).

$$\textbf{Heritability } h^2 b = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Where,

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

3.4.12.3 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al.*, (1955).

Genetic advance (GA) = h^2b x K x δp

Where,

h^2b = Heritability

δp = Phenotypic standard deviation

K = Selection intensity the value of which is 2.06 at 5% selection intensity.

3.4.12.4 Estimation of genetic advance in percent of mean GA(%)

Estimate by the following formula suggested by Comstock and Robinson (1952).

$$\textbf{Genetic advance in percent of mean GA (\%)} = \frac{GA}{\overline{X}}$$

Where,

GA = Expected Genetic Advance

$\overline{X}$ = Population mean

3.4.12.5 Genetic Analysis

Combining ability in relation to diallel cross*:*

Combining ability analysis was carried out following Method-2, Model 1 of Griffing (1956) in experiments 2. ANOVA for combining ability analysis in Method 2 Model 1 is as follows-

Source	Df	SS	MS	Expected mean squares
gca	p-1	SSg	Mg	$\delta^2 e + \frac{p+2}{p-1} \Sigma g^2 i$
Sca	$\frac{P(p-1)}{2}$	SSs	Ms	$\delta^2 e + \frac{2}{p(p-1)} \Sigma\Sigma s^2 ij$
Error	(b-1)(e-1)	Sse	Me′	$\delta^2 e$

p stands for number of parents

Model-1

The mathematical model for the combining ability analysis in model 1 was as bellows

$$Yij = \mu + gi + gj + Sij + \frac{1}{bc} \Sigma\Sigma e_{ij}k_1$$

Where,

ij = 1---------- n (n = no. of parents)

k = 1---------- b (b= no. of blocks/replications)

l = 1---------- c (c = no. of observation in each plot)

X ij is the mean of X_{ij}^{th} genotype over k and l ; μ is the population mean; g_i is the gca effect. S_{ij} is the sca effect such that $S_{ij} = S_{ji}$ and $e_{ij}k_l$ is the environment effect associated with $_{ij}kl^{th}$ observation.

Restriction imposed are $\Sigma_i g_i = 0$ and $\Sigma_j s_{ij} + s_{ji} = 0$ (for each i)

The sum of squares (SS) were calculated as:

$$SSg = \frac{1}{n+2} [\Sigma_i (Yi. + Yii)^2 - \frac{4}{n} Y^2..]$$

$$SSs = \Sigma\Sigma Y_{ij}^2 - \frac{1}{n+2}\Sigma(Yi. + Yii)^2 + \frac{2}{(n+1)(n+2)}Y^2..$$

Where,

SSg = sum of square due to gca

SSs = sum of square due to sca

Yi = array total of the i^{th} parent

Yii = mean value of the i^{th} parent

Y.. = grand total of the $\frac{1}{2n(n-1)}$ crosses and parental values

Yij = progeny mean values in the diallel table

Thus the effects were calculated as:

$$g_i = \frac{1}{(n+2)}[(Yi. + Yii) - \frac{2}{n}Y..]$$

$$Sij = Yij - \frac{1}{(n+2)}[Yi. + Yii + Y.j + Yjj] + \frac{2}{(n+1)(n+2)}Y..$$

Variance of effects was calculated as:

i) $Var(gi) = (n-1)\,\delta^2 e/n(n+2)$

ii) $Var(sij) = 2(n-1)\,\delta^2 e/(n+1)(n+2)$

SE (standard error) was calculated as the square root of the variance.

3.4.12.6 Vr- Wr analysis and graphical presentation

The Vr-Wr analysis facilitates study of major genetic features of quantitative characters, subjected to fulfillment of certain assumptions as listed by Hayman (1954). The assumptions are:

a) Diploid segregation
b) No differences between reciprocal crosses (exception environmental difference)
c) Independent action of non allelic genes

d) No multiple allilism

e) Homozygosity of parents

f) Independent distribution of genes.

The array variance (Vr) and parent offspring covarience (Wr) and regression of Wr on Vr were calculated to test the adequacy of the additive dominance genetic model to discern the relative proportion of dominant to recessive genes present in the common parents of the arrays and to find average level of dominance.

The parabola Wr = √ Vp.Vr in the Wr/Vr graph delimited the area which the coordinate (Vr, Wr) array data occur and the Wr intercept is an indicator of the average dominance, being positive with patial domonance and negative with over dominance. If there is no domonance, all the points on the Vr, Wr graph are estimates of single point (Wr, Vr) with Wr = 2Vr, there is no regression and the line is tangent to the limiting parabola, and with complete dominance, the regression line is of unit slope and passes through the origin.

The variance (Vr) and covariance (Wr) of array whose common parent bears most of the dominant genes will be relatively smaller in magnitude than the array whose common parent carries most of the recessive genes. Parents with dominant allele will have low Vr and Wr and will be near the origin while highly recessive parents have large Vr and Wr and will be farthest from the origin.

3.4.12.7 Estimation of components of variation in F_1

The components of genetic variation were calculated according to Hayman (1954) as:

$D = V_0 L_0 – E$ = variation due to additive effect

$F = 2V_0L_0 – 4 W_0 L_{01} – 2(n-2)E/n$ = the mean of 'Fr' values over the arrays

$H_1 = V_0L_0 - 4\ W_0\ L_{01} + 4\ V_0L_1 - (3n-2)E/n$ = component of variation due to the dominance effect of the genes.

$H_2 = 4V_1L_1 - 4\ V_0L_1 - 2E$ = proportion of positive genes 'u' and proportion of negative genes 'v'in the parents

$h^2 = 4(ML_1 - ML_0)^2 - 4(n-1)E/n^2$ = dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses).

E = environmental variance was derived from EMS of the ANOVA = expected environmental component of variation.

Where,

$V_0\ L_0$ = Variance of parents

V_1L_1 = Mean variance of the arrays

$W_0\ L_{01}$= The mean co-variance between the parents and the arrays

V_0L_1= The variance of the mean of arrays

$(ML_1- ML_0)$ = The difference between the mean of the parents and the mean of their n^2 progeny.

The standard errors, to test the significance of components listed above, are calculated as follows:

$$\text{SE of D} = \sqrt{\frac{S^2(n^5 + n^4)}{n^5}}$$

$$\text{SE of } H_1 = \sqrt{\frac{S^2(16n^5 + 656\ n^4 + 192n^3 + 64n^2)}{n^5}}$$

$$\text{SE of } H_2 = \sqrt{\frac{S^2(576\ n^4)}{n^5}}$$

$$\text{SE of F} = \sqrt{\frac{S^2(16n^5 + 80n^4 - 64n^3 + 6n^2)}{n^5}}$$

$$\text{SE of } h^2 = \sqrt{\frac{S^2(256n^4 + 256n^2 - 512n + 256)}{n^5}}$$

$$\text{SE of } E_2 = \sqrt{\frac{S^2(n^4)}{n^5}}$$

Where, n = Number of parents and S^2 = ½ Var. (Wr – Vr)

The significance of the various statistics wastestedby‘t’ test at n-2 degree of freedom as

$$t = \frac{\text{Parameter}}{\text{SE of parameter}}$$

The parents were divided by their respective standard errors and the resulting values which exceeded 2.776 were marked significant.

The following parameters were also calculated:

Proportion of the genetic components

The different proportions of the genetic components were worked out according to the procedure given below:

(a) Degree of dominance: $[H_1/D]^{½}$

If $[H_1/D]^{½} = 1$ (Complete dominance)

< 1 (Over dominance)

>1 (Partial dominance)

(b) Proportion of genes with positive and negetive effects in the parents:

$\mathbf{H_2 / 4H_1}$

(c) Proportion of dominant and recessive genes in the parents :

$$\frac{(4DH_1)^{½} + F}{(4DH_1)^{½} - F}$$

(d) Number of genes which control the character and exhibit dominance: h^2/H_2

(e) Heritability in narrow sense (h^2n): $$\frac{½D + ½ H_1 - ½ H_2 - ½F}{½D + ½ H_1 - ¼ H_2 - ½F + E}$$

(f) Heritability in broad sense (h^2 b): $$\frac{½D + ½ H_1 - ¼ H_2 - ½F}{½D + ½ H_1 - ¼ H_2 - ½F + E}$$

CHAPTER IV

RESULTS

To achieve the objectives of the study four separate experiments were conducted. The results of the research works are presented experiment wise with relevant sub heads as follows.

4.1 Experiment 1: Screening of salt tolerant and sensitive genotypes of groundnut based on shoot biomass and pod yield at different salinity levels.

The study was conducted to screening the salt tolerant and sensitive genotypes based on sixteen (six shoot-root characters, six pod yield and yield attributes and four nutrient elements up take) characters of 25 genotypes of groundnut at different salinity levels of 10dS/m, 8dS/m and control tap water 0.38 dS/m. Mean squares of shoot and root characters, pod yield, yield attributes and nutrient elements uptake in shoot tissues of 25 genotypes as influenced by salinity levels are presented in Table 4(a), Table 4(b) and Table 4(c), respectively. The genotypes (V) and salinity levels (SL) showed highly significant differences for plant height, branch number, shoot biomass, root biomass, root: shoot ratio, total biomass, peg number/plant, pod number/plant, pod: peg ratio, pod yield/plant, kernel weight/plant, shelling%, Na^+ content/plant, K^+ content/plant, Na^+/K^+ ratio and Ca^{+2} content/plant in shoot tissues. The interactions between genotypes and salinity levels, V x SL for all characters were highly significant. That indicated the presence of considerable variation among the genotypes as well as the effect of salinity levels on the genotypes.

4.1.1 Performance of the shoot-root characters of the genotypes at non-saline condition

The means of shoot and root characters under non-saline control condition are shown in Table 5a. The highest plant height showedin V18 (29.50 cm) and V25 (29.50 cm) followed

Table 4. Analysis of variance of different characteristics of 25 genotypes of groundnut as influenced by different salinity levels Imposed during flowering till harvest stages

(a) Shoot and root characters

SV	df	Plant height	Branch number	Shoot biomass	Root biomass	Root: shoot ratio	Total biomass
Genotypes(V)	24	169.83**	14.70**	8.89**	0.04**	0.002**	9.86**
Salinity levels (SL)	2	919.79**	37.67**	200.38**	1.12**	0.003**	231.07**
V x SL	48	89.09**	6.22**	4.37**	0.02**	0.0006**	4.74**
Error	150	6.50	1.31	1.28	0.01	0.0002	1.39

**Significant at 1%

Table4. Continued.

(b) Pod yield and yield attributes

SV	df	Peg no./plant	Pod no./plant	Pod: peg ratio	Pod yield/plant	Kernel wt./plant	Shelling (%)
Genotypes(V)	24	24.23**	19.50**	429.06**	4.58**	0.90**	2142.10**
Salinity levels (SL)	2	77.02**	151.93**	4620.36**	71.66**	20.72**	32407.90**
V x SL	48	13.65**	4.97**	412.98**	2.34**	0.71**	517.09**
Error	150	4.15	1.82	1.99	0.59	0.11	6.94

**Significant at 1%

(c) Na^+, K^+ and Ca^{++} contents in shoot tissues

SV	df	Na^+ (%)	K^+ (%)	Na^+: K^+ ratio	Ca^{2+} (%)
Genotypes(V)	24	0.21**	0.83**	2.68**	0.06**
Salinity levels (SL)	2	23.65**	24.79**	85.14**	1.03**
V x SL	48	0.10**	0.46**	1.25**	0.034**
Error	150	0.005	0.06	0.68	0.003

**Significant at 1%

Table 5a. Performance of shoot and root characters of 25 groundnut genotypes at non-saline condition

Code	Genotypes/ varieties	Plant height (cm)	No. of branches	Shoot biomass (g)	Root biomass (g)	Root : shoot ratio	Total biomass (g)
V1	Binachinabadam-1	21.33	5.17	6.10	0.55	0.10	6.65
V2	Binachinabadam-2	20.92	6.67	7.55	0.37	0.05	7.92
V3	Binachinabadam-3	17.25	4.83	5.34	0.55	0.10	5.89
V4	Binachinabadam-4	17.67	7.49	5.08	0.45	0.09	5.53
V5	Binachinabadam-5	20.50	7.50	5.19	0.42	0.08	5.61
V6	Binachinabadam-6	22.92	7.50	5.35	0.40	0.07	5.74
V7	Dhaka-1(Maizchar)	19.00	5.00	5.29	0.40	0.08	5.69
V8	Pk-1 (Pakshi local)	23.92	6.50	5.39	0.41	0.08	5.79
V9	Basantibadam (DG-2)	25.42	10.50	6.99	0.49	0.07	7.48
V10	Tridanabadam (DM-1)	19.08	6.33	4.46	0.45	0.10	4.91
V11	Jhingabadam	23.33	7.67	5.27	0.40	0.08	5.67
V12	Barichinabadam-5	25.83	9.78	7.25	0.54	0.08	7.79
V13	BARI Chinabadam-6	25.17	9.33	6.61	0.42	0.06	7.03
V14	BARI Chinabadam -7	23.17	9.67	5.45	0.45	0.08	5.89
V15	BARI Chinabadam -8	23.42	8.61	5.48	0.42	0.08	5.90
V16	BARI Chinabadam -9	22.00	9.31	6.11	0.46	0.08	6.57
V17	ICGV-96175	26.75	7.50	6.24	0.39	0.06	6.63
V18	ICGV-01249	29.50	9.83	7.88	0.43	0.06	8.31
V19	ICGV-00203	27.00	7.00	7.10	0.37	0.05	7.47
V20	ICGV-91068	27.08	9.36	6.98	0.51	0.07	7.49
V21	ICGV-97119	29.17	7.36	6.40	0.35	0.06	6.76
V22	ICGV-96178	25.50	7.50	6.41	0.48	0.08	6.89
V23	J-2001-14	20.33	5.00	5.37	0.39	0.08	5.77
V24	J-2001-6	20.67	6.50	7.17	0.42	0.06	7.59
V25	J-2001-22	29.50	4.00	2.86	0.38	0.10	3.24
Range		**17.25 - 29.50**	**4.00 - 10.50**	**2.86-7.88**	**0.35-0.55**	**0.05-0.10**	**3.24-8.31**
Average		**23.45**	**7.43**	**5.97**	**0.44**	**0.08**	**6.40**
LSD(0.05)		**4.53**	**2.03**	**2.06**	**0.13**	**0.02**	**2.14**

by V20, V19, V17, V12, V9 and V13 with non-significant differences. In contrast, V3 had the lowest plant height sharing equal statistical rank with V4, V7, V10, V23, V24, V2 and V1. The rest of the genotypes had intermediate plant height (17.25 cm) with significant differences from other genotypes.V8, V9, V12, V13, V17, V18, V19, V20, V21, V22 and V25 showed significantly higher plant height than the local variety/genotype, Dhaka-1(V7).

Genotype V9 had the maximum number of branches (10.50) followed by V18, V12, V14, V20, V13, V16 and V15 with non-significant differences. In contrast, V25 had the minimum number of branches (4.00) of all, shared equal statistical rank with V3, V7, V23 and V1. The rest of the genotypes had intermediate number of branches with significant differences from genotypes.

The highest shoot biomass (7.88g) was found in V18 followed by V2, V12, V24, V19, V9, V20, V13, V22, V21, V17, V16 and V1with non-significant differences. The lowest shoot biomass (2.86 g) was found in V25.

Genotypes V1and V3 had the highest root biomass (0.55 g) and V21 had the lowest root biomass (0.35 g) with non-significant differences with all genotypes. V1, V3, V10 and V25 had highest root: shoot ratio (0.10) followed by V4, V5, V7, V8, V11, V12, V14, V15, V16, V22 and V23 with non-significant differences. In contrast, V2and V19 had the lowest root: shoot ratio (0.05) sharing equal statistical rank with V6, V9, V13, V17, V18, V20, V21 and V24.

Like shoot biomass, the highest total biomass (8.31 g) was found in V18 followed by V2, V12, V24, V20, V9, V19, V13, V22, V1, V17 and V16 with non-significant differences. Interestingly, like shoot biomass V25 had the lowest total biomass (3.24 g) sharing equal statistical rank with V10 and significantly differences with all the rest genotypes.

4.1.2 Performance of the pod yield and yield attributes of the genotypes at non-saline condition:

The means of the pod yield and yield attribute sunder non-saline control condition are shown in Table 5b. All the traits were observed significantly different within the genotypes under non-saline control condition. Genotype V9 was observed maximum peg number (10.50) followed by V8, V5andV20with non-significant differences. In contrast, V25 had the minimum peg number (3.21) sharing equal statistical rank with V14, V10, V21, V24, V11, V17, V22 and V19. The rest of the genotypes had intermediate peg number with significant difference with other genotypes. Peg number showed a wide range of variation from 3.21 to 10.50 with average value of 6.66.

The maximum number of pods/plant (8.00) was found in V5 and V8 followed by V3, V20, V6, V1 and V15 with non-significant differences. In contrast, V24, V21, V19 and V17 had the minimum number of pods (2.00) sharing equal statistical rank with V23, V25, V22, V13, V16 and V7. The rest of the genotypes had intermediate number of pods with significant differences from other genotypes. Pod number showed a wide range of variation from 2.00 to 8.00 with average value of 4.40.

The highest and higher pod: peg ratio was found in V11 andV25 (0.97) followed by, V20, V3, V12, V8, V15, V16, V4 and V1 showing significant differences. The lowest pod: peg ratio (0.31) was found in V23 followed by V9 with significant differences with other rest genotypes. The rest of the genotypes had intermediate pod: peg ratio with significant differences from others. Pod:peg ratio showed a wide range of variation from 0.31 to 0.97 with average value of 0.63.

The highest pod weight/plant (5.81 g) was found in V14 followed by V18, V14 and V20 with non-significant differences. V24 had the lowest pod weight (0.36g) sharing

Table 5b. Performance of pod yield and yield attributes of 25 groundnut genotypes at non-saline condition

Code	Genotypes/ varieties	Peg no. /plant	Pod no. /plant	Pod :peg ratio	Pod wt. /plant (g)	Kernel wt. /plant (g)	Shelling (%)
V1	Binachinabadam-1	8.50	6.00	0.71	1.73	1.36	78.81
V2	Binachinabadam-2	6.83	4.70	0.61	1.14	0.72	63.23
V3	Binachinabadam-3	9.67	7.83	0.81	3.34	2.19	65.50
V4	Binachinabadam-4	6.33	5.00	0.79	3.29	1.56	47.46
V5	Binachinabadam-5	9.50	8.00	0.60	2.78	1.75	59.28
V6	Binachinabadam-6	7.00	6.30	0.76	2.49	1.42	57.00
V7	Dhaka-1(Maizchar)	7.00	4.50	0.64	1.77	0.88	49.41
V8	Pk-1 (Pakshi local)	10.17	8.00	0.78	2.23	1.23	55.16
V9	Basantibadam (DG-2)	10.50	3.33	0.32	2.35	1.53	65.09
V10	Tridanabadam (DM-1)	4.17	3.00	0.72	1.57	0.65	41.48
V11	Jhingabadam	4.83	4.67	0.97	2.99	1.41	47.12
V12	Barichinabadam-5	6.17	5.00	0.81	1.68	0.44	46.05
V13	BARI Chinabadam-6	7.00	3.00	0.43	1.82	0.71	86.59
V14	BARI Chinabadam -7	3.50	2.67	0.76	5.81	1.87	32.26
V15	BARI Chinabadam -8	7.83	6.00	0.77	4.48	1.65	36.91
V16	BARI Chinabadam -9	6.33	4.00	0.63	1.22	0.60	48.61
V17	ICGV-96175	5.00	2.00	0.40	0.72	0.34	41.46
V18	ICGV-01249	6.67	4.67	0.70	5.07	2.79	55.11
V19	ICGV-00203	5.17	2.00	0.39	0.98	0.46	47.52
V20	ICGV-91068	8.50	7.00	0.82	4.16	2.64	63.58
V21	ICGV-97119	4.33	2.00	0.46	0.74	0.30	42.85
V22	ICGV-96178	5.00	3.00	0.60	1.87	1.13	60.49
V23	J-2001-14	7.50	2.33	0.31	0.52	0.26	49.57
V24	J-2001-6	4.50	2.00	0.44	0.36	0.15	41.10
V25	J-2001-22	3.21	3.00	0.91	0.71	0.31	43.91
Range		**3.21-10.50**	**2.00-8.00**	**0.31-0.97**	**0.36-5.81**	**0.15-2.79**	**32.26-86.59**
Average		**6.66**	**4.40**	**0.63**	**2.23**	**1.09**	**53.45**
LSD(0.05)		**2.91**	**2.55**	**0.07**	**1.68**	**0.83**	**4.68**

equal statistical rank with V23, V25, V17, V21, V19, V2, V16, V10, V12, V1, V7, V13 and V22. The rest of the genotypes had intermediate pod weight/plant with significant differences from others. Pod weight/plant showed a wide range of variation from 0.36 g to 5.81g with average value of 2.23g.

Genotype V18 had the highest kernel weight/plant (2.79g) followed by V20 and V3 with non-significant differences. In contrast, V24 had the lowest kernel weight/plant (0.15g) sharing equal statistical rank with V23, V25, V17, V21, V19, V16, V10, V13, V2 and V7. The rest of the genotypes had intermediate kernel weight/plant with significant differences from others. Kernel weight/plant showed a wide range of variation from 0.15g to 2.79g with average value of 1.09g.

The highest shelling (%) was found only in V13 (86.39) followed by V1, V3, V9 and V2 showing significant differences. In contrast, V14 had the lowest (32.16) shelling (%) followed by V21, V24, V25, V17, V10 and V23 with significant difference. The rest of the genotypes had intermediate shelling (%) with significant differences from others. Shelling (%) showed a wide range of variation from 32.26 to 86.59 with average value of 53.45.

4.1.3 Performance of the shoot-root characters of the genotypes at 8dS/m salinity stress condition:

The means of shoot and root characters under 8dS/m salinity stress condition are shown in Table 6a. V18 showed the highest plant height (26.00 cm) despite non-significant difference with V20, V21, V13, V9, V12, V19 and V22. In contrast, V3 had the lowest plant height (15.50 cm) sharing equal statistical rankWith V17, V4, V7, V10, V24 and V23. The rest of the genotypes had intermediate plant height with significant differences from others. Plant height showed a wide range of variation from 15.50 cm to 26.00 cm with average value of 21.19 cm.

Table 6a. Performance of shoot and root characters of 25 groundnut genotypes at 8dS/m salinity stress

Code	Genotypes/ varieties	Plant height (cm)	No. of branches	Shoot biomass (g)	Root biomass (g)	Root : shoot ratio	Total biomass (g)
V1	Binachinabadam-1	20.33	5.00	3.17	0.32	0.10	3.49
V2	Binachinabadam-2	20.75	5.83	5.22	0.36	0.07	5.58
V3	Binachinabadam-3	15.50	4.83	4.03	0.25	0.06	4.28
V4	Binachinabadam-4	17.58	5.50	3.14	0.21	0.07	3.35
V5	Binachinabadam-5	19.83	5.50	4.06	0.32	0.08	4.52
V6	Binachinabadam-6	20.00	5.00	3.59	0.24	0.07	3.83
V7	Dhaka-1(Maizchar)	18.33	5.50	3.22	0.23	0.07	3.35
V8	Pk-1 (Pakshi local)	19.33	4.00	3.63	0.33	0.09	3.96
V9	Basantibadam (DG-2)	25.17	8.50	4.14	0.33	0.08	4.47
V10	Tridanabadam (DM-1)	18.42	6.33	3.58	0.25	0.07	3.83
V11	Jhingabadam	20.17	4.33	3.04	0.23	0.08	3.27
V12	Barichinabadam-5	24.67	7.57	4.00	0.42	0.10	4.42
V13	BARI Chinabadam-6	25.17	7.67	5.15	0.24	0.05	4.19
V14	BARI Chinabadam -7	22.17	7.33	4.83	0.29	0.06	5.12
V15	BARI Chinabadam -8	22.17	4.83	4.55	0.22	0.05	4.77
V16	BARI Chinabadam -9	21.50	7.00	5.21	0.33	0.06	5.54
V17	ICGV-96175	17.50	5.50	1.47	0.10	0.07	1.57
V18	ICGV-01249	26.00	4.83	5.05	0.30	0.06	5.35
V19	ICGV-00203	24.00	6.00	5.50	0.23	0.04	5.73
V20	ICGV-91068	25.67	4.67	4.22	0.34	0.08	4.56
V21	ICGV-97119	25.33	4.67	3.89	0.23	0.06	4.12
V22	ICGV-96178	23.00	5.00	4.75	0.35	0.07	5.10
V23	J-2001-14	18.58	1.50	1.92	0.17	0.09	2.09
V24	J-2001-6	18.50	5.67	3.96	0.32	0.08	4.28
V25	J-2001-22	20.00	3.00	0.52	0.05	0.10	0.57
Range		**15.50-26.00**	**1.50-8.50**	**0.52-5.50**	**0.05-0.42**	**0.04-0.10**	**0.57-5.73**
Average		**21.19**	**5.42**	**3.83**	**0.27**	**0.07**	**4.05**
LSD(0.05)		**3.48**	**2.07**	**1.87**	**0.11**	**0.03**	**1.94**

The maximum number of branches (8.50) was found in V9 followed by V13, V12, V14 and V16 with non-significant differences. In contrast, V23 had the minimum number of branches (1.50) of all, shared equal statistical rank only with V25. The rest of the genotypes had intermediate number of branches with significant differences from other genotypes. Number of branches showed a wide range of variation from 1.50 to 8.50 with average value of 5.42.

The highest shoot biomass (5.50g) was found in V19 followed by V2, V16, V13, V18, V14, V22, V15, V20, V9, V5, V3, V12, V24, V21, and V8 with non-significant differences. The lowest shoot biomass (0.52g) was found in V25 followed by V17 and V23 with non significant differences. The rest of the genotypes had intermediate shoot biomass with significant differences from others. Shoot biomass showed a wide range of variation from 0.52g to 5.50g with average value of 3.83g.

Genotype V12 had the highest root biomass (0.42g) followed by V2, V22, V20, V16, V9, V8, V5, V1 and V24 with non-significant differences. V25 had the lowest root biomass (0.05g) shared equal statistical rank only with V17 and significant differences with all genotypes. V1, V12 and V25 had the highest root: shoot ratio (0.10) followed by V23, V8, V5, V11, V9, V10 and V20 with non-significant differences. In contrast, V19 had the lowest root: shoot ratio (0.04) sharing equal statistical rank with V15, V13, V3, V14, V16, V17, V18 and V21.

Like shoot biomass, the highest total biomass (5.73g) was found in V19 followed by V2, V16, V18,V14,V22,V15,V20, V9,V5, V24, V3, V13, V21,V8,V5 and V10 with non-significant differences. Interestingly, like shoot biomass V25 had the lowest total biomass (0.57g) sharing equal statistical rank with V17, V23 and significantly differences with all the rest genotypes. Total biomass showed a wide range of variation from 0.57g to 5.73g with average value of 4.05g.

4.1.4 Performance of the pod yield and yield attributes of the genotypes at 8dS/m salinity stress condition:

The means of the pod yield and yield attributes under 8dS/m salinity stress condition are shown in Table 6b. All the traits were observed significantly different within the genotypes under 8dS/m salinity stress condition. In V12 showed the maximum peg number (10.33) followed by V5, V6, V1 and V14 with non-significant differences. In contrast, V25 had the minimum peg number (0.00) due to salinity effect sharing equal statistical rank with V22, V19, V21, V18, V17, V9 and V11. The rest of the genotypes had intermediate peg number with significant differences with other genotypes. Peg number showed a wide range of variation from 0.00 to 10.33 with average value of 4.49.

Genotypes V5 and V6 had the maximum number of pods/plant (7.00) with significant differences of all genotypes. In contrast, V25, V23, V22, V21 and V19 had the minimum number of pods (0.00) sharing equal statistical rank with V24, V17, V10, V18, V13, V9 and V11. Due to salinity effect genotypes V19, V21, V22, V23 and V25 did not produce any pods at 8dS/m salinity level. The rest of the genotypes had intermediate number of pods with significant differences from other genotypes. Pod number showed a wide range of variation from 0.00 to 7.00 with average value of 2.24.

The highest pod: peg ratio (0.79) was found in V2 followed by V5 with non-significant differences and significant differences with all the others genotypes. In contrast, V25, V23, V22, V21 and V19 had the lowest pod: peg ratio (0.00) with significant differences of all the other genotypes. The pod: peg ratio was found lowest (0.00) in those genotypes which produced no pods at 8dS/m salinity level. The rest of the genotypes had intermediate pod: peg ratio with significant differences from others.

Table 6b. Performance of pod yield and yield attributes of 25 groundnut genotypes at 8dS/m salinity stress

Code	Genotypes/ varieties	Peg no. /plant	Pod no. /plant	Pod : peg ratio	Pod wt. /plant (g)	Kernel wt. /plant (g)	Shelling (%)
V1	Binachinabadam-1	7.00	2.67	0.38	0.38	0.00	0.00
V2	Binachinabadam-2	5.67	4.50	0.79	0.69	0.32	46.38
V3	Binachinabadam-3	7.67	2.33	0.30	1.21	0.06	4.80
V4	Binachinabadam-4	6.50	3.67	0.56	0.24	0.00	0.00
V5	Binachinabadam-5	9.67	7.00	0.72	2.59	1.41	54.33
V6	Binachinabadam-6	9.50	5.50	0.58	1.60	0.89	55.80
V7	Dhaka-1(Maizchar)	6.50	2.30	0.36	0.40	0.00	0.00
V8	Pk-1 (Pakshi local)	5.00	3.00	0.60	0.07	0.03	48.31
V9	Basantibadam (DG-2)	3.00	2.00	0.67	0.52	0.00	0.00
V10	Tridanabadam (DM-1)	3.67	2.00	0.54	0.72	0.00	0.00
V11	Jhingabadam	3.33	2.00	0.30	1.12	0.00	0.00
V12	Barichinabadam-5	10.33	4.67	0.45	0.81	0.25	30.77
V13	BARI Chinabadam-6	4.00	2.00	0.75	1.05	0.41	38.87
V14	BARI Chinabadam -7	7.00	2.33	0.33	2.14	0.34	15.84
V15	BARI Chinabadam -8	3.50	2.20	0.52	1.32	0.48	36.56
V16	BARI Chinabadam -9	5.00	2.33	0.47	0.45	0.17	37.27
V17	ICGV-96175	3.00	1.00	0.33	0.41	0.00	0.00
V18	ICGV-01249	2.67	1.67	0.63	0.34	0.03	9.14
V19	ICGV-00203	0.00	0.00	0.00	0.00	0.00	0.00
V20	ICGV-91068	5.00	2.33	0.47	0.53	0.00	0.00
V21	ICGV-97119	2.33	0.00	0.00	0.00	0.00	0.00
V22	ICGV-96178	0.00	0.00	0.00	0.00	0.00	0.00
V23	J-2001-14	4.00	0.00	0.00	0.00	0.00	0.00
V24	J-2001-6	4.83	1.00	0.41	0.10	0.00	0.00
V25	J-2001-22	0.00	0.00	0.00	0.00	0.00	0.00
Range		**0.00-10.33**	**0.00-7.00**	**0.00-0.79**	**0.00-2.59**	**0.00-1.41**	**0.00-55.80**
Average		**4.49**	**2.24**	**0.42**	**0.67**	**0.18**	**15.13**
LSD(0.05)		**3.43**	**2.05**	**0.07**	**1.16**	**0.22**	**3.30**

Pod: peg ratio showed a wide range of variation from 0.00 to 0.79 with average value of 0.42.

Genotype V5 had highest pod weight/plant (2.59g) followed by V14 and V6 with non-significant differences. V25, V23, V22, V21 and V19 had the lowest pod weight (0.00g) sharing equal statistical rank with V24, V8, V4, V18, V1, V7, V17, V16, V20, V12, V13, V10, V9, V11, V2 and V15. In genotypes V19, V21, V22, V23 and V25 no pod formation happened at 8dS/m salinity level because of salinity effect. The rest of the genotypes had intermediate pod weight/plant with significant differences from the others. Pod weight/plant showed a wide range of variation from 0.00g to 2.59g with average value of 0.67g.

Genotype V5 had the highest kernel weight/plant (1.41g) followed byV6 with significant differences with all the others genotypes. In contrast, V24, V25, V23, V25, V22, V21, V20, V19, V17, V11, V10, V9, V7, V4 and V1 had the lowest kernel weight/plant (0.00g) sharing equal statistical rank with V18, V16, and V8. In genotypes V1, V4, V7, V9, V10, V11, V17, V19, V20, V21, V22, V23, V24 and V25 no kernel formation occured at 8dS/m salinity level because of salinity effect. Kernel weight/plant showed a wide range of variation from 0.00g to 1.41g with average value of 0.18g.

The highest shelling (%) found only inV6 (55.80) followed by V5 with significant differences with all the others genotypes. In contrast, V25, V24, V23, V22, V21, V20, V19, V17, V11, V10, V9, V7, V4 and V1 had the lowest shelling (%) (0.00) due to no kernels were produced in these genotypes at 8dS/m salinity level. Shelling (%) showed a wide range of variation from 0.00 to 55.80 with average value of 15.13.

4.1.5 Performance of the shoot-root characters of the genotypes at 10dS/m salinity stress condition

The means of shoot and root characters under 10dS/m salinity stress condition are shown in Table 7a. V9 showed highest plant height (24.75cm) despite non-significant difference with V18, V20, V13, V12, V14, V15 and V16. In contrast, V24 had the lowest plant height (14.00cm) sharing equal statistical rank with V10, V23, V3, V25, V8, V4, V17, V5, V21, V1, V6, V2 and V7. The rest of the genotypes had intermediate plant height with significant differences from other genotypes. Plant height showed a wide range of variation from 14.00cm to 24.75cm with average value of 19.00cm.

Genotype V9 had the maximum number of branches (6.55) followed by V12, V14, V10, V21 and V2 with non-significant differences. In contrast, V23 had the minimum number of branches (1.00) of all, shared equal statistical rank with V25 and V24. The rest of the genotypes had intermediate number of branches with significant differences from other genotypes. Number of branches showed a wide range of variation from 1.00 to 6.55 with average value of 4.45.

The highest shoot biomass was found in V9 (4.90g) followed by V18, V19, V11, V10, V22, V3, V1, V12, V8 andV13 with non-significant differences. The lowest shoot biomass (0.55g) was found in V25 followed by V23 andV21 with non significant differences. The rest of the genotypes had intermediate shoot biomass with significant differences from other genotypes. Shoot biomass showed a wide range of variation from 0.55g to 4.90g with average value of 3.12g.

Genotypes V1 and V9 had the highest root biomass (0.34g) followed by V12, V20, V18, V3, V16, V11, V8 and V4 with non-significant differences. V25 had the lowest root biomass (0.04) shared equal statistical rank with V24, V21, V19 and significant

Table 7a. Performance of shoot and root characters of 25 groundnut genotypes at 10dS/m salinity stress

Code	Genotypes/ varieties	Plant height (cm)	No. of branches	Shoot biomass (g)	Root biomass (g)	Root : shoot ratio	Total biomass (g)
V1	Binachinabadam-1	17.58	5.00	3.59	0.34	0.09	3.93
V2	Binachinabadam-2	18.00	5.23	2.56	0.15	0.06	2.71
V3	Binachinabadam-3	15.42	4.00	3.60	0.30	0.08	3.90
V4	Binachinabadam-4	16.67	4.53	3.16	0.24	0.07	3.39
V5	Binachinabadam-5	17.00	5.00	2.46	0.18	0.06	2.64
V6	Binachinabadam-6	17.67	4.55	3.04	0.20	0.07	3.24
V7	Dhaka-1(Maizchar)	18.17	7.89	2.58	0.21	0.08	2.79
V8	Pk-1 (Pakshi local)	16.33	4.00	3.45	0.26	0.07	3.71
V9	Basantibadam (DG-2)	24.75	6.55	4.90	0.34	0.07	5.25
V10	Tridanabadam (DM-1)	15.17	5.33	3.76	0.17	0.05	3.94
V11	Jhingabadam	18.67	4.33	4.17	0.27	0.06	4.44
V12	Barichinabadam-5	22.83	6.50	3.55	0.33	0.09	3.88
V13	BARI Chinabadam-6	23.00	5.00	3.44	0.18	0.05	3.62
V14	BARI Chinabadam -7	21.67	5.50	2.74	0.17	0.06	2.91
V15	BARI Chinabadam -8	21.00	4.50	3.23	0.23	0.07	3.47
V16	BARI Chinabadam -9	20.92	4.33	2.89	0.29	0.10	3.19
V17	ICGV-96175	17.00	5.00	3.11	0.18	0.06	3.29
V18	ICGV-01249	24.67	5.00	4.31	0.30	0.07	4.61
V19	ICGV-00203	20.00	5.00	4.20	0.13	0.03	4.33
V20	ICGV-91068	23.42	4.65	3.12	0.32	0.10	3.44
V21	ICGV-97119	17.42	5.33	1.92	0.13	0.07	2.05
V22	ICGV-96178	22.50	5.00	3.63	0.23	0.06	3.86
V23	J-2001-14	15.20	1.00	1.45	0.16	0.11	1.61
V24	J-2001-6	14.00	1.89	2.61	0.12	0.05	2.73
V25	J-2001-22	16.00	1.00	0.55	0.04	0.08	0.59
Range		**14.00-24.75**	**1.00-6.55**	**0.55-4.90**	**0.04-0.34**	**0.03-0.11**	**0.59-5.25**
Average		**19.00**	**4.45**	**3.12**	**0.22**	**0.07**	**3.34**
LSD(0.05)		**4.18**	**1.51**	**1.64**	**0.10**	**0.02**	**1.72**

differences with all the other genotypes. Root biomass showed a wide range of variation from 0.04g to 0.34g with average value of 0.22g.

The genotype V23 had the highest root: shoot ratio (0.11) followed by V20, V16, V1 and V12 with non-significant differences. In contrast, V19 had the lowest root: shoot ratio (0.03) sharing equal statistical rank with V24, V13 and V10. Root: shoot ratio showed a wide range of variation from 0.03 to 0.11 with average value of 0.07.

The highest total biomass (5.25g) was found in V9followed by V18, V11, V19, V10, V1, V3, V12, V22, V8 and V13 with non-significant differences. Interestingly, like shoot biomass V25 had the lowest total biomass (0.59g) sharing equal statistical rank with V23 and V21 and significantly differences with all the rest genotypes. Total biomass showed a wide range of variation from 0.59g to 5.25g with average value of 3.34g.

4.1.6 Performance of the pod yield and yield attributes of the genotypes at10dS/m salinity stress condition

The means of the pod yield and yield attributes under 10dS/m salinity stress condition are shown in Table 7b. All the traits were observed significantly different within the genotypes under 10dS/m salinity stress condition except kernel weight per plant. InV20 observed the maximum peg number (9.67) followed by, V11 and V22 with non-significant differences. In contrast, V25, V24, V23, V21, V19 had the minimum peg number (0.00) due to salinity effect sharing equal statistical rank with V17, V2, V3 and V14. No pegs were formed in V19, V21, V23, V24 and V25 because of increased salinity effect at 10dS/m salinity level. The rest of the genotypes had intermediate peg number with significant differences from other genotypes. Peg number showed a wide range of variation from 0.00 to 9.67 with average value of 3.69. Like as 8dS/m salinity level V5 and V6 had the maximum number of pods/plant (4.33) with significant differences of all genotypes. In contrast, V25, V24, V23, V22,

Table 7b. Performance of pod yield and yield attributes of 25 groundnut genotypes at 10dS/m salinity stress

Code	Genotypes/ varieties	Peg no. /plant	Pod no. /plant	Pod :peg ratio	Pod wt. /plant(g)	Kernel wt. /plant(g)	Shelling (%)
V1	Binachinabadam-1	4.50	1.33	0.30	0.07	0.00	0.00
V2	Binachinabadam-2	1.00	0.00	0.00	0.00	0.00	0.00
V3	Binachinabadam-3	2.50	2.30	0.93	0.52	0.03	5.77
V4	Binachinabadam-4	3.83	2.00	0.52	0.29	0.00	0.00
V5	Binachinabadam-5	4.83	4.33	0.90	0.56	0.28	50.00
V6	Binachinabadam-6	5.17	3.33	0.65	1.27	0.63	49.60
V7	Dhaka-1(Maizchar)	3.83	0.50	0.13	0.29	0.00	0.00
V8	Pk-1 (Pakshi local)	5.50	1.17	0.21	0.04	0.00	38.12
V9	Basantibadam (DG-2)	5.67	1.00	0.25	0.06	0.00	0.00
V10	Tridanabadam (DM-1)	4.67	2.00	0.43	0.56	0.00	0.00
V11	Jhingabadam	8.00	1.00	0.25	0.09	0.00	22.22
V12	Barichinabadam-5	5.67	2.00	0.35	0.22	0.00	0.00
V13	BARI Chinabadam-6	6.00	2.00	0.33	0.65	0.23	35.38
V14	BARI Chinabadam -7	1.83	1.33	0.73	0.33	0.00	0.00
V15	BARI Chinabadam -8	4.33	1.80	0.50	0.87	0.20	22.98
V16	BARI Chinabadam -9	5.00	1.83	0.37	0.32	0.03	09.38
V17	ICGV-96175	1.00	0.00	0.00	0.00	0.00	0.00
V18	ICGV-01249	3.00	1.33	0.44	0.26	0.00	0.00
V19	ICGV-00203	0.00	0.00	0.00	0.00	0.00	0.00
V20	ICGV-91068	9.67	0.00	0.00	0.00	0.00	0.00
V21	ICGV-97119	0.00	0.00	0.00	0.00	0.00	0.00
V22	ICGV-96178	6.33	0.00	0.00	0.00	0.00	0.00
V23	J-2001-14	0.00	0.00	0.00	0.00	0.00	0.00
V24	J-2001-6	0.00	0.00	0.00	0.00	0.00	0.00
V25	J-2001-22	0.00	0.00	0.00	0.00	0.00	0.00
Range		**0.00-9.67**	**0.00-4.33**	**0.00-0.93**	**0.00-1.27**	**0.00-0.63**	**0.00-50.00**
Average		**3.69**	**1.17**	**0.29**	**0.26**	**0.08**	**9.33**
LSD(0.05)		**3.47**	**1.86**	**0.03**	**0.70**	**0.37**	**1.58**

V21, V20, V19, V17 and V2 had the minimum number of pods (0.00) sharing equal statistical rank with V18, V16, V14, V9, V11, V8 and V1. The genotypes V2, V17, V19, V20, V21, V22, V23, V24 and V25 did not produce any podsdue to increased salinity effect at 10dS/m salinity level. The rest of the genotypes had intermediate number of pods with significant differences from other genotypes. Pod number showed a wide range of variation from 0.00 to 4.33 with average value of 1.17.

The highest pod: peg ratiowas found inV3 andV5 (0.93) with significant differences with all the others genotypes. In contrast, V25, V24, V23, V22, V21, V20, V19, V17 and V2 had the lowest pod: peg ratio (0.00) with significant differences of all the other genotypes. The pod: peg ratio was found lowest (0.00) in those genotypes which produced no pods at 10dS/m salinity level. The rest of the genotypes had intermediate pod; peg ratio with significant differences from other genotypes. Pod:peg ratio showed a wide range of variation from 0.00 to 0.93 with average value of 0.29.

In genotype V6 had the highest pod weight/plant (1.27g) followed by V15 and V13 with non-significant differences. In contrast, V25, V24, V23, V22, V21, V20, V19, V17 and V2 had the lowest pod weight (0.00g) sharing equal statistical rank with V18, V12, V16, V14, V10, V9, V11, V8, V7, V4, V1 and V5. In genotypes V2, V17, V19, V20, V21, V22, V23, V24 and V25 no pods were formed at 10dS/m salinity level because of increased salinity effect. Pod weight/plant showed a wide range of variation from 0.00g to 1.27g with average value of 0.26g.

The trait kernel weight per plant was found non-significance differences among the genotypes under 10dS/m salinity level. Genotype V6 had the highest kernel weight/plant (0.63g) followed byV5, V13 and V15 with non-significant differences. In contrast, V25, V24,V23,V22,V21,V20, V19,V18, V17, V14, V12,V11, V10, V9, V8, V7, V4, V2 and V1 had the lowest (0.00g) kernel weight because of no kernels

were formed in these genotypes with increased salinity effect at 10 dS/m salinity level. Kernel weight/plant showed a wide range of variation from 0.00g to 0.63g with average value of 0.08.

The highest shelling (%) found in V5 (50.00) and V6 with significant differences with all the others genotypes followed by V8, V13, V15, V11, V16, V3. In contrast, the remainder genotypes had the lowest (0.00) shelling (%). The shelling (%) showed lowest (0.00) in those genotypes which produced no kernels at 10dS/m salinity level. Shelling (%) showed a wide range of variation from 0.00 to 50.00 with average value of 9.33.

4.1.7 Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues at non-saline condition

The means of Na^+, K^+ and Ca^{++}content (%)/plant in shoot tissues under non-saline condition are shown in Table 8. All the uptake of nutrients was observed significantly different within the genotypes under non-saline condition. According to the data presented in Table 7, it was observed that the highest value (0.74) of Na^+content (%) found in V8with significant differences among the genotypes followed by V1, V19 and V3. In contrast, the lowest was (0.25) in V22 followed byV23 andV25 with non-significant differences. Na^+content (%) /plant showed a wide range of variation from 0.25 to 0.74 with average value of 0.39.

The highest value (1.91) of K^+content (%) found in V8 again with significant differences among the genotypes followed by V7, V5, V6 and V18. In contrast, the lowest was (0.63) in V9 with significant differences among the genotypes. K^+ content (%) /plant showed a wide range of variation from 0.63 to 1.91 with average value of 1.18.

The highest value (5.98) of K^+/Na^+ ratio found in V22 with significant differences among the genotypes followed by V5, V18, V25 and V7. In contrast, the lowest was

Table 7. Mean value of Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues of 25 groundnut genotypes at non-saline condition

Code	Genotypes/ varieties	Na^+ (%)	K^+(%)	K^+ / Na^+	Ca^{++}(%)
V1	Binachinabadam-1	0.68	1.25	2.00	0.51
V2	Binachinabadam-2	0.31	1.20	4.14	0.50
V3	Binachinabadam-3	0.53	1.24	2.31	0.35
V4	Binachinabadam-4	0.31	1.14	4.08	0.52
V5	Binachinabadam-5	0.35	1.56	4.69	0.39
V6	Binachinabadam-6	0.44	1.41	3.30	0.49
V7	Dhaka-1(Maizchar)	0.42	1.78	4.37	0.44
V8	Pk-1 (Pakshi local)	0.74	1.91	2.61	0.10
V9	Basantibadam (DG-2)	0.30	0.63	2.37	0.38
V10	Tridanabadam (DM-1)	0.34	1.33	3.96	0.33
V11	Jhingabadam	0.36	1.10	3.20	0.45
V12	Barichinabadam-5	0.35	0.97	2.91	0.45
V13	BARI Chinabadam-6	0.31	1.16	4.13	0.40
V14	BARI Chinabadam -7	0.35	1.10	3.30	0.38
V15	BARI Chinabadam -8	0.45	1.03	2.36	0.60
V16	BARI Chinabadam -9	0.32	0.97	3.22	0.50
V17	ICGV-96175	0.30	1.22	4.51	0.45
V18	ICGV-01249	0.32	1.41	4.66	0.68
V19	ICGV-00203	0.61	0.97	1.54	0.51
V20	ICGV-91068	0.34	0.98	2.64	0.43
V21	ICGV-97119	0.44	0.97	2.12	0.43
V22	ICGV-96178	0.25	1.16	5.98	0.47
V23	J-2001-14	0.26	0.94	4.18	0.46
V24	J-2001-6	0.33	0.91	2.74	0.46
V25	J-2001-22	0.28	1.10	4.45	0.41
Range		**0.25-0.74**	**0.63-1.91**	**1.54-5.98**	**0.10-0.68**
Average		**0.39**	**1.18**	**3.43**	**0.44**
LSD(0.05)		**0.03**	**0.08**	**1.13**	**0.02**

in V19 followed by V1, V3, V21, V15, V9 and V8 with non-significant differences. K^+/Na^+ ratio showed a wide range of variation from 1.54 to 5.98 with average value of 4.34.

Ca^{++} content (%) found the highest value (0.68) of in V18 with significant differences among the genotypes followed by V15, V4, V1, V19, V2 and V16. In contrast, the lowest Ca^{++} content was (0.10) in V8 with significant differences among the genotypes. Ca^{++} content (%)/plant showed a wide range of variation from 0.10 to 0.68 with average value of 0.44.

4.1.8 Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues at 8 dS/m salinity stress condition

The means of Na^+, K^+ and Ca^{++}content (%)/plant in shoot tissues at8 dS/m salinity stress condition are shown in Table 9. All the uptake of nutrients was observed significantly different within the genotypes under 8 dS/m salinity stress condition. According to the data presented in Table 8, it was observed that the highest value (1.54) of Na^+content (%) found in V24 followed by V1 and V3 with non-significant differences. In contrast, the lowest was (0.69) in V22 and V13 followed by V16 and V18 with significant differences among the genotypes. Na^+content (%) /plant showed a wide range of variation from 0.69 to 1.54 with average value of 1.09.

The highest value (1.96) of K^+content (%) found in V8 with significant differences among the genotypes followed by V3, V7, V19 and V5. In contrast, the lowest was (0.95) in V9 with significant differences among the genotypes. K^+ content (%) /plant showed a wide range of variation from 0.95 to 1.96 with average value of 1.56.

The highest value (2.58) of K^+/Na^+ ratio found in V22 followed by V13 (2.56) with non-significant differences. In contrast, the lowest was (0.76) in V24 followed by V9 with non-significant differences. K^+/Na^+ratio showed a wide range of variation from 0.76 to 2.58 with average value of 1.55.

Table 9. Mean value of Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues of 25 groundnut genotypes at 8 dS/m salinity stress

Code	Genotypes/ varieties	Na^+ (%)	K^+(%)	K^+/ Na^+	Ca^{++}(%)
V1	Binachinabadam-1	1.51	1.52	1.02	0.70
V2	Binachinabadam-2	1.02	1.65	1.65	0.66
V3	Binachinabadam-3	1.50	1.89	1.27	0.88
V4	Binachinabadam-4	1.25	1.62	1.31	0.51
V5	Binachinabadam-5	1.01	1.80	1.82	0.44
V6	Binachinabadam-6	1.45	1.68	1.17	0.47
V7	Dhaka-1(Maizchar)	1.19	1.88	1.60	0.56
V8	Pk-1 (Pakshi local)	1.15	1.96	1.73	0.60
V9	Basantibadam (DG-2)	0.98	0.95	0.99	0.50
V10	Tridanabadam (DM-1)	1.13	1.49	1.34	0.75
V11	Jhingabadam	1.12	1.14	1.03	0.48
V12	Barichinabadam-5	0.96	1.83	2.01	0.44
V13	BARI Chinabadam-6	0.69	1.70	2.56	0.72
V14	BARI Chinabadam -7	0.92	1.60	1.78	0.84
V15	BARI Chinabadam -8	1.21	1.49	1.28	0.73
V16	BARI Chinabadam -9	0.77	1.22	1.68	0.78
V17	ICGV-96175	1.10	1.35	1.29	0.88
V18	ICGV-01249	0.80	1.60	2.10	0.72
V19	ICGV-00203	1.00	1.82	1.93	0.70
V20	ICGV-91068	1.22	1.41	1.22	0.81
V21	ICGV-97119	0.89	1.39	1.59	0.69
V22	ICGV-96178	0.69	1.64	2.58	0.80
V23	J-2001-14	0.93	1.51	1.71	0.51
V24	J-2001-6	1.54	1.17	0.76	0.74
V25	J-2001-22	1.31	1.64	1.29	0.71
Range		**0.69-1.54**	**0.95-1.96**	**0.76-2.58**	**0.44-0.88**
Average		**1.09**	**1.56**	**1.55**	**0.67**
LSD(0.05)		**0.05**	**0.05**	**0.23**	**0.03**

Ca^{++} content (%) found the highest value (0.88) of in V3 and V17 with significant differences among the genotypes followed by V14, V20 andV22. In contrast, the lowest Ca^{++} content was (0.44) in V12 and V5 followed by V6 with non-significant differences. Ca^{++} content (%) /plant showed a wide range of variation from 0.44 to 0.88 with average value of 0.68.

4.1.9 Na^{+}, K^{+} and Ca^{++} content (%)/plant in shoot tissues at 10 dS/m salinity stress condition

The means of Na^{+}, K^{+} and Ca^{++}content (%)/plant in shoot tissues at10 dS/m salinity stress condition are shown in Table 10. All the uptake of nutrients was observed significantly different within the genotypes under 10 dS/m salinity stress condition. According to the data presented in Table 9, it was observed that the highest value (1.89) of Na^{+}content (%) found in V1 followed by V20 and V3 with non-significant differences. In contrast, the lowest was (1.05) in V7 with significant differences among the genotypes. Na^{+}content (%) /plant showed a wide range of variation from 1.05 to 1.89 with average value of 1.49.

The highest value (3.39) of K^{+}content (%) found in V6 with significant differences among the genotypes followed by V14, V5 and V12. In contrast, the lowest was (1.10) in V19 with significant differences among the genotypes. K^{+}content (%) /plant showed a wide range of variation from 1.10 to 3.39 with average value of 2.30.

The highest value (2.79) of K^{+}/Na^{+} ratio found in V7 with significant differences among the genotypes followed by V6, V14 and V12. In contrast, the lowest was (0.71) in V20 followed by V11, and V19 with non-significant differences. K^{+}/Na^{+}ratio showed a wide range of variation from 0.71 to 2.79 with average value of 1.58.

Ca^{++} content (%) found the highest value (0.79) of in V25 with significant differences among the genotypes followed by V10, V20, and V3. In contrast, the lowest Ca^{++} content was (0.39) in V9 followed by V7, V5 and V4 with non-significant differences. Ca^{++} content

Table 10. Mean value of Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues of 25 groundnut genotypes at 10 dS/m salinity stress

Code	Genotypes/ varieties	Na^+ (%)	K^+(%)	K^+ / Na^+	Ca^{++}(%)
V1	Binachinabadam-1	1.89	2.45	1.25	0.53
V2	Binachinabadam-2	1.23	2.16	1.77	0.48
V3	Binachinabadam-3	1.83	2.22	1.22	0.70
V4	Binachinabadam-4	1.42	1.80	1.27	0.40
V5	Binachinabadam-5	1.42	3.10	2.19	0.40
V6	Binachinabadam-6	1.50	3.39	2.27	0.45
V7	Dhaka-1(Maizchar)	1.05	2.91	2.79	0.40
V8	Pk-1 (Pakshi local)	1.19	2.11	1.72	0.53
V9	Basantibadam (DG-2)	1.51	2.79	1.79	0.39
V10	Tridanabadam (DM-1)	1.70	2.90	1.71	0.76
V11	Jhingabadam	1.63	1.20	0.72	0.48
V12	Barichinabadam-5	1.35	2.97	2.21	0.51
V13	BARI Chinabadam-6	1.17	2.41	1.94	0.45
V14	BARI Chinabadam -7	1.42	3.14	2.22	0.56
V15	BARI Chinabadam -8	1.71	2.42	1.42	0.49
V16	BARI Chinabadam -9	1.32	2.45	1.87	0.60
V17	ICGV-96175	1.73	2.46	1.43	0.56
V18	ICGV-01249	1.24	1.29	1.05	0.52
V19	ICGV-00203	1.55	1.10	0.73	0.46
V20	ICGV-91068	1.87	1.36	0.71	0.72
V21	ICGV-97119	1.66	2.46	1.49	0.55
V22	ICGV-96178	1.63	2.56	1.58	0.70
V23	J-2001-14	1.53	1.49	0.96	0.53
V24	J-2001-6	1.31	1.57	1.22	0.79
V25	J-2001-22	1.42	2.85	2.02	0.53
Range		**1.05-1.89**	**1.10-3.39**	**0.71-2.79**	**0.39-0.79**
Average		**1.49**	**2.30**	**1.58**	**0.54**
LSD(0.05)		**0.06**	**0.04**	**0..09**	**0.02**

(%) /plant showed a wide range of variation from 0.39 to 0.79 with average value of 0.54.

4.1.10 Relative performance of shoot-root characters of genotypes over different salinity levels:

The average value of different salinity levels of shoot-root characters shown by linear trends over genotypes have been presented in Fig.1 to Fig.6. And mean value of genotypes over different salinity levels of shoot-root characters also presented through bar graph in Fig. 1 to Fig. 6, concurrently.

In Fig.1, the linear trends showed that the increase of salinity stress condition reduced the plant height in groundnut. The bar graphs showed that the plant height reduced with the increase of salinity stress in each genotype. Under control / non-saline condition, the highest plant height observed in V18 and V25 genotype and lowest plant height observed in V3. Under 8dS/m salinity stress condition the highest plant height observed in V18 and lowest plant height in V17. Under 10dS/m salinity stress condition the highest plant height observed in V9 and lowest in V24 genotype.

The linear trends showed that the increase of salinity stress condition reduced the number of branches in groundnut in Fig.2. The bar graphs showed that the number of branches reduced with the increase of salinity stress in each genotype. Under control / non-saline condition, the highest number of branches observed in V9 genotype and lowest number of branches observed in V25. Under 8dS/m salinity stress condition the highest number of branches observed in V9 and lowest number of branches in V23. Under 10dS/m salinity stress condition the highest number of branches observed in V9 and lowest in V23 genotype.

In Fig. 3 the linear trends showed that the increase of salinity stress condition reduced the shoot biomass in groundnut. The bar graphs showed that the shoot biomass reduced with the increase of salinity stress in each genotype except V1, V9, V10, V11,

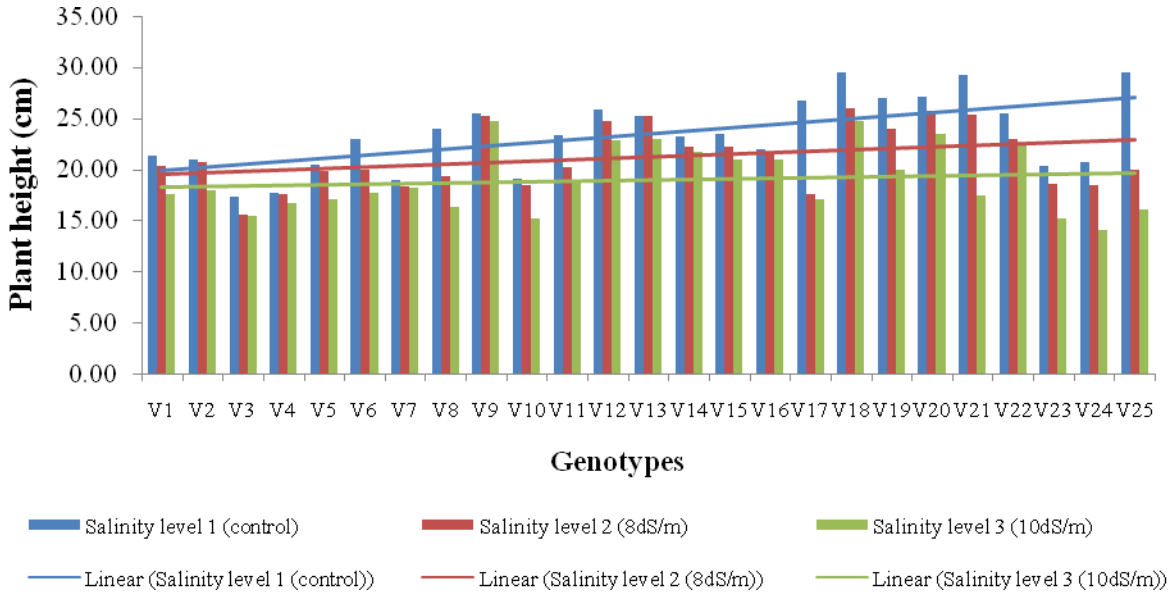


Fig.1. The effect of different salinity levelson plant height and its linear trends in 25 genotypes of groundnut

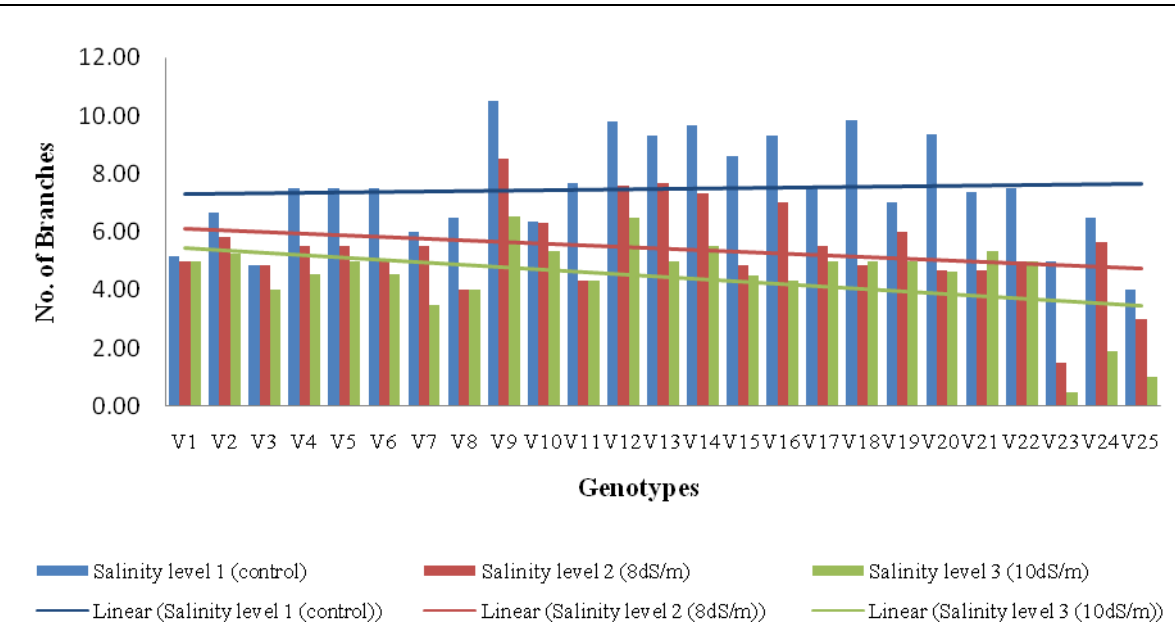


Fig.2. The effect of different salinity levelson number of branches and its linear trends in 25 genotypes of groundnut

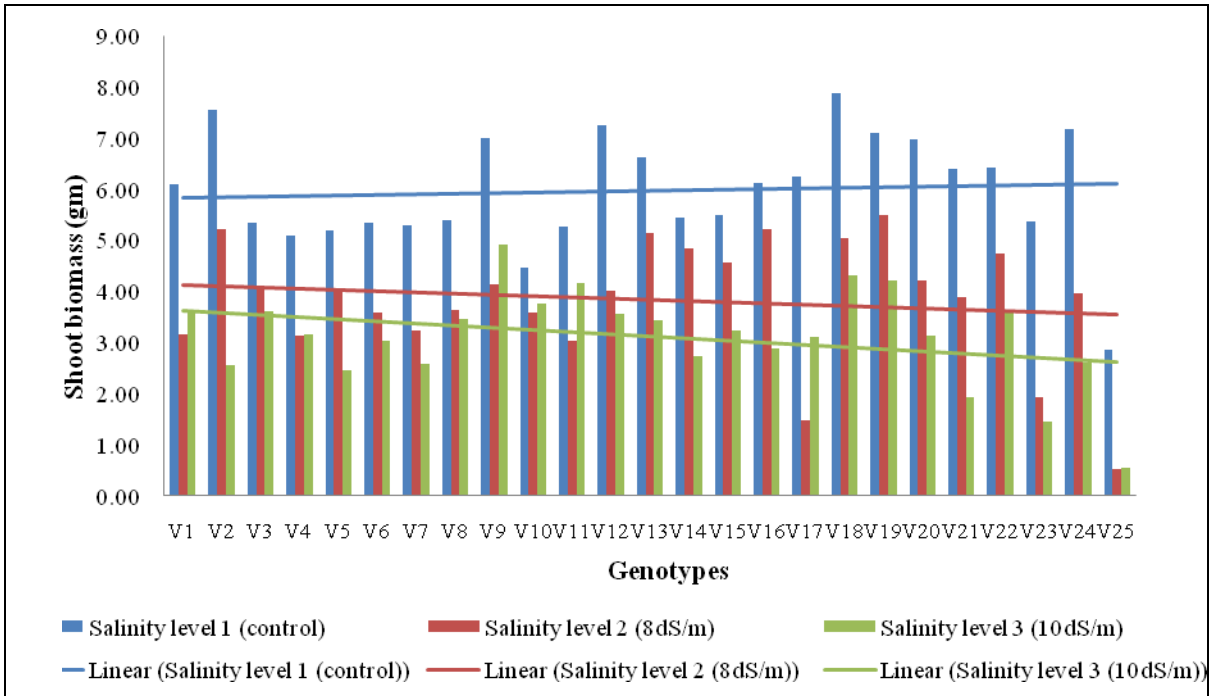


Fig. 3. The effect of different salinity levelson shoot biomass and its linear trends in 25 genotypes of groundnut

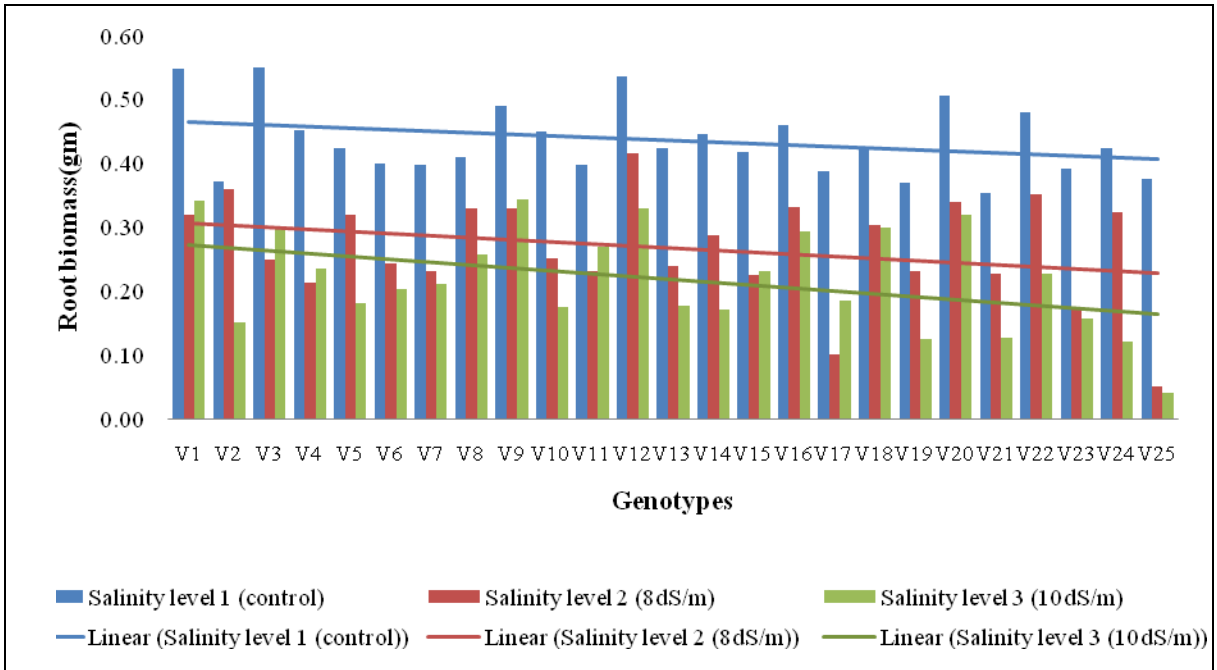


Fig. 4. The effect of different salinity levelson root biomass and its linear trends in 25 genotypes of groundnut

and V17. In these genotypes, shoot biomass not reduced in 10dS/m saline stress condition than in 8dS/m saline stress condition. But, in 8dS/m or 10dS/m salinity stress condition the shoot biomass reduced than the control or no-saline condition. Under control / non-saline condition, the highest shoot biomass observed in V18 genotype and lowest shoot biomass observed in V25. Under 8dS/m salinity stress condition the highest shoot biomass observed in V19 and lowest shoot biomass in V25. Under10dS/m salinity stress condition the highest shoot biomass observed in V9 and lowest in V25 genotype.

In Fig. 4 the linear trends showed that the increase of salinity stress condition reduced the root biomass in groundnut. The bar graphs showed that the root biomass reduced with the increase of salinity stress in each genotype except V1, V3, V4, V9, V11 and V17. In this case root biomass in 10dS/m saline stress condition not reduced less than the 8dS/m saline stress condition. But, in 8dS/m or 10dS/m salinity stress condition the root biomass reduced than the control or no-saline condition. Under control / non-saline condition, the highest root biomass observed in V1and V3 genotype and lowest root biomass observed in V21. Under 8dS/m salinity stress condition the highest root biomass observed in V12 and lowest root biomass in V25. Under10dS/m salinity stress condition the highest root biomass observed in V1 and V9 and lowest in V25 genotype.

The linear trends showed that the increase of salinity stress condition reduced the root/shoot ratio in groundnut in Fig.5. The bar graphs showed that the root/shoot ratio reduced or increased with the increase of salinity stress in genotypes. Under control / non-saline condition, the highest root/shoot ratio observed in V25 genotype and lowest root/shoot ratio observed in V19 and V2. Under 8dS/m salinity stress condition the highest root/shoot ratio observed in V1, V12 and V25 genotype and lowest

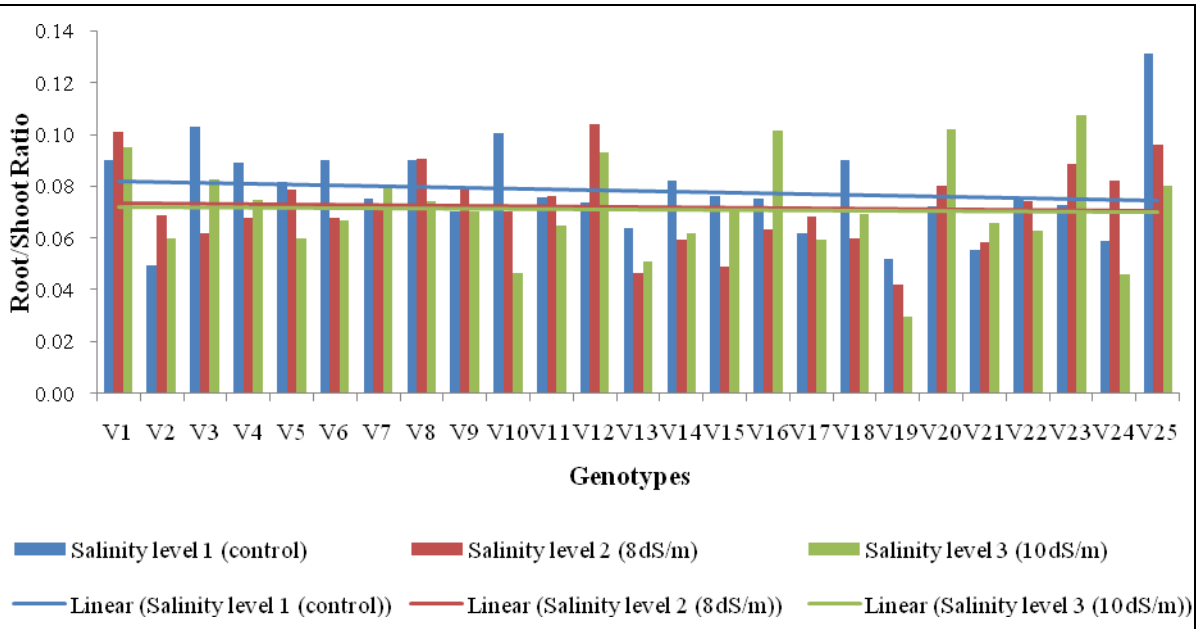


Fig.5. The effect of different salinity levelson root/shoot ratio and its linear trends in 25 genotypes of groundnut

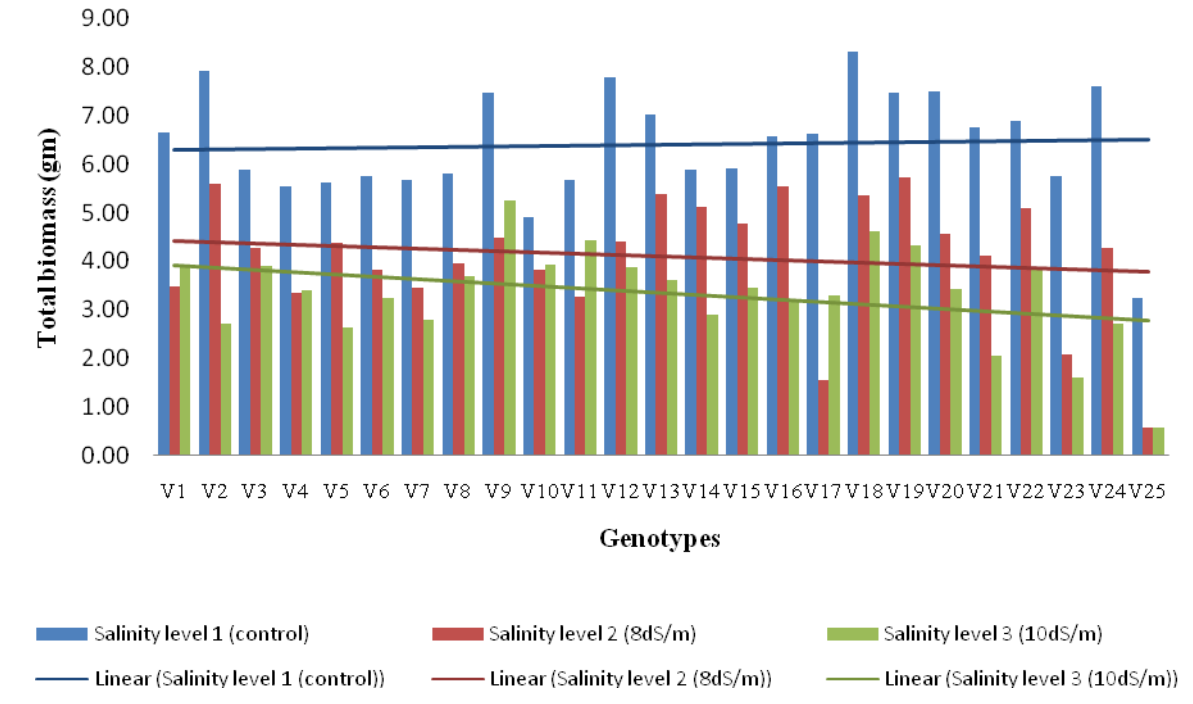


Fig. 6. The effect of different salinity levelson total biomass and its linear trends in 25 genotypes of groundnut

root/shoot ratio in V19. Under10dS/m salinity stress condition the highest root/shoot ratio observed in V23 and lowest in V19 genotype.

In Fig. 6 the linear trends showed that the increase of salinity stress condition reduced the total biomass in groundnut. The bar graphs showed that the total biomass reduced with the increase of salinity stress in each genotype except V1, V9, V10, V11 and V17. In genotypes, total biomass in 10dS/m saline stress condition not reduced less than the 8dS/m saline stress condition. But, in 8dS/m or 10dS/m salinity stress condition the total biomass reduced than the control or no-saline condition. Under control / non-saline condition, the highest total biomass observed in V18 genotype and the lowest total biomass observed in V25. Under 8dS/m salinity stress condition the highest total biomass observed in V19 and the lowest total biomass in V25. Under10dS/m salinity stress condition the highest total biomass observed in V9 and the lowest in V25 genotype.

4.1.11 Relative performance of yield and yield attributes of genotypes over different salinity levels:

The average value of different salinity levels of yield and yield attributes shown by linear trends over genotypes have been presented in Fig.7 to Fig.12. And mean value of genotypes over different salinity levels of yield and yield attributes also presented through bar graph in Fig.7 to Fig.12 concomitantly. In Fig.7 the linear trends showed that the increase of salinity stress condition reduced the number of peg/plant in groundnut. The bar graphs showed that the number of peg/plant reduced or increased with the increase of salinity stress in each genotype. Under control / non-saline condition, the highest number of peg/plant observed in V9 genotype and the lowest number of peg/plant observed in V25. Under 8dS/m salinity stress condition the highest number of peg/plant observed in V12 and the lowest number of peg/plant

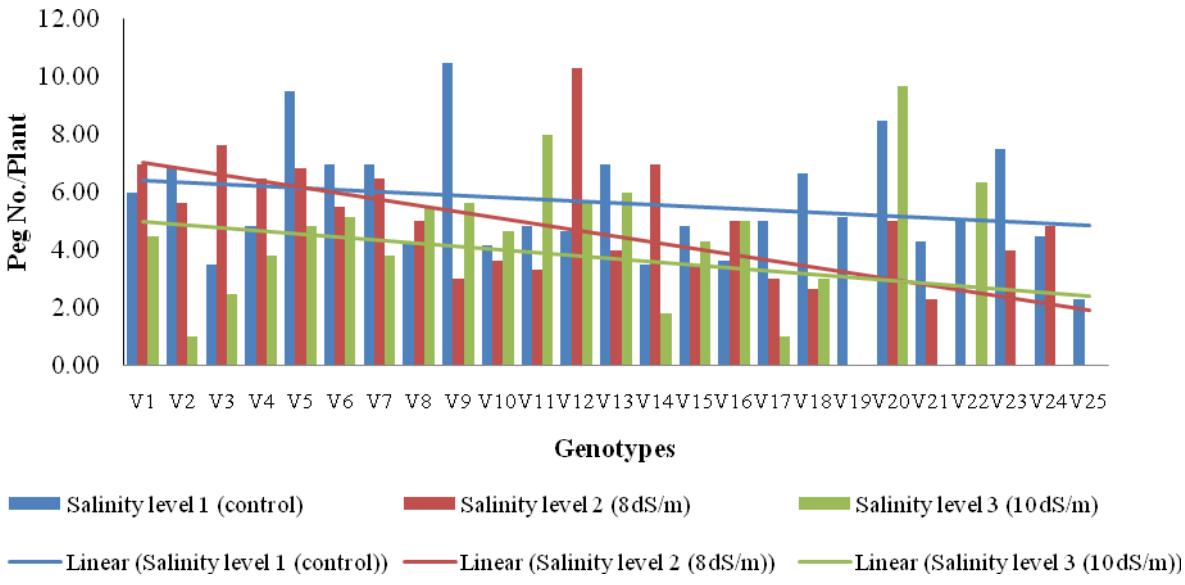


Fig.7 The effect of different salinity levelson peg number per plant and its linear trends in 25 genotypes of groundnut

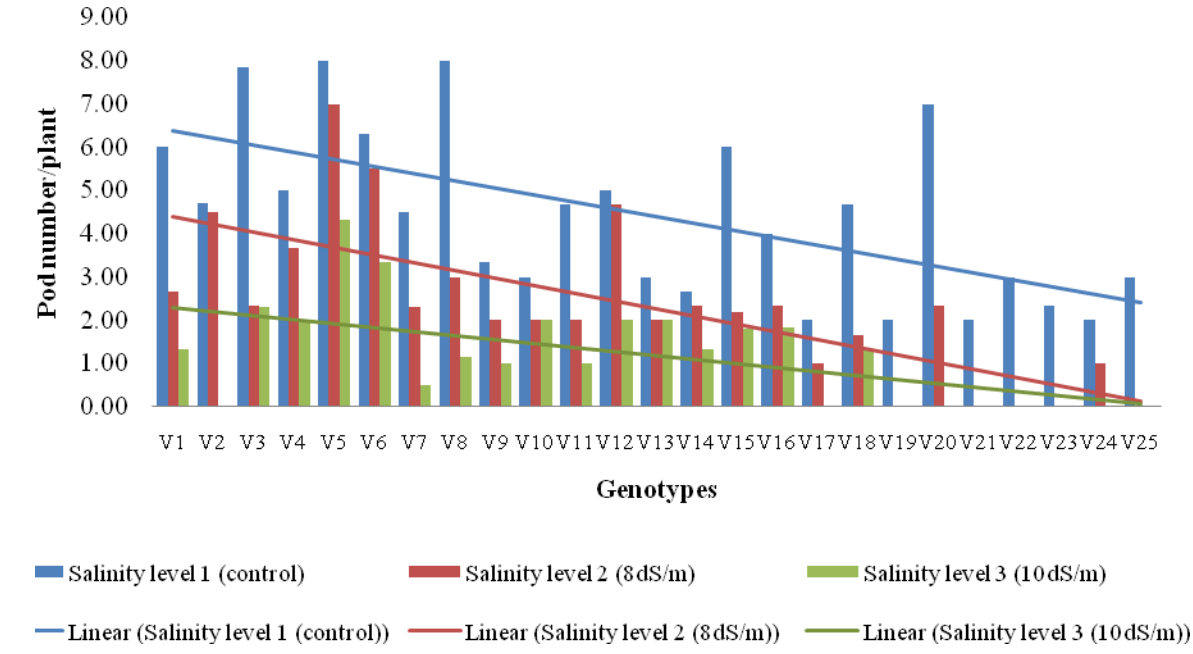


Fig. 8 The effect of different salinity levelson pod number per plant and its linear trends in 25 genotypes of groundnut

in V19, V22 and in V25. At 10dS/m salinity stress condition the highest number of peg/plant observed in V20 and the lowest in V19, V21, V23, V24 and in V25 genotype. The linear trends showed that the increase of salinity stress condition reduced the pod number/plant in groundnut in Fig.8. The bar graphs showed that the pod number/plant reduced with the increase of salinity stress in genotypes.

Under control / non-saline condition, the highest pod number/plant and the lowest pod number/plant observed in V17, V19, V21 and V24 genotype. Under 8dS/m salinity stress condition the highest pod number/plant observed in V5 genotype and the lowest pod number/plantin V19,V21,V22,V23 and in V25 genotype. Under 10dS/m salinity stress condition the highest pod number/plant observed in V5 and the lowest inV17, V19, V20, V21, V22, V23, V24 and in V25 genotype.

In Fig.9 the linear trends showed that the increase of salinity stress condition reduced the pod: peg ratio in groundnut. The bar graphs showed that the pod: peg ratio reduced or increased with the increase of salinity stress in genotypes. Under control / non-saline condition, the highest the pod: peg ratio observed in V3 and the lowest the pod: peg ratio observed in V23 genotype. Under 8dS/m salinity stress condition the highest the pod: peg ratio observed in V5 genotype and the lowest the pod: peg ratio in V19, V21, V22, V23 and V25 genotype. Under 10dS/m salinity stress condition the highest the pod: peg ratio observed inV3 and V5 and the lowest inV17, V19, V20, V21, V22, V23, V24 and in V25 genotype.

The linear trends showed that the increase of salinity stress condition reduced the pod weight /plant in groundnut in Fig.10. The bar graphs showed that the pod weight/plant reduced with the increase of salinity stress in genotypes. Under control / non-saline condition, the highest pod weight /plant observed in V14 and the lowest pod weight/plant observed in V24 genotype. Under 8dS/m salinity stress condition the

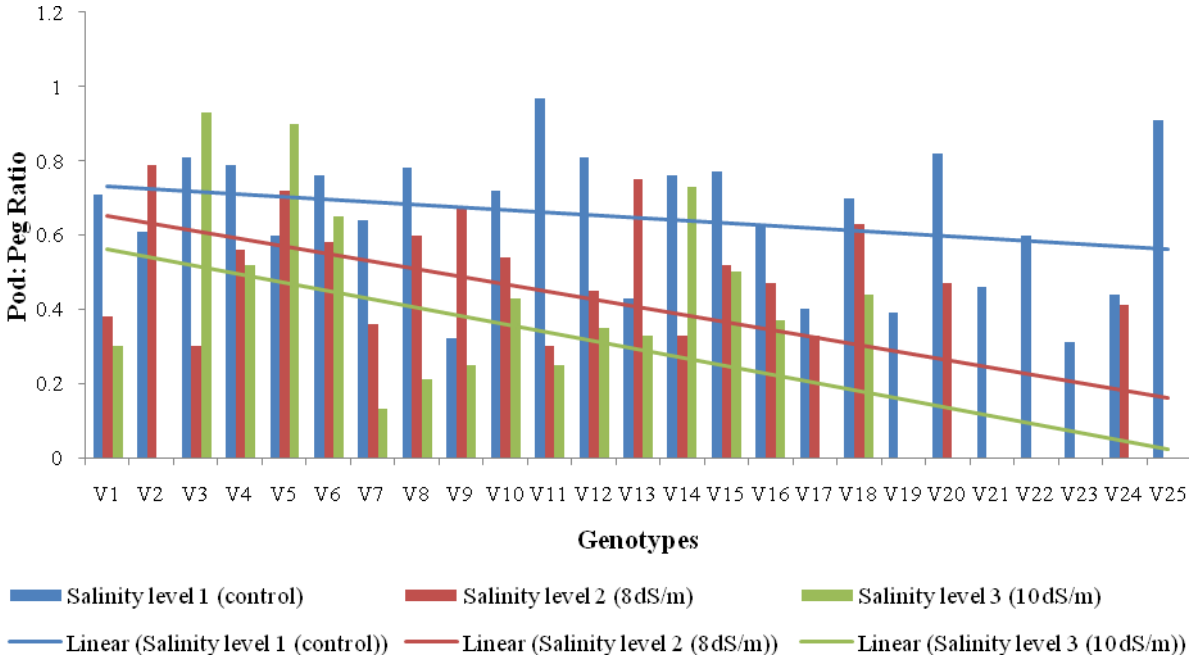


Fig. 9 The effect of different salinity levelson pod:peg ratio and its linear trends in 25 genotypes of groundnut

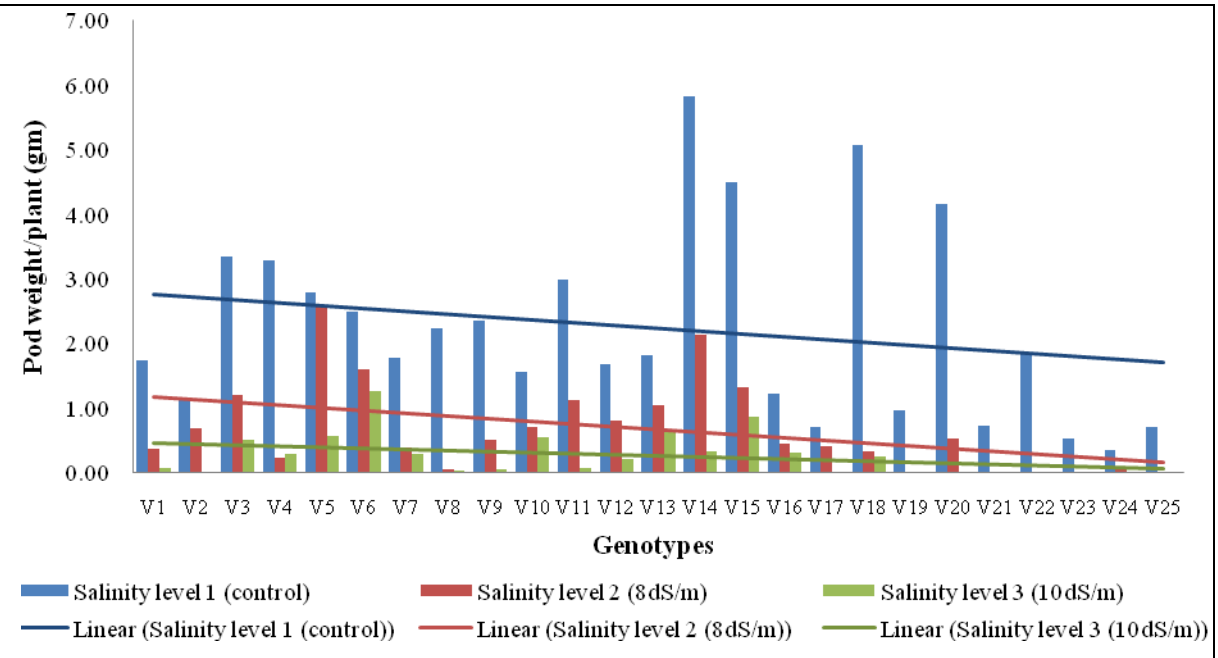


Fig. 10 The effect of different salinity levelson pod weight per plant and its linear trends in 25 genotypes of groundnut

highest pod weight/plant observed in V5 genotype and the lowest pod weight/plant in V19, V21, V22, V23 and in V25 genotype. Under10dS/m salinity stress condition the highest pod weight/plant observed in V6 and the lowest in V2, V17, V19, V20, V21, V22, V23, V24 and in V25 genotype.

In Fig.11 the linear trends showed that the increase of salinity stress condition reduced the kernel weight /plant in groundnut. The bar graphs showed that the kernel weight/plant reduced with the increase of salinity stress in genotypes. Under control / non-saline condition, the highest kernel weight /plant observed in V18 and the lowest kernel weight/plan to bserved in V24 genotype. Under 8dS/m salinity stress condition the highest kernel weight/plant observed in V5 genotype and the lowest kernel weight/plant in V1,V4,V7, V9, V10, V11, V17, V19, V20, V21, V22, V23 and in V25 genotype. Under 10dS/m salinity stress condition the highest kernel weight/plant observed in V6 and the lowest in V1, V2,V4, V7, ,V10, V12, V14, V17, V18, V19, V20, V21, V22, V23, V24 and V25 genotypes.

In Fig.12 the linear trends showed that the increase of salinity stress condition reduced the shelling percent (%) in groundnut. The bar graphs showed that the shelling percent (%) reduced with the increase of salinity stress in genotypes. Under control / non-saline condition, the highest shelling percent (%) observed in V13 and the lowest shelling percent (%) observed in V21 genotype. Under 8dS/m salinity stress condition the highest shelling percent (%) observed in V6 genotype and the lowest shelling percent (%) in V1, V4, V7, V9,V10, V11, V17, V19, V20, V21, V22, V23 and in V25 genotype. Under 10dS/m salinity stress condition the highest shelling percent (%) observed in V5 and the lowest in V1, V2,V4, V7, ,V10, V12, V14, V17, V18, V19, V20, V21, V22, V23, V24 and V25 genotypes.

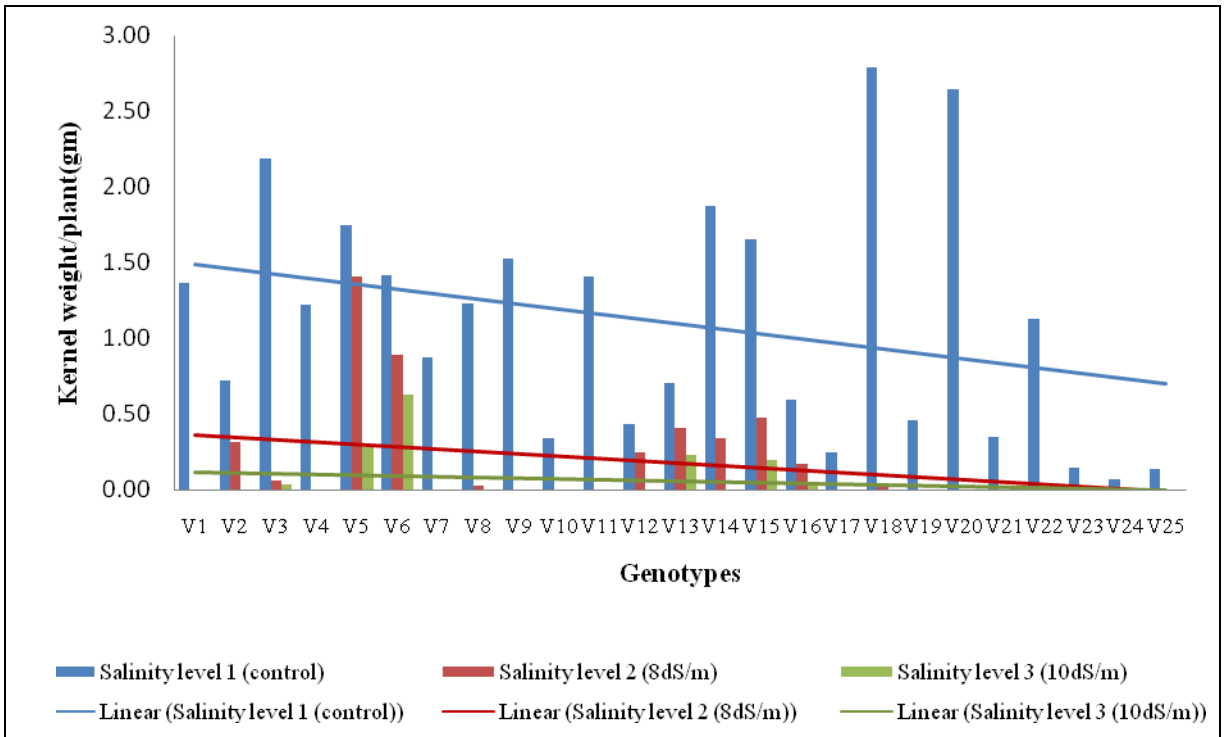


Fig. 11 The effect of different salinity levelson kernel weight per plant and its linear trends in 25 genotypes of groundnut

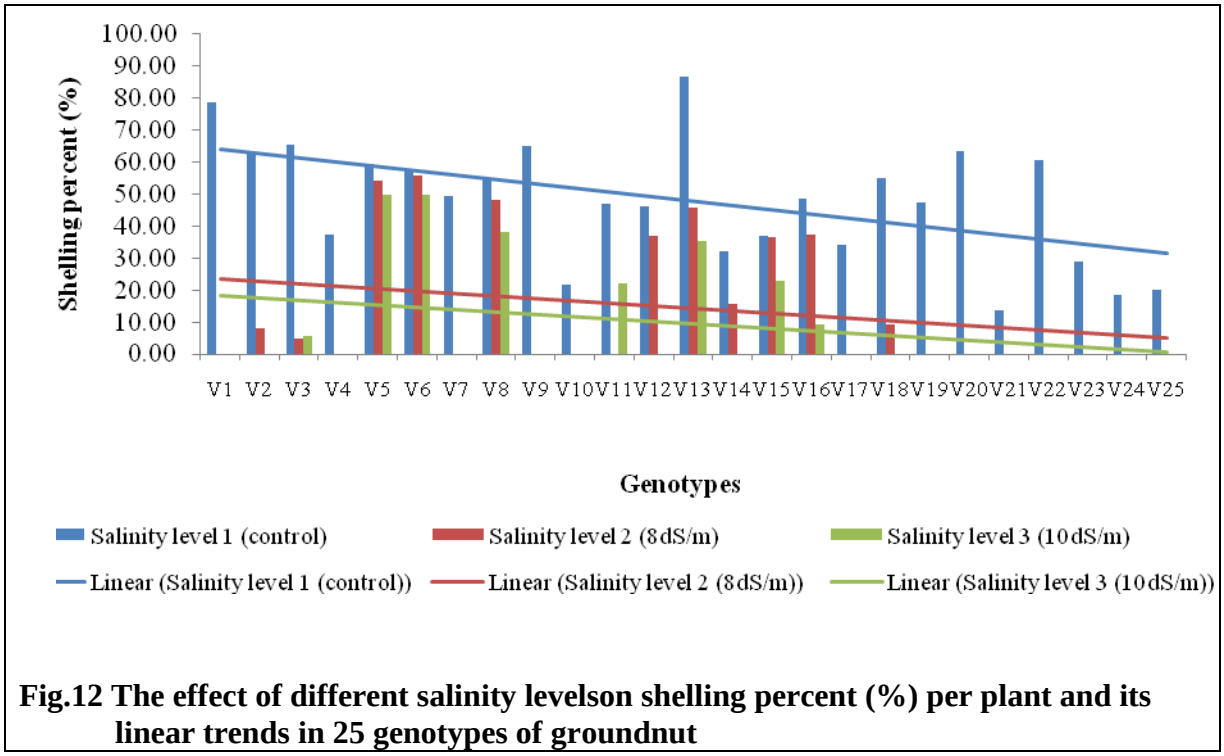


Fig.12 The effect of different salinity levelson shelling percent (%) per plant and its linear trends in 25 genotypes of groundnut

4.1.12 Relative performance of Na^+, K^+ and Ca^{++} content in shoot tissues of genotypes over different salinity levels

The average value of different salinity levels of Na^+, K^+ and Ca^{++} content in shoot tissues shown by linear trends over genotypes have been presented in Fig.13 to Fig.16. And mean value of genotypes over different salinity levels of Na^+, K^+ and Ca^{++} content (%) in shoot tissue salso presented through bar graph in Fig.13 to Fig.16 concurrently. In Fig.13 the linear trends showed that the increase of salinity stress condition increased Na^+ content (%) in the shoot tissuesin groundnut. The bar graphs showed that Na^+ content increased with the increase of salinity stress in each genotype except V7 and V8. Under control / non-saline condition, the highest Na^+ content observed in V8 genotype and the lowest number of Na^+ content in V22. Under 8dS/m salinity stress condition the highest Na^+ content observed in V24 and the lowest Na^+content in V22. Under 10dS/m salinity stress condition the highest Na^+ content observed in V1 and the lowest in V8 genotype.

The linear trends showed that the increase of salinity stress condition increased K^+ content (%) in the shoot tissues in groundnut in Fig.14. The bar graphs showed that K^{++} content increased with the increase of salinity stress in each genotype except V18 and V19. Under control / non-saline condition, the highest K^+ content observed in V8 genotype and the lowest number of K^+content in V9. Under 8dS/m salinity stress condition the highest K^+content observed in V8 and the lowest K^+content in V9. Under 10dS/m salinity stress condition the highest K^+content observed in V6 and the lowest in V19 genotype.

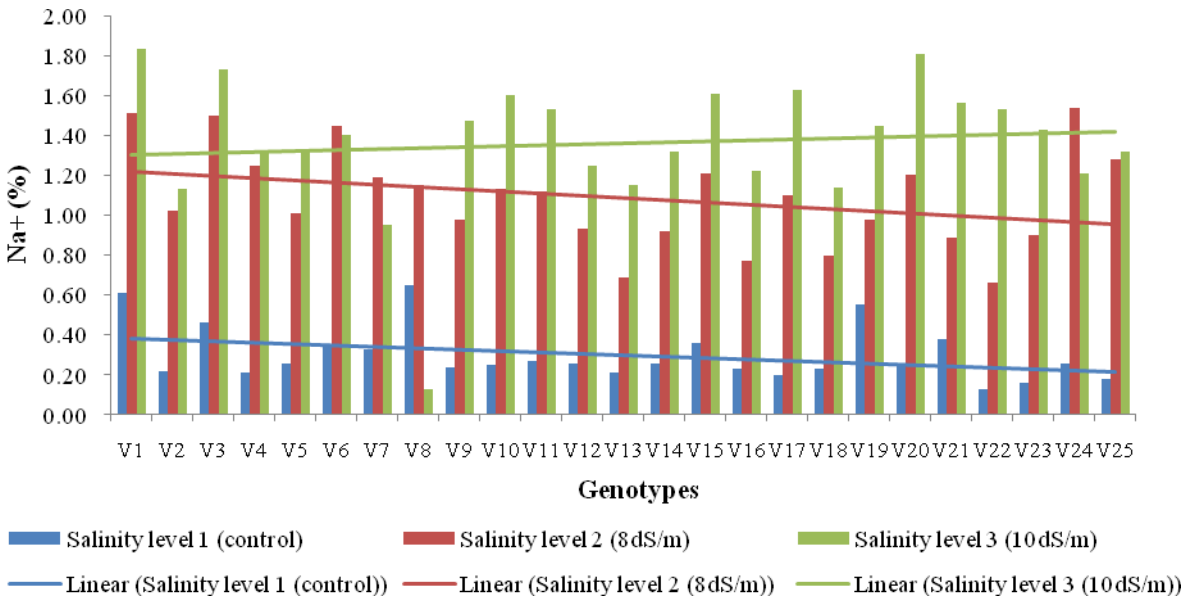


Fig.13 The effect of different salinity levelson Na^+ contents (%) and its linear trends in 25 genotypes of groundnut

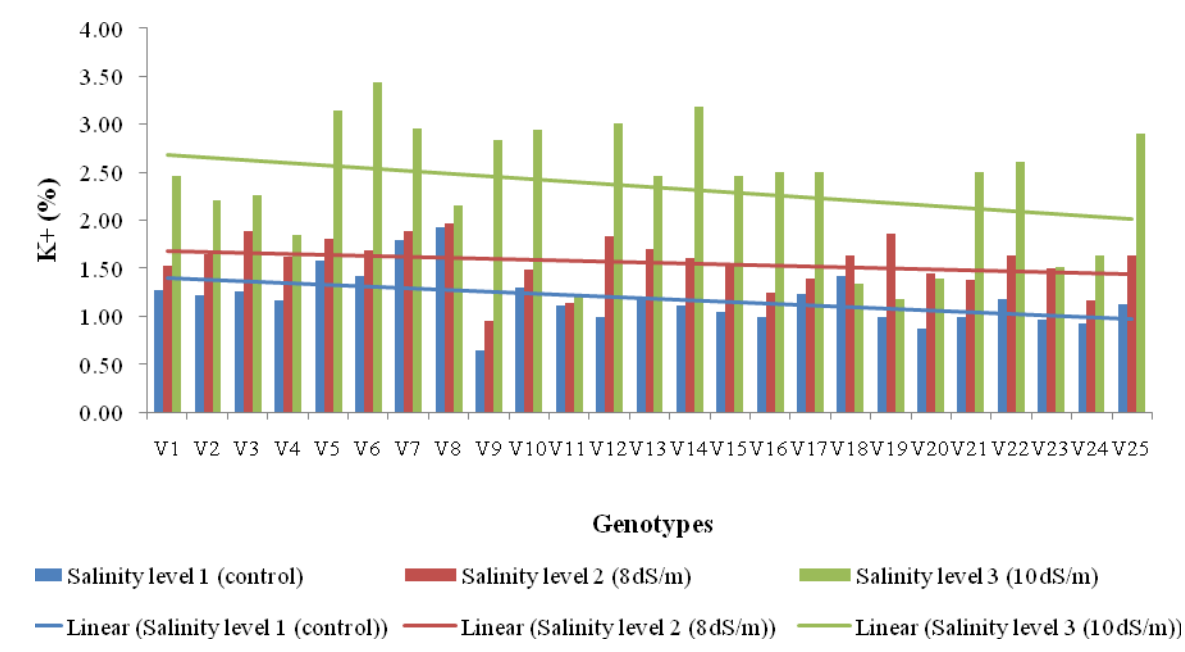


Fig. 14 The effect of different salinity levelson K^+ contents (%) and its linear trends in 25 genotypes of groundnut

In Fig.15 the linear trends showed that the increase of salinity stress condition increased Ca^{++} content (%) up to 8dS/m salinity, but decreased at 10dS/m salinity stress condition in the shoot tissues in groundnut. The bar graphs showed that Ca^{++} content increased up to 8dS/m with the increase of salinity stress in each genotype, but decreased at 10dS/m salinity stress condition. Under control / non-saline condition, the highest Ca^{++} content observed in V18 genotype and the lowest number of Ca^{++} content in V8. Under 8dS/m salinity stress condition the highest Ca^{++} content observed in V3 and the lowest Ca^{++} content in V5. Under10dS/m salinity stress condition the highest Ca^{++} content observed in V24 and the lowest in V4 genotype.

The linear trends showed that the increase of salinity stress condition the K^+/Na^+ ratio was not increased in the shoot tissuesin groundnutin Fig.14. The bar graphs showed that K^+/Na^+ratio not increased with the increase of salinity stress in each genotype. The K^+/Na^+ ratio showed higher only in non-saline/control condition. Under control / non-saline condition, the highest K^+/Na^+ ratio observed in V22 genotype and the lowest number of K^+/Na^+ratioin V19. Under 8dS/m salinity stress condition the highest K^+/Na^+ ratio observed in V13 and V22 and the lowest K^+/Na^+ratio in V24. Under 10dS/m salinity stress condition the highest K^+/Na^+ ratio observed in V7 and the lowest in V11 genotype.

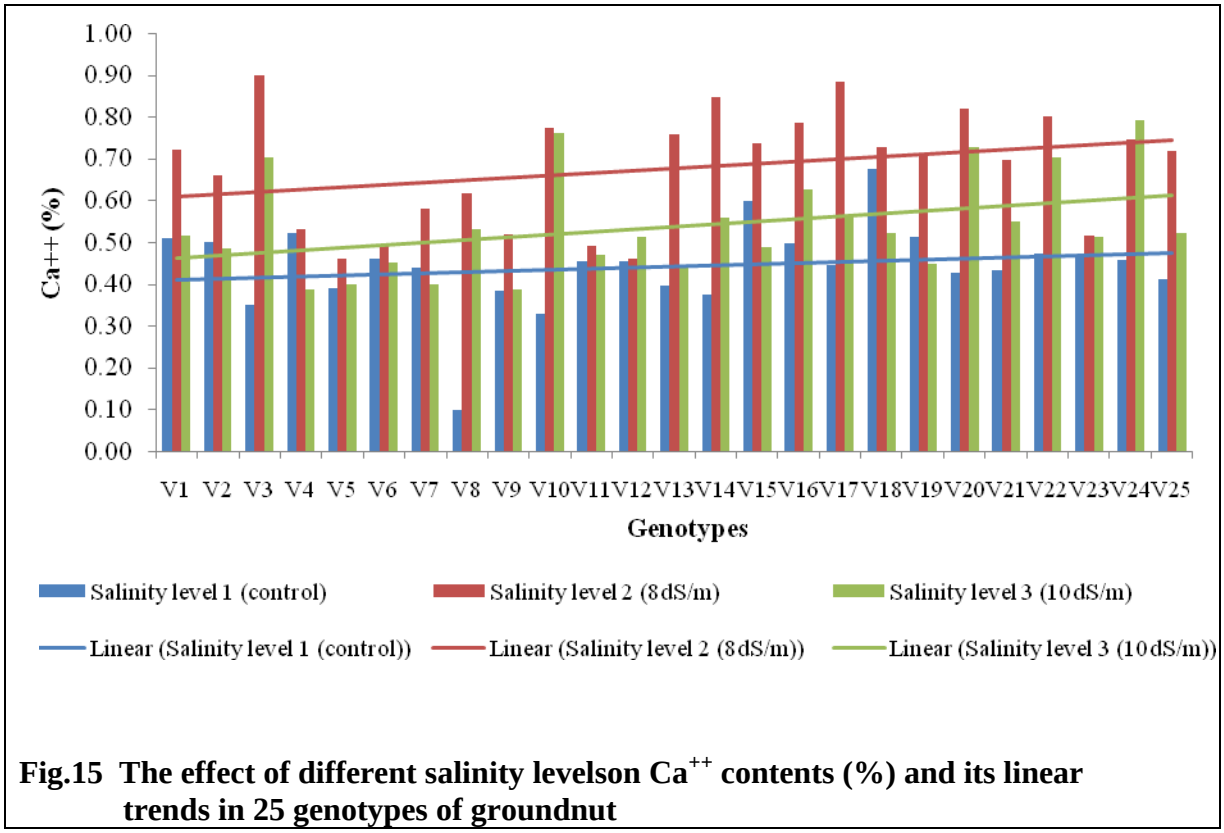


Fig.15 The effect of different salinity levelson Ca^{++} contents (%) and its linear trends in 25 genotypes of groundnut

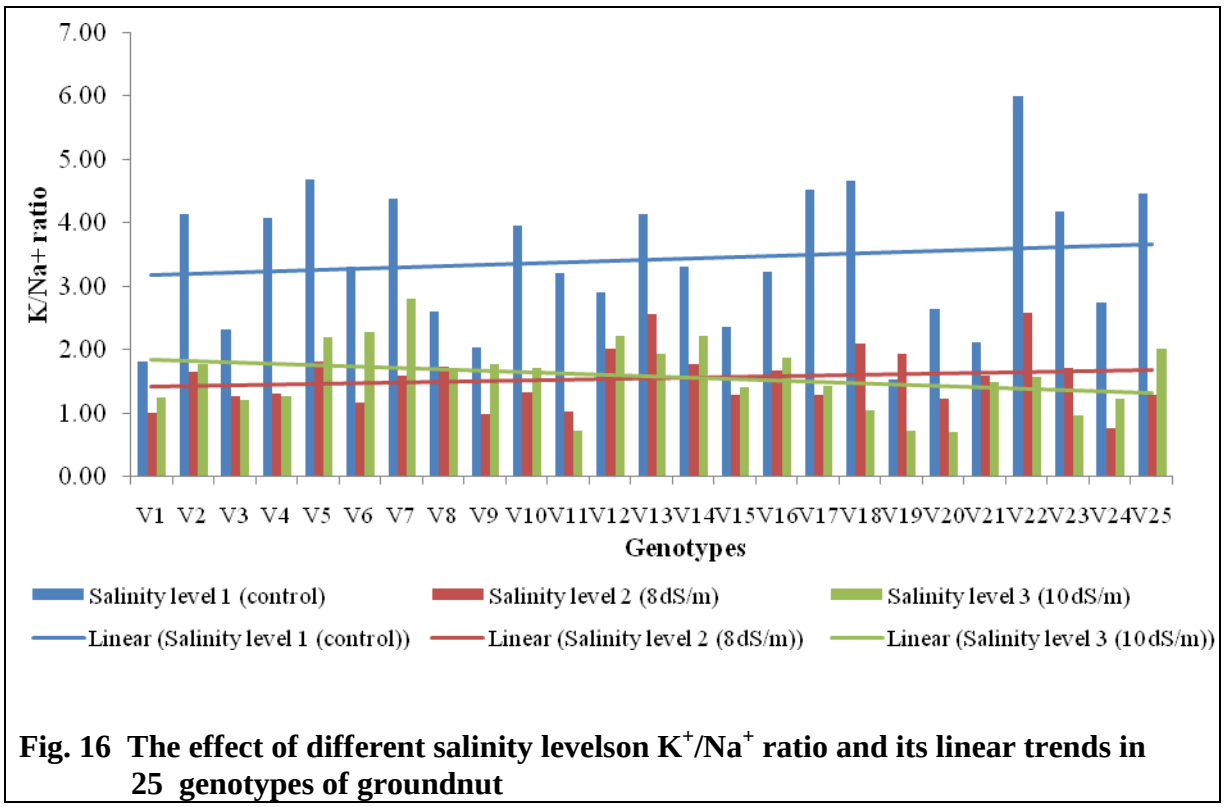


Fig. 16 The effect of different salinity levelson K^{+}/Na^{+} ratio and its linear trends in 25 genotypes of groundnut

4.1.13 Screening of genotypes of groundnut based on shoot biomass:

Shoot biomass of all the genotypes had significantly different under control condition and salinity stress condition. They showed higher shoot biomass under control condition than that of their respective saline stress condition (Table 11). Under control condition, the highest shoot biomass (7.88g) was found in V18 followed by V2, V12, V24, V19, V9, V20, V13, V22, V21, V17, V16 and V1 with non-significant differences. In contrast, the lowest shoot biomass (2.86g) was found in V25 followed by V10 with significant differences with all other rest genotypes.

Under saline condition the highest shoot biomass (5.50g) was found in V19 followed by V2, V16,V13,V18, V14, V22, V15,V20, V9, V5,V3,V12,V24, V21, and V8 with non-significant differences. The lowest shoot biomass (0.58g) was found in V25 followed by V17 and V23 with non significant differences. The rest of the genotypes had intermediate shoot biomass with significant differences from individuals of inter and intra groups. Shoot biomass showed a wide range of variation from 0.52 to 5.50.

Percent reduction in saline condition over control ranged 11.38 to 81.82% with V25 being the highest whilst V14 the lowest. As per classification using the equation mentioned in section 3.4.11 four and thirteen genotypes appeared tolerant (T) and moderately tolerant (MT), respectively (Table11). In contrast, five and three genotypes appeared moderately sensitive (MS) and sensitive (S) correspondingly. Different phenotypic appearances of tolerant, moderately tolerant, moderately sensitive and sensitive genotypes are shown in Plate 15 and Plate 16.

Table 11. Shoot biomass of 25 genotypes of groundnut undersalinity stress and non-saline conditions along with reduction in percent of control and salinity tolerance classes

Code	Genotypes/ varieties	Shoot biomass plant^{-1}(g)		Reduction (% of control) under Salinity 8dS/m	Salinity tolerance* classes
		Control	Salinity 8dS/m		
V1	Binachinabadam-1	6.10	3.17	48.03	MS
V2	Binachinabadam-2	7.55	5.22	30.86	MT
V3	Binachinabadam-3	5.34	4.03	24.53	MT
V4	Binachinabadam-4	5.08	3.14	38.19	MT
V5	Binachinabadam-5	5.19	4.06	21.77	MT
V6	Binachinabadam-6	5.35	3.59	32.90	MT
V7	Dhaka-1(Maizchar)	5.29	3.22	39.13	MT
V8	Pk-1 (Pakshi local)	5.39	3.63	32.65	MT
V9	Basantibadam (DG-2)	6.99	4.14	40.77	MS
V10	Tridanabadam (DM-1)	4.46	3.58	19.73	T
V11	Jhingabadam	5.27	3.04	42.31	MS
V12	Barichinabadam-5	7.25	4.00	44.83	MS
V13	BARI Chinabadam-6	6.61	5.15	22.09	MT
V14	BARI Chinabadam -7	5.45	4.83	11.38	T
V15	BARI Chinabadam -8	5.48	4.55	16.97	T
V16	BARI Chinabadam -9	6.11	5.21	14.73	T
V17	ICGV-96175	6.24	1.47	76.44	S
V18	ICGV-01249	7.88	5.05	35.91	MT
V19	ICGV-00203	7.10	5.50	22.54	MT
V20	ICGV-91068	6.98	4.22	39.54	MT
V21	ICGV-97119	6.40	3.89	39.22	MT
V22	ICGV-96178	6.41	4.75	25.90	MT
V23	J-2001-14	5.37	1.92	64.25	S
V24	J-2001-6	7.17	3.96	44.77	MS
V25	J-2001-22	2.86	0.52	81.82	S
LSD (0.05)		2.06	1.87		

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive

*Scale: <20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, >60% reduction= S (Azad *et al*., 2012).

Plate 15. Phenotypic appearance showing tolerant and moderately tolerant genotypes at 8dS/m salinity level

Plate 16. Phenotypic appearance showing moderately sensitive and sensitive genotypes at 8dS/m salinity level

4.1.14 Screening of genotypes of groundnut based on total biomass

Total biomass of all the genotypes had significantly different under control condition and salinity stress condition. They showed higher total biomass under control condition than that of their respective saline stress condition (Table 12). Under control condition, like shoot biomass, the highest total biomass (8.31g) was found in V18 followed by V2, V12, V24, V20, V9, V19, V13, V22, V1, V17 and V16 with non-significant differences. Interestingly, like shoot biomass V25 had the lowest total biomass (3.24g) sharing equal statistical rank with V10 and significantly differences with all the rest genotypes.

Under saline condition, like shoot biomass, the highest total biomass (5.73g) was found in V19 followed by V2, V16, V18,V14,V22,V15,V20, V9,V5, V24, V3, V13, V21,V8,V5 and V10with non-significant differences. Interestingly, like shoot biomass V25 had the lowest total biomass (0.57g) sharing equal statistical rank with V17, V23 and significantly differences with all the rest genotypes. Total biomass showed a wide range of variation from 0.57g to 5.73g.

Percent reduction in saline condition over control ranged 13.07 to 82.41% with V25 being the highest whilst V14 the lowest as like as shoot biomass. As per classification using the equation mentioned in section 3.4.11 four and thirteen genotypes appeared tolerant (T) and moderately tolerant (MT), respectively similar to shoot biomass (Table 11). In contrast, five and three genotypes appeared moderately sensitive (MS) and sensitive (S), correspondingly.

Table 12. Total biomass of 25 genotypes of groundnut under salinity stress and non-saline conditions along with percent reductionand salinity tolerance classes

Code	Genotypes/ varieties	Total biomassplant^{-1}(g)		Reduction (%of control) under Salinity 8dS/m	Salinity tolerance* classes
		Control	Salinity 8dS/m		
V1	Binachinabadam-1	6.65	3.49	47.52	MS
V2	Binachinabadam-2	7.92	5.58	29.55	MT
V3	Binachinabadam-3	5.89	4.28	27.33	MT
V4	Binachinabadam-4	5.53	3.35	39.42	MT
V5	Binachinabadam-5	5.61	4.52	19.43	T
V6	Binachinabadam-6	5.74	3.83	33.28	MT
V7	Dhaka-1(Maizchar)	5.69	3.35	41.12	MS
V8	Pk-1 (Pakshi local)	5.79	3.96	31.61	MT
V9	Basantibadam (DG-2)	7.48	4.47	40.24	MT
V10	Tridanabadam (DM-1)	4.91	3.83	22.00	MT
V11	Jhingabadam	5.67	3.27	42.33	MS
V12	Barichinabadam-5	7.79	4.42	43.26	MS
V13	BARI Chinabadam-6	7.03	4.19	40.40	MT
V14	BARI Chinabadam -7	5.89	5.12	13.07	T
V15	BARI Chinabadam -8	5.9	4.77	19.15	T
V16	BARI Chinabadam -9	6.57	5.54	15.68	T
V17	ICGV-96175	6.63	1.57	76.32	S
V18	ICGV-01249	8.31	5.35	35.62	MT
V19	ICGV-00203	7.47	5.73	23.29	MT
V20	ICGV-91068	7.49	4.56	39.12	MT
V21	ICGV-97119	6.76	4.12	39.05	MT
V22	ICGV-96178	6.89	5.1	25.98	MT
V23	J-2001-14	5.77	2.09	63.78	S
V24	J-2001-6	7.59	4.28	43.61	MS
V25	J-2001-22	3.24	0.57	82.41	S
LSD (0.05)		2.14	1.94		

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive

*Scale: <20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, >60% reduction= S(Azad *et al*., 2012)

4.1.15 Screening of genotypes of groundnut based on pod number

Pod numberof all the genotypes had significantly different under control condition and salinity stresscondition. It showed higher pod number under control condition than that of their respective saline stress condition (Table 13). Under control condition, V3 and V8 had the maximum number of pods/plant (8.0) followed by V3, V20, V6, V1 and V15with non-significant differences. In contrast, V24, V21, V19 and V17 had the minimum number of pods (2.0) sharing equal statistical rank with V23, V25, V22, V13, V16 and V7. The rest of the genotypes had intermediate number of pods with significant differences from individuals of inter and intra groups.Pod number showed a wide range of variation from 2.00 to 8.00.

Under saline condition, V5 and V6 had the maximum number of pods/plant (7.00) with significant differences of all genotypes. In contrast, V25, V23, V22, V21 and V19 had the minimum number of pods (0.00) sharing equal statistical rank with V24, V17, V10, V18, V13, V9 and V11. The rest of the genotypes had intermediate number of pods with significant differences from individuals of inter and intra groups. Pod number showed a wide range of variation from 0.00 to 7.00.

Percent reduction in pod number under saline condition over control ranged 4.26 to 100% with V2 being the lowest while the highest in those that had zero pod weight under saline condition. Following the same classification basisfive and three genotypes appeared tolerant (T) and moderately tolerant (MT), respectively (Table 12). In contrast, seven and ten genotypes appeared moderately sensitive (MS) and sensitive (S) correspondingly. On the basis of pod formation tolerant, moderately tolerant, moderately sensitive and sensitive genotypes are shown in Plate 17 and Plate 18.

Table 13. Pod number of 25 genotypes of groundnut under salinity stress and non-saline conditions along with percent reductionand salinity tolerance classes

Code	Genotypes/ varieties	Pod number plant^{-1}		Reduction (%of control) under Salinity 8dS/m	Salinity tolerance* classes
		Control	Salinity 8dS/m		
V1	Binachinabadam-1	6.0	2.7	55.50	MS
V2	Binachinabadam-2	4.7	4.5	4.26	T
V3	Binachinabadam-3	7.8	2.3	70.24	S
V4	Binachinabadam-4	5.0	3.7	26.60	MT
V5	Binachinabadam-5	8.0	7.0	12.50	T
V6	Binachinabadam-6	6.3	5.5	12.70	T
V7	Dhaka-1(Maizchar)	4.5	2.3	48.89	MS
V8	Pk-1 (Pakshi local)	8.0	3.0	62.50	S
V9	Basantibadam (DG-2)	3.3	2.0	39.94	MT
V10	Tridanabadam (DM-1)	3.0	1.5	50.00	MS
V11	Jhingabadam	4.7	2.0	57.17	MS
V12	Barichinabadam-5	5.0	4.7	6.60	T
V13	BARI Chinabadam-6	3.0	2.0	33.33	MT
V14	BARI Chinabadam -7	2.7	2.3	12.73	T
V15	BARI Chinabadam -8	6.0	2.2	63.33	S
V16	BARI Chinabadam -9	4.0	2.3	41.75	MS
V17	ICGV-96175	2.0	1.0	50.00	MS
V18	ICGV-01249	4.7	1.7	64.24	S
V19	ICGV-00203	2.0	0.0	100.00	S
V20	ICGV-91068	7.0	2.3	66.71	S
V21	ICGV-97119	2.0	0.0	100.00	S
V22	ICGV-96178	3.0	0.0	100.00	S
V23	J-2001-14	2.3	0.0	100.00	S
V24	J-2001-6	2.0	1.0	50.00	MS
V25	J-2001-22	3.0	0.0	100.00	S
LSD(0.05)		2.55	2.05		

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive

*Scale: <20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, >60% reduction= S (Azad *et al*., 2012)

Plate 17. Pod formation status showing tolerant and moderately tolerant genotypes at8dS/m salinity level after harvest

Plate 18. Pod formation status showing moderately sensitive and sensitive genotypes at8dS/m salinity level after harvest

4.1.16 Screening of genotypes of groundnut based on pod yield

Pod weight of all the genotypes had significantly different under control condition and salinity stress condition. It showed higher pod weght under control condition than that of their respective saline stress condition (Table 14). Under control condition, V14 had highest pod weight/plant (5.81g) followed by V18, V14 and V20 with non-significant differences. V24 had the lowest pod weight (0.36g) sharing equal statistical rank with V23, V25, V17, V21, V19, V2, V16, V10, V12, V1, V7, V13 and V22. The rest of the genotypes had intermediate pod weight/plant with significant differences from individuals of inter and intra groups. Pod weight/plant showed a wide range of variation from 0.36g to 5.81g.

Under saline condition, V5 had highest pod weight/plant (2.59g) followed by V14 and V6 with non-significant differences. V25, V23, V22, V21 and V19 had the lowest pod weight (0.00g) sharing equal statistical rank with V24, V8, V4,V18, V1, V7, V17, V16, V20, V12, V13, V10, V9, V11, V2, and V15. The rest of the genotypes had intermediate pod weight/plant with significant differences. Pod weight/plant showed a wide range of variation from 0.00g to 2.59g.

Percent reduction in pod weight under saline condition over control ranged 6.83 to 100% with V5 being the lowest while the highest in those that had zero pod weight under saline condition. Following the same classification basisone (V5) and two (V6 and V2) genotypes appeared tolerant (T) and moderately tolerant (MT), respectively (Table 14). In contrast, four genotypes appeared moderately sensitive (MS) and the remainders sensitive (S).

Table 14. Pod yield of 25 genotypes of groundnut under salinity stress and non-saline conditions along with percent reductionand salinity tolerance classes

Code	Genotypes/ Varieties	Pod weight plant^{-1}(g)		Reduction (% of control) under Salinity 8dS/m	Salinity tolerance* classes
		Control	Salinity 8dS/m		
V1	Binachinabadam-1	1.73	0.38	78.03	S
V2	Binachinabadam-2	1.14	0.69	39.47	MT
V3	Binachinabadam-3	3.34	1.21	63.77	S
V4	Binachinabadam-4	3.29	0.24	92.71	S
V5	Binachinabadam-5	2.78	2.59	6.83	T
V6	Binachinabadam-6	2.49	1.60	35.74	MT
V7	Dhaka-1(Maizchar)	1.77	0.40	77.40	S
V8	Pk-1 (Pakshi local)	2.23	0.07	96.86	S
V9	Basantibadam (DG-2)	2.35	0.52	77.87	S
V10	Tridanabadam (DM-1)	1.57	0.72	54.14	MS
V11	Jhingabadam	2.99	1.12	62.54	S
V12	Barichinabadam-5	1.68	0.81	51.79	MS
V13	BARI Chinabadam-6	1.82	1.05	42.31	MS
V14	BARI Chinabadam -7	5.81	2.14	63.17	S
V15	BARI Chinabadam -8	4.48	1.32	70.54	S
V16	BARI Chinabadam -9	1.22	0.45	63.11	S
V17	ICGV-96175	0.72	0.41	43.06	MS
V18	ICGV-01249	5.07	0.34	93.29	S
V19	ICGV-00203	0.98	0.00	100.00	S
V20	ICGV-91068	4.16	0.53	87.26	S
V21	ICGV-97119	0.74	0.00	100.00	S
V22	ICGV-96178	1.87	0.00	100.00	S
V23	J-2001-14	0.52	0.00	100.00	S
V24	J-2001-6	0.36	0.10	72.22	S
V25	J-2001-22	0.71	0.00	100.00	S
LSD (o.o5)		1.68	1.16		

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive

*Scale: <20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, >60% reduction= S (Azad *et al*., 2012)

4.1.17 Screening of genotypes of groundnut based on kernel weight

Kernel weightof all the genotypes had significantly different under control condition and salinity stress condition. It showed higher kernel weight under control condition than that of their respective saline stress condition (Table 15).Under control condition, V18 had the highest kernel weight/plant (2.79g)followed byV20 andV3 with non-significant differences.In contrast, V24had the lowest (0.07g) kernel weight/plant sharing equal statistical rank withV25,V23, V17, V10,V21,V19,V16,V13,V2, V7.The rest of the genotypes had intermediate kernel weight/plant with significant differences from individuals of inter and intra groups.Kernel weight/plant showed a wide range of variation from 0.07g to 2.79g.

Under saline condition, V5 had the highest kernel weight/plant (1.41g) followed byV6 with non-significant differences and significant differences with all the others genotypes.In contrast, V24, V25,V23,V25,V22,V21,V20,V19,V17, V11, V10, V9, V7, V4 and V1had the lowest (0.00)kernel weight/plant sharing equal statistical rank with V18, V16, and V8. Kernel weight/plant showed a wide range of variation from 0.00g to 1.41g.

Percent reduction in kernel weight under saline condition over control ranged 19.43 to 100% with V5 being the lowest while the highest in those that had zero pod weight under saline condition. Following the same classification basisone (V5) and one (V6) genotype appeared tolerant (T) and moderately tolerant (MT), respectively (Table 15). In contrast, three genotypes appeared moderately sensitive (MS) and the remainders sensitive (S).

Table 15. Kernel weight of 25 genotypes of groundnut under salinity stress and non-saline conditions along with percent reductionand salinity tolerance classes

Code	Genotypes/ varieties	Kernel weight plant^{-1}(g)		Reduction (%of control) under Salinity 8dS/m	Salinity tolerance* class
		Control	Salinity 8dS/m		
V1	Binachinabadam-1	1.36	0.00	100.00	S
V2	Binachinabadam-2	0.72	0.32	55.56	MS
V3	Binachinabadam-3	2.19	0.06	97.26	S
V4	Binachinabadam-4	1.23	0.00	100.00	S
V5	Binachinabadam-5	1.75	1.41	19.43	T
V6	Binachinabadam-6	1.42	0.89	37.32	MT
V7	Dhaka-1(Maizchar)	0.88	0.00	100.00	S
V8	Pk-1 (Pakshi local)	1.23	0.03	97.56	S
V9	Basantibadam (DG-2)	1.53	0.00	100.00	S
V10	Tridanabadam (DM-1)	0.34	0.00	100.00	S
V11	Jhingabadam	1.41	0.00	100.00	S
V12	Barichinabadam-5	0.44	0.25	43.18	MS
V13	BARI Chinabadam-6	0.71	0.41	42.25	MS
V14	BARI Chinabadam -7	1.87	0.34	81.82	S
V15	BARI Chinabadam -8	1.65	0.48	70.91	S
V16	BARI Chinabadam -9	0.6	0.17	71.67	S
V17	ICGV-96175	0.25	0.00	100.00	S
V18	ICGV-01249	2.79	0.03	98.92	S
V19	ICGV-00203	0.46	0.00	100.00	S
V20	ICGV-91068	2.64	0.00	100.00	S
V21	ICGV-97119	0.35	0.00	100.00	S
V22	ICGV-96178	1.13	0.00	100.00	S
V23	J-2001-14	0.15	0.00	100.00	S
V24	J-2001-6	0.07	0.00	100.00	S
V25	J-2001-22	0.14	0.00	100.00	S

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive
*Scale: <20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, >60% reduction= S (Azad *et al*., 2012)

4.1.18 Salinity tolerance classes and selection of parents for hybridization

After calculation of percent reduction under saline condition over control of different important traits like shoot biomass, total biomass, pod number, pod weight and kernel weight it was observed that the salinity tolerance classes of those traits are not alike over genotypes (Table 16). Some genotypes found tolerant incase of shoot biomass but not in pod number or pod weight or in kernel weight and vice versa. All the salinity tolerance classes of those traits were presented together in the Table 16. Among the genotypes V5 had observed moderately tolerant in shoot biomass trait but tolerant in total biomass, pod number, pod weight and kernel weight under saline condition. So, it was treated as saline tolerant.

Within the five traits, genotype V6 found moderately tolerant in four traits except pod number/plant which was showed tolerance in this trait only. Hence, it considered as moderately tolerant genotype. Genotype V2 also considered as moderately tolerant because, in the three traits it observed moderately tolerant though it showed tolerant and sensitive in pod number and kernel weight traits, respectively. Genotype V13 also considered as moderately tolerant because within the five traits it showed moderately tolerant in three traits viz. shoot biomass, total biomass and pod number. It was showed moderately sensitive in two other traits viz. pod weight and kernel weight.

Within the five traits, V12 showed moderately sensitive in four traits except pod number that showed tolerant. Thus, V12 considered as moderately sensitive. On the other hand, local variety V7 showed moderately tolerant in one trait, moderately sensitive in two traits and sensitive in two traits. So, it was considered as sensitive genotype.

Finally, V5 (Binachinabadam-5) selected as tolerant, V6 (Binachinabadam-6), V2 (Binachinabadam-2) and V13 (BARI Chinabadam-6) selected as moderately tolerant, V12 (BARI Chinabadam-5) selected as moderately sensitive and V7 (Dhaka-1) selected as sensitive genotype for hybridization in diallel mating system. The list of selected parents for diallel cross has mentioned in Table 2 in materials and methods chapter.

Table 16. Salinity tolerance classes based on shoot biomass, total biomass, pod number, pod yield and kernel yield of 25 genotypes of groundnut at 8 dS/m salinity imposed during flowering till harvest stages

Code	Genotypes/Varieties	Salinity tolerance class as per salinity 8dS/m				
		Shoot biomass plant^{1}	Total biomass plant^{1}	Pod number plant^{1}	Pod weight plant^{1}	Kernel weight plant^{1}
V1	Binachinabadam-1	MS	MS	MS	S	S
V2	Binachinabadam-2***	MT	MT	T	MT	MS
V3	Binachinabadam-3	MT	MT	S	S	S
V4	Binachinabadam-4	MT	MT	MT	S	S
V5	Binachinabadam-5****	MT	T	T	T	T
V6	Binachinabadam-6***	MT	MT	T	MT	MT
V7	Dhaka-1*	MT	MS	MS	S	S
V8	PK-1	MT	MT	S	S	S
V9	Basantibdam	MS	MT	MT	S	S
V10	Tridanabadam	T	MT	MS	MS	S
V11	Jhingabadam	MS	MS	MS	S	S
V12	BARI Chinabadam-5**	MS	MS	T	MS	MS
V13	BARI Chinabadam-6***	MT	MT	MT	MS	MS
V14	BARI Chinabadam-7	T	T	T	S	S
V15	BARI Chinabadam-8	T	T	S	S	S
V16	BARI Chinabadam-9	T	T	MS	S	S
V17	ICGV-96175	S	S	MS	MS	S
V18	ICGV-01249	MT	MT	S	S	S
V19	ICGV-00203	MT	MT	S	S	S
V20	ICGV-91068	MT	MT	S	S	S
V21	ICGV-97119	MT	MT	S	S	S
V22	ICGV-96178	MT	MT	S	S	S
V23	J-2001-14	S	S	S	S	S
V24	J-2001-6	MS	MS	MS	S	S
V25	J-2001-22	S	S	S	S	S

T= Tolerant, MT= Moderately Tolerant, MS= Moderately Sensitive and S= Sensitive

Here, the genotypes with super scripted asterisks (****), (***), (**) and (*) signs were selected parents for their tolerant, moderately tolerant, moderately sensitive and sensitive reactions respectively based on shoot biomass, total biomass, pod number, pod yield and kernel yield for hybridization and genetic studies, next.

4.2 Experiment 2: Combining ability and genetic analysis of salinity tolerance in 7x7 F_1 diallel population

Analysis of variance for biomass, pod yield and related traitsin a 7x7 F_1 diallel population under 8dS/m salinity stress imposed during flowering till harvest stage is presented in Table 17(a) and Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues of those population is also presented in Table 17(b). Results revealed highly significant ($P \leq 0.01$) differences due to genotypes for all characters viz, plant height, branch number, shoot biomass, total biomass, pod number per plant, pod yield per plant and kernel weight per plant. Among parental genotypes highly significant ($P \leq 0.01$) differences were observed for pod number per plant, pod yield per plant and kernel weight per plant. In contrast, significant ($P \leq 0.05$) differences were recorded for plant height, shoot biomass, total biomass and non-significant for branch number only. Among F_1's highly significant variation was observed for all the traits except kernel weight per plant that showed significant variation. But, the term P vs F_1's was highly significant for branch number and pod yield per plant; significant for shoot biomass and kernel weight per plant; and non-significant for total biomass, pod number per plant and plant height. Nutrient contents (% of Na^+, K^+ and Ca^{2+}) in leaf and stem tissues showed highly significant for genotypes, parents, F_1's and P Vs F_1's.

Means of biomass, pod yield and related traits in a 7x7 F_1 diallel population under 8dS/m salinity stress imposed during flowering till harvest stage is presented in Table 18(a) and Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues of those population is also presented in Table 18(b).

Table 17. Analysis of variance for biomass, pod yield and related traits in a 7x7 F_1population of groundnut at 8dS/m salinity imposed during flowering till harvest stages

(a) Biomass, pod yield and yield attributes

SV	df	Plant height (cm)	Branch number	Shoot biomass(g)	Total biomass(g)	Pod no./plant	Pod yield (g) /plant	Kernel wt.(g) /plant
Genotypes	27	61.92**	2.34**	13.14**	14.54**	31.10**	0.24**	0.07**
Parents(P)	6	49.46*	0.77^{ns}	9.27*	9.86**	25.86**	0.78**	0.22**
F_1s	20	68.62**	2.57**	13.95**	15.57**	34.04**	0.06**	0.02*
P Vs F_1s	1	2.69^{ns}	7.00**	20.17*	22.11**	3.57^{ns}	0.55**	0.05*
Error	54	16.21	0.89	3.19	2.93	6.97	0.02	0.01

*,**Significant at 5% and 1% level, respectively

Table 17. Continued

(b) Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues

SV	df	Leaf tissues				Stem tissues			
		Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+}	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+}
Genotypes	27	0.56**	4.31**	0.93**	1.44**	0.19**	0.39**	0.49**	1.77**
Parents(P)	6	0.17**	0.11**	0.03**	0.67**	0.05**	0.42**	0.79**	0.45**
F_1s	20	0.63**	5.10**	1.14**	1.53**	0.23**	0.06**	0.05**	0.73**
P Vs F_1s	1	1.52**	13.54**	2.30**	4.09**	0.17**	7.01**	6.61**	30.45**
Error	54	0.001	0.001	0.001	0.02	0.002	0.001	0.003	0.002

*,**Significant at 5% and 1% level, respectively

Among the parental genotypes plant height ranged from 17.67 cm in P3 to 30.00 cm in P1 (Table 18a). Among the F_1 progeny, P2xP4 showed the tallest plant height (38.50 cm) while P2xP6 exhibited the lowest plant height (17.92 cm). The maximum branch number was recorded in the parent P1, P4 and P5 (5.83) and the minimum branch number was recorded in P3 (4.67). The cross P2xP5 showed the maximum branch number (6.33) while the minimum branch number was in P4xP7 and P5xP6 (3.00).

Among the parental genotypes highest shoot biomass per plant was obtained in parent P1 (8.79 g) followed by P2 (7.49g) and minimum shoot biomass was in parent P6 (3.47 g). Among the hybrids the maximum shoot biomass was found in cross P1xP4 (11.52g) followed by P2xP4 (10.87 g), and the lowest shoot biomass per plant was in cross P5xP6 (3.38 g). The maximum total biomass per plant was observed in the parent P1 (9.34 g) followed by P4 (7.90 g) and the minimum total biomass was recorded in parent P7 (4.45 g). The cross P1xP5 showed the highest total biomass (12.23 g) followed by cross P2xP4 (11.84 g) while the lowest total biomass was in cross P5x P6 (3.76 g).

Among the parental genotypes maximum pod number per plant was found in parent P1 (10) followed by P2 (6.17) and the minimum pod number per plant was in parent P6 (2). Among the F_1 progeny, the maximum pod number was found in cross P2xP4 (15.50) and the minimum pod number was in cross P3xP6, P4xP7, P5xP6 and P5xP7 (0.67).

The highest pod yield per plant was obtained in parent P1 (1.44 g) followed by P2 (0.29 g) and minimum pod yield per plant was in parent P4 (0.03 g). Among the hybrids the highest pod yield per plant was found in cross P2xP4 (0.65g) followed by P1xP. (0.22 g), and the lowest pod yield per plant was in cross P5xP6 (0.01 g).

Table 18. Mean values of biomass, pod yield and related traits in a 7x7 F_1 population of groundnut at 8dS/m salinity imposed during flowering till harvest stages

(a) Biomass, pod yield and yield attributes

Characters / Crosses	Plant height (cm)	Branch number	Shoot biomass (g)	Total biomass (g)	Pod no../ plant	Pod yield (g) /plant	Kernel wt.(g) /plant
P1	30.00	5.83	8.79	9.34	10.00	1.44	0.74
P2	23.00	4.83	7.49	7.63	6.17	0.29	0.14
P3	17.67	4.67	5.67	5.08	3.83	0.11	0.06
P4	26.50	5.83	6.11	7.90	2.00	0.03	0.01
P5	25.17	5.83	4.68	5.52	2.17	0.18	0.05
P6	20.25	5.67	3.47	5.38	2.00	0.04	0.01
P7	24.50	5.17	5.47	4.45	3.67	0.05	0.01
P1xP2	23.17	5.00	7.79	8.41	4.50	0.13	0.13
P1xP3	23.92	5.00	9.74	10.51	3.17	0.13	0.01
P1xP4	28.92	5.67	10.03	10.77	5.50	0.15	0.13
P1xP5	30.25	5.67	11.52	12.23	5.33	0.11	0.00
P1xP6	24.42	5.00	7.75	8.21	6.00	0.22	0.05
P1xP7	22.42	4.67	7.48	8.01	5.17	0.09	0.01
P2xP3	23.17	5.67	6.54	7.11	6.17	0.20	0.35
P2xP4	38.50	5.83	10.87	11.84	15.50	0.65	0.05
P2xP5	26.25	6.33	6.02	6.56	4.00	0.09	0.01
P2xP6	27.42	5.17	6.56	7.15	6.67	0.18	0.14
P2xP7	21.50	4.83	6.92	7.57	3.33	0.06	0.13
P3xP4	23.42	4.50	6.34	6.97	2.00	0.03	0.02
P3xP5	23.92	4.67	6.01	6.43	2.00	0.08	0.03
P3xP6	23.00	4.83	6.94	7.55	0.67	0.16	0.08
P3xP7	18.77	3.50	5.09	5.62	1.50	0.02	0.19
P4xP5	29.75	5.33	8.82	9.35	3.00	0.02	0.01
P4xP6	24.25	4.50	5.68	6.24	2.17	0.03	0.01
P4xP7	20.50	3.00	6.78	7.24	0.67	0.02	0.01
P5xP6	17.92	3.00	3.38	3.76	0.67	0.01	0.01
P5xP7	20.33	3.83	4.20	4.54	0.67	0.02	0.01
P6xP7	18.17	3.50	4.33	4.71	0.83	0.02	0.01
Mean	**24.18**	**4.90**	**6.80**	**7.36**	**3.90**	**0.16**	**0.08**
SE(±)	**0.86**	**0.17**	**0.40**	**0.42**	**0.61**	**0.05**	**0.03**

Table 18. Continued

(b) Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues

Characters / Crosses	Leaf tissues				Stem tissues			
	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+} (%)	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+} (%)
P1	1.77	0.84	0.49	1.51	1.08	0.75	0.70	3.55
P2	1.80	0.81	0.45	1.75	1.12	1.25	1.12	4.37
P3	1.95	0.72	0.37	2.33	1.04	0.68	0.66	3.62
P4	1.70	0.75	0.46	2.07	1.15	0.81	0.70	3.29
P5	1.52	0.79	0.54	1.82	0.81	1.63	2.04	3.43
P6	2.27	1.16	0.51	2.94	0.89	0.69	0.77	3.59
P7	1.78	1.18	0.66	1.86	1.10	0.66	0.60	4.12
P1xP2	2.15	1.07	0.50	2.48	1.05	0.60	0.58	3.69
P1xP3	1.57	0.79	0.50	1.45	1.27	0.67	0.53	2.78
P1xP4	1.60	1.52	0.95	1.86	0.77	0.29	0.38	2.30
P1xP5	1.54	1.44	0.94	1.78	0.61	0.20	0.34	1.80
P1xP6	1.69	1.10	0.65	2.22	0.61	0.17	0.28	1.94
P1xP7	1.78	2.01	1.13	2.10	0.90	0.18	0.20	2.02
P2xP3	2.11	0.92	0.44	1.50	0.88	0.20	0.23	2.55
P2xP4	1.55	3.08	1.99	1.65	0.62	0.15	0.25	1.44
P2xP5	2.03	1.54	0.76	2.55	0.34	0.16	0.47	1.84
P2xP6	1.89	1.29	0.68	1.89	0.81	0.26	0.32	2.75
P2xP7	2.25	6.13	2.73	2.70	0.57	0.30	0.52	1.74
P3xP4	2.37	1.10	0.46	2.85	1.09	0.31	0.28	2.36
P3xP5	2.26	4.33	1.92	2.58	0.98	0.31	0.32	2.37
P3xP6	2.56	2.86	1.12	2.75	1.24	0.17	0.14	1.79
P3xP7	2.62	0.81	0.31	3.04	1.21	0.21	0.18	2.28
P4xP5	1.98	1.21	0.61	3.04	1.26	0.23	0.18	2.47
P4xP6	2.05	1.68	0.82	3.32	0.71	0.19	0.27	2.61
P4xP7	2.68	1.18	0.44	3.04	0.84	0.19	0.22	2.21
P5xP6	3.08	1.36	0.44	3.92	1.19	0.19	0.16	2.38
P5xP7	3.02	1.54	0.51	3.88	1.30	0.21	0.16	2.80
P6xP7	2.09	1.31	0.63	2.95	1.09	0.19	0.17	2.57
Mean	**2.06**	**1.59**	**0.79**	**2.42**	**0.95**	**0.42**	**0.46**	**2.67**
SE(±)	**0.08**	**0.23**	**0.11**	**0.13**	**0.05**	**0.07**	**0.07**	**0.15**

Among the parental genotypes maximum kernel weight per plant was found in parent P1 (0.74g) followed by P2 (0.14 g) and the minimum kernel weight per plant was in parent P4, P6, and P7 (0.01 g). Among the F_1 progeny, the maximum kernel weight per plant was found in cross P2xP3 (0.35 g) and the minimum kernel weight per plant was in cross P1xP5 (0.00) followed by P1xP3**,** P1xP7, P2xP5, P4xP6, P4xP7, P5xP6, P5xP7 and P6xP7 (0.01 g).

In leaf tissues Table 18(b), among the parental genotypes the highest Na^+ content was recorded (2.27%) in P3 and the lowest (1.70%) in P4. Amongst the F_1 progeny, P5xP7 showed highest Na^+ content (3.08%) followed by P5xP6 (3.02%),while P1xP5 exhibited the lowest Na^+ content (1.54%) followed by P2xP4 (1.55%) and P1xP3 (1.57%). The maximum K^+ content was recorded in the parent P7 (1.18%) followed by P6 (1.16%) and the minimum K^+ content was recorded in P3 (0.72%). The cross P2xP7 showed the maximum K^+ content (6.13%) followed by cross P2xP7 (4.33%), while the minimum K^+ content was in P1xP3 (0.79%) followed by P3xP7 (0.81%).

In leaf tissues Table 18(b), among the parental genotypes the highest Ca^{++} content was recorded (2.94%) in P6 and lowest (1.51%) in P1. Amongst the F_1 progeny, P5xP6 showed highest Ca^{++} content (3.92%) followed by P5xP7 (3.88%), while P1xP3 exhibited the lowest Ca^{++}content (1.45%) followed by P2xP3 (1.50%). The maximum K^+/Na^+ ratio was recorded in the parent P7 (0.66) and the minimum K^+/Na^+ ratio was recorded in the parent P3 (0.37). The cross P2xP7 showed the maximum K^+/Na^+ ratio (6.13%) followed by cross P2xP7 (4.33%), while the minimum K^+/Na^+ ratiowas in P3xP7 (0.31).

In stem tissues Table 18(b), among the parental genotypes the highest Na^+ content was recorded (1.15%) in P4 and lowest (0.81%) in P5. Amongst the F_1 progeny, P5xP7 showed highest Na^+ content (1.30%) followed by P1xP3 (1.27%), while P2xP5

exhibited the lowest Na^+ content (0.34%) followed by P2xP7 (0.57%). The maximum K^+ content was recorded in the parent P5 (1.63%) followed by P2 (1.25%) while the minimum K^+ content was recorded in P7 (0.66%). The cross P1xP3 showed the maximum K^+ content (0.67%) followed by cross P1xP2 (0.60%), while the minimum K^+ content was in P2xP4 (0.15%) followed by P2xP5 (0.16%).

In stem tissues Table 18(b), among the parental genotypes the highest Ca^{++} content was recorded (4.37%) in P2 followed by P7 (4.12%) and the lowest in P4 (3.29%). Amongst the F1 progeny, P1xP2 showed highest Ca^{++} content (3.69%) followed by P5xP7 (2.80%), while P2xP4 exhibited the lowest Ca^{++}content (1.44%). The maximum K^+/Na^+ ratio was recorded in the parent P5 (2.04) and the minimum K^+/Na^+ ratio was recorded in the parent P7 (0.60). The cross P1xP2 showed the maximum K^+/Na^+ ratio (0.58%) followed by cross P1xP3 (0.53%), while the minimum K^+/Na^+ ratio was in P3xP6 (0.14).

4.2.1 Combining ability varience

Analysis of variance for combining ability is presented in Table 19(a) and Table 19(b). Results showed highly significant differences for gca and sca variance for all the traits except, shoot biomass which showed only significant sca variance. Such results indicated the importance of additive type of gene action involved in the inheritance of almost all the characters.

GCA variance were 2 to 3 times higher than SCA variance, as reflected by mean squares for all the traits in Table 19(a) and in Table 19(b) GCA variance were higher than SCA variance for Na^+ and Ca^{++} contents in leaf tissues only indicating the predominance of additive gene action for these traits. The estimated components of SCA variance (δ^2s) were higher than GCA variance (δ^2g) for all the traits in Table 19(a) and in Table 19(b).

Table 19. Analysis of variance for combining ability of biomass, pod yield and related traits in an F_1 diallel population of groundnut at 8dS/m imposed during flowering till harvest stages

(a) Biomass, pod yield and yield attributes

Item	df	Plant height	Branch number	Shoot biomass	Total biomass	Pod no./plant	Pod yield/ plant	Kernel wt./plant
gca	6	46.41**	1.17**	11.95**	13.71**	22.75**	0.15**	0.04**
sca	21	13.28**	0.67**	2.22*	2.31**	6.83**	0.06**	0.02**
Error	54	5.40	0.30	1.06	0.98	2.32	0.01	0.01
Variance components								
$\delta^2 g$		3.68	0.06	1.08	1.27	1.77	0.01	0.002
$\delta^2 D$		7.36	0.11	2.16	2.53	3.54	0.02	0.005
$\delta^2 s = \delta^2 H$		7.87	0.37	1.15	1.34	4.50	0.05	0.015
$\delta^2 g : \delta^2 H$		0.47	0.15	0.93	0.95	0.39	0.21	0.167

*,** Significant at 5% and 1% level, respectively

(b) Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues

Item	df	Leaf tissues				Stem tissues			
		Na^+(%)	K(%)	K^+/Na^+ ratio	$Ca2^+$	Na^+(%)	K(%)	K^+/Na^+ ratio	$Ca2^+$
gca	6	0.26**	0.52**	0.10**	0.95**	0.05**	0.07**	0.14**	0.09**
sca	21	0.17**	1.70**	0.37**	0.35**	0.07**	0.15**	0.16**	0.73**
Error	54	0.001	0.0003	0.0002	0.006	0.001	0.0004	0.001	0.001
Variance components									
$\delta^2 g$		0.01	-0.13	-0.03	0.07	-0.001	-0.01	-0.002	-0.07
$\delta^2 D$		0.02	-0.26	-0.06	0.13	-0.003	-0.02	-0.004	-0.14
$\delta^2 s = \delta^2 H$		0.17	1.70	0.37	0.34	0.07	0.15	0.16	0.73
$\delta^2 g : \delta^2 H$		0.06	-0.07	-0.08	0.20	-0.02	-0.06	-0.01	-0.10

*,** Significant at 5% and 1% level, respectively

gca= General combining ability $\delta^2 g$= gca variance $\delta^2 D$= Additive genetic variance
sca= Specific combining ability $\delta^2 s$= sca variance $\delta^2 H$= Dominance genetic variance

Additive and non-additive genetic components were concluded on the basis of δ^2g : δ^2s rather than GCA MS : SCA MS, because δ^2g and δ^2s represent the additive and non-additive genetic components respectively as suggested by Iftehkeruddaula (2003). Since, the ratio of additive genetic variance by dominance genetic variance is less than unity (one), all the traits are governed by dominance gene action. The dominance gene action is responsible for inheritance of these traits.

4.2.2 gca effects of parental genotypes for different genotypes

Estimates of gca effects at 8 dS/m salinity stress imposed during flowering till harvest stages are presented in Table 20(a) and Table 20(b). For plant height, the parents P4 and P1 were identified as good general combiner as the gca effects for these parents were positive and significant. Parent P3, P6 and P7 were considered as poor general combiner as they showed significant negative gca effects.Two parents P1 and P2 exhibited positively significant gca effects for branch number as they were thus the best general combiner for branch number while parent P7 was the worst. For shoot biomass the parent P1 followed by P4 was the best general combiner and the parent P6 followed by P7 was poor general combiner. Considering significant gca effects for shoot biomass the parents P1 and P4 were the best general combiner while parent P7 followed by P6 was poor general combiner due to significant negative GCA effect. For pod number per plant parents P2 and P1 were showed significant positive GCA effect thus they were the best general combiner for pod number. While, parents P7, P5 and P6 were poor general combiner due to significant negative GCA effect. For pod yield per plant, that parent P1 followed by P2 was the best general combiner as the gca effects showed significant positive (Plate 19). Parent P7, P6, P5 and P3 were poor general combiner as they were significant negative. As like pod yield per plant, for the kernel yield per plant, parent P1followed by P2 was the best general combiner as the gca effects showed significant positive. Parents P7, P6, P5 and P3 were poor general combiner as they were negatively significant.

Table 20. gca effect of biomass, pod yield and related traits in an F_1 population of groundnut at 8dS/m imposed during flowering till harvest stages

(a) Biomass, pod yield and yield attributes

Item	Plant height	Branch number	Shoot biomass	Total biomass	Pod no./plant	Pod yield/plant	Kernel wt./plant
P1	2.18**	0.38*	1.94**	1.99**	2.05**	0.27**	0.13**
P2	1.40	0.36*	0.58	0.56	2.36**	0.07**	0.04*
P3	-2.44**	-0.19	-0.27	-0.50	-0.90	-0.05*	0.01
P4	2.77**	0.14	0.70*	1.04**	0.18	-0.04	-0.05**
P5	0.59	0.14	-0.57	-0.55	-1.25**	-0.07**	-0.06**
P6	-1.97**	-0.21	-1.43**	-1.17**	-1.14*	-0.07**	-0.04*
P7	-2.53**	-0.62**	-0.97**	-1.37**	-1.30**	-0.11**	-0.04*

*,** Significant at 5% and 1% level, respectively

(b) Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues

Item	Leaf tissues				Stem tissues			
	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+}	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+}
P1	-0.29**	-0.35**	-0.07**	-0.50**	-0.02**	0.03**	0.01	0.03**
P2	-0.10**	0.33**	0.19**	-0.35**	-0.12**	0.09**	0.11**	0.16**
P3	0.10**	-0.05**	-0.09**	-0.06*	0.13**	-0.02**	-0.07**	0.004
P4	-0.09**	-0.16**	-0.01*	0.06*	0.002	-0.05**	-0.07**	-0.15**
P5	0.05**	0.03**	0.003	0.22**	-0.03**	0.13**	0.23**	-0.09**
P6	0.16**	-0.09**	-0.10**	0.39**	-0.02**	-0.09**	-0.08**	-0.01
P7	0.17**	0.29**	0.09**	0.23**	0.06**	-0.09**	-0.11**	0.06**

*,** Significant at 5% and 1% level, respectively

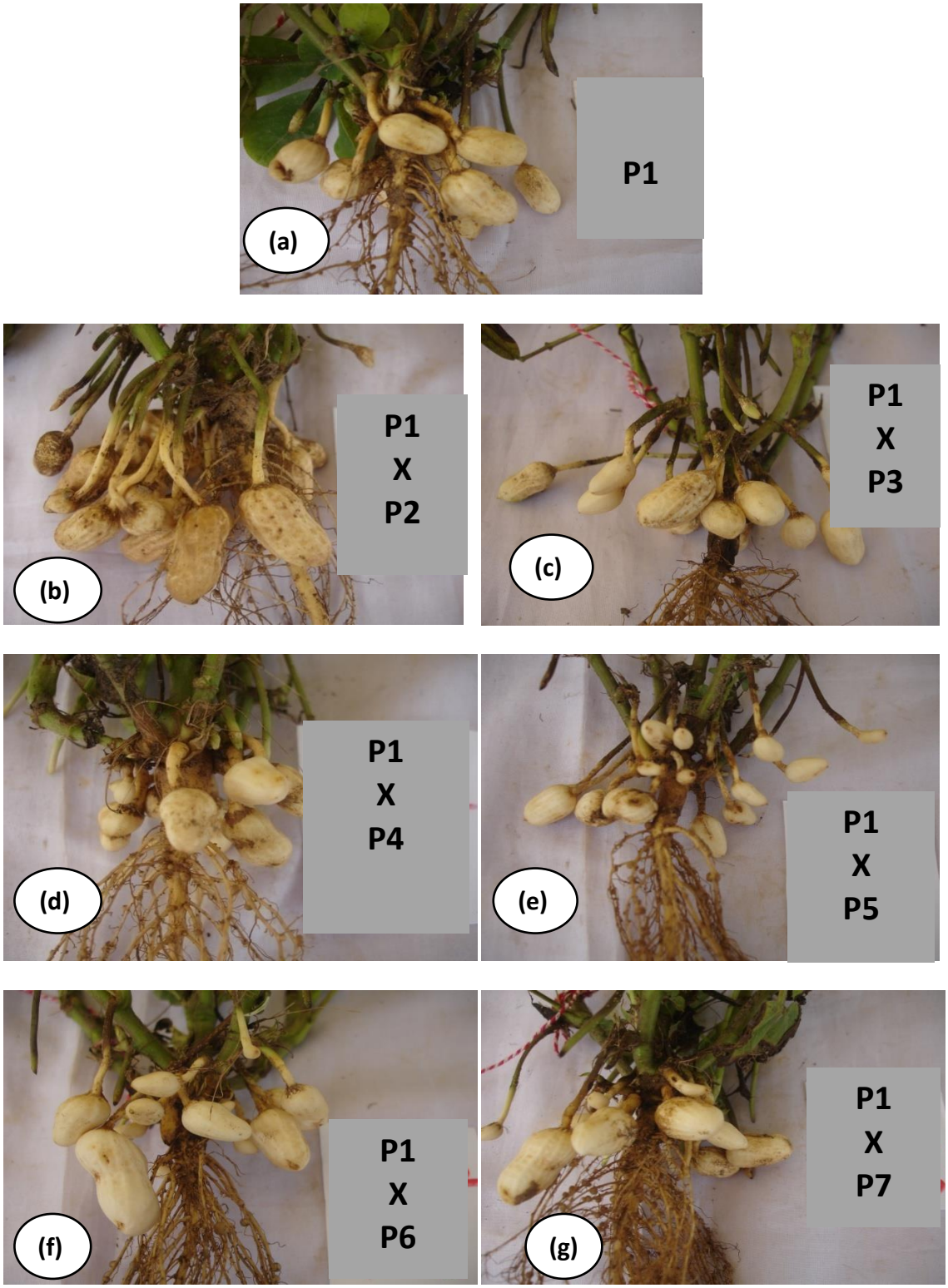


Plate 19. General combining ability of (a) Binachinabadam-6 (P1) with (b) Binachinabadam-5 (P2), (c) Binachinabadam-2(P3), (d) BARI Chinabadam-5(P4),(e) BARI Chinabadam-6 (P5), (f) Dhaka-1 (P6) and (g) ICGV-00309 (P7) for pod production at 8dS/m salinity imposed during flowering till harvest stages

In Table 20(b), for Na^+ contents (%) in leaf tissues parent P3 and P7 were positively significant and parent P1, P2 and P4 were the negatively significant general combiner. For K^+ contents (%) parent P2, P7, P3 and P5 were positively significant and parent P1, P3 and P4 were the negatively significant general combiner. In contrast, for Ca^{++} contents (%) P6, P7, P5 and P4 were positively significant and parent P1, P2 and P3 were the negatively significant general combiner. For K^+/Na^+ ratio parent P2, P7 and P5 were positively significant and rest of all were negatively significant general combiner. On the other hand, for Na^+ contents (%) in stem tissues parent P3 and P7 were positively significant and parent P1, P2, P5 and P6 were the negatively significant general combiner. For K^+ contents (%) parent P1, P2 and P5 were positively significant and parent P6, P7, P3 and P4 were the negatively significant general combiner. In contrast, for Ca^{++} contents (%) P1, P2 and P7 were positively significant and parent P6, P5 and P4 were the negatively significant general combiner. For K^+/Na^+ ratio parent P2 and P5 were positively significant and rest of all were negatively significant general combiner in stem tissues.

Considering all these physiological and yield traits parent P1, P2, P4, P5 and P6 could be considered as potential combiners which could be used in the hybridization in order to enrich the physiological efficiency of future groundnut varieties having salt tolerance with higher yield potential.

4.2.3 sca effect of hybrid genotypes

Estimates of sca effects at 8 dS/m salinity stress imposed during flowering till harvest stages are presented in Table 21(a) and Table 21(b). For plant height, the cross P2xP4 appeared as the best specific combiner among the crosses. That originated from crossing between parents having high and low gca effects.

Table 21. sca effect of biomass, pod yield and related traits in an F_1 population of groundnut at 8dS/m imposed during flowering till harvest stages

(a) Biomass, pod yield and yield attributes

Item	Plant height	Branch number	Shoot biomass	Total biomass	Pod no./plant	Pod yield/plant	Kernel wt./plant
P1xP2	-4.59*	-0.65	-1.54	-1.50	-3.82**	-0.36**	-0.13*
P1xP3	-0.01	-0.09	1.27	1.66	-1.89	-0.25**	-0.21**
P1xP4	-0.21	0.24	0.58	0.38	-0.63	-0.24**	-0.03
P1xP5	3.30	0.24	3.34**	3.43**	0.63	-0.26**	-0.15**
P1xP6	0.03	-0.07	0.44	0.02	1.19	-0.14	-0.13*
P1xP7	-1.42	0.01	-0.29	0.03	0.52	-0.23**	-0.17**
P2xP3	0.03	0.59	-0.58	-0.31	0.80	0.02	0.02
P2xP4	10.16**	0.43	2.78**	2.88**	9.06**	0.46**	0.23**
P2xP5	0.08	0.96*	-0.80	-0.80	-1.02	-0.07	-0.07
P2xP6	3.82	0.11	0.60	0.40	1.54	0.02	0.05
P2xP7	-1.55	0.19	0.50	1.03	-1.63	-0.06	0.04
P3xP4	-1.09	-0.35	-0.90	-0.92	-1.19	-0.04	-0.03
P3xP5	1.58	-0.19	0.05	0.13	0.24	0.04	-0.01
P3xP6	3.23	0.33	1.83*	1.86*	-1.20	0.12	0.02
P3xP7	-0.45	-0.59	-0.48	0.13	-0.20	0.01	0.13*
P4xP5	2.21	0.15	1.88*	1.51	0.17	-0.03	0.03
P4xP6	-0.72	-0.33	-0.40	-0.99	-0.78	-0.02	0.01
P4xP7	-3.92	-1.43**	0.24	0.21	-2.11	0.01	0.01
P5xP6	-4.88*	-1.83**	-1.43	-1.89*	-0.85	-0.01	0.02
P5xP7	-1.91	-0.59	-1.07	-0.91	-0.69	0.03	0.02
P6xP7	-1.51	-0.57	-0.08	-0.12	-0.63	0.03	-0.01

*,**Significant at 5% and 1% level, respectively

Table 21. Continued

(b) Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues

Item	Leaf tissues				Stem tissues			
	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+} (%)	Na^+(%)	K^+(%)	K^+/Na^+ ratio	Ca^{2+} (%)
P1xP2	0.48**	-0.50**	-0.41**	0.90**	0.25**	0.07**	0.01**	0.83**
P1xP3	-0.30**	-0.40**	-0.12**	-0.41**	0.22**	0.24**	0.14**	0.08**
P1xP4	-0.07**	0.44**	0.24**	-0.12	-0.16**	-0.12**	-0.01	-0.25**
P1xP5	-0.28**	0.16**	0.22**	-0.37**	-0.28**	-0.38**	-0.35**	-0.81**
P1xP6	-0.24**	-0.06**	0.04**	-0.10	-0.30**	-0.18**	-0.10**	-0.75**
P1xP7	-0.16**	0.47**	0.33**	-0.05	-0.08**	-0.18**	-0.15**	-0.74**
P2xP3	0.05**	-0.94**	-0.45**	-0.52**	-0.08**	-0.29**	-0.26**	-0.28**
P2xP4	-0.32**	1.32**	1.02**	-0.48**	-0.21**	-0.31**	-0.24**	-1.23**
P2xP5	0.02	-0.41**	-0.21**	0.25**	-0.46**	-0.48**	-0.32**	-0.89**
P2xP6	-0.23**	-0.54**	-0.19**	-0.58**	0.004	-0.16**	-0.16**	-0.06**
P2xP7	0.12**	3.92**	1.66**	0.39**	-0.32**	-0.12**	0.07*	-1.14**
P3xP4	0.30**	-0.28**	-0.22**	0.43**	0.01	-0.05**	-0.03	-0.16**
P3xP5	0.05**	2.76**	1.22**	0.01	-0.07**	-0.23**	-0.29**	-0.21**
P3xP6	0.24**	1.41**	0.52**	-0.01	0.18**	-0.14**	-0.16**	-0.87**
P3xP7	0.29**	-1.02**	-0.47**	0.45**	0.07**	-0.11**	-0.10**	-0.45**
P4xP5	-0.04*	-0.25**	-0.16**	0.34**	0.34**	-0.28**	-0.43**	0.04*
P4xP6	-0.07**	0.34**	0.15**	0.44**	-0.22**	-0.09**	-0.03	0.11**
P4xP7	0.55**	-0.54**	-0.42**	0.33**	-0.17**	-0.10**	-0.05	-0.36**
P5xP6	0.81**	-0.17*	-0.24**	0.88**	0.29**	-0.27**	-0.44**	-0.18**
P5xP7	0.74**	-0.37**	-0.36**	1.01**	0.32**	-0.26**	-0.42**	0.16**
P6xP7	-0.30**	-0.48**	-0.14**	-0.09	0.10**	-0.05**	-0.09**	-0.14**

*,** Significant at 5% and 1% level, respectively

In contrast, the cross P5xP6 had the worst sca effect followed by P1xP2. The parents of these crosses had non-significant positive versus highly significant negative and highly significant positive versus non-significant positive gca effects, respectively. For branch number, cross P2xP5 was the only the best specific combiner which was obtained from crossing between parents with non-significant positive versus non-significant positive gca. In contrast, the cross P5xP6 had the worst sca effect followed by P4xP7. These crosses were obtained from crossing between the parents having gca effects with non-significant positive versus non-significant negative and non-significant positive versus highly significant negative, respectively.

For shoot biomass, four cross combinations showed highly or just significant positive sca with P1xP5 being the best followed by P2xP4, P4xP5 and P3xP6. These crosses were obtained from crossing between parents with highly significant positive versus non-significant negative, non-significant positive versus just significant positive, non-significant negative versus significant positive and non-significant negative versus highly significant negative gca effects, respectively. On the other hand, cross P1xP2 had the worst sca effect followed by P5xP6, P5xP7, P3xP4, P2xP5, P2xP3, P3xP7, P1xP7 and P6xP7 having non-significant negative sca effects. These crosses were obtained from crossing between parents with highly significant positive versus non-significant positive, non-significant negative versus highly significant negative, non-significant negative versus highly significant negative, non-significant negative versus just significant positive, non-significant positive versus non-significant positive, non-significant positive versus non-significant negative, non-significant negative versus highly significant negative, highly significant positive versus highly significant negative and highly significant negative versus highly significant negative gca effects, respectively. For total biomass, two cross combinations showed highly significant

positive sca effect with P1xP5 being the best followed by P2xP4. These crosses were obtained from crossing between parents with highly significant positive versus non-significant negative and non-significant positive versus highly significant positive, gca effects respectively. In contrast, cross P5xP6 had the worst sca effect among the remaining crosses having non-significant negative sca. The cross P5xP6 were obtained from crossing between parents with highly significant negative versus highly significant negative gca effect, respectively.

For pod number per plant, the cross P2xP4 showed the best sca effect with highly significant positive value followed by P2xP6, P1xP6, P2xP3, P1xP5, P1xP7, P3xP5 and P4xP5 which are with non-significant positive sca effects. These crosses were obtained from crossing between parents with highly significant positive versus non-significant positive, highly significant positive versus significant negative, highly significant positive versus significant negative, highly significant positive versus non-significant negative, highly significant positive versus highly significant negative, highly significant positive versus highly significant negative, non-significant negative versus highly significant negative and non-significant positive versus highly significant negative gca, respectively. In contrast, cross P1xP2 had the worst sca effect among the remaining crosses having highly significant negative sca. The cross P1xP2 were obtained from crossing between parents with highly significant positive versus highly significant positive gca effect, respectively.

For pod yield per plant, the cross P2xP4 again showed the best sca with highly significant positive followed by P3xP6, P3xP5, P5xP7, P6xP7, P2xP3 and P2xP6 which are non-significant with positive sca.These crosses were obtained from crossing between parents with highly significant positive versus non-significant negative, significant negative versus highly significant negative, significant negative

versus highly significant negative, highly significant negative versus highly significant negative, highly significant negative versus highly significant negative, highly significant positive versus significant negative and highly significant positive versus highly significant negative gca, respectively. In contrast, cross P1xP2 had the worst sca effect followed by P1xP5, P1xP3, P1xP4 and P1xP7 crosses having highly significant negative sca. The crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant positive versus highly significant negative, highly significant positive versus significant negative, highly significant positive versus non-significant negative and highly significant positive versus highly significant negative gca effect, respectively. Specific combining ability of different cross combination for pod production under 8dS/m salinity imposed during flowering till harvest stages are shown in Plate 20.

For kernel yield per plant, the cross P2xP4 again showed the best sca with highly significant positive followed by P3xP7. These crosses were obtained from crossing between parents with highly significant positive versus highly significant negative and non-significant negative versus significant negative gca, respectively. In contrast, cross P1xP3 had the worst sca effect followed by P1xP7, P1xP5, P1xP6 and P1xP2 crosses having highly significant negative sca.The crosses were obtained from crossing between parents with highly significant positive versus non-significant negative, highly significant positive versus significant negative, highly significant positive versus highly significant negative, highly significant positive versus significant negative and highly significant positive versus significant positive gcaeffect, respectively.

Plate 20. Specific combining ability of different cross combination for pod production at 8dS/m salinity imposed during flowering till harvest stages

In table 21(b), for Na^+ content in leaf tissues the cross P5xP6 appeared as the best specific combiner with highly significant positive followed by P5xP7, P4xP7, P1xP2, P3xP4, P3xP7, P3xP6 and P2xP7.These crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant positive versus highly significant positive, highly significant negative versus highly significant positive, highly significant negative versus highly significant negative, highly significant positive versus highly significant negative, highly significant positive versus highly significant positive, highly significant positive versus highly significant positive andhighly significant negative versus highly significant positive gcarespectively.In contrast, cross P2xP4 had the worst sca effect followed by P1xP3, P6xP7, P1xP5, P1xP6, P2xP6 and P1xP7 crosses having highly significant negative sca.The crosses were obtained from crossing between parents with highly significant negative versus highly significant negative,highly significant negative versus highly significant positive, highly significant positive versus highly significant positive, highly significant negative versus highly significant positive, highly significant negative versus highly significant positivehighly significant negative versus highly significant positive and highly significant negative versus highly significant positive gca effect, respectively.

For K^+ content in leaf tissues, the cross P2xP7 appeared as the best specific combiner with highly significant positive followed by P3xP5, P3xP6, P2xP4, P1xP4 and P1xP5. These crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant negative versus highly significant positive, highly significant negative versus highly significant negative, highly significant positive versus highly significant negative, highly significant negative versus highly significant negative and highly significant negative versus

highly significant positive gca, respectively. In contrast, cross P3xP7 had the worst sca effect followed by P2xP3, P4xP7, P1xP2, P6xP7 P2xP5, P1xP3 and P5xP7crosses having highly significant negative sca. The crosses were obtained from crossing between parents with highly significant negative versus highly significant positive, highly significant positive versus highly significant negative, highly significant negative versus highly significant positive, highly significant negative versus highly significant positive, highly significant negative versus highly significant positive,highly significant positive versus highly significant positive ,highly significant negative versus highly significant negative and highly significant positive versus highly significant positive gca effect, respectively.

For K^+/Na^+ ratio in leaf tissues, the cross P2xP7 appeared as the best specific combiner with highly significant positive followed by P3xP5, P2xP4, P3xP6, P1xP7,P1xP4 and P1xP5. These crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant negative versus non-significant positive, highly significant positive versus significant negative, highly significant negative versus highly significant negative, highly significant negative versus highly significant positive,highly significant negative versus significant negative and highly significant negative versus significant positivegcarespectively.In contrast, cross P3xP7 had the worst sca effect followed by P2xP3, P4xP7, P1xP2, P5xP7, P5xP6, P2xP5 and P2xP6 crosses having highly significant negative sca.The crosses were obtained from crossing between parents with highly significant negative versus highly significant positive, highly significant positive versus highly significant negative, significant negative versus highly significant positive, highly significant negative versus highly significant positive, non-significant positive versus highly significant positive, non-significant positive

versus highly significant positive, highly significant positive versus non-significant positive and highly significant positive versus highly significant negative gca effect, respectively.

For Ca^{+} content in leaf tissues, the cross P5xP7 appeared as the best specific combiner with highly significant positive followed by P1xP2, P5xP6, P3xP7, P4xP6, P3xP4 and P2xP7. These crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant negative versus highly significant negative, highly significant positive versus highly significant positive, significant negative versus highly significant positive, significant positive versus highly significant positive, significant negative versussignificant positive and highly significant negative versus highly significant positive gca, respectively. In contrast, cross P2xP6 had the worst sca effect followed by P2xP3, P2xP4, P1xP3, P1xP5 and P1xP6 crosses having highly significant negative sca. The crosses were obtained from crossing between parents with highly significant negative versus highly significant positive, highly significant negative versus significant negative, highly significant negative versus significant positive, highly significant negative versus highly significant negative, highly significant negative versus highly significant positive and highly significant negative versus highly significant positive gca effect, respectively.

In table 21(b), for Na^{+} content in stem tissues the cross P4xP5 appeared as the best specific combiner with highly significant positive followed by P5xP7, P5xP6, P1xP2, P1xP3, P3xP6 and P3xP7. These crosses were obtained from crossing between parents with non-significant positive versus highly significant negative, highly significant negative versus highly significant positive, highly significant negative versus highly significant negative, highly significant negative versus highly

significant negative, highly significant negative versus highly significant positive, highly significant positive versus highly significant negative andhighly significant positive versus highly significant positive gca respectively. In contrast, cross P2xP5 had the lowest sca effect followed by P2xP7, P1xP6, P1xP5, P4xP6, P4xP7and P1xP4 crosses having highly significant negative sca.The crosses were obtained from crossing between parents with highly significant negative versus highly significant negative, highly significant negative versus highly significant positive, highly significant negative versus highly significant negative, highly significant negative versus highly significant negative,non-significant positive versus highly significant negative, non-significant positive versus highly significant negative and highly significant negative versus non-significant positive gca effect, respectively.

For K^+ content in stem tissues, the cross P1xP3 appeared as the best specific combiner with highly significant positive followed by P1xP2.These crosses were obtained from crossing between parents with highly significant positive versus highly significant negative, highly significant positive versus highly significant positive gcarespectively.In contrast, cross P2xP5 had the worst sca effect among the remaining crosses having highly significant negative sca.The cross was obtained from crossing between parents with highly significant positive versus highly significant positive gca effect,respectively.

For K^+/Na^+ ratio in stem tissues, the cross P1xP3 appeared as the best specific combiner with highly significant positive followed by P2xP7 and P1xP2. These crosses were obtained from crossing between parents with non-significant positive versus highly significant negative, highly significant positive versus highly significant negative and non-significant positive versus highly significant positive gca, respectively. In contrast, cross P5xP6 had the worst sca effect among the remaining

crosses having highly significant negative sca. The cross was obtained from crossing between parents with highly significant positive versus highly significant negative gca effect, respectively.

For Ca^{+} content in stem tissues, the cross P1xP2 appeared as the best specific combiner with highly significant positive followed by P5xP7, P4xP6 and P1xP3. These crosses were obtained from crossing between parents with highly significant positive versus highly significant positive, highly significant negative versus highly significant positive, highly significant negative versus non-significant positiveand highly significant positive versus non-significant positive gcarespectively. In contrast, cross P2xP4 had the worst sca effect among the remaining crosses having highly significant negative sca. The cross was obtained from crossing between parents with highly significant positive versus highly significant negative gca effect, respectively.

4.2.4 Variance-covariance (Vr-Wr) analysis

Hayman (1958) showed that in the absence of non allelic interaction and with independent of the genes among the parents, the linear regression of Wr on Vr would have a unit slope and the Wr, Vr, array point would be lie along the lines. The array points would be within an area delimited by parabola limit, $Wr^2 = V_0 l_0$ x Vr where $V_0 I_0$ is the variance of parental means. Further, magnitude and sign of intercept cut off by the regression line showed the level of dominance.

Variance-covariance (Vr-Wr) analysis shows that salinity tolerance based on biomass, yield and yield attributes followed the simple additive-dominance genetic model. Since the regression coefficient (b) was close to unity and significantly different from zero and unity (Appendix-1V). The non-significant t^2 value satisfied the uniformity of covariance and variance (Wr,Vr) and thus supported the validation of assumptions made by Hayman (1954a) for the character.

Plant height:

From the Vr-Wr analysis (Fig.17) showed the regression line intersected the Wr axis above the origin indicating partial dominance of genes controlling this trait. The slope of the regression line did not differ significantly from zero but significantly differ from unity suggesting inadequate additive dominance genetic model. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest the origin. In contrast, those with most recessives fall furthest from the origin. The parent P7 was the nearest whilst P4 the farthest from the origin. This means higher proportion of dominant and recessive genes was involved for the expression of plant height in P7 and P4, respectively. Moreover, none of the points coincide the limiting parabola line at the upper or lower ends of the regression line suggesting no single parent possessed completely dominant or recessive genes.

Branch Number:

From the Vr-Wr analysis (Fig. 18) showed the regression line intersected the Wr axis above the origin indicating partial dominance of genes controlling this trait. The slope of the regression line did not differ significantly from zero but significantly differ from unity suggesting inadequate additive dominance genetic model. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessives fall furthest from the origin. The parent P1 was the nearest whilst P5 the farthest from the origin. This means higher proportion of dominant and recessive genes was involved for the expression of branch number in P1 and P5, respectively. Moreover, none of the points coincide the limiting parabola line at the upper or lowerends of the regression line suggesting no single parent possessed completely dominant or recessive genes.

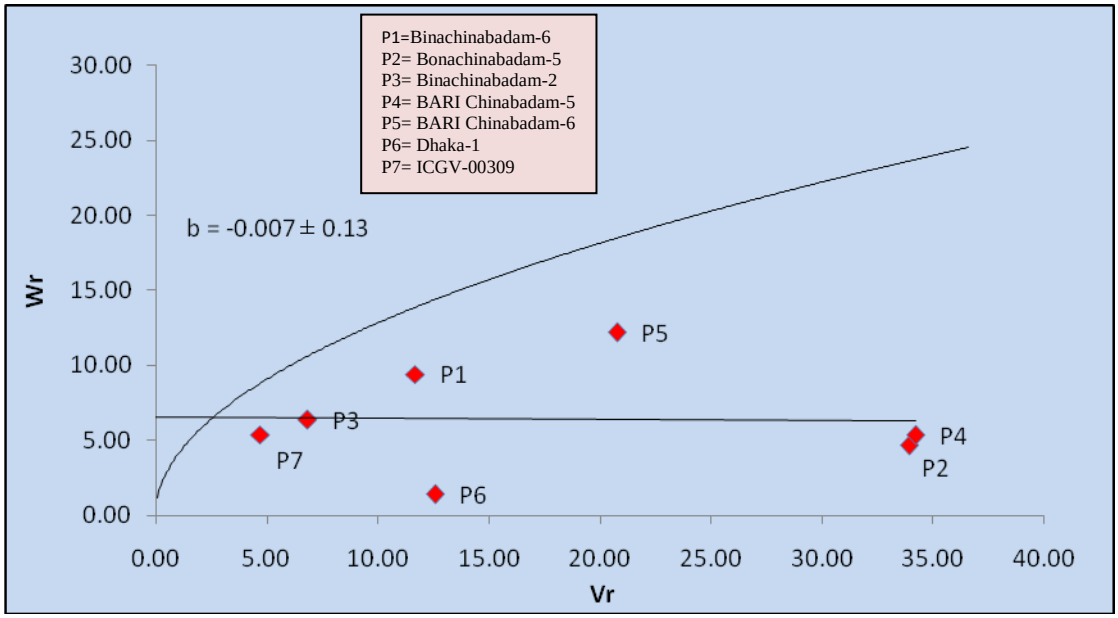


Fig. 17. Wr-Vr graph for plant height of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

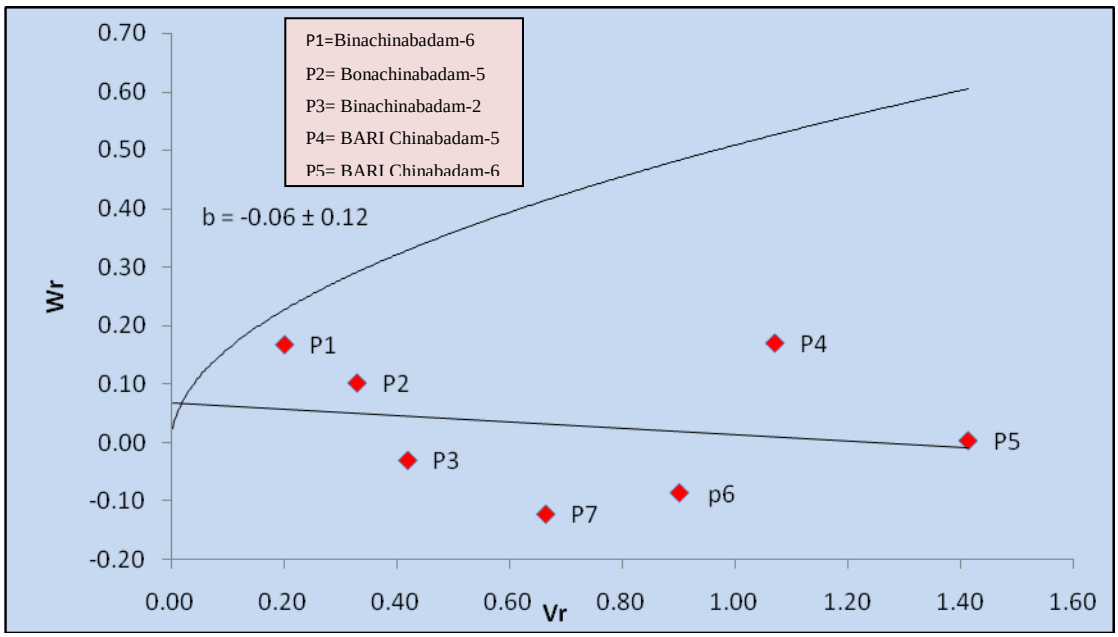


Fig.18. Wr-Vr graph for branch number of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

Shoot biomass:

From the Vr-Wr analysis (Fig. 19) showed the regression line intersected the Wr axisabove the origin indicating partial dominance of genes controlling this trait. The slope of the regression line did not differ significantly from zero but significantly differ from unity suggesting inadequate additive dominance genetic model. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessives fall furthest from the origin. The parent P7 was the nearest whilst P5 the farthest from the origin. This means higher proportion of dominant and recessive genes was involved for the expression of shoot biomass in P7 and P5, respectively. Moreover, none of the points coincided the limiting parabola line at the upper or lower ends of the regression line suggesting no single parent possessed completely dominant or recessive genes.

Total biomass:

From the Vr-Wr analysis (Fig. 20) showed the regression line intersected the Wr axis above the origin indicating partial dominance of genes controlling this trait. The slope of the regression line did not differ significantly from zero and unity suggesting adequate additive dominance genetic model. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessives fall furthest from the origin. The parent P1, P6 and P3 were the nearest whilst P5 the farthest from the origin. This means higher proportion of dominant and recessive genes was involved for the expression of total biomass in P1 and P5, respectively. Moreover, none of the points coincided the limiting parabola line at the upper or lower ends of the regression line suggesting no single parent possessed completely dominant or recessive genes.

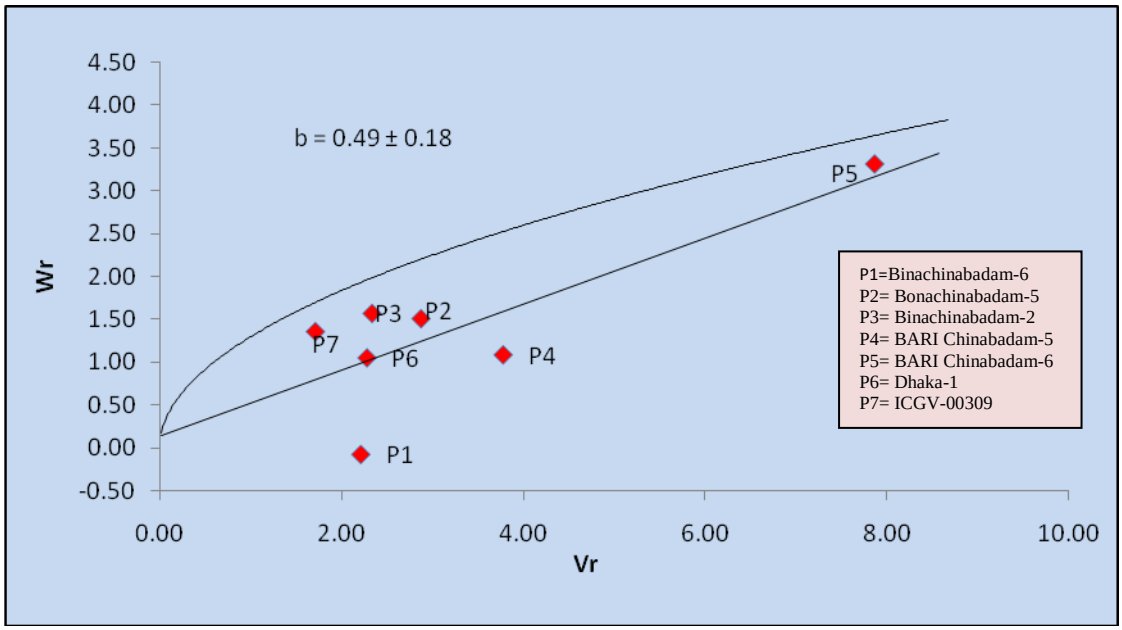


Fig. 19.Wr-Vr graph for shoot biomass of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

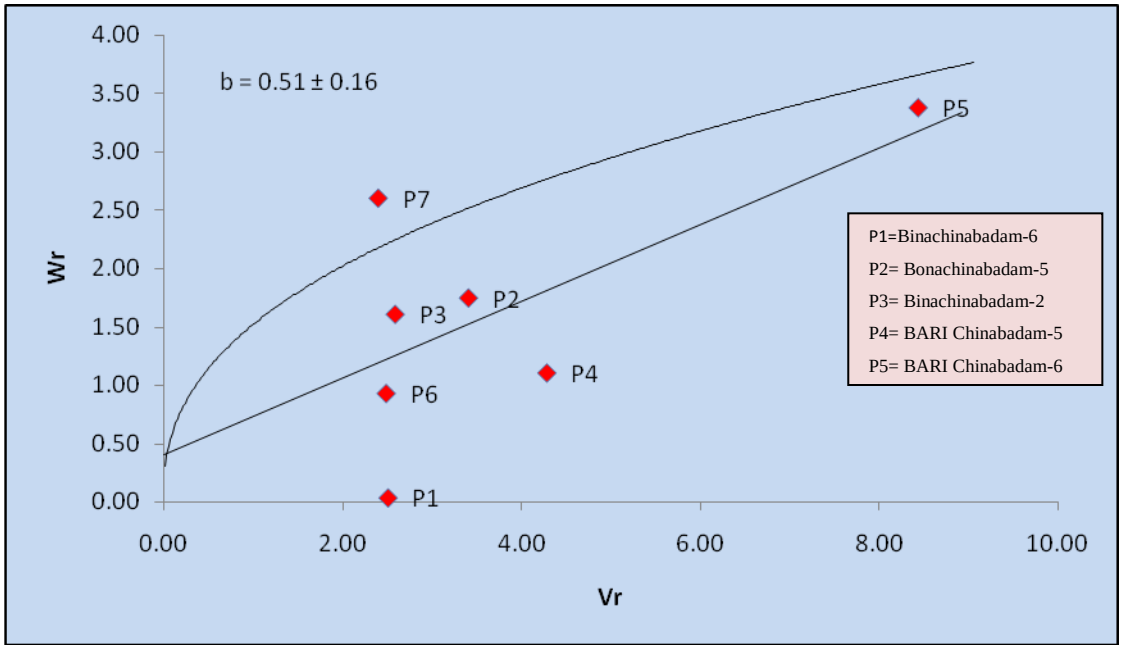


Fig. 20. Wr-Vr graph for total biomass of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

Pod number:

From the Vr-Wr analysis (Fig. 21) showed the regression line intersected the Wr axis above the origin indicating partial dominance of genes controlling this trait. The slope of the regression line did not differ significantly from zero and unity suggesting adequate additive dominance genetic model. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessives fall furthest from the origin. The parent P5, P7 and P3 were the nearest whilst P4 the farthest from the origin. This means theparents P5, P7 and P3 contained major proportion of dominant genes while recessive genes were involved for the expression of pod number in P4. No parent appeared to contain completely dominant or recessive genes, as there was no point touching the limiting parabola either at the lower or upper end.

Pod yield:

From the Vr-Wr analysis (Fig. 22) showed the regression line intersected the Wr axis just below the origin indicating over dominance of genes controlling this trait. The slope of the regression line did not differ significantly from unity suggesting adequate additive dominance genetic model and absence of non-allelic interaction. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessive fall furthest from the origin. The parent P5, P3, P7 and P6 were the nearest whilst P1 the farthest from the origin. This means theparents P5, P3, P7 and P6 contained major proportion of dominant genes while recessive genes were involved for the expression of pod yield inP1. Parent P5 and P1 appeared to contain completely dominant and recessive genes as their points were touching the limiting parabola at the lower and upper end, respectively.

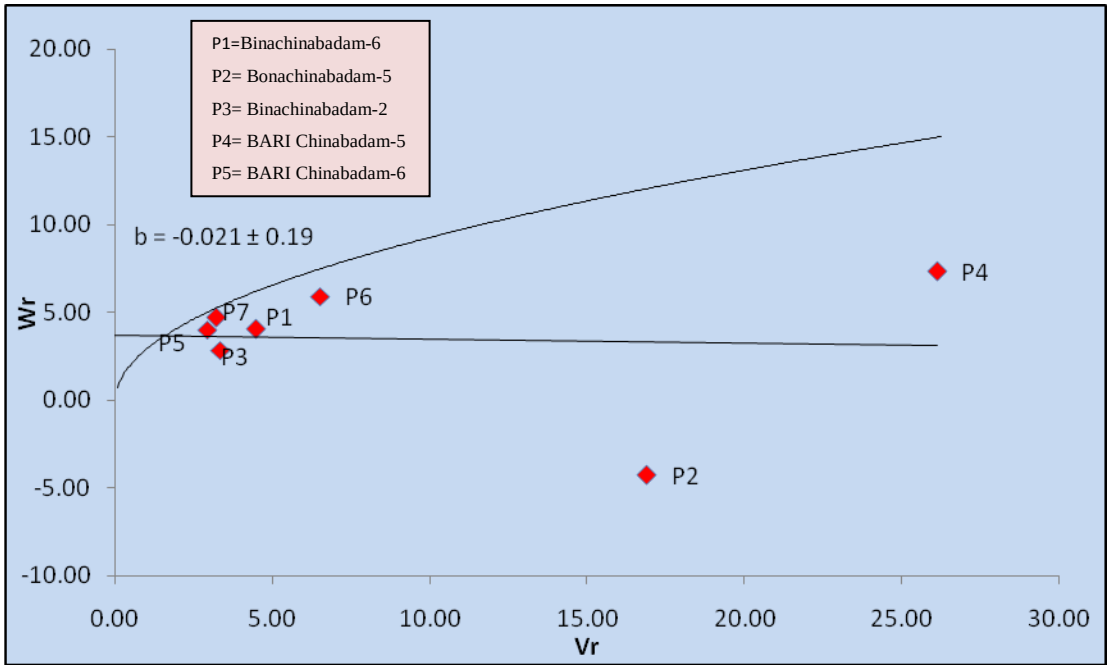


Fig. 21. Wr-Vr graph for pod number of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

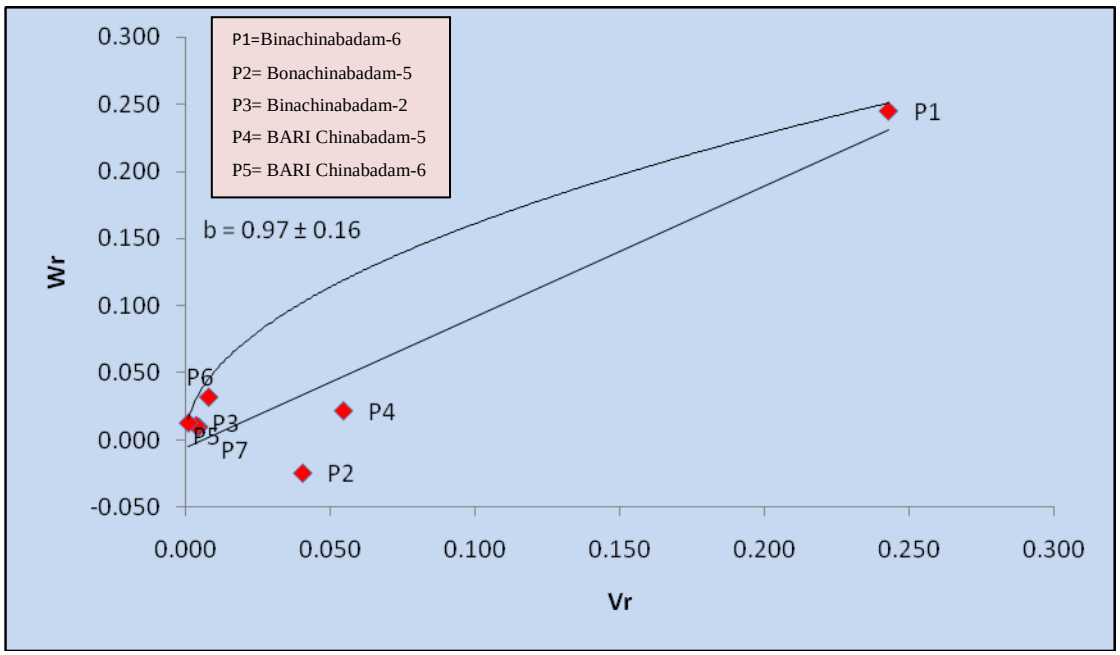


Fig.22.Wr-Vr graph for pod yield of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

Kernel weight:

From the Vr-Wr analysis (Fig. 23) showed the regression line intersected the Wr axis just below the origin indicating over dominance of genes controlling this trait. The slope of the regression line did not differ significantly from unity suggesting adequate additive dominance genetic model and absence of non-allelic interaction. The distribution of array points in the graph showed the dominance order of the parents. Parent(s) with most dominant alleles have their points nearest to the origin. In contrast, those with most recessive fall furthest from the origin. The parent P5, P5, P7 and P4 were the nearest whilst P1 the farthest from the origin. This means the parents P5, P5, P7 and P4 contained major proportion of dominant genes while recessive genes were involved for the expression of kernel in P1. Parent P4 and P1 appeared to contain completely dominant and recessive genes as their points were touching the limiting parabola at the lower and upper end, respectively.

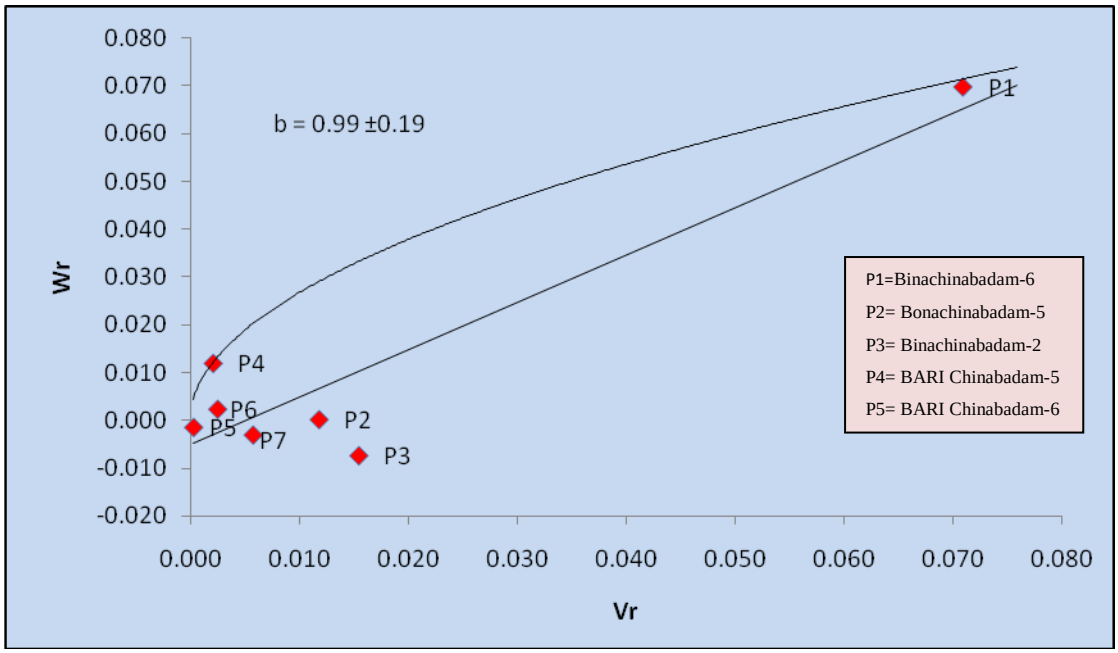


Fig. 23. Wr-Vr graph for kernel weight of a 7x7 diallel population of groundnut at 8 dS/m salinity stress imposed during flowering till harvest stages

4.2.5 Components of variations and their ratios

Of the components; D, H_1, H_2 and F are genetic while E is the environmental estimates (Mather and Jinks, 1971). D measures additive effects, H_1 and H_2 measures for the dominance effects while H1 is the same coefficient as D and that $(H1/D)^{½}$ measures the degree of dominance. The ratio $H_2/4H_1$ measures the mean product uv over all loci and in that 'u' and 'v' are frequencies of positive and negative alleles. The sign and magnitude of F reveals the relative frequencies of dominant to recessive alleles in the parent. F is positive when there are excess dominant alleles in the parent and in contrast it becomes negative when excess in recessive alleles exists in the parent. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ determines the type of allele which is most frequent. This ratio measures total number of dominant to recessive alleles in all parents. The estimates of components of variations and ratios are presented in Table 22. The components of variation are interpreted character wise as follows:

Plant height:

The non-significant and significant values of D and H_1, respectively, indicated preponderance of dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 2.12, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$ was 0.18, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 1.38, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by

Table 22. Estimates of genetic and environmental components of variance and ratio in a 7x7 F_1 diallel population for pod yield and related traits at 8dS/m imposed during flowering till harvest stages

Parameter	Plant height	Branch number	Shoot biomass	Total biomass	Pod no./plant	Podyield/ plant	Kernel wt./plant
D	9.84±9.67	-0.04±0.36	0.23±1.08	0.16±1.04	6.27±7.49	0.25^{**}±0.02	0.07^{**}±0.002
F	6.65±23.19	0.30±0.86	1.46±2.59	1.53±1.61	2.35±17.98	0.01±0.06	0.004±0.004
H_1	44.06^{*}±22.27	2.20^{*}±0.87	5.32^{*}±2.60	6.42^{**}±1.61	24.45±18.04	0.27^{**}±0.06	0.08^{**}±0.004
H_2	32.50±20.50	1.46^{*}±0.73	4.58^{*}±2.29	5.34^{**}±1.51	19.63±15.90	0.15^{**}±0.05	0.04^{**}±0.003
h^2	400.95^{**}±14.58	26.94^{**}±0.54	24.33^{**}±1.63	31.21^{**}±1.28	15.34^{*}±7.31	0.17^{**}±0.04	0.04^{**}±0.002
$(H_1/D)^{½}$	2.12	7.63	4.78	6.30	1.97	1.03	1.10
$H_2/4H_1$	0.18	0.17	0.22	0.21	0.20	0.14	0.13
$\frac{(4DH_1)^{½} + F}{(4DH_1)^{½} - F}$	1.38	3.11	4.79	7.10	1.21	1.03	1.04
h^2/H_2	12.34	18.40	5.32	5.84	0.78	1.17	0.81
$\mathbf{h^2_n}$	0.33	0.23	0.10	0.06	0.38	0.80	0.78
$\mathbf{h^2_b}$	0.70	0.66	0.38	0.44	0.80	0.97	0.94

*,**Significant at 5% and 1% level, respectively

approximately eleven to twelve groups of dominant genes as the ratio of h^2/H_2 was 12.34. Heritability estimates, narrow and broad sense, were 0.33 and 0.70, respectively.

Branch Number:

The non-significant value of D and the significant values of H_1, H_2 and h^2 indicated the control of dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 7.63, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$was 0.17, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 3.11, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately seventeen to eighteen groups of dominant genes as the ratio of h^2/H_2 was 18.40. Heritability estimates, narrow and broad sense, were 0.23 and 0.66, respectively.

Shoot biomass:

The non-significant value of D and significant values of H_1, H_2 and h^2 indicated preponderance of dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 1.10, indicating over-dominance effect of the genes

involved. The value $H_2/4H_1$was 0.13, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 1.00, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately four to five groups of dominant genes as the ratio of h^2/H_2 was 5.32. Heritability estimates, narrow and broad sense, were 0.10 and 0.38, respectively.

Total biomass:

The non-significant value of D and significant values of H_1, H2 and h^2 indicated preponderance of dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 6.30, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$ was 0.21, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 7.10, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately five to six groups of dominant genes as the ratio of h^2/H_2 was 5.84. Heritability estimates, narrow and broad sense, were 0.06 and 0.44, respectively.

Pod number:

The non-significant value of D and significant values of h^2 respectively, indicated preponderance of dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant

alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 1.97, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$was 0.20, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 1.21, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately one to two groups of dominant genes as the ratio of h^2/H_2 was 0.74. Heritability estimates, narrow and broad sense, were 0.38 and 0.80, respectively.

Pod yield:

The significant values of D, H_1, H_2 and of h^2 indicated the control of both additive and dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 1.03, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$was 0.14, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 1.03, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately one to two groups of dominant genes as the ratio of h^2/H_2 was 1.17. Heritability estimates, narrow and broad sense, were 0.80 and 0.97, respectively.

kernel weight:

The significant values of D, H_1, H_2 and of h^2 indicated the control of both additive and dominant gene actions in the inheritance of this character under salinity stress (Table 22). The positive value of F indicated more number of dominant alleles in the parents than recessive alleles, which was also supported by the estimates $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$. The mean degree of dominance averaged over all loci, estimated by $(H_1/D)^{½}$, was 1.10, indicating over-dominance effect of the genes involved. The value $H_2/4H_1$was 0.13, less than the theoretical value 0.25, indicating the positive and negative alleles were asymmetrically distributed in the parents. The ratio $[(4DH_1)^{½} + F]/[(4DH_1)^{½} - F]$ measures the total number of dominant to recessive alleles in all the parents. The ratio was 1.04, greater than one and thus indicated that the parents mostly carry dominant genes. This trait appeared to be controlled by approximately one to two groups of dominant genes as the ratio of h^2/H_2 was 0.81. Heritability estimates, narrow and broad sense, were 0.78 and 0.94, respectively.

4.3 Experiment 3. Genetic variability of yield and yield attributing characters of F_2 7x7 diallel population of groundnutin non-saline field condition

The experiment was conducted with parents and F_2 7x7 diallel population of groundnut in the non-saline field condition during August to December 2013 at SAU campus. In this experiment, the analysis of variance (ANOVA) presented in Table 23. Analysis of variance (Table23.) shows highly significant ($P< 0.01$) differences due to genotypes for all the characters viz., plant height, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage (%), while branch number showed only significant ($P< 0.05$) differences. This result indicated the presence of wide range of variation among the genotypes for all characters in non-saline field condition. The mean performance and the variations as estimated by DMRT are presented in Table 24. The Genetic parameters of yield and yield contributing characters of F_2 7x7diallel populations of groundnut in non saline field condition are presented in Table 25. The pictorial view of experiment in non-saline field condition is presented in Plate 21 and Plate 22.

Plant height:

The analysis of variance for plant height indicated highly significant variation among the genotypes (Table 23). P4 was found to be the tallest genotype (97.10 cm) and was significantly different from all other genotypes. On the other hand P5 was the shortest genotype (65.26 cm). Plant height showed a wide range of variation from 65.26cm to 97.10 cm with mean value of 81.45 cm (Table 24). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (10.93) and genotypic (10.17) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. Very high heritability (86.60) coupled with high genetic advance in percentage of mean (19.50) was observed for plant height

Table 23. Analysis of variance of yield and yield attributing characters in F_2 7x7 diallel population of groundnut in non-saline field condition

SV	df	Plant height	Branch number	Shoot biomass	Pod no./plant	100 pod wt.	Podyield /plant	Kernel wt./plant	Shelling %
Replication	2	852.58	1.14	51.94	17.27	14.47	38.46	2.46	41.94
Genotypes	27	216.67**	1.18*	353.65**	135.76**	329.79**	52.68**	26.31**	106.03**
Error	54	10.63	0.63	15.78	8.55	30.08	8.22	1.22	25.42

*,**Significant at 5% and 1% level, respectively

Table 24. Mean performance of yield and yield attributing characters in F_2 7x7 diallel population of groundnut in non-saline field condition

Code	Genotypes /varieties	Plant height (cm)	Branch number	Shoot biomass (g)	Pod no./plant
1	P1	82.36 hi	6.47 a-e	61.83 c	45.19 b
2	P2	84.83 f	6.28 a-e	46.58 ij	38.72 d-g
3	P3	68.15 n	7.35 a-c	41.50 lm	31.60 hi
4	P4	97.09 a	7.74 a	57.51d	25.96 jk
5	P5	65.26 o	7.00 a-d	50.38 gh	29.91i
6	P6	80.18 j	6.33 a-e	46.59 ij	39.15 d-g
7	P7	84.38 fg	5.65 de	44.05 j-l	32.36 hi
8	P1xP2	83.11 gh	7.61 ab	53.76 ef	45.25 b
9	P1xP3	74.29 l	6.76 a-d	50.02 gh	39.90 c-f
10	P1xP4	95.38 b	5.90 c-e	61.46 c	35.26 gh
11	P1xP5	88.68 de	6.61 a-e	52.52 e-g	30.68 i
12	P1xP6	84.65 f	6.02 c-e	35.07 n	45.21b
13	P1xP7	78.81 j	6.67 a-e	48.62 hi	36.47 fg
14	P2xP3	89.62 cd	6.03 c-e	46.11 ij	39.13 d-g
15	P2xP4	96.56 ab	5.90 c-e	52.22 fg	24.16 k
16	P2xP5	74.12 l	5.90 c-e	35.85 n	29.71 ij
17	P2xP6	82.66 hi	5.87 c-e	34.17 n	37.47 e-g
18	P2xP7	90.75 c	5.83 c-e	30.93 o	37.51e-g
19	P3xP4	81.56 i	6.17 b-e	39.14 m	28.99 ij
20	P3xP5	65.67 o	5.63 de	42.17 kl	29.20 ij
21	P3xP6	72.47 m	5.11 e	42.84 kl	41.56 b-d
22	P3xP7	76.90 k	5.93 c-e	44.11 j-l	32.58 hi
23	P4xP5	75.31 l	6.22 a-e	44.74 jk	29.96 i
24	P4xP6	85.70 f	6.70 a-e	77.33 a	50.62 a
25	P4xP7	87.71 e	6.57 a-e	68.67 b	38.90 d-g
26	P5xP6	75.50 l	5.81 c-e	55.33 de	43.14 bc
27	P5xP7	80.02 j	5.83 c-e	61.00 c	44.55 b
28	P6xP7	78.88 j	5.50 de	60.67 c	41.51b-e
Range		**65.26-97.10**	**5.11-7.74**	**30.93-77.33**	**24.16-50.62**
Average		**81.45**	**6.26**	**49.47**	**36.59**
SE(±)		**0.64**	**0.65**	**1.36**	**1.74**

Same letter in a column do not differ significantly at P≤0.05 as per DMRT

Table 24. (Continued)

Code	Genotypes /varieties	100 pod wt.	Pod yield /plant	Kernel wt./plant	Shelling %
1	P1	65.75 e-h	29.63 b-f	15.73 d-h	53.32 de
2	P2	62.63 gh	24.14 g-i	14.31h-j	60.08 b-d
3	P3	81.70 b-d	25.93 e-h	14.86 f-i	57.98 b-e
4	P4	72.32 d-g	18.66 jk	7.580 m	40.72 f
5	P5	89.99 b	27.04 d-g	15.61d-h	57.83 b-e
6	P6	68.14 e-h	26.60 e-g	12.65 jk	48.21ef
7	P7	67.14 e-h	21.60 h-j	11.45 kl	53.32 de
8	P1xP2	68.26 e-h	26.29 e-h	17.35 cd	66.65 ab
9	P1xP3	67.90 e-h	27.06 d-g	16.52 c-g	61.15 b-d
10	P1xP4	67.65 e-h	23.72 g-i	13.44 ij	56.82 b-e
11	P1xP5	87.61 b	26.80 e-g	14.66 g-j	54.71c-e
12	P1xP6	59.16 h	26.62 e-g	15.44 d-h	58.14 b-d
13	P1xP7	81.92 b-d	29.89 b-e	18.29 bc	61.11b-d
14	P2xP3	73.58 c-f	27.44 d-g	19.73 b	72.14 a
15	P2xP4	67.36 e-h	16.25 k	9.93 l	61.29 b-d
16	P2xP5	104.20 a	34.81a	15.09 e-i	57.14 b-e
17	P2xP6	67.19 e-h	25.15 f-i	14.59 g-j	58.65 b-d
18	P2xP7	62.25 gh	23.26 g-j	14.04 h-j	60.44 b-d
19	P3xP4	83.15 bc	24.03 g-i	12.71 jk	53.30 de
20	P3xP5	87.39 b	25.57 e-i	14.97 f-i	59.15 b-d
21	P3xP6	64.51 f-h	26.86 e-g	16.90 c-f	62.83 b-d
22	P3xP7	87.27 b	29.05 c-f	17.20 c-e	59.74 b-d
23	P4xP5	69.08 e-h	21.12 ij	13.87 h-j	66.33 ab
24	P4xP6	66.76 e-h	33.80 ab	21.79 a	64.30 a-c
25	P4xP7	75.73 c-e	29.43 b-f	16.62 c-g	59.47 b-d
26	P5xP6	73.63 c-f	31.72 a-d	17.20 c-e	54.18 de
27	P5xP7	72.15 d-g	32.16 a-c	19.99 ab	62.25 b-d
28	P6xP7	67.26 e-h	27.82 c-g	15.86 d-h	57.12 b-e
Range		**59.15-104.20**	**16.25-34.81**	**7.58-21.79**	**40.72-72.14**
Average		**73.63**	**26.52**	**15.30**	**58.51**
SE(±)		**4.47**	**2.34**	**0.90**	**4.11**

Same letter in a column do not differ significantly at P≤0.05 as per DMRT

Table 25. Genetic parameters of yield and yield contributing characters of F_2 populations of groundnut in non saline field condition

Characters	Genotypic variance	Phenotypic variance	Genotypic coefficient of variance (GCV%)	Phenotypic coefficient of variance (PCV%)	Heritability h^2b (%)	GA	GA in % of mean
Plant height	68.68	79.31	10.17	10.93	86.60	15.89	19.50
Branch number	0.18	0.82	6.84	14.41	22.51	0.42	6.68
Shoot biomass	112.62	128.40	21.45	22.91	87.71	22.47	41.39
Pod no./plant	42.40	50.95	17.79	19.51	83.22	12.24	33.44
100 pod wt	99.90	129.98	13.57	15.48	76.86	18.05	24.52
Pod yield/plant	14.82	23.04	14.52	18.10	64.32	6.36	23.99
Kernel wt./plant	8.36	9.58	18.90	20.24	87.25	5.56	36.37
Shelling %	26.87	52.29	8.86	12.36	51.39	7.65	13.08

Plate21. Growing of F_2 7x7 diallel population of groundnut in non-saline field condition at SAU campus

Plate 22 . Field experiment of F_2 7x7 diallel population of groundnut in non-saline field condition at SAU campus

(Table 25) which indicating additive gene effects and therefore effective selection may be made for this trait.

Number of branches

A significant difference among the genotypes was observed for the number of branches per plant (Table 23). The highest number of branches was obtained from the genotype P4 (7.74) followed by P1xP2 (7.61), P3 (7.35) and P5 (7.00). The lowest value (5.11) was observed in P3xP6. Number of branches showed a wide range of variation from 5.11 to 7.74with mean value of 6.26 (Table 24). The genotypic variance (0.18) and phenotypic variance (0.82) was low for this trait. Phenotypic coefficient of variance (14.41) was higher than genotypic coefficient of variance (6.84). Low heritability (22.51%) with low genetic advance (0.42) and low genetic advance in percentage of mean (6.68) was observed for number of branches was observed (Table 25). These results indicated low genetic variability and limited scope of improvement.

Shoot Biomass

The analysis of variance for shoot biomass indicated highly significant variation among the genotypes (Table 23). Cross P4xP6 was found to be the maximum shoot biomass (77.33g) and was significantly different from all other genotypes. On the other hand P2xP7 was the minimum shoot biomass (30.93g). Shoot biomass showed a wide range of variation from 30.93g to 77.33g with mean value of 49.47g (Table 24). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (22.91) and genotypic (21.45) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. Very high heritability (87.71) coupled with high genetic advance in percentage of mean (41.39) was observed for shoot biomass (Table 25), which indicating additive gene effects and therefore effective selection may be made for this trait.

Pod number per plant

The analysis of variance for pod number per plant indicated highly significant variation among the genotypes (Table 23). Cross P4xP6 was found the highest pod number per plant (50.62) and was significantly different from all other genotypes. On the other hand P2xP4 was the lowest pod number per plant (24.16). pod number per plant showed a wide range of variation from 24.16 to 50.62 with mean value of 36.59 (Table 24). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (19.51) and genotypic (17.79) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. Very high heritability (83.22) coupled with high genetic advance in percentage of mean (33.44) was observed for pod number per plant (Table25), which indicating additive gene effects and therefore effective selection may be made for this trait.

100 pod weight

The analysis of variance for 100 pod weight indicated highly significant variation among the genotypes (Table 23). Cross P2xP5 was found the highest100 pod weight (104.20g) and was significantly different from all other genotypes. On the other hand P1xP6 was the lowest 100 pod weight (62.25g). 100 pod weights showed a wide range of variation from 59.16 to 104.2g with mean value of 73.63g (Table 24). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (15.48) and genotypic (13.57) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. High heritability (76.86) coupled with high genetic advance in percentage of mean (24.52) was observed for 100 pod weigh (Table 25), which indicating additive gene effects and therefore effective selection may be made for this trait.

Pod yield per plant

The analysis of variance for pod yield per plant indicated highly significant variation among the genotypes (Table 23). Cross P2xP5 was found the highestpod yield per plant (34.81g) and was significantly different from all other genotypes. On the other hand P2xP4 was the lowest pod yield per plant (16.25g). Pod yield per plant showed a wide range of variation from 16.25g to 34.81g with mean value of 26.52g (Table 24). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (18.10) and genotypic (14.52) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. High heritability (64.32) coupled with high genetic advance in percentage of mean (23.99) was observed for pod yield per plant (Table 25), which indicating additive gene effects and therefore effective selection may be made for this trait. Pod yield of different crosses presented in Plate 23.

Kernel weight per plant

The analysis of variance for Kernel weight per plant indicated highly significant variation among the genotypes (Table 22). Cross P4xP6 was found the highestkernel weight per plant (21.79g) and was significantly different from all other genotypes. On the other hand P4 was the lowest Kernel weight per plant (7.58g). Kernel weight per plant showed a wide range of variation from 7.58g to 21.79g with mean value of 15.13g (Table 23). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (20.24) and genotypic (18.90) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. High heritability (87.25) coupled with high genetic advance in percentage of mean (36.37) was observed for kernel weight per plant (Table 24), which indicating additive gene effects and therefore effective selection may be made for this trait.

Plate 23. Pod yield of different crosses of $F_2$7x7 diallel population in non-saline field condition at SAU campus

Shelling percentage

The analysis of variance for shelling percentage indicated highly significant variation among the genotypes (Table 23). Cross P2xP3 was found the highestshelling percentage (72.14) and was significantly different from all other genotypes. On the other hand P4 was the lowest shelling percentage (40.72). Shelling percentage showed a wide range of variation from 40.72 to 72.14 with mean value of 58.51 (Table 24). Considerable environmental influence was observed from the difference between genotypic variance (26.87) and phenotypic variance (52.29) and also the differences between genotypic coefficient of variation (8.86) and phenotypic coefficient of variation (12.36) which indicated considerable environmental effect on this trait. Moderate heritability (51.39) coupled with low genetic advance (7.65) and moderategenetic advance in percentage of mean (13.08) was observed for shelling percentage (Table 25), which indicating the limited scope for the improvement of this trait.

In non-saline field condition cross P2xP5 showed highest pod yield per plant followed by cross P4xP6, P5xP7, P5xP6, P1xP7, P4xP7 and P3xP7 (Table 24). Among them, P4xP6 showed highest kernel weight and higher shelling %, higher 100 pod weight, highest shoot biomass and pod number per plant. On the other hand, P2xP5 showed highest 100 pod yield and pod yield, but in kernel weight, shelling %, pod number and shoot biomass appeared below average value. The yield and 100 pod weight may be increased due to bigger pod size and contrary, kernel weight, shelling % reduced due to samller size of seeds or kernels. On the other hand, P4xP7, P5xP6, P5xP7, P3xP7, P1xP7 showed higher pod yield with higher or around average value in 100 pod weight, kernel weight, shelling %, pod number and shot biomass. Cross P2xP3, P1xP2, P1xP3 showed higher kernel weight, shelling %, but in pod yield, 100 pod weight, pod number and shoot biomass showed average or more than average value. From above results, cross P2xP5, P4xP6, P4xP7, P5xP7, P1xP7, P2xP3 and P1xP2 can be selected for next improvement and trial to develop high yielding variety for non-saline field condition.

4.4 Experiment 4. Genetic variability of yield and yield attributing characters of F_2 7x7 diallel population of groundnut in saline field condition

The experiment was conducted with parents and F_2 7x7 diallel population of groundnut in the saline field condition during September 2013 to February 2014 at Agriculture Research Station, BARI, Benarpota, Shatkhira (Plate 24). In this experiment, the analysis of variance (ANOVA) presented in Table 26. Analysis of variance (Table 26) shows highly significant ($P< 0.01$) differences due to genotypes for all the characters viz., plant height, branch number, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage (%). This result indicated the presence of wide range of variation among the genotypes for all characters in saline field condition. The mean performance and the variations as estimated by DMRT are presented in Table 27. The Genetic parameters of yield and yield contributing characters of F_2 7x7 diallel populations of groundnut in saline field condition are presented in Table 28.

Plant height: The analysis of variance for plant height indicated highly significant variation among the genotypes (Table 26). Cross P2Xp4 was found to be the tallest genotype (84.25 cm) followed by cross P1Xp4 (84.88 cm) and was significantly different from all other genotypes. On the other hand cross P3Xp5 was the shortest genotype (53.53 cm) followed by P3 (53.23 cm). Plant height showed a wide range of variation from 53.23 cm to 84.25 cm with mean value of 65.50 cm (Table 27). Phenotypic and genotypic variance were high with relatively higher amount of phenotypic (13.70) and genotypic (12.89) coefficient of variance indicating the existence of inherent variability with low environmental effect among the genotypes. Very high heritability (88.74) coupled with high genetic advance in percentage of

Table 26. Analysis of variance of yield and yield attributing characters in F_2 7x7 diallel population of groundnut in saline field condition

SV	df	Plant height	Branch number	Shoot biomass	Pod no./plant	100 pod wt.	Podyield /plant	Kernel wt./plant	Shelling %
Replication	2	49.50	0.98	110.93	63.01	493.67	68.41	152.92	137.50
Genotypes	27	223.16**	0.86**	53.23**	124.45**	250.10**	40.11**	7.24**	85.28**
Error	54	9.29	0.27	6.68	15.31	35.38	11.68	2.50	40.05

**Significant at 1% level

Table 27. Mean performance of yield and yield attributing characters in F_2 7x7 diallel population of groundnut in saline field condition

Code	Genotypes /varieties	Plant height	Branch number	Shoot biomass	Pod no./plant
1	P1	66.40 f-h	4.54 b-i	32.86 a	18.87 a-d
2	P2	71.02 c-e	4.33 b-i	24.57 b-e	12.50 d-g
3	P3	53.23 j	3.73 f-i	21.01 c-f	6.05 g-i
4	P4	69.70 d-f	4.67 a-f	23.03 b-f	4.00 hi
5	P5	53.96 j	5.65 a	20.69 c-f	3.82 i
6	P6	63.86 gh	4.41b-i	18.28 f-h	4.86 hi
7	P7	72.10 cd	4.19 c-i	19.78 e-g	5.96 g-i
8	P1Xp2	67.84 e-g	5.14 a-c	26.16 b	24.38 ab
9	P1Xp3	63.16 h	4.67 a-f	25.04 b-d	20.88 a-c
10	P1Xp4	84.88 a	4.98 a-e	31.37 a	10.84 e-h
11	P1Xp5	74.77 bc	4.63 b-g	24.41b-e	7.87 f-i
12	P1Xp6	64.08 gh	4.18 c-i	14.62 h	13.73 d-f
13	P1Xp7	76.35 b	4.72 a-f	22.38 b-f	6.33 g-i
14	P2Xp3	67.88 e-g	4.52 b-i	20.33 d-f	24.74 a
15	P2Xp4	84.25 a	3.53 i	25.56 bc	23.64 ab
16	P2Xp5	56.84 ij	3.62 g-i	15.18 gh	15.30 c-e
17	P2Xp6	63.06 h	4.07 d-i	18.18 f-h	18.10 b-d
18	P2Xp7	69.38 d-f	3.57 hi	15.48 gh	10.92 e-h
19	P3Xp4	73.54 b-d	4.93 a-e	22.97 b-f	6.75 g-i
20	P3Xp5	53.53 j	4.47 b-i	19.91 d-g	6.33 g-i
21	P3Xp6	55.93 ij	4.60 b-h	22.84 b-f	4.33 hi
22	P3Xp7	58.25 i	4.00 e-i	21.04 c-f	7.34 f-i
23	P4Xp5	55.42 ij	4.00 e-i	21.59 b-f	6.46 g-i
24	P4Xp6	67.73 e-g	4.33 b-i	24.88 b-e	9.03 e-i
25	P4Xp7	67.14 e-h	5.33 ab	26.42 b	12.87 d-g
26	P5Xp6	64.26 gh	4.33 b-i	24.80 b-e	10.61e-i
27	P5Xp7	58.83 i	5.07 a-d	22.84 b-f	7.76 f-i
28	P6xP7	56.73 ij	4.99 a-e	22.05 b-f	10.84 e-h
Range		**53.23-84.88**	**3.53-5.65**	**14.62-32.86**	**3.82-24.74**
Average		**65.50**	**4.47**	**22.44**	**11.25**
SE(±)		**1.87**	**0.43**	**2.11**	**2.86**

Same letter in a column do not differ significantly at P≤0.05 as per DMRT

Table 27. (Continued)

Code	Genotypes /varieties	100 pod wt.	Pod yield /plant	Kernel wt./plant	Shelling %
1	P1	60.31 a-d	10.74 a-e	5.32 a-f	49.45 a-e
2	P2	55.65 b-f	6.453 c-f	4.17 b-f	44.66 b-e
3	P3	33.43 j	5.13 d-f	3.22 c-f	45.91b-e
4	P4	31.26 j	3.74 f	2.67 d-f	57.12 ab
5	P5	37.97 ij	4.04 ef	2.33 ef	54.29 a-c
6	P6	48.13 e-i	4.21 ef	2.33 ef	51.46 a-d
7	P7	44.59 f-i	4.43 ef	2.14 f	51.26 a-d
8	P1xP2	68.73 a	15.95 a	6.94 ab	41.38 de
9	P1xP3	60.11 a-d	12.65a-c	5.15 a-f	37.75 e
10	P1xP4	48.81d-i	5.30 d-f	2.60 d-f	50.61 a-d
11	P1xP5	50.02 d-h	4.83 d-f	2.42 ef	59.26 a
12	P1xP6	49.70 d-i	6.14 d-f	3.76 c-f	46.99 a-e
13	P1xP7	61.68 a-c	5.18 d-f	3.33 c-f	48.60 a-e
14	P2xP3	64.15 ab	15.27 a	7.95 a	47.94 a-e
15	P2xP4	55.59 b-f	13.16 ab	6.19 a-c	45.71 b-e
16	P2xP5	56.47 b-e	10.06 a-f	5.38 a-e	50.74 a-d
17	P2xP6	60.30 a-d	11.46 a-d	5.67 a-d	52.99 a-d
18	P2xP7	47.09 e-i	5.82 d-f	3.21 c-f	53.41 a-d
19	P3xP4	45.33 e-i	4.29 ef	2.75 d-f	41.80 c-e
20	P3xP5	46.22 e-i	4.33 ef	2.74 d-f	53.05 a-d
21	P3xP6	47.12 e-i	4.19 ef	3.10 d-f	37.63 e
22	P3xP7	46.06 e-i	3.41f	2.35 ef	54.93 ab
23	P4xP5	38.37 h-j	5.27 d-f	3.03 d-f	53.35 a-d
24	P4xP6	44.66 f-i	6.17 d-f	2.48 ef	50.73 a-d
25	P4xP7	49.16 d-i	7.20 b-f	3.14 c-f	47.19 a-e
26	P5xP6	51.05 c-g	5.52 d-f	3.10 d-f	48.47 a-e
27	P5xP7	40.09 g-j	4.75 d-f	2.87 d-f	51.56 a-d
28	P6xP7	46.59 e-i	5.38 d-f	2.81 d-f	54.09 a-d
Range		**31.26-68.73**	**3.41-15.95**	**2.14-7.95**	**37.63-59.26**
Average		**49.59**	**6.97**	**3.68**	**49.37**
SE(±)		**4.85**	**2.79**	**1.29**	**5.16**

Same letter in a column do not differ significantly at P≤0.05 as per DMRT

Table 28. Genetic parameters of yield and yield contributing characters of F_2 populations of groundnut in saline field condition

Characters	Genotypic variance	Phenotypic variation	Genotypic coefficient of variance (GCV%)	Phenotypic coefficient of variance (PCV %)	Heritability h^2b (%)	GA	GA in % of mean
Plant height	71.29	80.58	12.89	13.70	88.47	16.35	24.98
Branch number	0.19	0.47	9.84	15.29	41.40	0.58	13.04
Shoot biomass	15.52	22.19	17.56	21.00	69.91	6.78	30.24
Pod no./plant	36.38	51.68	53.60	63.88	70.40	10.43	92.64
Pod yield/plant	9.48	21.16	44.19	66.02	44.79	4.24	60.92
Kernel wt./plant	1.58	4.08	34.13	54.84	38.74	1.61	43.77
Shelling %	15.08	55.13	7.86	15.04	27.35	4.18	8.47
100 pod wt	71.58	106.95	17.06	20.85	66.92	14.26	28.75

Plate 24. Experimental plot of F_2 7x7 diallel population of groundnut in saline field condition at Agriculture Research Station (ARS), Benarpota, Satkhira, BARI

mean (24.97) was observed for plant height (Table 28) which indicating additive gene effects and therefore effective selection may be made for this trait.

Number of branches

A highly significant difference among the genotypes was observed for the number of branches per plant (Table 26). The highest number of branches was obtained from the genotype P5 (5.65) and was significantly different from all other genotypes. The lowest value (3.53) was observed in P2xP4. Number of branches showed a wide range of variation from 3.53 to 5.65 with mean value of 4.47 (Table 27). The genotypic variance (0.19) and phenotypic variance (0.47) was low for this trait. Phenotypic coefficient of variance (15.29) was higher than genotypic coefficient of variance (9.84). Medium heritability (41.40%) with low genetic advance (0.58) and low genetic advance in percentage of mean (13.04) was observed for number of branches (Table 28). These results indicated low genetic variability and limited scope of improvement.

Shoot Biomass

The analysis of variance for shoot biomass indicated highly significant variation among the genotypes (Table 26). P1 was found to be the maximum shoot biomass (32.86g) followed by cross P1xP4 (31.37g) without significant difference. On the other hand cross P1xP6 was the minimum shoot biomass (14.62g). Shoot biomass showed a wide range of variation from 14.62g to 32.86g with mean value of 22.44g (Table 27). Phenotypic and genotypic variance were high with considerable differences between phenotypic (21.00) and genotypic (17.56) coefficient of variance indicating the existence of inherent variability with moderate environmental effect among the genotypes. Very high heritability (69.91) coupled with moderate genetic advance in percentage of mean (30.4) was observed for shoot biomass (Table 28)

which indicating the action of both additive and non-additive gene effects in the expression of this trait.

Pod number per plant

The analysis of variance for pod number per plant indicated highly significant variation among the genotypes (Table 26). Cross P2xP3 was found the highest pod number per plant (24.74) and was significantly different from all other genotypes. On the other P5 was the lowest pod number per plant (3.82). pod number per plant showed a wide range of variation from 3.82 to 24.74with mean value of 11.25 (Table 27). Phenotypic and genotypic variance were high with considerable differences between phenotypic (63.88) and genotypic (53.60) coefficient of variance indicating the existence of inherent variability with intermediate environmental effect among the genotypes. High heritability (70.40) coupled with high genetic advance in percentage of mean (92.64) was observed for pod number per plant (Table 28), which indicating additive gene effects and therefore effective selection may be made for this trait.

100 pod weight

The analysis of variance for 100 pod weight indicated highly significant variation among the genotypes (Table 26). Cross P1xP2 was found the highest100 pod weight (68.73g) and was significantly different from all other genotypes. On the other hand P4 was the lowest 100 pod weight (31.26g). 100 pod weights showed a wide range of variation from 31.26g to 68.73g with mean value of 49.59 (Table 27). Phenotypic and genotypic variance were high with considerable differences between phenotypic (20.85) and genotypic (17.06) coefficient of variance indicating the existence of inherent variability with intermediate environmental effect among the genotypes. High heritability (66.92) coupled with high genetic advance in percentage of mean (28.75) was observed for 100 pod weigh (Table 28), which indicating additive gene effects and therefore effective selection may be made for this trait.

Pod yield per plant

The analysis of variance for pod yield per plant indicated highly significant variation among the genotypes (Table 26). Cross P1xP2 was found the highestpod yield per plant (15.95g) and was significantly different from all other genotypes. On the other hand cross P3xP7 was the lowest pod yield per plant (3.41g). Pod yield per plant showed a wide range of variation from 3.41g to 15.95g with mean value of 6.95 (Table 27). Phenotypic and genotypic variance were high with considerable differences between phenotypic (66.02) and genotypic (44.19) coefficient of variance indicating the existence of inherent variability with intermediate environmental effect among the genotypes. Intermediate heritability (44.79) coupled with high genetic advance in percentage of mean (60.92) was observed for pod yield per plant (Table 28), which indicating the action of both additive and non-additive gene effects in the expression of this trait. Pod yield of different crosses of F_2 population is presented in Plate 25.

Kernel weight per plant

The analysis of variance for Kernel weight per plant indicated highly significant variation among the genotypes (Table 26). Cross P2xP3 was found the highestkernel weight per plant (7.95g) and was significantly different from all other genotypes. On the other hand P7 was the lowest Kernel weight per plant (2.14g). Kernel weight perplant showed a wide range of variation from 2.14g to 7.95g with mean value of 3.68g (Table 27). Phenotypic and genotypic variance were low with considerable differences between phenotypic (54.84) and genotypic (34.13) coefficient of variance indicatingthe existence of inherent variability with intermediate environmental effect among the genotypes. Intermediate heritability (38.74) coupled with high genetic advance in percentage of mean (43.77) was observed for kernel weight per plant (Table 28), which indicating the limited scope of non-additive gene effect, genotype environment interactions and micro environmental influence.

Plate 25. Pod yield of different crosses of F_2 7x7 diallel population in saline field condition at Agriculture Research Station (ARS), Benarpota, Satkhira, BARI

Shelling percentage

The analysis of variance for shelling percentage indicated highly significant variation among the genotypes (Table 26). Cross P1xP5 was found the highestshelling percentage (59.26) and was significantly different from all other genotypes. On the other hand cross P3xP6 was the lowest shelling percentage (37.63). Shelling percentage showed a wide range of variation from 37.63 to 59.26 with mean value of 49.37 (Table 27). Considerable environmental influence was observed from the difference between genotypic variance (15.08) and phenotypic variance (55.13) and also the differences between genotypic coefficient of variation (7.86) and phenotypic coefficient of variation (15.04) which indicated considerable environmental effect on this trait. Low heritability (27.35) coupled with low genetic advance (4.18) and lowgenetic advance in percentage of mean (8.47) was observed for shelling percentage (Table 28), which indicating the limited scope for the improvement of this trait.

In saline field condition cross P1xP2 showed highest pod yield per plant followed by cross P2xP3, P2xP4, P1xP3, P2xP6, P1 and P2xP5 (Table 27). Among them, P2xP3 and P1xP2 showed highest/higher kernel weight and higher shelling %, higher 100 pod weight, higher pod number per plant, higher/average shoot biomass and pod number per plant. In contrary, cross P1xP5 showed highest shelling %, but in kernel weight, pod yield and pod number appeared below average value with average yield and 100 pod weight. Shelling % may be increased due to bigger kernel size. Cross P1xP4 showed highest shoot biomass and plant height but, in pod yield, kernel weight, 100 pod weight showed below average value.

From the above results, crosses of F_2 population viz. P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 can be selected for next improvement and trial to develop high yielding salt tolerant variety in saline field condition.

CHAPTER V

DISCUSSION

In Bangladesh about 1.0 million hectares of land is affected by varying degree of soil salinity which remain fallow round the year due to lack of salinity tolerant crop varieties. Now groundnut is grown on marginal lands due to pressure of cereal crops. To increase the cultivable area of groundnut in the costal belt, it is important to develop salt tolerant varieties with high yield potentiality. In this context, the present study was carried out with four separate experiments. Results were presented in previous chapter and discussed experimentwise as follows:

5.1 Screening of salt tolerant and sensitive genotypes of groundnut at different salinity levels

The study was conducted to screening the salt tolerant and sensitive genotypes based on sixteen (six shoot-root characters, six pod yield and yield attributes and four nutrient elements up take) characters of 25 genotypes of groundnut at different salinity levels of 10dS/m, 8dS/m and control tap water 0.38dS/m. Analysis of variance of sixteen characters of 25 genotypes of groundnut at different salinity levels (Table 4a; 4b; 4c) indicated that presence of considerable variation among the genotypes, the effect of salinity levels on genotypes as well as the interaction between genotypes and salinity levels. From the study it was found that shoot-root characters viz. plant height, branch number, shoot biomass, root biomass, root/shoot ratio and total biomass were reduced with the increase of salinity levels (Table 5a; 5b). The relative performance of shoot-root characters of genotypes over different salinity levels (Fig.1 to Fig.6) showed that the linear trends and bar graphs reduced with the

increase of salinity inshoot-root characters viz. plant height, branch number, shoot biomass, root biomass, root/shoot ratio and total biomass. These results corroborate with that of many others (Hermandez *el al*., 1995; Cherian *et a*l., 1999, Takemura et *al*., 2000; Vadez *et al*., 2005; Haque, 2006; Azad, 2006; Gupta and Yadav, 1986; Silberbush and Lips, 1988; Lauter *et al*., 1988). The gradual reduction ofshoot-root characters could be due to decrease in number of leaves, growth retard by disruption in photosynthetic process through stomata collapse. Azad (2006) observed decreased leaf number in salinity stress groundnut. Plant when subjected to salt stress cannot absorb water for low water potential in soil medium, this message is transmitted to the leaf possibly via ABA signaling routs. This is reasonably proper since the increased production of abscisic acid (ABA) result in salt stressed condition (Munns and Cramer, 1996). Therefore, ABA is considered as the potent candidate of signal transduction pathway that forces stomata to close thereby reduce water expense via transpiration (Cramer and Quarrie, 2002; Sauter *et al*., 2001; Ren *et al*., 2006). The closure of stomata also limits parallelly CO_2 intake by the plant and result in reduce growth via reduced photosynthesis.

It was found that yield and yield attributing characters viz. peg number per plant, pod number, plant, pod: peg ratio, pod yield per plant, kernel weight per plant and shelling percentage were reduced with the increase of salinity levels (Table 5b; 6b; 7b). The relative performance of yield and yield attributing characters of genotypes over different salinity levels (Fig.7 to Fig.12) showed that the linear trends and bar graphs reduced with the increase of salinity in yield and yield attributing characters viz. peg number per plant, pod number, plant, pod: peg ratio, pod yield per plant, kernel weight per plant and shelling percentage, except peg number per plant in some genotypes. These results are in agreement with many earlier findings: Joshi *et al*.

(1990), Hunshal *et al*. (1991), Patel *et al*. (1992), Hebbera *et al*. (1992), Janila *et al*. (1999) and Nautiyal *et al*. (2000) who also reported significant difference amongst the genotypes for yield under salinity stress in their experiments with different crops including groundnut.

Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissuesfound that Na^+ and K^+ up take increased with the increase of salinity, but Ca^{++} up take increased with the increase of salinity up to 8 dS/m and reduced again with the increase of salinity at 10dS/m level. K^+/Na^+ ratio reduced with the increase of salinity (Table 8 to 10 and Fig.13 to16). These results agree with earlier findings (Shalhavet *et al*., 1969; Shabala *et al*., 1998 Saha and Gupta, 1997 and Azad, *et al*., 2013), who reported similar results in their experiments with different crops. The growth reduction results from the toxic effect of salt inside the plants. It is a general agreement that plants always transpire more water than they actually need for exit of heat generated in metabolic pathways apart from CO_2diffusion through opened stomata. This means excessive amounts of salt from the external solution enter into the transpiration stream. During transpiration, plants transpire water as vapour and salts accumulate in leaves and rapidly build up to 'toxic level'. This is being known as 'salt or ion specific effect' (Munns et al., 2006). The presence of excess salt inside the cell imposes the osmotic stress in the cellular environments of leaves (Jeschke *et al*., 1986). In the present study, shoot (leaves & stems) Na^+, K^+, Ca^{++} concentration gradually and significantly increased (Table 8 to 10). A low Na^+/K^+ or high K^+/Na^+ ratio in the cytosol is essential for normal cellular functions. Na^+ competes with K^+ uptake through Na^+, K^+ co-transporters, and may also block the K^+ specific transporters of root cells when salinity is experience (Zhu, 2003). This results in sodium toxicity and insufficient K^+ concentration for attending enzymatic reactions and osmotic adjustment. Moreover, higher Na^+ concentration

reduces turgidity of guard cells that leads to partial stomatal opening and in turn limits transpiration and CO_2 assimilations (James *et al*., 2002). This results in reduced shoot, root and total biomass growth and yield attributes (Table 6a, 6b, 7a, 7b). It is generally and widely accepted that increased Na^+ uptake inhibits K^+ entry into the cytoplasm and that it results in Na^+ toxicity and dysfunction of metabolic reactions. However, in this study both Na^+, K^+ and Ca^{++} uptake increased parallel with increased salinity (Table 8, 9, 10) except Ca^{++} which increased up to 8dS/m and decreased at 10 dS/m level.It might be the cause of the increase of Na^+ uptake inhibits the entry of Ca^{++} in to cytoplasm of leaf tissues at this salinity level. As a result, the influx of Ca^{++} ions was reduced than the influx of Na^+ ions to the leaf tissues of the plant.

The ultimate target of any breeding program under stress or unstressed environments is economic yield. This means, for assessing salinity tolerance in groundnut economic yield should be considered rather than biological yield (Azad *et al*., 2012; Azad *et al*., 2013). The flowering stage was the most sensitive stage for both biomass growth and yield and salinity level between 7-9 dS/m appropriate for screening program in plant breeding applications as maximum dispersion amongst varieties appeared in this salinity range (Azad, 2008). In this study, screening of salt tolerant and sensitive genotypesfind out by imposing salinity stress during flowering till harvest stages at 8dS/m level both biomass growth and yield. The salinity tolerance classes obtained by using the equation mentioned in sub-section3.4.11 and the scale: >20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS,<60% reduction= S (Azad *et al*., 2012).

In shoot biomass, the total number of 4, 13, 5 and 3 genotypeswere showed as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 10). Based on total biomass, 4, 13, 5 and 3 number of genotypes

were appeared as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 12). A total number of 5, 3, 7 and 10 genotypeswere appeared as tolerant, moderately tolerant, moderately sensitive and sensitive, respectively among 25 genotypes based on pod number per plant (Table 13). Based on pod weight per plant a number of 1, 2, 4 and 17 genotypes were appeared as tolerant, moderately tolerant, moderately sensitive and sensitive, respectively among 25 genotypes (Table 14). Based on kernel weight per plant a number of 1, 1, 3 and 20 genotypes are appeared as tolerant, moderately tolerant, moderately sensitive and sensitive, respectively among 25 genotypes (Table 15).

It was observed that some genotypes like V10 and V5 appeared tolerant and moderately tolerant at 8dS/m in shoot biomass but in total biomass they showed moderately tolerant and tolerant, respectively. On the other hand, V7 showed moderately tolerant in shoot biomass but in total biomass showed moderately sensitive. However, remaining genotypes appeared same tolerance classes which they showed in shoot biomass and total biomass (Table 16). This could be attributed to differential micro climates particularly day length (Nigam *et al*., 1994 and 1998; Nagnall and King, 1991; Bell *et al*., 1991), temperature (Prasad *et al*., 2000 and 2003; Talwar *et al*., 1999; Craufurd *et al*., 2002), humidity (Karunakar, *et al*., 2002) within the experimental area. In case of yield attributing traits like pod number, pod weight and kernel weight per plant only V5 appeared as tolerant, V6 showed tolerant in pod number but moderately tolerant showed in pod weight and kernel weight per plant. V2 showed tolerant in pod number but moderately tolerant and moderately sensitive showed in pod weight and kernel weight per plant, respectively. V12 and V14 appeared tolerant in pod number per plant but showed moderately sensitive and sensitive in pod weight and kernel weight per plant, respectively. Genotypes V4, V9

and V13 showed moderately tolerant in pod number per plant but they showed sensitive and moderately sensitive in pod weight, kernel weight per plant, respectively. Genotypes V1, V7, V11, V16 and V24 showed moderately sensitive, sensitive and sensitive in pod number, pod weight and kernel weight per plant, respectively. On the other hand, V10 and V17 appeared moderately sensitive, moderately sensitive and sensitive in pod number, pod weight and kernel weight per plant, respectively. The remaining genotypes showed sensitive to salinity in pod number, pod weight and kernel weight per plant (Table 16). Pod yield is the final end product of all physiological processes and proportional to the assimilate translocation efficiency to reproductive sink of the varieties/genotypes. The genotypes V2, V4, V5, V6, V13,, V14 had higher/ moderately higher biomass yield produce higher/ moderately higher number of pods per plant, of which only V5, V6, V2 produced higher/moderate pod weight per plant and among them V5 and V6 had higher and moderately higher kernel weight per plant. Conversely, V15, V16, V10, V8, V18, V19, V22, V21 and V20 although produce higher/, moderately higher biomass yield (Table 11, 12) yet had very low/ zero assimilate translocation for pod and kernel formation at imposed salinity level (Table 13,14, 15).

When a pod is formed, it needs continuous supply of assimilates for maturation. This depends on the assimilate translocation efficiency to reproductive sink of the genotype. The assimilate translocation efficiency differ in the genotypes to genotypes in groundnut in saline condition. The tolerant variety/genotype accumulated increased total sugar contents to that of unstressed control treatment when exposed to salinity stresses during flowering and pod filling stages. Free amino acid during pod filling stage helped maintaining turgor of guard cell and intake of CO_2 through opened stomata. This CO_2 in presence of undamaged chloroplast helped maintaining

photosynthesis and mobilization of assimilates to reproductive organs, particularly kernel (Azad *et al*., 2013).

Finally, based on shoot biomass, total biomass, pod number, pod yield and kernel yield six genotypes viz. V5 (Binachinabadam-5) selected as tolerant; V6 (Binachinabadam-6), V2 (Binachinabadam-2) and V13 (BARI Chinabadam-6) selected as moderately tolerant; V12 (BARI Chinabadam-5) selected as moderately sensitive and V7 (Dhaka-1) selected as sensitive parent for hybridization in diallel mating system (Table 16). The selected genotypeswere crossed all possible combinations excluding reciprocals to study the combining ability and gene action, followed in experiment 2.

5.2 Combining ability and genetic analysis of salinity tolerance in 7x7 F_1diallel population

To determine the mode of inheritance of traits a detailed genetic study is the prerequisite, which ultimately helps adopt better planning and execution in a varietal improvement program. In breeding program for development of salt tolerant groundnut variety, selected seven diverse genotypes were crossed in half diallel fashion and their 21 F_1 progenies along with their parents were evaluated in pot culture with saline soil. The significant variation in general and specific combining ability estimated for all the characters were observed which indicated the importance of both additive and non-additive gene actions in inheritance of these characters (Table 19a, 19b). This result is in conformity with that of many workers (Moeljopawiro and Ikehashi, 1981; Akbar *et al*., 1986; Muralia and Satry, 2001; Ali *et al.,* 2006; Azad *et al*., 2014) who investigated salinity tolerance in many different crops. Baker (1978) suggested that general and specific combining ability should be assessed by estimating the components of variance, expressing as δ^2g/δ^2s ratio. The closer the ratio to unity the greater would be the magnitude of additive genetic effects.

The ratios computed in these studies were much less than unity (Table 19a and 19b), suggesting predominant role of non-additive gene effects in their inheritance. This result corroborates with that of many workers (Subbarao *et al*., 1990; Azhar and McNeilly, 1988; Saranga *et al*., 1991; Tal and Shannon, 1983) working with salinity tolerance in many different crops. The higher values of sca than gca component could be due to presence of repulsion phase linkage and linkage disequilibrium (Sokol and Baker, 1977). Verma and Srivastava (2004) observed high sca effects which resulting from the dominance and interaction or epistatic effects that existed between the hybridizing parents. Additionally, higher sca than gca can be explained in many different ways (i) negative associations between genes (Sokol and baker, 1977) (ii) previous selection that narrowed down the genetic base of the lines tested (Plaisted *et al.*, 1962) (iii) directional selection (Killick and Malcolmson, 1973) and (iv) use of closely related parents (Neele *et al.*, 1991).

In case of biomass, pod yield and yield attributes parent P1showed highest/higher positive general combining ability for plant height, branch number, shoot biomass, total biomass, pod number. Pod yield and kernel yield. Parent P2 showed higher/highest positive general combining ability for branch number, pod number. Pod yield and kernel yield. Parent P4 appeared highest and higher positive general combining ability for plant height and shoot biomass & total biomass respectively. Parent P5, P6 and P7 showed lower and/or negative general combining ability for plant height, branch number, shoot biomass, total biomass, pod number. Pod yield and kernel yield. In contrast, Na^+, K^+ and Ca^{2+} contents in leaf and stem tissues parent P2 showed highest positive general combining ability for K^+, K^+/Na^+ content in leaf and stem tissues and Ca^{2+} contents in stem tissues. Parent P3 appeared highest/higher positive general combining ability for Na^+ content in both leaf and stem tissues.

Parent P5showed higher/highest Ca^{2+} content in leaf tissues; K^+ and K^+/Na^+ content in stem tissues. Parent P6 showed higher/highest Na^+ and Ca^{2+} content in leaf tissues. Parent P7 showed highest/ higher Na^+, K^+ and K^+/Na^+ content in leaf tissues. This suggests that these characters in these parents are governed by either additive genes or genes with additive x additive interaction effects and represents a fixable portion of genetic variation. Furthermore, it would be worthwhile to use these genotypes as parent for the development of improved salt tolerant varieties, particularly with shoot biomass/ total biomass, pod number, Pod yield, kernel yield; and K^+/Na^+ and Ca^{2+} content in stem tissues. The parents for the remaining characters appeared lowest/ lower gca values to be controlled by non-additive genes. The discussion above suggests that the studied characters with higher gca values under salinity stress is governed by additive genes depending on parents and with that of lower gca values controlled by non-additive genes.

The higher specific combining ability (sca) for different characters were obtained from the crosses with high x low or high x average or average x average or average x low or low x low gca effects (Table 20a,20b and 21a, 21b). The high sca effects from crosses between high x low gca or high x average or low x low or vice versa parents were due to additive x dominant or additive x additive interactions (Verma and Srivastava, 2004). Moreover, they had the opinion that such higher sca could be due to complementary interaction apart from additive effect of the high parent. Conversely, the superiority of average x average or average x low or low x lowcombines could be due to concentration of and/or interaction between favorable genes contributed by the relevant parents (Verma and Srivastava, 2004).

Parent P1with the highest or higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight had high gca for these characters.

Contrary, parent P2 with the highest or higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight had high gca forbranch number, pod number, pod yield and kernel weight; and parent P4 with the highest or higher plant height, branch number, shoot biomass, total biomasshad high gca for plant height, shoot biomass and total biomass (Table 17a). This indicates that higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight under salinity stress controlled by additive x dominant or additive x additive interaction genes in some parents and in some parents by non-additive genes. The high sca effects for plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight were obtained in cresses with high x low or low x high or low x low gcas (Table 20a and 21a). It means the characters are controlled either by additive x dominant or by dominant x dominant type gene interaction and thus non-fixable.

Covariance (Wr) and variance (Vr) is relevant when traits show non-additive variation (Kearsey and Pooni, 1996). All traits were controlled by both additive and non-additive genes (Table 19a; 19b) and justified the use of Wr/Vr analysis. The adequacy of the additive-dominance model and its validity stem from assumptions that are non-allelic interaction, no multiple allelism and uncorrelated gene distribution assessed using joint regression analysis and Wr/Vr analysis. Here, significant deviation of the regression coefficient from zero but not from unity indicates adequacy of model. For total biomass, pod yield and kernel weight regression coefficient were significantly greater than zero but from unity (Appendix 1V); and the non-significant t^2 value satisfied the additive-dominance model (Fig. 20, 22 and 23). For shoot biomass regression coefficient was not significantly greater than zero and unity but the non-significant t^2 value satisfied the uniformity of covariance and variance (Wr,Vr) (Fig.

19). This suggests that the additive-dominance model was partially adequate. For pod number regression coefficient was not significantly greater than zero but from unity; and the non-significant t^2 value satisfied the uniformity of covariance and variance (Wr,Vr) (Fig. 21).This also means that the additive-dominance model was partially adequate. In contrast, for plant height and branch number regression coefficient was not significantly greater than zero but from unity; and the significant t^2 value not satisfied the additive-dominance model (Fig. 17 and 18). This means the independent distribution of genes amongst the parents was hindered by epistatic and dominance gene effects. Epistasis is not considered in most genetic models, as estimates of additive and dominance variation are biased to an unknown extent (Upadhyaya and Nigam, 1999). This may affect a breeding program by choosing inappropriate breeding methods. However, Singh (1990) observed little effect of epistasis on the additive and dominance components. Sharma (1999) had the opinion that the characters governed by epistatic effect could be improved by following reciprocal recurrent selection in the early segregating generations. However, as this epistatic effect disappears in the advanced generation (Sharma, 1999), advancing of segregating material through bulk, pedigree, single seed/pod descent methods would be rewarding (Gupta and Dahiya, 1986).

All traits in genetic studies appeared to be controlled by poly genes with preponderance of dominance effect and the genes with positive and negative effects followed asymmetrical distribution amongst the parents. Heritability estimates, narrow and board sense, ranged 0.06 to 0.80 and 0.38 to 0.97, respectively. Pod yield, kernel weight and pod number had highest, higher and moderate narrow sense heritability respectively (Table 22). This means simple progeny selection could be effectively followed in the segregating generations for these traits under salinity.

5. 3 Genetic variability of yield and yield attributing characters of F_2 7x7 diallel population of groundnut in non-saline field condition

The experiment was conducted with parents and F_2 7x7 diallel population of groundnut in the non-saline field condition during August to December 2013 at SAU campus. This investigation has been conducted to determine the genotypic effects and comparative performance of F_2 7x7 diallel population of groundnut in non-saline field condition. In this experiment, the analysis of variance (ANOVA) shows highly significant ($P< 0.01$) differences due to genotypes for all the characters viz., plant height, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage(%), while branch number showed only significant ($P< 0.05$) differences (Table 23). This result indicated the presence of wide range of variation among the genotypes for all characters in non-saline field condition.The mean performance and the variations as estimated by DMRT (0.05) are presented in Table 24. Parent P4 was found to be the tallest genotype followed by P2xP4, P1xP4 and P2xP7. The highest number of branches was obtained from the genotype P4 followed by P1xP2, P3 and P5. Cross P4xP6 was found to be the maximum shoot biomass followed by P4xP7, P1, P1xP4, P5xP7, P6xP7 and P4. Cross P4xP6 was found the highest pod number per plant followed by P5xP7, P1xP2, P1xP6, P1, P5xP7, P3xP6 and P6xP7. Cross P2xP5 was found the highest 100 pod weight followed by P5, P1xP5, P3xP7, P3xP5, P3xP4 and P1xP7. Cross P2xP5 was found the highestpod yield per plant followed by P4xP6, P5xP7, P5xP6, P1xP7 and P4xP7. Cross P4xP6 was found the highest kernel weight per plant followed by P5xP7, P2xP3, P1xP7 and P1xP2. Cross P2xP3 was found the highest shelling percentage and followed by P1xP2, P4xP5, P4xP6, P5xP7 and P1x P7.

In non-saline field condition cross P2xP5 showed highest pod yield per plant followed by cross P4xP6, P5xP7, P5xP6, P1xP7, P4xP7 and P3xP7 (Table 24). Among them, P4xP6 showed highest kernel weight and higher shelling %, higher 100 pod weight, highest shoot biomass and pod number per plant. On the other hand, P2xP5 showed highest 100 pod yield and pod yield, but in kernel weight, shelling %, pod number and shoot biomass appeared below average value. The yield and 100 pod weight may be increased due to bigger pod size and contrary, kernel weight, shelling % reduced due to samller size of seeds or kernels. On the other hand, P4xP7, P5xP6, P5xP7, P3xP7, P1xP7 showed higher pod yield with higher or around average value in 100 pod weight, kernel weight, shelling %, pod number and shot biomass. Cross P2xP3, P1xP2, P1xP3 showed higher kernel weight, shelling %, but in pod yield, 100 pod weight, pod number and shoot biomass showed average or more than average value. It may due to seeds size are bold but pod number per plant are smaller with thick shell structure.

From above discussion, cross P2xP5, P4xP6, P4xP7, P5xP7, P1xP7, P2xP3 and P1xP2 can be selected for next improvement and trial to develop high yielding variety for non-saline field condition.

The values of phenotypic coefficient of variation (PVC) and genotypic coefficient of variation (GCV) indicated that there were considerable variations for all the traits while number of branches and shelling % showed minimum amount of variations (Table 25). GCV was highest for shoot biomass followed by kernel weight per plant, pod number per plant, pod yield per plant and 100 pod weight indicating high degree of genetic variability in these traits. Similar results have also been obtained by Alam *et al.* (1985a and b), Patil and Bhapker (1987), Reddy and Gupta (1992), Pathak *et al.* (1993) and Latif *et al.* (1995). Heritability estimated in broad sense were relatively

high for all the characters except number of branches. Johnson,*et al.* (1955) and Panse (1957) suggested that heritability estimates along with genetic gain is due to additive gene effect and more useful in predicting the effect for selecting the best individuals. Moderate to high estimates of heritability along with high genetic advance in percentage of mean for shoot biomass per plant, kernel weight per plant, pod number per plant, 100 pod weight, pod yield per plant and plant height suggests that improvement of these would be effective through phenotypic selection. Selection for these yield contributing characters was found effective as reported by Alam *et al.* (1985a and b), Kandaswami *et al.* (1986), Reddi *et al*. (1991) and Latif *et al.* (1995).

5. 4 Genetic variability of yield and yield attributing characters of F_2 7x7 diallel population of groundnut in saline field condition

The experiment was conducted with parents and F_2 7x7 diallel population of groundnut in the saline field condition during September 2013 to February 2014 at Agriculture Research Centre, BARI, Benarpota, Shatkhira. This investigation has been conducted to determine the genotypic effects and comparative performance of F_2 7x7 diallel population of groundnut in saline field condition. In this experiment, the analysis of variance (ANOVA) shows highly significant ($P<0.01$) differences due to genotypes for all the characters viz., plant height, branch number, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage (Table 26). This result indicated the presence of wide range of variation among the genotypes for all characters in saline field condition.The mean performance and the variations as estimated by DMRT (0.05) are presented in Table 27. Cross P1xP4 was found the tallest genotype followed by P2xP4 and P1xP7. The highest number of branches was obtained from the parent P5 followed by P4xP7 and cross P1xP2. Parent P1 was obtained the maximum shoot biomass followed by

P1xP4, P1xP2, P4xP7, P2xP4, P1xP3, P4xP6, P1xP5 and P1xP7. Cross P2xP3 was found the highestpod number per plant followed by P1xP2, P2xP4, P1xP3, P1 and P2xP6. Cross P1xP2 was found the highest 100 pod weight followed by P2xP3, P1xP7, P1, P2xP6 and P1xP3. Cross P1xP2 was found the highestpod yield per plant followed by P2xP3, P2xP4, P1xP3, P2xP6, P1 and P2xP5. Cross P2xP3 was found the highestkernel weight per plant followed by P1xP2, P2xP4, P2xP6, P2xP5 and P1xP3. Cross P1xP5 was found the highestshelling percentage and followed by P3xP7, P4, P2xP7, P4xP5, P2xP6, P2xP5 and P1xP4.

In saline field condition cross P1xP2 showed highest pod yield per plant followed by cross P2xP3, P2xP4, P1xP3, P2xP6, P1 and P2xP5 (Table 27). Among them, P2xP3 and P1xP2 showed highest/higher kernel weight and higher shelling %, higher 100 pod weight, higher pod number per plant, higher/average shoot biomass and pod number per plant. On the other hand, cross P1xP5 showed highestshelling %, but in kernel weight, pod yield and pod number appeared below average value with average yield and 100 pod weight. Shelling % may be increased due to bigger kernel size. Cross P1xP4 showed highest shoot biomass and plant height but, in pod yield, kernel weight, 100 pod weight showed below average value. It may due to lower photosynthetic ability and lower assimilate translocation efficiency to reproductive sink of the genotype. The average values of all traits studied in non-saline and saline field condition revealed that the average values are smaller in saline field condition than in non-saline field condition in spite individual performance is different to each other to different field conditions. The result corroborates with that of many workers (Hurd,1974; Singh and Jain, 1989 and Abdul-Halim *et al*., 1988) indicates that under salinity stress, plants tend to record low yields because of adverse effects of salinity on such parameters as relative water content, total dry weight, plant height and shoot

biomass of plant. This is because salinity inhibits plant growth by exerting low water potentials, ion toxicity andion imbalance (Greenway and Munns, 1980; Sharma, 1997). The ability of any genotypes to maintain agronomic parameters at near control levels therefore confers salt tolerance.

From above discussion, cross P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 can be selected for next improvement and trial to develop high yielding variety in saline field condition.

The values of phenotypic coefficient of variation (PVC) and genotypic coefficient of variation (GCV) indicated that there were considerable variations for all the traits while number of branches and shelling % showed minimum amount of variations (Table 28). GCV was highest for pod number per plant followed by pod yield per plant, kernel weight per plant, shoot biomass and 100 pod weight indicating high degree of genetic variability in these traits. Heritability estimated in broad sense was relatively high for all the characters except shelling %. Johnson *et al*. (1955) and Panse (1957) suggested that heritability estimates along with genetic gain is due to additive gene effect and more useful in predicting the effect for selecting the best individual. Moderate to high estimates of heritability along with high genetic advance in percentage of mean for pod number per plant, pod yield per plant, kernel weight per plant, shoot biomass per plant, 100 pod weight, and plant height suggests that improvement of these would be improve through selection. Selection for these yield contributing characters could be a source for salt tolerant variants in groundnut was reported by Mensah,*et al*. (2006).

The results showed that even though there were significant changes within the non-saline and saline field condition means performance (Table 24 and 27), genetic parameters such as heritability and genetic gain were not adversely affected by the

different field conditions. The possible explanation is that the changes in the mean values of the traits as observed in the present investigations are mainly physiological in nature and would be reversed when grown under environments with lower electrical conductivities/salinity. It could therefore be inferred from the study that the yield characters under investigations could successfully be selected among the genotypes for improvement in saline environments.

The F_2 population derived from the crosses P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 as the most salt tolerant genotypes could serve as a source of genetic material for the development of salt tolerant varieties.

CHAPTER VI

SUMMARY AND CONCLUSION

Salinity is the most wide spread adverse soil problem which affects crop production. In Bangladesh more than 30% of the net cultivable area, and about 1.02 million hectare land is in the costal belts. To increase the groundnut growing area towards the costal belt, it is need to be developed salinity stress tolerant groundnut varieties. The tolerance is relative term depending mainly upon the intensity of salinity and relative performance of the genotypes. The knowledge on genetics of salinity tolerance is a prerequisite in designing effective breeding program to develop groundnut variety with higher ability to cope with salt stress.

The objectives of this study were (i) to screening the groundnut genotypes against salinity and discriminate salt tolerant and sensitive groups; (ii) to assess combining ability and genetic behavior of salinity tolerance in groundnut and (ii) to identify the high yielding and salt tolerant genotype (s) in non- saline and saline field condition respectively. To fulfill these objectives, the present investigation was carried out with four separate experiments during the period from August 2010 to January 2014 at the net house premises and the field experimental plot of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka; laboratory of Soil Resources Development Institute, Dhaka and Agricultural Research Station of Bangladesh Agricultural Research Institute, Benarpota, Satkhira. Summary of the research works is presented experiment wise as follows:

A considerable variation among 25 genotypes of groundnut in response to different salinity levels was observed for sixteen (six shoot-root characters, six pod yield and

yield attributes and four nutrient element uptake) characters under study (Table 4a,4b,4c). The effect of salinity levels on genotypes as well as the interaction between genotypes and salinity levels were also highly significant ($P<0.01$). From the study it was observed that shoot-root characters viz. plant height, branch number, shoot biomass, root biomass, root/shoot ratio and total biomass were reduced with the increase of salinity levels (Table 5a,6a,7a). The relative performance of shoot-root characters of genotypes over different salinity levels (Fig.1 to 6) showed that the linear trends and bar graphs reduced with the increase of salinity in shoot-root characters viz. plant height, branch number, shoot biomass, root biomass, root/shoot ratio and total biomass.The gradual reduction of shoot-root characters could be due to decrease in number of leaves, growth retarded by disruption in photosynthetic process through stomata collapse. For yield and yield attributing characters it was found that peg number per plant, pod number per plant, pod: peg ratio, pod yield per plant, kernel weight per plant and shelling percentage were reduced with the increase of salinity levels (Table 5b,6b,7b). The relative performance of yield and yield attributing characters of genotypes over different salinity levels (Fig.7 to12) showed that the linear trends and bar graphs reduced with the increase of salinity in yield and yield attributing characters viz. peg number per plant, pod number per plant, pod: peg ratio, pod yield per plant, kernel weight per plant and shelling percentage, except peg number per plant in some genotypes. Na^+, K^+ and Ca^{++} content (%)/plant in shoot tissues indicated that Na^+ and K^+ up take increased with the increase of salinity, but Ca^{++} up take increased with the increase of salinity up to 8 dS/m and reduced again with the increase of salinity at 10dS/m level. K^+/Na^+ ratio reduced with the increase of salinity (Table 8 to 10 and Fig.13 to16).In the present study, shoot (leaves & stems) Na^+, K^+, Ca^{++} concentration gradually and significantly increased (Table 6 to 8). A

low Na^+/K^+ or high K^+/Na^+ ratio in the cytosol is essential for normal cellular functions. Na+ competes with K+ uptake through Na^+, K^+ co-transporters, and may also block the K^+ specific transporters of root cells when salinity is experienced. It is generally and widely accepted that increased Na^+ uptake inhibits K^+ entry into the cytoplasm and that it results in Na+ toxicity and dysfunction of metabolic reactions. However, in this study both Na^+, K^+ and Ca^{++} uptake increased parallel with increased salinity (Table 8, 9, 10) except Ca^{++} which increased up to 8dS/m and decreased at 10 dS/m level. It might be the cause of the increase of Na^+ uptake inhibits the entry of Ca^{++} in to cytoplasm of leaf tissues at this salinity level. As a result, the influx of Ca^{++} ions was reduced than the influx of Na^+ ions to the leaf tissues of the plant.

In this study, screening of salt tolerant and sensitive genotypes was done by imposing salinity stress during flowering till harvest stages at 8dS/m level for both biomass growth and yield. The salinity tolerance classes were obtained by using the equation mentioned in sub-section 3.4.11 and the scale: >20% reduction =T, 20-40% reduction = MT, 41-60% reduction = MS, <60% reduction= S (Azad *et al*., 2012). In shoot biomass, total number of 4, 13, 5 and 3 genotypes were identified as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 11). Based on total biomass, total number of 4, 13, 5 and 3 genotypes appeared as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 12). Total number of 5, 3, 7 and 10 genotypes appeared as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes based on pod number per plant (Table 13). Based on pod weight per plant total number of 1, 2, 4 and 17 genotypes appeared as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 14). Based on kernel weight per plant, total number of 1, 3 and

20 genotypes appeared as tolerant, moderately tolerant, moderately sensitive and sensitive respectively among 25 genotypes (Table 15). It was observed that some genotypes like V10 and V5 appeared as tolerant and moderately tolerant at 8dS/m in shoot biomass but in total biomass they showed moderately tolerant and tolerant respectively. On the other hand, V7 showed moderately tolerant in shoot biomass but in total biomass showed moderately sensitive. However, remaining genotypes appeared same tolerance classes which they showed in shoot biomass and total biomass (Table 16). In case of yield attributing traits like pod number, pod weight and kernel weight per plant only V5 appeared as tolerant, V6 showed tolerant for pod number but moderately tolerant showed for pod weight and kernel weight per plant. V2 showed tolerant for pod number but moderately tolerant and moderately sensitive showed for pod weight and kernel weight per plant respectively. V12 and V14 appeared tolerant for pod number per plant but showed moderately sensitive and sensitive for pod weight and kernel weight per plant respectively. V4, V9 and V13 showed moderately tolerant for pod number per plant but they showed sensitive and moderately sensitive for pod weight, kernel weight per plant respectively. V1, V7, V11, V16 and V24 showed moderately sensitive and sensitive for pod number, pod weight and kernel weight per plant respectively. On the other hand, V10 and V17 appeared moderately sensitive and sensitive for pod number, pod weight and kernel weight per plant respectively. The remaining genotypes showed sensitive to salinity for pod number, pod weight and kernel weight per plant (Table 16). Pod yield is the final end product of all physiological processes and proportional to the assimilate translocation efficiency to reproductive sink of the varieties/genotypes. The genotypes V2, V4, V5, V6, V13, V14 had higher/ moderate higher biomass yield produced higher/ moderate higher number of pods per plant, of which only V5, V6, V2

produced higher/moderate pod weight per plant and among them V5 and V6 had higher and moderate higher kernel weight per plant. Conversely, V15, V16, V10, V8, V18, V19, V22, V21 and V20 although produce higher/, moderate higher biomass yield (Table 11, 12) yet had very low/ zero assimilate translocation for pod and kernel formation under imposed salinity condition (Table 13,14, 15).

Continuous supply of assimilates for maturation is needed after pod formation. This depends on the assimilate translocation efficiency to reproductive sink of the genotype. The assimilate translocation efficiency differs from genotype to genotype in groundnut under saline condition. Finally, based on shoot biomass, total biomass, pod number, pod yield and kernel yield six genotypes viz. V5 (Binachinabadam-5) selected as tolerant; V6 (Binachinabadam-6), V2 (Binachinabadam-2) and V13 (BARI Chinabadam-6) selected as moderately tolerant; V12 (BARI Chinabadam-5) selected as moderately sensitive and V7 (Dhaka-1) selected as sensitive parent for hybridization in diallel mating system (Table 16). Then, the selected genotypes were crossed in all possible combinations excluding reciprocals to study the combining ability and gene action, followed in experiment 2.

A 7x7 diallel experiment was carried out for genetic analysis of salt tolerance in groundnut. The significant variation in general and specific combining ability estimated for all the characters were observed which indicated the importance of both additive and non-additive gene actions in inheritance of these characters (Table 19a,19b). The δ^2g/δ^2s ratios computed in these studies were much less than unity (Table 19a and 19b), suggesting predominant role of non-additive gene effects in their inheritance.

In biomass, pod yield and yield attributes parent P1 showed highest/higher positive general combining ability for plant height, branch number, shoot biomass, total

biomass, pod number, pod yield and kernel yield. Parent P2 showed higher/highest positive general combining ability for branch number, pod number. Pod yield and kernel yield. Parent P4 appeared highest and higher positive general combining ability for plant height and shoot biomass & total biomass respectively. Parent P5, P6 and P7 showed lower and/or negative general combining ability for plant height, branch number, shoot biomass, total biomass, pod number, Pod yield and kernel yield. The parent P2 showed the highest positive general combining ability for K^+, K^+/Na^+ content in leaf and stem tissues and Ca^{2+} contents in stem tissues. The parent P3 showed highest/higher positive general combining ability for Na^+ content in both leaf and stem tissues. The parent P5 showed higher/highest Ca^{2+} content in leaf tissues; K^+ and K^+/Na^+ content in stem tissues. The parent P6 showed higher/highest Na^+ and Ca^{2+} content in leaf tissues. The parent P7 showed highest/ higher Na^+, K^+ and K^+/Na^+ content in leaf tissues. This suggests that these characters in these parents are governed by either additive genes or genes with additive x additive interaction effects and represents a fixable portion of genetic variation. Furthermore, it would be worthwhile to use these genotypes as parent for the development of improved salt tolerant varieties, particularly with shoot biomass/ total biomass, pod number, Pod yield, kernel yield; and K^+/Na^+ and Ca^{2+} content in stem tissues. The parents for the remaining characters showed lowest/ lower gca values to be controlled by non-additive genes. The discussion above suggests that the studied characters with higher gca values under salinity stress is governed by additive genes depending on parents and with that of lower gca values controlled by non-additive genes.

The higher specific combining ability (sca) for different characters were obtained from the crosses with high x low or high x average or average x average or average x low or low x low gca effects (Table 20a, 20b and 21a, 21b). The high sca effects from

crosses between high x low gca or high x average or low x low or vice versa parents were due to additive x dominant or additive x additive interactions. Parent P1with the highest or higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight had high gca effects for these characters. Contrary, parent P2 with the highest or higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight had high gca effect for branch number, pod number, pod yield and kernel weight; and parent P4 with the highest or higher plant height, branch number, shoot biomass, total biomass had high gca effect for plant height, shoot biomass and total biomass (Table 20a). This indicates that higher plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight under salinity stress controlled by additive x dominant or additive x additive interaction genes in some parents and in some parents by non-additive genes. The high sca effects for plant height, branch number, shoot biomass, total biomass, pod number, pod yield and kernel weight were obtained in cresses with high x low or low x high or low x low gcas (Table 20a and 21a). It means the characters are controlled either by additive x dominant or by dominant x dominant type gene interaction and thus non-fixable.

All traits were controlled by both additive and non-additive genes (Table 19a; 19b) and justified the use of Wr/Vr analysis. The adequacy of the additive-dominance model and its validity stem from assumptions that are non-allelic interaction, no multiple allelism and uncorrelated gene distribution assessed using joint regression analysis and Wr/Vr analysis. Here, significant deviation of the regression coefficient from zero but not from unity indicates adequacy of model. For total biomass, pod yield and kernel weight regression coefficient were significantly greater than zero but from unity (Appendix 1V); and the non-significant t^2 value satisfied the additive-

dominance model (Fig. 20, 22 and 23). For shoot biomass regression coefficient was not significantly greater than zero and unity but the non-significant t^2 value satisfied the uniformity of covariance and variance (Wr,Vr) (Fig. 19). This suggests that the additive-dominance model was partially adequate. For pod number regression coefficient was not significantly greater than zero but from unity; and the non-significant t^2 value satisfied the uniformity of covariance and variance (Wr,Vr) (Fig. 21). This also means that the additive-dominance model was partially adequate. In contrast, for plant height and branch number regression coefficient was not significantly greater than zero but from unity; and the significant t^2 value not satisfied the additive-dominance model (Fig. 18 and 19). This means the independent distribution of genes amongst the parents was hindered by epistatic and dominance gene effects.The characters governed by epistatic effect could be improved by following reciprocal recurrent selection in the early segregating generations. Moreover, the disappearance of epistatic effect in the advanced generation suggests that advancing of segregating material through bulk, pedigree, single seed/pod descent methods would lead to effective selection.

The genetic studies of all traits appeared to be controlled by poly genes (two to five groups) with preponderance of dominance effect and the genes with positive and negative effects followed asymmetrical distribution amongst the parents. Heritability estimates, in narrow and board sense, ranged from 0.06 to 0.80 and 0.38 to 0.97, respectively. Pod yield, kernel weight and pod number had highest, higher and moderate narrow sense heritability, respectively (Table 22). This means simple progeny selection could be effectively followed in the segregating generations for these traits under salinity.

This investigation has been conducted to determine the genotypic effects and comparative performance of $F_2$7x7 diallel population of groundnut in non-saline field condition. In the study,the analysis of variance indicated that genotypic effects were highly significant ($P< 0.01$) for all the characters viz., plant height, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage(%), while branch number showed only significant ($P< 0.05$) differences (Table 23). It indicated the presence of wide range of variation among the genotypes for all characters in non-saline field condition.The mean performance estimated by DMRT (0.05) showed the variations (Table 24). In non-saline field condition cross P2xP5 showed highest pod yield per plant followed by cross P4xP6, P5xP7, P5xP6, P1xP7, P4xP7 and P3xP7 (Table 24). Among them, P4xP6 showed highest kernel weight and higher shelling %, higher 100 pod weight, highest shoot biomass and pod number per plant. On the other hand, P2xP5 showed highest 100pod yield and pod yield, but in kernel weight, shelling %, pod number and shoot biomass appeared below average value. The yield and 100 pod weight may be increased due to bigger pod size and contrary, kernel weight, shelling % reduced due to samller size of seeds or kernels. On the other hand, crosses P4xP7, P5xP6, P5xP7, P3xP7 and P1xP7 showed higher pod yield with higher or around average value in 100 pod weight, kernel weight, shelling %, pod number and shot biomass. Cross P2xP3, P1xP2, P1xP3 showed higher kernel weight, shelling %, but in pod yield, 100 pod weight, pod number and shoot biomass showed average or more than average value. It may be due to seeds size are bold but pod number per plant are smaller with thick shell structure.

The values of phenotypic coefficient of variation (PVC) and genotypic coefficient of variation (GCV) indicated that there were considerable variations for all the traits while number of branches and shelling % showed minimum amount of variations

(Table 25). GCV was highest for shoot biomass followed by kernel weight per plant, pod number per plant, pod yield per plant and 100 pod weight indicating high degree of genetic variability in these traits. Heritability estimated in broad sense was relatively high for all the characters except number of branches. It is suggested that heritability estimates along with genetic gain is due to additive gene effect and more useful in predicting the effect for selecting the best individual. Moderate to high estimates of heritability along with high genetic advance in percentage of mean for shoot biomass per plant, kernel weight per plant, pod number per plant, 100 pod weight, pod yield per plant and plant height suggests that improvement of these would be effective through phenotypic selection.

From above discussion, F_2 population generated from the crosses viz. P4xP6, P4xP7, P5xP7, P1xP7, P2xP3 and P1xP2 can be selected for next improvement and trial to develop high yielding variety for non-saline field condition.

Another experiment was conducted to determine the genotypic effects and comparative performance of F_2 7x7 diallel population of groundnut in saline field condition. The analysis of variance showed that genotypes effects were highly significant ($P< 0.01$) for all the characters viz., plant height, branch number, shoot biomass, pod number per plant, 100 pod weight, pod yield per plant, kernel weight per plant and shelling percentage (Table 26). This indicated the presence of wide range of variation among the genotypes for all characters in saline field condition. The mean performance showed the variations as estimated by DMRT (0.05) (Table 27).

In saline field condition cross P1xP2 showed the highest pod yield per plant followed by cross P2xP3, P2xP4, P1xP3, P2xP6, P1 and P2xP5 (Table 27). Among them, P2xP3 and P1xP2 showed highest/higher kernel weight and higher shelling %, higher 100 pod weight, higher pod number per plant, higher/average shoot biomass and pod

number per plant. On the other hand, cross P1xP5 showed highest shelling %, but in kernel weight, pod yield and pod number appeared below average value with average yield and 100 pod weight. Shelling % may be increased due to bigger pod size. Cross P1xP4 showed highest shoot biomass and plant height but, in pod yield, kernel weight, 100 pod weight showed below average value. It may due to lower photosynthetic ability and lower assimilate translocation efficiency to reproductive sink of the genotype. The average values of all traits studied in non-saline and saline field condition revealed that the average values are smaller in saline field condition than in non-saline field condition in spite individual performance is different to each other to different field conditions. The results indicates that under salinity stress, plants tend to record low yields because of adverse effects of salinity on such parameters as relative water content, total dry weight, plant height and shoot biomass of plant. This is because of salinity inhibits plant growth by exerting low water potentials, Ion toxicity and ion imbalance. The ability of any genotypes to maintain agronomic parameters at near control levels therefore confers salt tolerance.

The values of phenotypic coefficient of variation (PVC) and genotypic coefficient of variation (GCV) indicated that there were considerable variations for all the traits while number of branches and shelling % showed minimum amount of variations (Table 28). GCV was highest for pod number per plant followed by pod yield per plant, kernel weight per plant, shoot biomass and 100 pod weight indicating high degree of genetic variability in these traits. Heritability estimated in broad sense was relatively high for all the characters except shelling %. It is suggested that heritability estimates along with genetic gain is due to additive gene effect and more useful in predicting the effect for selecting the best individual. Moderate to high estimates of heritability along with high genetic advance in percentage of mean for pod number

per plant, pod yield per plant, kernel weight per plant, shoot biomass per plant, 100 pod weight, and plant height suggests that improvement of these would be improve through selection. Selection for these yield contributing characters could be a source for salt tolerant variants in groundnut.

The results showed that even though there were significant changes within the non-saline and a saline field condition means performance (Table 24 and 27), genetic parameters such as heritability and genetic gain were not adversely affected by the different field conditions. The possible explanation is that the changes in the mean values of the traits as observed in the present investigations were mainly physiological in nature and would be reversed when grown under environments with lower electrical conductivities or salinity. It could therefore be inferred from the study that the yield characters under investigations could successfully be selected among the genotypes for improvement and suitable for saline environments. The F_2 crosses P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 as the most salt tolerant genotypes could serve as a source of genetic material for the improvement of salt tolerant variants.

From above discussion, F_2 population generated from the crosses viz. P2xP3, P1xP2, P2xP4, P1xP3, P2xP6 and P2xP5 can be selected for next improvement and trial to develop high yielding varieties in saline field condition.

CHAPTER VII

REFERENCES

Abdul-Halim R.K., Salih H.M., Ahmed A.A. and Abdulrahim, A.M.(1988). Growth and Development of Maxipak wheat as affected by soil salinity and moisture levels. *Plant and Soil.***112**(2):255-259.

Abrol I.P.(1986). Salt affected soils: An overview in approaches for incorporating drought and salinity resistance in crop plants. pp. 1-23

Adams,P.,Thomas,J.C.,Vernon,D.M.,Bohnert,H.J. andJensen,R.G.(1992).Distinctcellular and organismic responses to salt stress.*Plant Cell Physiol*. **33**(8):1215- 1223

Ahmed, E.M. and Young, C.T.(1982).Composition, quality and flavor ofpeanuts.In: Peanut Science and Technology. H. Pattee and C.T.Young (Editors), American Peanut Research and EducationSociety,Yoakum, Texas, pp 655-688.

Akbar, M. (1986).Breeding for Salinity Tolerance in Rice. In: Prospects for Biosaline Research-Proceedings of US-Pakistan Biosaline Research Workshop. Karachi,Pakistan, pp. 38-54.

Akbar, M. and Yabuno, T. (1977). Breeding saline-resistant varieties of rice. V. Inheritance of delayed type panicle sterility induced by salinity. *Japan. J. Breed*.**27**(3):237-240.

Akbar, M., Khush, G. S. and HilleRisLambers,D.(1986).Genetics of salt tolerance in rice.In:Proceedings of the international rice genetics symposium, IRRI, May 1985, pp. 399-409.

Akbar, M., Yabuno,T. and Nakao,S.(1972).Breeding for saline-resistant varieties of rice.I.Variability for salt tolerance among some rice varieties.*Japan. J. Breed*. **22**(5):277-284.

Alam, M.S., Begum,D.and. Khair, A.B.M.A. (1985a).Study of genetic parametersand character interrelationship in groundnut. *Bangladesh J. Agric. Res.***10**(2):111-117.

Alam, M.S., Rahman, A.R.M.S. and Khair, A.B.M.A. (1985b). Genetic variability and characterassociation in groundnut (*Arachishypogaea* L.).*Bangladesh J. Agric.Res.***10**(4)9-16.

Alam M.K., Nath, U.K., Azad M.A.K., Alam, M.A. and Khan A.A. (2013).Genetic analysis of some agronomic traits in groundnut (*Arachis hypogaea* L.).*Int. J. Agril. Res. Innov. &Tech*. **3**(2): 31-35.

Aldoss, A.A. and Smith, S.E. (1998). Registration of AZ-97MEC and AZ-97MEC-ST very non dormant alfalfa germplasm pools with increased shoot weight and differential response to saline irrigation. *Crop Sci*. **38** (1): 568-568.

Ali, G.M., Murtaza, M., Collins,J.C. and McNeilly, T.(2006). Study of salt tolerance parameters in pearl millet *Pennisetumamericanum*L. *J. Cent. Eur. Agric.***7**(2):365-376.

Apse, M.P., Aharon, G.S.,Snedden,W.A. and Blumwald, E. (1999). Salt toleranceconferred by overexpression of a vacuolar Na^+/H^+antiport in Arabidopsis.*Science.* **285** (5431):1256-1258.

Araya, F., Abarca, O., Zuniga, G. E. and Corcuera, L. J (1991).Effects of NaCl on glycinebetaine and on aphids in cereal seedlings.*Phytochem*.**30**(8): 1793-1795.

Arjunan, A. andGopalakrishnan, S. (1987).Cationic content of groundnut shell as influenced by calcium-sodium interaction.*MadrasAgril. J.***74** (2): 84-88.

Asada, K. (2006). Production and scavenging of reactive oxygen species in chloroplasts and their functions.*Plant Physiol*. **141**(1): 391-396.

Ashihara, H., K. Adachi, M. Otawa, E. Yasumoto, Y. Fukushima, M. Kato, H. Sano, Sasamoto, H. and. Baba, S.(1997). Compatible solutes and inorganic ions in the mangrove plant *Avicennia marina* and their effects on the activities of enzymes.*Z. Naturforsh*.**52**(1): 433-440.

Ashraf, M., (1999).Breeding for salinity tolerance proteins in plants. Crit. Rev. *Plant Sci.***13**(1):17-42 .

Ashraf M., Harris, P.J.C. (2005). Abiotic streses: plant resistance through breeding and molecular approaches, Haworth Press. New York, pp.701-725

Ayoub, A. T. (1976). Salt tolerance of lentil *(Lens esculenta).J. Hort. Sci*. **52** (1): 163-168.

Azad, M. A.K. and Hamid, M.A. (2000).Genetic variability, Character association and pathanalysis in groundnut (*Arachis hypogaea* L.).*Thai. J. Agric. Sci*.**33**(3/4):153-157.

Azad, M. A. K., (2006). Effect of salt stress on growth and some biochemical attributes in two groundnut genotypes. MS thesis, Dept. of Crop Botany, Bangladesh Agricultural University, Mymensingh.

Azad, M.A.K., Hamid, M.A., Islam, M.Z. and Islam, M.A. (2000).Genotype-environment interaction on pod yield stability in groundnut.*Bangladesh J. Agril. Sci*. **27**(2): 239-242.

Azad, M.A.K., Alam, M.S., Hamid, M.A, Rafii, M.Y. and Malek, M.,A. (2014). Combining ability of pod yield and related traits of groundnut (*Arachis hypogaea* L.) under salinity stress. The Scientific World Journal. Hindawi Publishing Corporation.Volume 2014, Article ID 589586, 7 p.

Azad, M.A.K., Alam M.S., Hamid, M.A. and Hossain, M.A. (2013). Low Ca^{2+}/Na^{+} ratioand efficiency of mobilization of Ca^{2+} from shoot tissues to kernel determine salinity tolerance in groundnut (*Arachis hypogaea* L.). *Legume Res.***36**(5) : 396-405.

Azad, M.A.K., Haque, M.M. Hamid, M.A., Yasmin, F. and Golder, M.A.W. (2012).Tolerance to salinity stress in groundnut (*Arachis hypogaea* L.) through osmotic adjustment and undamaged choloroplast. *Legume Res*. **35**(4): 271-284.

Azad, M.A.K. (2008). Genetics of salt tolerance in groundnut (*Arachis hypogaea* L.)Ph.D. dissertation, Dept. of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh.

Azad, M.A.K., Alam M.S. and Hamid, M.A. (2013). Modification of salt tolerance level in groundnut (*Arachis hypogaea* L.) through induced mutation. *Legume Res.***36**(3):224-233.

Azhar, FM. and McNeilly, T. (1988).The genetic basis for salt tolerance in *Sorghum bicolor* (L) Moenchseedlings.*PlantBreed*.**101**(2): 114-121.

Badigannavar, A.K., Kale, D.M. and Murty, G.S.S. (2002).Genetic variability and diversity in groundnut genotypes.*Plant Breed*.**121** (4): 348-353.

Bangladesh Economic Survey, (1998). Ministry of Finance, Finance Division, Economic Advisor Wing, Government of the People's of Republic of Bangladesh. pp.32.

Bagnall, D.J. and King, R.W. (1991).Response of peanut *(Arachishypogaea*L.) totemperature, photoperiod and irradiance. 2. Effect on peg and pod development. *Field Crops Res*. **26**(2): 279-293.

Baker, RJ. (1978). Issues in diallelanalysis.*CropSci.***18**(4):533-536.

BARC, (2005). Fertilizer Recommendation Guide-2005, Bangladesh Agricultural Research Council, Dhaka

BBS.(2012).Year Book of Agricultural Statistics of Bangladesh. Bangladesh Bureau of Statistics, Ministry of Planning. Government of the People's of Republic of Bangladesh, Dhaka, Bangladesh.

Bell, M.J., Bagnall, D.J. and Harch, G. (1991).The effects of photoperiod on reproductive development of peanut *(Arachishypogaea*L.) in a cool subtropicalenvironment. 2. temperature interactions. *Australian J. Agric. Res*. **42**(7): 1151-1161.

Benavides, M.P., Marconi, P.L., Gallego, S.M. Comba,M.E. and Tomaro, M.L. (2000).Relationship between antioxidant defence systems and salt tolerance in *Solanumtuberosum. Australian. J. Plant Physiol*. **27**(3): 273-278.

Beresford, Q., Bekle, H., Phillips, H.andMulcock, J. (2001).The Salinity Crisis Landscapes, Communities and Politics, University of Western Australia, Crawley, Western Australia.pp.324.

Bohnert, H.J. andJensen, R.G. (1996).Strategies for engineering water-stress tolerance in plants.*Trends Biotechnol*.**14**(3):89-97.

Bohnert, H.J., Nelson D.E. and Jensen, R.G.(1995).Adaptations to environmental stresses.*Plant Cell.***7**(7): 1099-1111.

Boshou, L., Young, L., Huifang, J., Shenyu,W. and Peiwu, L. (2003).Development of groundnut cultivars with high oil content.*IAN.* 23:11-12.

Bray EA, Bailey-Serres J. Weretilnyk, E. (2000). Responses to abiotic stress In: Buchanan B. GWajR(eds) Biochemistry and molecular biology of plants. American Society of Plant Physiology, Rockville.

Bunting, A.H. and Elston, J. (1980). Eco-physiology of growth and adaptation in thegroundnut: and essay on structure, partition and adaptation. In: Advance inlegume science, RJ. Summerfield and A.H. Bunting (eds.), Univ. Reading, England, pp.495-500.

Burman, U., Garg, B.K. and Kathju, S. (2002). Interactive effects of saline water irrigationand nitrogen fertilization on growth and metabolism of isabgol*(Plantagoovata*Forsk). *Plant BioI*.**29**(3): 249-255.

Burton, G.W, (1952). Quantitative inheritance in grasses.Proc.Sixth Int. Grassland.pp. 277-283.

Cheeseman, J.M. (1988). Mechanism of salinity tolerance in plants.*Plant Physiol*. **87**(3):547-550.

Cherian, S., Reddy, M.P. and Pandya, J.B. (1999).Studies on salt tolerance in *Avicenniamarina*(Forstk.)Vierh: effect of NaCl salinity on growth, ion accumulation andenzyme activity. *Indian J. Plant Physiol*. **4**(4): 266-270.

Chinnusamy, V., Jaqendorf, A.andZhu, J.K.(2005). Understanding and improving salt tolerance in plants.*Crop Sci*. **45**(1):437-448.

Climate Change Cell (2007).Climate Change and Bangladesh. Climate Change Cell, Dhaka, Department of Environment, Government of the People's Republic of Bangladesh, with support from Comprehensive Disaster Management Programme of the Government of the People's Republic of Bangladesh and its developmentpartners,UNDPandDFID);
vailableat:http://www.climatechangecellbd.org/publications/others/ccbd.pdf.

Cramer, G.R. and Ouarrie, S.A. (2002).Abscisic acid is correlated with leaf growthinhibition of four genotypes of maize differing in their response to salinity. *Func.Plant.Biol*. **29**(1):111-115.

Craufurd, P.O., Prasad P.V.V. and Summerfield,R J. (2002). Dry matter production and rate of change harvest index at high temperature in peanut. *Crop Sci*.**42**(1): 146-151.

Dasberg, S., Bielorai, H., Haimowitz, A. and Erner, Y. (1991).The effect of saline irrigation water on 'Shamouti' orange trees.*Irrig.Sci*.**12**(4): 205-211.

Dhindsa, R.S. and Matowe, W. (1981). Drought tolerance in two mosses correlated with enzymaticdefense against lipid peroxidation. *J. Exp. Bot*. **32**(1): 79-91.

Dierig, D.A., Shannon, M.C. and Grieve, C.M. (2001). Registration of WCL-SL 1 salt tolerant *Lesquerel/a fend/eri*germplasm .*Crop Sci*. **41**(2): 604-605.

Dobrenz, A.K., (1999). Salt tolerant alfalfa. US: Agripro Seeds, Inc, Shawnee Mission, K.S.

Dopp, M., Larther, F. and Weigel, P. (1985).Osmotic adaptation in Australian mangroves.*Vegetation*.**61**(1):247-254.

Dubois, M., Gilles,K.A., Hamilton, J.K., Robers, P.A. and Smith, F. (1956).Colorimetric method for determination of sugars and related substances.*Anal.Chem*.**28**(3): 350-356.

Esechie, H. A., AI-Saidi,A. and AI-Khanjari, S.(2002).Effect of sodium chloride salinity of seedling emergence in chickpea.*J. Agron. Crop Sci*. **188**(3): 155-160 .

Evans, L.T.(1998). Feeding the Ten Billion.Cambridge University Press.pp.247.

FAO.(1990).Food Outlook, 1990. Rome, Italy.

FAO, (2005).Global network on integrated soil management for sustainable use of salt-affected soils. Rome, Italy.FAO Land and plant nutrition management service.http://www.fao.org/ag/agllagll/spush

FAO, (2006).FAO Production Year book, Vo1.60, Rome, Italy.

FAO.(2008).Land and plant nutrition management service. htpp://www.fao. org/ ag/ agl/agll/spush.

FAO. (1996). Fact sheets: World Food Summit-November 1996. Rome, Italy.

FAO. (1989). Production Yearbook: Vol. 42. FAO, Rome.

FAO, (1984).Year Book of Production.Food and Agriculture Organization of the United Nations. Rome. Vol. 57 (177).pp 118.

FAO-UNESCO (1974). FAO-UNESCO Soil Map of the world. Vol.1 Legend, Paris.

Field, D.1. (1995). Land evaluation for crop diversification. Crop Diversification Program (CDP), Department of Agricultural Extension, Dhaka .

Flowers, T.J. and Yeo, A.R. (1995).Breeding for salinity resistance in crop plants-where next.*Australian J. Plant.Physiol.***22**(6): 875-884.

Flowers, Y.J, Troke P.F. and Yeo A.R. (1977).The mechanism of salt tolerance in halophytes.*Ann. Rev. Pl. Physiol*. **28**(1): 89-121.

Flowers, T.J. (1988).Chloride as a nutrient and as osmoticum. In: Advances in Plant Nutrition by B.Tinker and A Lauchli (eds.) vol, 3. New York: Praeger, 55-78.

Flowers, T.J. (2004). Genetics of plant mineral nutrition: Improving crop salt tolerance. *J.Exp.Bot*. **55**(396):307-319.

Flowers,T.J. and Flowers, S.A. (2005). Why does salinity pose such a difficult problem for plant breeders? *Agric. Water Manage*. **78** (1-2):15-24

Foolad, M.R.(1997). Genetic basis of physiological traits related to salt tolerance in tomato, *Lycopersiconesculentum* Mill. *Plant Breed*.**116** (1): 53-58

Foolad, M.R. (2004). Recent advances in genetics of salt tolerance in tomato. *Plant CellTiss. Org. Cult*. **76**(2): 101-1

Ford, C.W. (1984). Accumulation of low molecular solutes in water stress tropical legumes. *Phytochem*.**23**(1):1007-1015.

Fridovich, I. (1986). Biological effects of the superoxide radical.*Arch.Biochem.Biophys.***247**(1):1-11.

Frimpong, A. (2004).Characterization of groundnut (*Arachis hypogaea* L.) in Northern Gana.*PakistanJ.Biol.Sci*.**7(**5):338-842.

Fukuda, A., Nakamura, A.,Tagiri, A.,Tanaka, H., Miyao, A.,HirochikaH. andTanaka,Y.(2004).Function, intracellular localization and importance in salt tolerance of avacuolar Na^+/H^+antiporter from rice.*Plant Cell Physiol***.** **45**(1):146-159.

Garcia, A., Rizzo, C.A., Uddin, J.,Bartos, S.L.,Senadhira, D.,Flowers,T.J. and Yeo, A.R. (1997).Sodium and potassium transport to the xylem are inherited independently in rice, and the mechanism of sodium: potassium selectivity differs between rice and wheat. *Plant Cell Environ*.**20**(9):1167-1174.

Garcia, A., Senadhira, D., Flowers,T.J. and Yeo, A.R. (1995).The effects of selection forsodium transport and of selection for agronomic characteristics upon salt resistance in rice (*Oryza sativa*L.).*Theor. Appl. Genet*. **90**(7-8): 1106-1111.

Garg, B.K., Kathju, S., Vyas, S.P. and Lahiri, A.N. (1997).Sensitivity of clusterbean to salt stress at various growth stages.*Indian J. Plant Physiol*. **2**(1):49-53.

Ghassemi, F., Jakeman, A.J.and Nix, H.A. (1995).Salinisation of Land and Water Resources.Human causes, Extent Management & Case Studies, University of New South Wal,Sydney.526 pp.

Giller, K.E., Nambiar, P.T.C.,SrinivasaRao, B.,DartP.J.and. Day, J.M. (1987).Acomparison of nitrogen fixation in genotypes of groundnut (*Arachishypogaea*L) using 15N dilution.*Biol.Fert. Soils*.**5**(1):23-25.

Girija, C., Smith, B. N. and Swamy, P. M. (2002).Interactive effect of sodium chloride and calcium chloride on the accumulation of proline and glycinebetaine in peanut (*Arachishypogaea*L.).*Environ. Exp. Bot*. **47** (1): 1-10.

Golakia, P.R.; Makne, V.G. and Monpara, B.A. (2005).Heritable variation and associationin Virginia runner and Spanish bunch of groundnut.*Nat. J. PI. Improv*.**7** (1): 50-53.

Gomez, K. A. and Gomez,A. A. (1984).Statistical Procedure for Agricultural Research.SecondEdition.A Willey Inte-Science Publication, John Wiley and Sons, New York.p. 680.

Gossett, D.R., Millhollon,E.P. and Lucas, M.C. (1994).Antioxidant response to NaCIstress in salt tolerant and salt sensitive cultivars of cotton.*Crop Sci*. **34**(3): 706- 714.

Grattan, S.R. and Grieve,C.M. (1999). Salinity-mineral nutrient relations in horticultural crops.*Sci. Hort*., **78**(1): 127-157.

Greenway, H. and Munns,R. (1980).Mechanisms of salt tolerance in non-halophytes.*Annu.Rev.Plant Physiol*. **31**:149-190.

Gregorio, G.B. and Senadhira, D. (1993).Genetic analysis of salinity tolerance in rice.*Theor.Appl.Gen*.**86**(21):333-338.

Griffing, B. (1956).A generalized treatment of the use of daillel cross in quantitative inheritance.*Heredity*.**10**(1): 31-50.

Gu, R., Fonseca, S., Puskas, L.G., Hackler, L. Jr.,Zvara, A., Dudits,D. and Pais,M.S. (2004).Transcript identification and profiling during salt stress and recovery of *Populuseuphratica.Tree Physiol*. **24**(1):265-76

Gupta, I. C. and Yadav, J. S. P. (1986).Crop tolerance to saline irrigation waters.*J. Indian Soc. Soil Sci*. **34** (2): 379-386.

Gupta, K.R. and. Dahiya, B.S. (1986).Inheritance of pod yield traits in pea.*Crop Improv*.**13**(1): 45-48.

Halliwell, B. and Gutteridge,J.M.C. (1985).Free Radicals in Biology and Medicine,Clarendon Press, Oxford.

Halward, TM., Stalker, I.T., LaRue,E.A. and Kochert, G. (1991).Genetic variationtectablewith molecular markers among unadapted germ-plasm resources of cultivated peanut and related wild species.*Genome*.**34**(6):1013-

1020.

Hamid, M.A., Peat,W.E. and Azad, M. A. K. (1996). Pod yield stability in bold seededgroundnut*(Arachishypogaea*L) mutants. *Progress. Agric*. **7**(2): 197-201

Hammons, R.C. (1963). Artificial cross-pollination of *Arachishypogaea* L. with bee collected pollen. *Crop Sci*. **3**(2):562-563.

Haque, M.M. (2006). Salinity stress in groundnut.MS thesis, Dept. of Crop Botany,Bangladesh Agricultural University, Mymensingh, 60p.

Harper, D.B. and Harvey, B.M.R.(1978).Mechanisms of paraquat tolerance in perennial ryegrass II.Role of superoxide dismutase, catalase, and peroxidase.*Plant Cell Environ.***1**(2): 211-215.

Hassegawa, P.M., Bressan, R.A.,Zhu,J.K. and Bohnert, H.J. (2000).Plant cellular and molecular responses to high salinity. Ann. Rev. *Plant. Physio. Plan Mol. Bio.***51(**1):463-499.

Hayman, B.1. (1958). The separation of epistatic from additive and dominance variation in generation means. Heredity **12**(3): 371-390.

Hayman, B.I.(1954). The theory and analysis of diallel crosses.*Genetics*.**39**(6): 789-809.

Hebbara, M., Patil, S.G. and Srinivas, S. (1992).Evaluation of groundnut (*Arachis hypogaea*L.) genotypes.*Karnataka J. Agric. Sci*. **5**(4): 396-398.

Heenan, D.P., Lewin,L.G. and Mccaffery,D.W. (1988).Salinity tolerance in rice varieties at different growth stages.*Australian J. Exp. Agric*. **28**(3):343-349.

Hernandez, J., Jimenez, A.,Mullineaux,P. and Sevilla, F. (2000). Tolerance of pea plants (*Pisumsativum*) to long-term salt stress is associated with induction of antioxidantdefences. *Plant Cell Environ.***23**(8):853-862.

Hernandez, J., Olmos, A.E., Corpas, F.J., Sevilla, F. and Adel Rio, L. (1995).Salt-induced oxidative stress in chloroplasts of pea plants.*Plant Sci.***105**(2): 151-167.

Hibino, T., Lee, B.H., Rai, A.K., Ishikawa, H.,Kojima, H., Tawada, M., Shimoyama,H. and Takabe, T. (1996). Salt EnhancesPhotosystemI Contentand Cyclic Electron Flow via NAD(P)H Dehydrogenase in the HalotolerantCyanobacterium*Aphanothecehalophytica*.*Australian. J. Plant. Physiol*. **23**(1):321-330.

Hossain, M.A., Hossain, A.K.M.Z., Koyoma, H. and Hara, T. (2006).Alleviation of AI-induced oxidative damage by supplying Ca^{+} in wheat seedlings.*BJ.CropSci.***17**(2):427-435.

Hunshal, C.S., Viswanath,D.P., Chimmad, V.P. and Gali, S.K. (1991).Performance of groundnut genotypes undersaline water irrigation.*J. Maharashtra*

*Agric.Univ.***16** (1): 116-117.

Hurd, K.A. (1974). Phenotype and drought tolerance in wheat. Agric. Method.**14**(1-2): 39-55.

Iftekharuddaula, K.M.(2003). Genetic analysis of morpho-physiological characters in diallel crossof rice. MS Thesis. Dept. of Genet. And Plant Breeding. Bangladesh Agril.Univ.Mymensingh.

Imlay, J.A. and Linn, S. (1988).DNA damage and oxygen radical toxicity.*Science* **240**(4857):1302-1309.

Islam, M.M. (2004). Mapping salinity tolerance in rice *(Oryza sativa* L.).Ph.D. dissertation, University of the Philippines, Los Banos, Laguna, Philippines,150p.

Islam, M.N., Islam M.N. and Mowla, G. (1997).Importance of salinity management toprotect environmental degradation in the coastal ecosystem of Bangladesh.Joint IntI.Conf. on Agril.Engg.& Tech. Exhibition '97, Bangladesh Institution of Engineers, Dhaka, pp. 663-669.

Islam, M.S. and Noor, S. (1982). Performance of groundnut under different levels of phosphate fertilizer in grey flood plain soils of Jamalpur. *Bangladesh J. Agril.***7**(1):35-50.

Islam, M.T. (2003). Study on genetic diversity, selection index and relationship of yield and yield attributes of groundnut (*Arachishypogaea* L.). MS Thesis. Department of Genetics and Plant Breeding, Mymensingh.

Iyengar, E.R.R. and Reddy, M.P. (1996). Photosynthesis in highly salt-tolerant plants In: M. Pesserkali (eds), Handbook of photosynthesis, Marshal Dekar, Baten Rose, USA.*J. Agric. Res*.**28** (2): 149-158.

Jain, M., Choudhary,O., Kale, R.K.andSarin, N.B. (2002). Salt and glyphosphate-induced increase in glyoxalate I activity in cell lines of groundnut *(Arachishypogaea*L.) *Physiol.Plant*. **114**(4):499-505.

Jain, M., Mathur, G.,Koul, S. and Sarin, N. B (2001).Ameliorative effects of proline on salt stress-induced lipid peroxidation in cell lines of groundnut *(Arachishypogaea*L.).*Plant CellReports*.**20** (5): 463-468.

James, R.A., Rivelli, A.R.,MunnsR.and von Caemmerer, S. (2002).Factors affecting CO_2 assimilation, leaf injury and growth in salt-stressed durum wheat.*Func.Plant.Biol.***29**(12): 1393-1403.

Janila, P., Rao,T.N., Kumar, A.A. (1999). Germination and early seedling growth of groundnut *(Arachishypogaea*L.)varieties under salt stress.*Annals of Agricultural Research.***20**(2):180-182.

Jeschke, W.O., Aslam, Z. and Green way, H. (1986).Effect of NaCL on ion relations andcarbohydrate status of roots and on osmotic regulation of roots and shoots

ofAtriplexamnicla.Plant Cell Environ. **9**(7):559-569.

Jinks, J.L. (1956).The F_2 and backcross generations from a set of diallel crosses. *Heredity*.**10**(1):1-30.

John, K., Vasanth, R.P. and Venkateswarly, O. (2006).Variability and heritability studies in groundnut (*Arachis hypogaea* L.).*Legume Res*. **29** (3): 225-227.

Johnson, C.M. and Ulrich, A. (1959).Analytical method for use in plant analysis.*Callifornia Agricultural Experimental Station Bulletin.***766**(1): 26-77.

Johnson, H.W., Robinson, H.F. and Comstock,R.E. (1955).Estimates of genetic and environmental variability in soybean.*Agron. J*. 47(7): 314-318.

Joshi, Y.C., Ravindra, V.,NautiyalP.C.andZala, P.V. (1990).Screening for salt tolerance in groundnut.*Groundnut News.***2** (1): 4.

Kadam, P.S. and Panwar, D.V.S. (1999).Genetic divergence in rice.Annals of Biology, Ludhiana.**15**(1): 35-39.

Kaul, A.K. and Das, M.L. (1986).Oilseeds in Bangladesh.Canada-Bangladesh Agriculture Sector Team, Ministry of Agriculture, Government of the People's of Republic of Bangladesh. pp.92-112.

Karim, Z. and Iqbal, A. (2001).Impact of land degradation in Bangladesh Changing Scenario in Agricultural Land Use, Bangladesh Agricultural Research Council, pp.46-47.

Karunakar, AP., Jiotode, O.J. and Nalamvar, R.V. (2002). Basis of variation in pod yield ofkharif groundnut under delayed sowings. *Res. Crops*.**3** (3): 546-550. 133

Khan, M.R.A. (2004). Genetic diversity analysis and its use in yield related characters in groundnut (*Arachishypogaea* L.) M.S. Thesis. Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh.

Kearsey, M.J. and Pooni, S.(1996).The genetic analysis of quantitative traits.Chapman and Hall. London

Keating, B.A. and Fisher, M.J. (1985).Comparative tolerance of grain legumes.*Australian J.Agric. Res.***36**(3): 373-383.

Kennedy, B.F. and De Fillippis, L.F. (1999).Physiological and oxidative response to NaCl of the salt tolerant *Grevilleailicifolia*and the salt sensitive *Grevillea arenaria.J. Plant Physiol*. **155**(6): 746-754

Kerepesi, I. and Galiba, G. (2000).Osmotic and salt stress-induced alteration in soluble carbohydrate content in wheat seedlings.*CropSci*.**40**(2)**:** 482-487.

Khan, M.A., Ungar, I.A. and Showalter, A.M. (2000). Effects of sodium chloride treatments on growth and ion accumulation of the halophyte *Haloxylonrecurvum.*Commun.*Soil Sci. Plant Anal*. **31**(17-18) :2763-2774.

Khatkar, D. and Kuhad, M.S. (2000). Short-term salinity induced changes in two

wheat cultivars at different growth stages. *Biol.Plant*. **43**(4): 629-632.

Killick, R.J. and. Malcolmson, J. K.(1973).Inheritance in potatoes of field resistance to late blight (*Phytophthorainfestans). Physiol.Plant.Pathol*. **3**(1): 1221-1231.

Knight, H., TrewavasA.J.and Knight, M.R. (1997).Calcium signaling in *Arabidopsis thaliana* responding to drought and salinity.*Plant J.***12**(5):1067-1078.

Krapovickas, A. and Gregory, W.C. (1994). Taxonomĭadelgėnero *Arachis* (Leguminodae). *Bonplandia.* **8**(1): 1-186

Krause, G.H. (1994). The role of oxygen in photoinhibition of photosynthesis. In: Causes of photooxidative stress, amelioration of defense system in plants. pp. 40-62.

Krishna, T.M., John, K.,Vasanthi, R.P.,Ramaiah, M.,Venkateswarly, O. and Naidu, P.N. (2006). Variability studies in groundnut germplasm. *Legume Res*. **29** (3): 219-220.

Krishnamurty, L., Reddy, B.V.S. and Serraj, R. (2003a).Screening pearl millet germplasmfor tolerance to salinity.*International Sorghum and Millets Newsletter*.**44**(6):90-92.

Krishnamurty, L., Rai, K.N., HashC.T. and Serraj, R. (2003b). Screening sorghum germ plasmfortolerance to salinity.*International Sorghum and MilletsNewsletter*.**44**(5):155-157.

Kumar, C.V.S. and Rajmani, S. (2004). Genetic variability and heritability in groundnut (*Arachishypogaea* L.).*Prog.Agric*.**4** (1): 69-70.

Kumar, R.,Ghos, J. and Sah, J.N. (1998).Variability and correlation studies in mutant cultures of groundnut.*J. Appl. Biol*. **8**(2): 20-23.

Kumar, S. and Patel, S.(1996).Crossing technique in groundnut *(Arachishypogaea*L.).*Indian J. .Agric. Sci*. **66** (10):589-593.

LatifAkanda, M.A.,Alam, M.S. and Shamsuddin, A. K. M. (1995).Genetic variability, correlation and path coefficient of yield and its components in groundnut (*Arachis hypogaea* L.).*Bangladesh J. Pl. Breed.Genet.***8**(1&2) : 39-44.

Lauchli, A. and Schubert, S. (1989). The role of calcium in the regulation of membrane and cellular growth processes under salt stress. NATO ASI Ser. G19, pp. 131-137.

Lauter, D., Meiri, A., Federman, A. and Plaut, Z. (1988). The growth and development of peanut pods in a saline pod zone. *Hassadeh*.**68** (9): 1689-1691.

Lee, D.H., Kim,Y.S. and Lee, C.B. (2001).The inductive responses of the antioxidantenzymesby salt stress in the rice *(Oryza sativa* L.).*J. Plant Physiol*.

158(6): 737-745.

Lee, H., Lee, H.S. and Lee, S.H. (1998). Introduction, development and characterization of supernodulatingsoybeanincefantnitrate inhibition of nodulation and nitrogen fixation in supernodulating soybean mutant. *Korea J. of Crop Sci*. **43** (1): 23-27.

Liu, J. and Zhu, J.K. (1997). An *Arabidopsis* mutant that requires increased calcium for potassium nutrition and salt tolerance. Proc. Natl. Acad. Sci. USA 94, pp. 14960-14964.

Lyon, C. (1941). Responses of two species of tomatoes and the F_1 generation to sodium sulphate in the nutrient medium.*Bot. Gaz*.**103**(1): 107-122.

Makhan, L., Roy, D. and Ojha, O.P. (2003).Genetic variability and selection response for root and other characters in groundnut (*Arachishypogaea* L.).*Legume Res*. **26** (2): 128-130.

Maliwal, G.L.(1997). Response of wheat varieties to chloride and sulphatedominantsalinity.*IndianJ.Plant Physiol*. **2**(3):225-228.

Manzoor, A., Mohammad,A. and Niazi, B. H. (1986).Effect of Rhizobia inoculation on growth and crude protein/nitrogen contents of lentil in relation to soil salinity.*Lens-News l*.**13** (2): 16-19.

Mass, E.V. and Hoffman, G.J. (1977).Crop salt tolerance- current assessment.*Journal of Irrigation and Drainage Division, ASCE,***103** (IR2):115-134.

Mather, K. and Jinks, J.L. (1971).Introduction to Biometrical Genetics.Chapman and Hall, London, UK.

Maurel, C. and Chrispeels, M.J. (2001).Aquaporins, a molecular entry into plant water relations. *Plant Physiol*. **125**(1): 135-138

Mehler, A.H. (1951). Studies on reactivity of illuminated chloroplasts. I. Mechanism of the reduction of oxygen and other Hill reagents. *Arch. Biochem. Biophys*.**33**(1):65-77.

Mendoza, I., Rubio, F., Rodriguez-Navarro A. and Prado, J.M. (1994). The proteinphosphatase calcineurin is essential for NaCl tolerance of *Saccharomyces cerevisiae.J. Biol.Chem.***269**(12):8792-8796.

Mensah J. K., Akomeah P.A., Ikhajiagbe B. and Ekpekurede E.O. (2006).Effects of salinity on germination, growth and yield of five groundnut genotypes.*African Journal of Biotechnology*.**5**(20):1973-1979.

Mittova, V., Tal, M., Volokita, M. and Guy, M. (2002). Salt stress induces up-regulation of an efficient chloroplast antioxidant system in the salt-tolerant wild tomato species *Lycopersiconpennellii*but not in the cultivated species. *Physiol. Plant*. **115**(3): 393-400.

Mittova, V., Tal, M., Volokita,M. and Guy,M. (2003).Up-regulation of the leaf

mitochondrial and peroxisomal anti oxidative systems in response to salt-induced oxidative stress in the wild salt-tolerant tomato species *Lycopersiconpennellii.Plant Cell Environ*. **26**(6): 845-856.

Moeljopawiro, S. andIkehashi, H. (1981).Inheritance of salt resistance in rice.*Euphytica*.**30**(2): 291-300

Montero, E., Cabot, C., Poschenrieder,Ch. and Barcelo,J. (1998).Relative importance of osmoticstress and ion-specific effects on ABA-mediated inhibition of leaf expansion growth in *Phaseolusvulgaris.Plant Cell Environ*. **21**(1): 54-62.

Munns, R., James, R.A. and Lauchli, A. (2006).Approach to increasing the salt tolerance of wheat and other cereals.*J. Exp. Bot*. **57**(5):1025-1030.

Munns, R. and Cramer, G.R.(1996). Is coordination of leaf and root growth mediated byabscisic acid? (Opinion).*Plant and Soil*.**185**(1):33-49.

Munns, R. and James, R.A. (2003). Screening methods for salinity tolerance: a case studywithtetraploid wheat. *Plant and Soil*.**253**(1):201-218.

Munns, R., Husain, S., Rivelli, A.R.,James, R.A., Condon, A.G.,Lindsay, M.P.,Lagudah, E.S., SchachtmanD.P. and Hare,R.A. (2002). Avenues for increasing salt tolerance of crops, and the role of physiological based selection traits. *Plant and Soil*.**247**(1): 93-105.

Muralia, S. and DivakaraSastry, E.V.(2001).Combining ability for germination and seedling establishment characters in bread wheat *(Triticumaestivum)* under normal and saline environments.*Indian J. Genet*.**60**(1):69-70.

Naazar, A., Malik, S.N.,Khurram, B. and Mirza.M.Y.(2000).Genetic variability, heritability and correlation studies in groundnut.*Sarhad J. Agric*. **16** (5): 533-536.

Nath, U.K. (2001). Study on genetic diversity and in vitro regeneration potentiality of groundnut. MS Thesis. Department of Genetics and Plant Breeding, Mymensingh.

Nautiyal, P. C., Ravindra, V. and Joshi, Y.C. (1989).Germination and early seedling growth of some groundnut (*Arachishypogaea* L.) cultivars under salt stress.*Indian J. Plant Physiol*.**32** (3): 251-253.

Nautiyal, P.C., Bandyopadhyay, A., Koradia, V.G., Madhubhai, M. and Makad, M. (2000).Performance of groundnut germ plasm and cultivars under saline waterirrigation in thesoils of Mundra in Gujarat, *India. IAN*, **20**(1): 80-82.

Neele, A. E. F., Nab H.J. and Lowes, K.M. (1991). Identification of superior parents in a potato breedingprogramme.*Theor. Appl. Genet*. **82**(3):264-272.

Nelson, N. (1944).A photometric adaptation of theSomogyi method for determination of glucose.*J. BioI. chern*. **153**(2): 375-380.

Nelson, T. (1991).Leaf vascularpattern formation.*Plant Cell*.**9**(7): 121-135.

Nigam, S.N.,NageswaraRao, R. C. and Wynne, J. C (1998).Effect of temperature and photoperiod on vegetative and reproductive growth of groundnut *(Arachishypogaea*L.).*J. Agron. Crop. Sci*. **181**(2):117-124.

Nigam, S.N., NageswaraRao, R. C., Wynne, J. C.,Williams, J.H., FitznerM. andNagabhushanam, G. V. S (1994).Effect and interaction of temperature and photoperiod on growth and partitioning in three groundnut *(Arachishypogaea*L.) genotypes.*Annals Appl. Biol*.**125**(3): 541-552.

Orthen, B., Popp, M. and Smirnoff, N. (1994).Hydroxyl radical scavenging properties of cyclitols. Proc. R. Soc. Edinburg Sect. B **102**(1): 269-272.

Owen, P.A., Nickell, C.D., Noel,G.R.,Thomas D.J. and Frey, K.(1994).Registration of saline soybean.*Crop Sci*. **34**(6):1689.

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding.*Indian J. genet.Pl.Breed.***17**(1):318-38.

Patel, M.S., Gundalia, J.D. and Polara,K.B. (1992).Evaluation of salt tolerance of different groundnut*(Arachishypogaea*L.) genotypes.*Gujarat Agricultural UniversityResearch Journal*.**18**(1): 17-23.

Pathak, V.D., Patel C.V.J.and Pathani, K.V. (1993). Variability studies in bunch and spreading types of groundnut in high and low fertility levels. *Gujarat Agricultural University Research Journal*.**19**(1): 164-168.

Patil, S. L., Hunshal, C. S., Nadagouda, B.T., Kori, R. N. and Salakinakop, S. R. (1996). Dry matter accumulation in gram as influenced by saline water irrigation.*Advances in Agric. Res. India*, **6**(23): 78-87.

Pattee, H.E., Jones, EB.,Singleton,J.A. and Sanders, T.A. (1974).Composition Changes of Peanut Fruit Parts DuringMaturation. *Peanut Science*.**1**(2): 57- 62.

Petersen, L. and Shireen, S. (2001). Soil and water salinity in the coastal area of Bangladesh.SRDI.

Peraz-Alfocea, F., Estan, M.T.,Caro, M. and Guerrier, G. (1993).Osmotic adjustment in *Lycopersiconesculentum* L penelliundrNaCI and PEG 6000 iso-osmotic stresses.*Physiol.Plant*. **87**(2):493-498.

Pilon-Smits, EA.H.,Ebskamp, M.J.M.,Paul, M.J.,Jeuken, M.J.W. , Weisbeek, P.J. andSmeekens, S.C.M. (1995). Improved performance of transgenic fructan-accumulating tobacco under drought stress. *Plant Physiol*. **107**(1):125-130.

Plaisted, R.L.L., Sandorf, W.T., Federer,W.T., Kehr,A.E. and Peterson, L.C. (1962).Specific and general combining ability for yield in potatoes.*Am. Potato J.* **39**9(1):185-197.

Ponnamperuma, F.N. and Bandyopahya, A.K. (1980). Soil salinity as a constraints on food production in the humid tropics. In soil related constraints to food production in the tropics. IRRI. Philippines. pp. 203-216

Prakash, B.G.; Khanure, S.K. and Sajjanavar, G.M. (2000). Variability studies in spreading groundnut. *Karnataka J.Agril.Sci*.**13**(4): 988-990.

Prasad, P.V.V., Boote, K.J.,Allen,L.H. Jr. and Thomas, J.M.G. (2003). Super-optimaltemperatures are detrimental to peanut *(Arachishypogaea*L.) reproductive processes and yield at both ambient and elevated carbon dioxide. *Global Change Biol.***9**(12): 1775-1787.

Prasad, P.V.V., Craufurd, P.Q. and Summerfield, RJ.(2000).Effect of high air and soil temperature on dry matter production, pod yield components of groundnut.*Plant and Soil.***222**(1-2): 231-239.

Rahman, M.M. and Ahsan, M. (2001). Salinity constraints and agricultural productivity in coastal saline area of Bangladesh, Soil Resources in Bangladesh: Assessment and Utilization.

Rahman, S.M. (1992). Salinity problems and crop production in Bangladesh.Proceedings of the first Biennial conference of the crop science society of Bangladesh.pp.198-204.

Reddy, L.J.andKaul, A.K. (1986).Status and prospects of groundnut in Bangladesh.Bangladesh Agricultural Research Council, Dhaka pp.9-10.

Reddy, M.P., Sanish,S. and lyengar,E.R.R. (1992). Photosynthetic studies and compartmentation of ions in different tissues of *Salicomia brachiate* Roxb. under saline conditions. *Photosynthetica.***26**(1):173-179.

Reddy, K.R. and Gupta,R.V.S. (1992).Variability and interrelationship of yield and its components of characters in groundnut.*J. Maharashtra Agric. Univ*. **17**(2): 224-226.

Ren, H., Gao, Z.,Chen, L.,Wei, K.,Liu, J.,Fan, Y.,Davies, W.J.,JiaW. and Zhang, J. (2006). Dynamics of ABA accumulation in relation to the rate of ABA catabolism in maizetissues under water deficit.*J.Exp. Bot*. **57**(2):1-9.

Rhodes, D. and Hanson, A.D. (1993). Quaternary ammonium and tertiary sulphonium compounds in higher plants. Annu.Rev. Plant Physiol. *Plant Mol. Biol*.**44**(1):357- 384.

Rhodes, J.D. and Loveday (1990).Salinity in irrigated agriculture.American Society of Engineers.Irrigation of Agricultural Crops (EDS). Steward BA, Nilson DR. *Am. Soc. Agron. Mono*.**30**(1): 1089-1142.

Robbelen, G. (1991). Mutation breeding for quality improvement- a case study for oil seed cropsIn: Plant mutation breeding for crop improvement. Vo1.2. Proc. Symp.18-22 June, 1990, FAOIIAEA, Vienna, Austria.

Saha, K. and Gupta,K. (1997). Effect of NaCI Salinity on ethylene production and metabolism in sunflower seedlings. *Indian J.Plant Physiol.***2**(2):127-130.

Singh, M. and Jain, R. (1989). Factors affecting goatweed (*Scopariadulcis*) seed germination. Weed Sci. **37**(6): 766-770.

SAIC (SAARC Agricultural Information Center).(2000). Statistical Bulletin of SAARC, Dhaka, Bangladesh.

SAIC (SAARC Agricultural Information Center).(2003). Statistical Bulletin of SAARC, Dhaka, Bangladesh.

SAIC (SAARC Agricultural Information Centre). (2005).Statistical Bulletin of SAARC, Dhaka, Bangladesh.

Sakurai, J., Ishikawa, F.,Yamaguchi, T.,Uemura,M. and Maeshima, M. (2005).Identification of 33 rice aquaporin genes and analysis of their expression and function.*Plant Cell Physiol*. **46**(9): 1568-77

Saranga, Y., D.Zamir.,Marani,A and Rudich,J. (1991). Breeding tomatoes for salt tolerance-field-evaluation of Lycopersicongermplasm for yield and dry-matter production.*Journal of the American Society for Horticultural Science*.**116**(6),1067-1071.

Sarkar, P. (2001). Study on the variation o morphological traits of 15 groundnut genotypes. MS Thesis. Department of Genetics and Plant Breeding, Mymensingh.

Satakopan, V. N. and Rajendran, L. (1989). Changes inproline levels in germinating groundnut seeds under different stress conditions. *Current Res. Univ. Agril. Sci. Banglore.* **18** (1): 8-10.

Sauter, A., Davies, W.J. and Hartung, W. (2001). The long distance abscisic acid signal in thedroughted plant: the fate of the hormone in its way from root to shoot. *J. Exp. Bot.* **52**(363): 1991-1997.

Schroeder, J.I., Allen, G.J.,Hugouvieux, V., Kwak, J.M. and Waner, D. (2001). Guard cell signal transduction. *Ann. Rev. Plant Physiol. Plant Mol. BioI.***52**(1):627-658.

Sehmer, L., Alaoui-Sosse,B. and Dizengremel, P. (1995).Effect of salt stress on growth and on the detoxyfying pathway of pedunculate oak seedlings *(Quercusrobur*L.).*J. Plant Physiol.***147**(1): 144-151

Sekhar, M. R. (1994). Salt tolerance of mungbean*(Vignaradiata*L.Wilczek) at germination stage.*Annals Agric. Res.***15** (1): 90-91.

Shabala, S., Shabala, L., Van Volkenburgh, E.and Newmann, I. A.(2005). Effect of divalentcationson ion fluxes and leaf photochemistry in salinized barley leaves. *J. Exp. Bot.***56**(415):1369-1378.

Shabala, S.N., Shabala, S.1.,Martynenko, A.I.,Babourina,O. and Newmann, L.A.(1998).Salinity effect on bioelectric activity, growth, Na^+ accumulation and chlorophyll fluorescence of maize leaves: a comparative survey and prospects for screening. *Aust. J. Plant PhysioI*.**25**(5):609-616.

Shalhevet, J., Reiniger, P. and Shimsi, D. (1969).Peanut response to uniform and non-uniform soil salinity.*Agronomy Journal*.**61**(3) :384-387.

Sharma, A.K. and Saran, B. (1994).Effect of salinity on germination and seedling growth in black gram (*Phaseolusmungo* L.).*Neo-Botanica*.**2** (1): 57-59.

Sharma, S.K. (1997). Plant growth, photosynthesis and ion uptake in chickpea as influenced by salinity.*Indian J. Plant Physiol*. **2**(1): 171-173.

Sharma, J.R. (1999).Principles and practice of plant breeding. Tata McGrawhili Publishing Company Limited, New Delhi.

Sharma, Y., Tiwari, C.,Verma, B.L. and Singhania, R.A.(2003).Effect of mixing of saline and canal water on yield of groundnut and wheat.*Crop Res. Hisar*. **26** (2): 249- 253.

Sibole, J.V., Cabot, C., Poschenrieder, C. and Barcelo, J. (2003).Efficient leaf ion partitioning, an overriding condition for abscisic acid-controlled stomatal and leaf growth responses to NaCI salinization in two legumes.*J. Exp. Bot*. **54**(390):2111-2119

Sibole, JV., Montero, E., Cabot, C., Poschenrieder, C. and Barcelo, J. (1998). Role of sodium in the ABAmediated long-term growth response of bean to salt stress.*Physiol.Plant.***104**(3): 299-305.

Sibole, JV., Montero, E., Cabot, C., Poschenrieder, C. and Barcelo, J. (2000). Relationship between carbon partitioning and Na^+, cr and ABA allocation in fruits of salt- stressed bean. *J. Plant Physiol*.**157**(6): 637-642

Silberbush, M. and Ben, A. J. (1989).The effect of NaCI concentration on NO_3^-, K^+ and orthophosphate-P influx to peanut roots.*ScientiaHorticulturae*, **39** (4): 279- 287.

Silberbush, M. and Lips, S. H. (1988).Nitrogen concentration, ammonium nitrate ratio and NaCI interaction in vegetative and reproductive growth of peanuts.*PhysiologiaPlantarum.***74** (3): 493-498.

Singh, S.(1990). Bias caused by epistasis in the estimates of additive and dominance components and their interaction with environment in wheat. *Indian J. Genrt.***50**(2): 157-160.

Singh, S.B. and Chaubey, A.K. (2003). Variability and association amongst quantitative characters in Pea nut (*Arachis hypogaea* L.). *New Agrist*.**14** (1/2): 97-101.

Singh, S.B. and Singh, J.P. (1999).Correlation analysis of growth and yield components in groundnut.*J. Maharastra Agric. Univ*. **17**(2): 224-226.

Singh, R.K. and Chaudhury, B.D.(1985).Biometrical methods in quantitative genetic analysis.Kalyani Publishers, New Delhi.pp.239-267.

Singh, S.K., Sharma, H.C.,Goswami, A.M.,Dattaand,S.P. and Singh, S.P. (2000).In vitro growth and leaf composition of grapevine cultivars as affected by sodium

chloride.*BioI.Plant.***43**(2):283-286.

Sinha, T.S. and Haque, A. (1999).Effect of salinity on ionconcentration in the leaves of Indian mustard *(Brassica juncea*L.). In: Plant physiology for sustainable Agriculture by G.C. Srivastava, Karan Singh and Madan Pal (eds.). Pointer Publishers, Jaipur, India, pp.370-379.

Sokol, M.J. and Baker, R.J. (1977). Evaluation of the assumptions required for the genetic interpretation of diallel experiments in self pollinating crops. *Can.J.PlantSci*.**57**(4):1185-1191.

Spychalla, J.P. and Desborough, S.L. (1990).Superoxide disrnutase, lcatalase and alpha- tocopherol content of stored potato tubers.*Plant Physiol.* **94**(3):1214-1218.

SRDI.(2003). Soil salinity in Bangladesh 2000. Soil Resource Development Institute,Ministry of Agriculture, V7215. pp. 90-91.

Sreenivasulu, N., Grimm, B.,Wobus,U. and Weschke, W. (2000).Differential response of antioxidant compounds to salinity stress in salt-tolerant and salt-sensitive seedlings of fox-tail millet *(Setariaitalica). PhysioL Plant*. **109**(4): 435-442.

Srivastava, N., Sharma, V. Srivastava, N. and Sharma, V. (1998).Effect of salinity on growth, Na^+ and Cl^- ion content and membrane ATPases in peanut *(Arachishypogaea*L).*Plant PhysioL and Biochemistry*.**25**(2): 83-88.

Srivastava, N. (2006). Identification and field-testing of salinity tolerant groundnut in saline areas of India.Progress Report for IFAR, ICRISAT, Patancheru 502324,Andhra Pradesh, India.pp.1-4.

Subbarao, G.V., C. Johansen, J.V., Kumar Rao, D.K. and. Jana. M.K. (1990).Salinity tolerance in F_1 hybrids of pigeonpea and a tolerant wild relative.*Crop Sci*. **30**(4), 785-788.

Suga, S., Komatsu,S. and Maeshima, M. (2002). Aquaporin isoforms responsive to salt and water stresses and phytohormones in radish seedlings. *Plant Cell Physiol*. **43**(10): 1229-1237

Szaboles, I. (1987). The global problems of salt affected soils. *ActaAgronomicaHunarica*.**36**(1):159-172.

Takemura, T., Hanagata, N.,Sugihara, K.,Baba, S.,Karube,I. and Dubinsky, Z. (2000).Physiological and biochemical responses to salt stress in the mangrove, *Bruguieragymnorrhiza, Aquat.Bot*. **68**(1): 15-28.

Tal, M. and Shannon,M.C. (1983). Salt tolerance in two wild relatives of the cultivated tomato: Responses of *Lycopetsiconesculentum, L. cheesmani, L. peruvianum, Solanumpennelli,* and F_1 hybrids of high salinity. *Australian J. Plant Physiol*.**10**(1): 109-117.

Talwar, H.S., Takeda, H.,Yashima,S. and Senboku, T. (1999).Growth and photosynthetic responses of groundnut genotypes to high temperature.*Crop*

Sci.**39**(2): 460-466.

Tester, M. and Davenport, R.(2003). Na^+ tolerance and Na^+ transport in higher plants. *Annals Bot*. **91**(5):503-527.

Tyerman, S.D. and Skerrett, I.M. (1998). Root ion channels and salinity. *Sci. Hort*. **78**(1-4):175-235

Uddin, M.J., Chowdhury, M.A.Z., Sultan, M.K. and Mitro, B.N. (1995).Genetic variability, correlation and path analysis in groundnut.(*Arachis hypogaea* L.).*Bangladesh J. Sci. Ind. Res*.**30** (2-3): 235-241.

Upadhyaya, H.D. and Nigam, S.N. (1999).Detection of epistasis for protein and oil contents in oil quality parameters in peanut.*Crop Sci*. **39**(1): 115-118.

Vadez, V., Krishnamurthy, L., Serraj, R., Gaur, P.M.,Upadhyaya, H.D., Hoisington,D.A., Varshoey, R.K.,Turner,N.C. and Siddique, K. H. M. (2007). Large variation in salinity tolerance in chickpea is explained by differences in sensitivity at the reproductive stage. *Field Crops Res*. **104**(1-3):123-129.

Vadez, V., Srivastava, N., Krishnamurthy, L., Aruna, R. and Nigam, S. N. (2005).Standardization of a protocol to screen for salinity tolerance in groundnut.*IAN*.**25**(1):42-47.

Valls, J.F.M. and Simpson, CE. (2005). New species of *Arachis* L. (Leguminosae) from Brazil, Paraguay and Bolivia.*Bonplandia*.**14**(1/2): 35-64.

Venkataramana, P. (2001). Variability and correlation studies in groundnut.*Crop Res. His*.**21**(1): 81-83.

Verhalen, L.M., Walter, C.M., AI-RaweeBaha, A., Kwee-chong, F. and Murray, J.C. (1971).A diallel analysis of seversl agronomic traits in upland cotton *(Gossypiumhirsutum*L.).*Crop Sci*. **11**(1):92-96.

Verma, O.P. and Srivastava, H.K (2004).Genetic component and combining ability analyses in relation to heterosis for yield and associated traits using three diverse rice growing ecosystems.*Field Crop Res*. **88**(2): 91-102.

Very, A.A., Robinson, M.F., Mansfield, T.A. and Sanders, A. (1998). Guard cells cationchannels are involved in Na-induced stomatal closure in halophyte. *Plant J*.**14**(5):509-521.

Wahhab, M.A., Mondal, M.R.I., Alam, M.S., Ahmed, M.U. and Begum, F. (2002).Status of oil crop production in Bangladesh, Oilseed Research centre. BARI. Joydevpur, Gazipur-1701, Bangladesh.pp.83.

Wang,Y. and Nil, N. (2000). Changes in chlorophyll ribulosebiphosphate carboxylase-oxygenase.Glycinebetainecontent.photosynthesis and transpiration in *Amaranthus tricolor* leaves during salt stress.*J. Hortic. Sci. Biotechnol*. **75**(6): 623-627.

Wild, A.(2003). Soils, land and food: managing the land during the twenty- first century. Cambridge, UK, Cambridge University Press.

Wise, R.R. and Naylor, A.W. (1987).Chilling-enhanced photooxid~tion evidence for the role of singlet oxygen and endogenous antioxidants.*Plant Physiol*. **83**(2): 278-282.

Woodroof, L.G. (1983). Peanuts, processing, products (3rd.ed.). AVI Publishing,Connecticut.

Yamme, K., Rahman, M.S., Kawasaki, M., Taniguchi M. and Miyaqke, H. (2004). Pretreatment with antioxidants decreases the effects of salt stress on chloroplast ultra structure in rice leaf segments (*Oryzasativa*L.). *Plant Prod. Sci*. **7**(1):292-300.

Yancey, P., Clark, M.E., Had, S.C., Bowlus, R.D. and Somero, G.N. (1982). Living with water stress evolution of osmolyte system. *Science*.**217**(4566):1214-1222 .

Yasin, M., Zahid, M. A.,Ghafoor, A., Ahmad, Z., Ahmad, R. and Malik, K.A. (2002).Genotypic behavior of lentil *(Lens culinaris*Medik) towards salinity.Prospects for saline agriculture.National Agricultral Research Center, Islamabad,Pakistan. pp. 231-235.

Yemm, E.W. and Cocking, E.C. (1955). Determination of amino acids with ninhydrin: *Analyst*.**80**(948):209-230.

Yeo, A.R. and Flowers,T.J. (1986).Salinity Resistance in Rice and a Pyramiding Approach to Breeding Varieties for Saline Soils. In: Plant Growth, Drought, andSalinity. N.C. Turner and J.B. Passioura. (ed.). Growth, Drought, and Salinity.CSIRO, Melbourne, Australia.pp.161-173.

Yeo, A.R. (1998). Molecular biology of salt tolerance in the context of whole plant physiology.*J. Exp. Bot*.**49**(323), 915-929.

Yeo, A.R.(1999). Predicting the interaction between the effects of salinity and climate change on crop plants.*Sci.Hortic*. (Amsterdam) **78**(1-4):159-174

Yogendra, P.L.,Verma, A.K., Haider, Z.A., Mahto, J., Prasad, Y. and Mahto, J. (2002). Variability studies in Spanish bunch groundnut. *J. Res.***14**(1): 91-93.

Young ND, Weeden NF and Kochert, G. (1996).Genome mapping in legumes (Family Fabaceae). In: Genome mapping in plants (Paterson AH, Ed.). Landes Biomedical Press, Austin, 212-227.

Yupsanis, T., Kefalas, P. S., Eleftheriou, P. and Kotinis, K. (2001).RNase and DNaseactivitiesinthe alfalfa and lentil grown in iso-osmotic of NaCI and manitol.*J. Plant Physiol.* **158**(7):921-927 .

Zhifang, G. and Loescher, W.H. (2003). Expression of a celery mannose 6-phosphatereductase in *Arabidopsis thaliana* enhances salt tolerance and induces biosynthesis of both mannitol and a glucosyl-mannitol dimmer. *Plant CellEnviron*. **26**(2): 275-283.

Zhu, J.K. (2003).Regulation of ion homeostasis under salt stress.*Curr.Opin.Plant Biol*.**6**(5): 441-445.

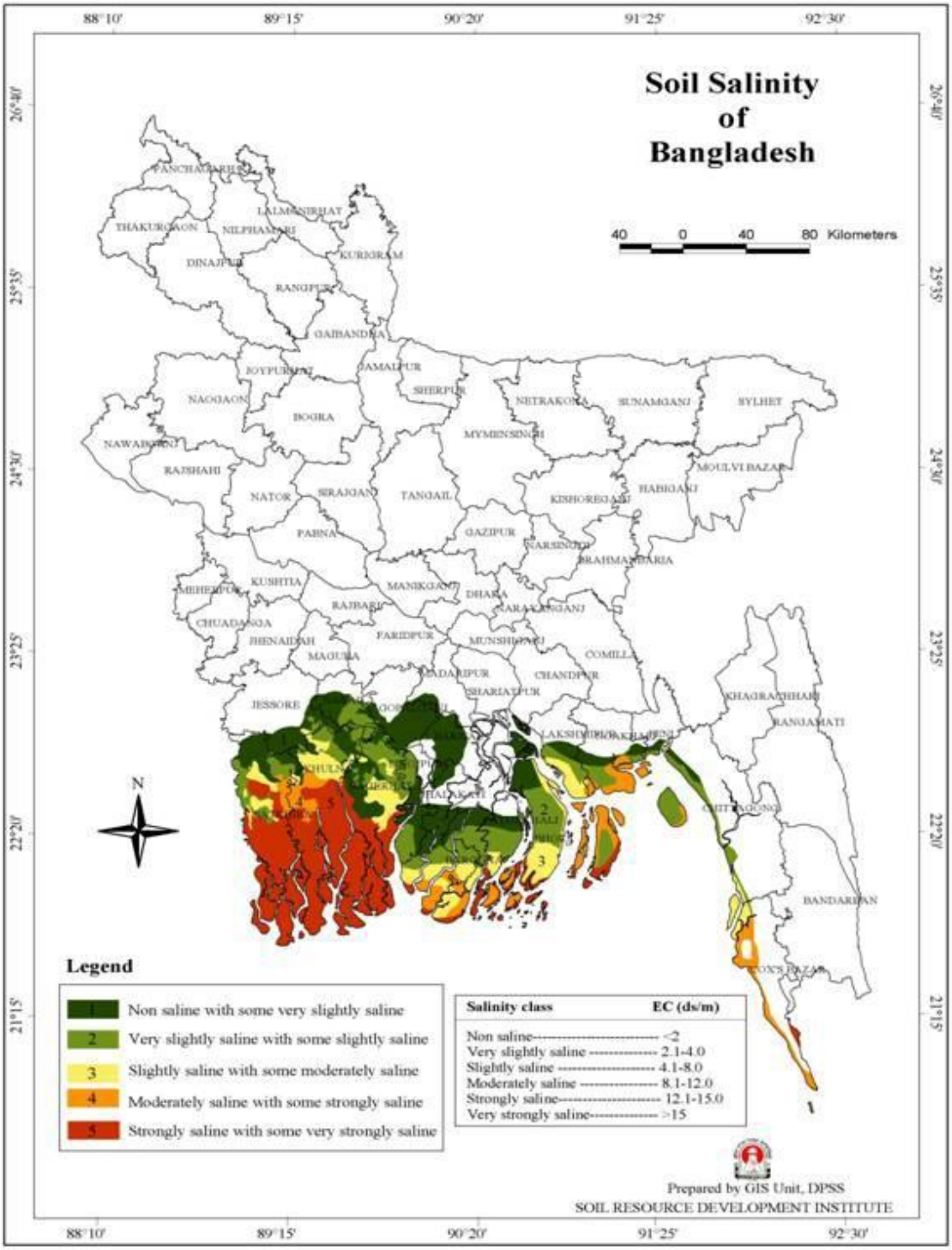
Zhu, J.K., Shi, J.,Singh, U.,Wyatt, S.E.,Bressan, R.A.,Hasegawa P.M. and Capita,N.C. (1993).Enrichment of vitronectin and fibronectin like proteins in NaCI-adapted plant cells and evidence for their involvement in plasma membrane-cell wall adhesion.*Plant J*.**3**(5):637-646.

.

CHAPTER VIII

APPENDICES

Appendix I. Saline prone area of Bangladesh



Appendix II. Salinity affected areas in the coastal and offshore region of Bangladesh.

Description	Total cultivated area	Saline area	Area of each salinity class (ha) (dS/m)				
			S_1 (2.0-4.0)	S_2 (4.1-8.0)	S_3 (8.1-12.0)	S_4 (12.1-16.0)	S_5 (>16.0)
Non-saline with very slightly saline	4,25,490	1,15,370 (27%)	82,260 (72%)	31,590 (27%)	1,520 (1%)	0	0
Very slightly saline with slightly saline	4,20,420	3,09,190 (73%)	1,70,380 (55%)	1,10,390 (35%)	29,420 (10%)	0	0
Slightly saline with moderately saline	2,57,270	2,40,220 (93%)	35,490 (15%)	1,13,890 (47%)	61,240 (26%)	25,870 (11%)	2,650 (1%)
Moderately saline with strongly saline	1,98,890	1,98,890 (100%)	1,630 (1%)	36,060 (18%)	73,400 (37%)	55,130 (28%)	32,750 (16%)

Source: Soil salinity in Bangladesh (SRDI) 2000

Appendix III. Soil salinity classes on the basis of EC (dS/m)

Class	EC (dS/m)	Salinity level	Plant growth
0	0-2	Non-Saline	Salinity effect most negligible
S1	2.1-4	Slightly Saline	Growth and yield of sensitive crops may be restricted
S2	4.1-8	Moderately Saline	Yield of many crops restricted
S3	8.1-15	Saline	Only tolerant crops yield satisfactory
S4	>15	Strongly Saline	Only very tolerant crops yield satisfactory

Source: Rahman, 1992

Appendix IV. Homogeneity test for hypothesis validity for different characters of groundnut in a F_2 7x7 diallel crosses

Characters	a	b	SE(b)	1-b (2.571(5%), 4.032(1%)	b=0 (2.571(5%), 4.032(1%)	t^2(6.26 at5%,15.52 at 1%)
Pt. height	6.54	-0.007	0.13	7.90**	-0.06^{ns}	12.96*
No. Branches	0.07	-0.06	0.12	8.88**	-0.45^{ns}	15.20*
Shoot wt	0.29	0.49	0.18	2.47^{ns}	2.49^{ns}	2.70^{ns}
Total dry wt	0.41	0.51	0.16	2.51^{ns}	3.09*	3.49^{ns}
No. of Pod	3.72	-0.02	0.19	5.51**	-0.12^{ns}	4.99^{ns}
Pod wt.	-0.01	0.97	0.16	0.18^{ns}	6.13**	0.05^{ns}
Kernel wt.	-0.01	0.99	0.19	0.06^{ns}	5.35**	0.16^{ns}

*Significant at 5%, **Significant at 1% level and^{ns}Non-singificant

Appendix V. Maximum and minimum temperature, total rainfall and humidity of Dhaka in the year 2011

Month	Temperature (°C)		Rainfall (mm)	Humidity (%)
	Min.	Max.		
January	9.6	29.0	0	71
February	12.0	31.2	48	56
March	18.4	37.3	22	59
April	20.8	37.9	37	67
May	21.3	36.9	177	71
June	23.2	35.8	308	79
July	25.3	35.1	167	77
August	25.0	35.1	340	78
September	24.8	34.0	169	79
October	21.5	35.7	174	74
November	16.6	33.2	0	68
December	11.0	29.7	81	66

Source: The Metrological Department, Agargaon, Dhaka.

Appendix VI. Maximum and minimum temperature, total rainfall and humidity of Dhaka in the year 2012

Month	Temperature (°C)		Rainfall (mm)	Humidity (%)
	Min.	Max.		
January	8.2	27.8	0	69
February	13.0	31.0	0	54
March	16.0	34.5	20	57
April	20.2	35.8	123	64
May	21.3	35.3	235	76
June	23.2	36.0	314	80
July	23.9	35.4	356	79
August	24.5	35.0	409	82
September	23.7	36.2	207	77
October	22.0	34.5	112	73
November	17.2	32.4	0	67
December	11.0	30.0	0	73

Source: The Metrological Department, Agargaon, Dhaka.

Appendix VII. Maximum and minimum temperature, total rainfall and humidity of Dhaka in the year 2013

Month	Temperature (°C)		Rainfall (mm)	Humidity (%)
	Min.	Max.		
January	10.5	28.5	10	66
February	12.2	33.0	1	52
March	18.3	37.3	37	57
April	19.0	37.1	269	69
May	20.5	36.2	137	70
June	23.2	36.7	175	77
July	25.2	34.3	226	79
August	24.4	34.5	282	78
September	24.9	36.5	81	79
October	20.3	34.4	38	71
November	14.8	32.4	0	68
December	9.6	28.5	0	77

Source: The Metrological Department,Agargaon, Dhaka.

Appendix VIII. Maximum and minimum temperature, total rainfall and humidity of Agriculture Research station, BARI, Benarpota, Satkhira in the year 2013-14.

Month	Temperature (°C)		Rainfall (mm)	Humidity (%)
	Min.	Max.		
January'13	8.7	28.2	0	79
February'13	9.6	33.4	0	72
March'13	16.4	37.2	5	71
April'13	19.4	38.4	14	72
May'13	20.5	39.0	36	70
June'13	23.7	39.2	72	77
July'13	24.6	34.4	199	84
August'13	25.0	35.0	239	85
September'13	24.6	35.0	314	85
October'13	18.6	35.0	282	79
November'13	15.5	31.2	53	78
December'13	10.0	29.6	5	81
January'14	9.0	28.5	0	77
February'14	9.8	33.8	0	74

Source: The Metrological Department, Agargaon, Dhaka.

Appendix IX. Month wise soil salinity (EC dS/m) levels during growing period in the experimental field of ARS, BARI, Benarpota, Satkhira in the year 2013-14.

Month	Depth of Soil (cm)	Soil Salinity (dS/m)	
		15^{th} day of month	30^{th} day of month
January'13	0.30	12.2	12.5
February'13	0.30	12.5	12.8
March'13	0.30	14.2	14.4
April'13	0.30	14.3	14.5
May'13	0.30	13.3	13.2
June'13	0.30	11.8	9.0
July'13	0.30	5.8	5.5
August'13	0.30	3.4	3.5
September'13	0.30	2.9	3.0
October'13	0.30	6.2	6.4
November'13	0.30	7.8	7.9
December'13	0.30	8.5	8.7
January'14	0.30	10.5	10.6
February'14	0.30	11.4	11.5

Source: Agricultural research Station (ARS), BARI, Benarpota, Satkhira.