"In the name of ALLAH, the most merciful, the most gracious"
Genetics of Salt Tolerance in Maize (Zea mays. L)

By

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FAISALABAD, PAKISTAN
2017
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I hereby declare that the contents of this thesis “Genetics of salt tolerance in Maize (Zea mays L.)” are product of my own research and no part has been copied from any published source except the references, standard mathematical or genetic models/equations/formulate/protocols, etc. I further declare that this work has not been sent for the award of any other degree/diploma. The university may take action if the information provided found inaccurate at any stage.

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TO

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THIS HUMBLE EFFORT IS DEDICATED TO

My Affectionate and Beloved

Father (Late)
Who live in my mind
In my heart
Throughout the life span
And is
Nearest, dearest and deepest
To me
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LIST OF ABBREVIATIONS

[d] = Additive
[h] = Dominance
[i] = Additive × additive
[j] = Dominance × dominance
[l] = Additive × dominance
[m] = Mean effect
100G W= 100 grain weight
A = Photosynthetic rate
ANOVA = Analysis of Variance
BC1 = 1st Back cross
BC2 = 2nd Back cross
Chl a = Chlorophyll-a
Chl b = Chlorophyll-b
Cl⁻ = Chloride concentration
CRD = Completely randomized design
CUG = Coefficient of uniformity of germination
dsm⁻¹ = Desi Siemens per meter
E = Transpiration rate
EC = Electrical Conductivity
F1 = 1st filial generation
F2 = 2nd filial generation
FGP = Final germination percentage
GE = Energy of germination
GI = Germination index
GPC = Number of grains per cob
Gs = Stomata conductance
GYPP = Grain yield per plant
K⁺ = Potassium concentration
LA = Leaf area
LFW = Leaf fresh weight
MGT = Mean germination time
Na⁺ = Sodium concentration
Na⁺/K⁺ = Sodium potassium ratio
NaCl = Sodium Chloride
NARC = National Agricultural Research Centre
P1 = 1st parent
P2 = 2nd parent
PBG = Plant Breeding and Genetics
PCA = Principal Component Analysis
PGRI = Plant Genetic Resources Institute
PH = Plant height
PRO = Proline contents
PROT = Protein contents
RCBD = Randomized complete block design
RDW = Root dry weight
RFW = Root fresh weight
RL = Root length
RWC = Relative water contents
S = Salinity
SDW = Shoot dry weight
SFW = Shoot fresh weight
SL = Shoot length
T50 = Time to 50% germination
TSG = Time to start germination
TSS = Total soluble sugars
UAF = University of Agriculture, Faisalabad
Ψw = Water potential
ABSTRACT

Abiotic stresses are dangerous to crop productivity. Climate of Pakistan is arid to semi-arid for which salinity is major problem. As population is increasing, food requirement is also increasing, salt tolerant varieties must available for cultivation in saline areas to meet this demand. Current investigation was done in screenhouse of the department of PBG, UAF, Pakistan and saline soil research institute (SSRI), Pindi Bhattian following split plot arrangement to search for salinity tolerance among available maize germplasm, to determine the mode of gene action involved in the control of different standards related to salinity stress tolerance and to assess the extent of association of different standards with grain yield. Research comprised of screening, hybridization and evaluation experiments. Two experiments were conducted for screening of 40 maize genotypes i) hydroponic screening and ii) field screening to screen the material for identification of better and poor parents against different physiological, morphological, growth and yield related standards following triplicated CRD and RCBD under split plot arrangement respectively. In screenhouse experiment, maize genotypes were screened under different salinity concentrations $S_{0.8 \text{ dSm}^{-1}}$ (T1; Control), $S_{4 \text{ dSm}^{-1}}$ (T2), $S_{6 \text{ dSm}^{-1}}$ (T3) and $S_{10 \text{ dsm}^{-1}}$ (T4) against various standards which include shoot length, shoot fresh weight, shoot dry weight, root length, root fresh weight, root dry weight, sodium concentration, potassium concentration, chloride concentration, proline contents, sodium potassium ratio in hydroponic system. In field, genotypes were screened under $S_{0.89 \text{ dSm}^{-1}}$ (T1; Control), $S_{5.2 \text{ dSm}^{-1}}$ (T2), $S_{6.7 \text{ dSm}^{-1}}$ (T3) and $S_{11 \text{ dsm}^{-1}}$ (T4) in natural saline conditions against different standards like chlorophyll-$a$ contents, chlorophyll-$b$ contents, relative water contents, water potential, protein contents, total soluble sugar and some growth and yield related traits like leaf fresh weight, leaf area, photosynthetic rate, plant height, stomata conductance, transpiration rate, number of grains per cob, 100 grain weight and grain yield per plant. On the basis of performance in both experiments, UAF-0024 was selected as a most tolerant and UAF-0028 was selected as a most susceptible genotype using biplot based on principal component analysis (PCA). Grain yield per plant, number of grains per cob, 100 grain weight, leaf area, relative water contents and photosynthetic rate were reported as best standards for selection criteria. Most tolerant and sensitive genotypes were used as parents in hybridization program of generation mean analysis to rise generations $P_1$, $P_2$, $F_1$, $F_2$, BC1 and BC2. These generations were evaluated in screenhouse and field under the same salinity concentrations used in screening experiments to find gene expression involved in the control of salinity stress related standards. Generation means analysis showed that mostly additive [d] and dominance $\times$ dominance [l] types of inheritances were present in the traits under normal and saline conditions. Association among yield contributing traits was computed to know the interrelationship among them. Positive association was found among leaf area, number of grains per cob, 100 grain weight, grain yield per plant and plant height. Information drawn from experiments done in screening phase, computation of association and genetic effects disclosed that genetic diversity among maize germplasm is quite evident at allelic level and there is available genetic potential to improve salinity stress tolerance in maize. The additive and epistatic effects in the control of different salinity stress related standards can be exploited in different breeding programs to improve maize genetic potential against salinity stress.
CHAPTER 1

INTRODUCTION

Maize is a highest grain producing important cereal. It was originated 9000 years ago as a wild grass. Maize can be grown in variety of environments like tropical to temperate regions. Globally, maize is used as a staple food and raw material in many products of industry. It is most important after wheat and rice and globally it plays vital role in industry. All parts of plant are useful for food and non-food items (Haddadi et al., 2012). Being a C₄, maize has good ability of photosynthesis than C₃ plant (Ashrafuzzaman et al., 2000).

Nutritive value of maize seed is 3% sugar, 72% starch, 8.5% fiber, 10% protein, 4.8% oil and 17% ash (Ahsan et al., 2007). Important use of its grain is in food and textile industry for making corn flour, corn syrup, starch, lactic acid, corn flakes, acetone and edible oil. Paper, card boards and insulating material is manufactured by its stalk while pipes, plastics, paste, paint, beverages and automotive fuels like gasohol, alcohol and biogas are manufactured by its rachis.

Globally its cultivation was on an area of 177.76 million hectares and its production was 961.10 million metric tons during year 2015-16 in which USA and China produce approximately 60% of the world maize (Foreign Agricultural Service/USDA Office of Global Analysis, 2017). In Pakistan, maize is grown twice a year i.e. during Spring and Kharif seasons. In Pakistan, it was cultivated on 1.144 million hectares and its production was of 4.920 million tons (Economic survey of Pakistan, 2015-16). In total production, share of Punjab and Khyber Pakhtunkhwa (KPK) is 97% while contribution of Sindh and Baluchistan is 3%. Khyber Pakhtunkhwa shows 69% production by using 60% area while production of Punjab is 40% from 30% area of total cultivated area. As its yield potential increased, maize is known as important source of food and feed for humans and animals respectively. For biodiesel production, it is second most important to soybean (Vasudevan and Briggs, 2008) in coming times production should be increased to meet the challenges of increasing population.

Maize fulfills up to 60% of the demand of poultry industry in Pakistan (Tariq and Iqbal, 2010). It is well adapted in variable agro-climatic conditions in the same year and is short duration crop therefore is grown in two seasons (Spring & Autumn) per year in most of the maize growing area of Pakistan. Internationally population is increasing at alarming rate and at the end of year 2050 it likely to reach at 9.7 billion (UN population prospects, 2015-2016); this is a big warning to food security and will be a challenge to increase production. Crop production must be doubled till 2050 to fulfill the projected loads. In contrast, many
Biotic and abiotic adverse climatic factors are reducing food production. Mahajan and Tuteja, 2005 reported, mentioned adverse factors are alarming peoples; so peoples wanted to reduce said losses. Among abiotic stresses, salinity plays vital role in reduction of crop growth particularly in maize. However, it is moderately susceptible to salinity; it is most susceptible to salinity than other crops (Isla and Aragues, 2010).

Abiotic stresses are major threats to crop production all over the world reducing 50% crop yield (Rodriguez et al., 2005; Acquaah, 2007). Plants have to face several environmental stresses like heat, salinity and drought. Many other stresses (herbicides and pesticides, ultraviolet radiations, heavy metals, ozone) also play major role to damage plant growth and development among the world (Ahmad and Prasad, 2012). Crop growth, biomass production and yield seriously affected by their adverse effects which ultimately reduce nearly 70% crop productivity (Ahmad et al., 2012). Consequently, these stresses are dangerous for food security globally (Flowers et al., 2010).

As Shannon, 1998 confirmed, amongst many environmental stresses, salinity pose dangerous hazard to agricultural yield and economy, predominantly of arid and semiarid areas. In 2400 BC, lands of Iraq were found salt affected; ancient societies were damaged by salinity which succeeded for centuries (Rengasamy, 2006). Approximately 6.5% of the total land of world (831 Mha) has affected by salinity and sodicity (FAO, 2008). Australasia followed by Northern and Central Asia has large proportion of salt affected soil which is (357568 Mha) and (211448 M ha) among different continents. In all over the world, 20% of the irrigated lands are damaged due to salinity (Prochazkova et al., 2013). Mostly areas with humid, sub humid, arid, semiarid climate, rivers are badly affected by salts (Rashid, 1996).

About 6.8 Mha out of total 80 Mha area of Pakistan is salt affected. Suitable area for agricultural farming is 19.30 Mha. In this suitable area, 16.00 Mha is practiced with irrigated agriculture (Alam et al., 2000). Among total saline area of Pakistan, 56% is saline-sodic. Mostly Punjab province is salt affected which is 84% due bad ground water having increased SAR and EC by which crops are badly affected (Ghafoor et al., 2001).

Definition of salt stress is the gathering of soluble salts in soil, forming saline soils (Ibraheem et al., 2011). Salinity defined as property of soil or water showing dissolved solutes in higher concentrations above a dangerous limit (Steppuhn and Wall, 1999). When soluble salts accumulated more than the need of plants, this is called salinity. Normal soil has EC 2 dS m\(^{-1}\) whereas salts with increased level (EC. 4 dS m\(^{-1}\)) is termed as saline soil (Weisany et al., 2012). Salt concentration is equals to 0.5% of dry land is termed as suitable definition of salinity (Street and Heigi, 1984).
Several salts, like NaCl, MgSO$_4$, Na$_2$SO$_4$, CaSO$_4$, KCl, MgCl$_2$ and NaCO$_3$ cause soil salinity (Flowers et al., 1977). Crop productivity is mainly reduced by two ions i.e. sodium and chloride, due to specific ion toxicity and reduction in soil osmotic potential (Munns and Tester, 2008).

Soluble salts aggregated naturally for long period referred as primary while human activities gathered soluble salts termed as secondary salinity which cause imbalance in water availability for crops. Soluble salts subjected to weathering are primary type of salinity. Major accelators for dumping sea salt to lands are wind and rain. 6-50 mg/kg of sodium chloride present in rainwater, its amount dependent on distance from coast. 10 kg salt is added in one hectare of land due to 10 mg/kg NaCl in rain (Muuns and Tester, 2008). Secondary salinity causes imbalance in applied and consumed water due to transpiration (Munns 2005; Garg and Manchanda, 2008). FAO and UNESCO estimated, globally 50% systems are facing secondary salinity, sodicity and water logging (SzaboIcs, 1987). Secondary salinity is increasing; globally 70 Mha of agricultural soils are affected with salts (FAO, 2005). Salinity of arid and semi-arid areas is reducing productivity consistently in these areas (Noreen and Ashraf, 2008). Due to salinity, soil is becoming unproductive for crop production. Wind and rain play major role in transportation of salts in coastal areas.

Salinity impos negative impacts like reduced osmotic potential and toxic ions (sodium and chlorine) on maize plant (Abdulzadeh et al., 2006). Three major effects are (i) lowering of water potential; (ii) ion cytotoxicity; (iii) nutrients imbalance. Generally, essential nutrients are reserved in cells of plants which can be available when needed. Consequently, bad impact of salinity is only seen when their movement towards plant is considerably stucked (Flowers and Flowers, 2005).

Growth of maize plant is reduced in two phases (Munns, 1993). In first phase, due to availability of salts on external side of root, reduction in the outer water potential is observed. In second phase, salts moved in plant which senescanced old leaves. As more salts accumulated in salt susceptible than salt tolerant maize ultimately cause death of plant. (Munns, 2002).

Salinity mainly affects growth, development, physiological, biochemical and molecular characteristics of plants (Munns, 2002). Mostly osmotic and specific ion effect impact plants (Hamza et al., 2006). Reduction in osmotic potential and ion cytotoxicity is eventually result of osmotic and specific ion effect respectively (Brady and Weil, 2002). Uptake of water and different essential ions is reduced due to salinity which ultimately causes ion toxicity (Saqib et al., 2005) eventuayl disturb membranes, enhanced ROS generation and
disruption in toxicity of metabolites (Joseph and Jini, 2011). Drastic impact of salinity causes conformational modifications in structure of membrane, particularly the lipid matrix and its surrounded proteins (Hurkman, 1988; Dupont, 1992; Kerkeb et al., 2001). Prime measures under saline environment are to maintain the functions of membrane. Membrane fluidity is dependent on the degree of saturation of fatty acid (Rochester, 1987). Balance and stability of lipids reveal the membrane strength (Quinn, 1983). Extents of phosphatidylcholine and phosphatidylethanolamine are disturbed by salts which cause drastic impacts on structure of membrane (Mansour, 1994; Kerkeb, 2001) ultimately reduces plant growth due to considerable reduction in photosynthetic activities (Agong et al., 2004).

Normally, plants can minimize or hinder the effect of salinity by causing remarkable reduction in osmotic potential and gathering of organic solutes (Hasegawa et al., 2000). Decreased level of Na⁺ and Cl⁻ and increased level of Ca²⁺ and K⁺ play important role to improve the growth under saline environment. Consequently, for identification tolerant and sensitive genotypes of maize under salinity, increased Ca²⁺/Na⁺ or K⁺/Na⁺ ratios are mostly used as good indicators under salinity (Song et al., 2006).

Many scientists introduced different approaches to cope with salinity problem. Reclamation of salinity remained effective, however, due to shortage of good water, less soil permeability and higher cost inputs for amendments, it is difficult to adopt practically on large scale (Qureshi et al., 1990). In these approaches, use of salt tolerant varieties in saline areas remained popular due to its quality and low cost and being efficient way to cultivate saline lands (Ashraf, 1994). There is large saline area available and utilization of this area and salty water with salt tolerant varieties is very cost effective for farmers than reclamation in developing countries (Qureshi and Barrett-Lennard, 1998). Breeding to develop salt tolerant varieties for saline areas is gaining importance to overcome the problem of salinity (Hollington, 2000).

Improvement in maize plant against salinity stress play important role to cultivate salty soils. For this purpose, there must be study the genetics of salinity tolerance at seedling as well as maturity stages. There must be study the genetic components and their role to control variation in salinity tolerance. For the development of salinity tolerant varieties, genetics of salt tolerance is must known by the scientists. It must be start development of inbred lines and hybrids of maize with increased tolerance and growth under saline area.

Present study was design to evaluate maize germplasm under different concentrations of salinity for tolerance on the basis of several morphological and physiological traits. For the generation of F₁, F₂, BC₁ and BC₂, most tolerant and susceptible genotypes were mated.
Following objectives were accomplished.

- Identification of salt tolerant and salt sensitive maize genotypes.
- Assessment of genetic diversity based on salinity tolerance levels.
- To determine the genetic inheritance and association of salt tolerant indicators in maize.
- To work out the best selection standard against salinity stress.
CHAPTER 2

REVIEW OF LITERATURE

2.1. General overview of abiotic stresses

Conditions of environment which impact badly on plants to reduce growth and ultimately yield are known as abiotic stresses (Skirycz and Inze, 2010). There are many biotic and abiotic stresses which reduce crop productivity. Major abiotic stresses are drought, salinity, heat, water logging etc. (Nishida and Murata, 1996). Problems beneath the soil like physical (compaction), chemical (salinity, sodicity, acidity, deficiencies and toxicities of nutrients) or biological (microbial activity) and hinderance in movement of water and nutrients in plants reduced the growth (Dang et al., 2006). There are different ways in which plants show their response towards abiotic stresses (Cramer, 2010). Strength of stress (acute or chronic) and duration of exposure to stress is important (Tattersall et al., 2007; Pinheiro and Chaves, 2011). Limited irrigation resources, increase level of global warming and drastic change in climate are major problems cause reduction in arable land ultimately reduced crop production (Lobell et al., 2011). Many problems have been reported due to abrupt increase in population and unnecessary use of natural resources. These problems are salinity, acidity, heat, shortage of water, flooding and different diseases. Crop production reduced drastically due to these stresses. It is estimation that salinity caused 20% yield losses. Approximately 17%, 40%, 20% and 8% reduction in crop productivity is reported by drought, heat, cold stress and other factors (Rehman et al., 2005; Ashraf et al., 2008). Globally, 51-82 % annual yield of crops is reduced by many abiotic stresses (Bray et al., 2000).

2.2. What is Salinity Stress?

Salinity refers to accumulation of excessive amount of soluble salts in soil which alter plant normal physiological processes and hinders plant growth. Water having 4 ds\textsuperscript{1} (40 mM NaCl) electric conductivity or greater (Cramer, 1993) is termed as saline one. Crops are affected drastically by environmental contaminants particularly having salt radicals (Kijne, 2006). Crop production and environmental health is damaged by gathering of salts in soil (Rengasamy, 2006). According to estimation, up to 2050, environmental problems will reduce half of the total fertile land (Manchanda and Garg, 2008). It must be 38% increased in crop production to feed the increasing population till 2025 which should further increased upto 50% till 2050. Global demands are limited by different factors mainly salinity and erosions which cause degradation of soil (Wild, 2003).
Type of source divides salinity into primary and secondary salinity. Rocks decaying are the major source of primary salinity that releases several salts. Human activities (overgrazing, deforestation, intensive cropping and irrigation) cause secondary salinity (Ashraf, 1994).

2.3. Global scenario of Salinity

Salinity is major issue of irrigated areas. Out of total area under cultivation, 17% area is irrigated which contributes 30% in total crop production (Hillel, 2000). Globally, salt stress is severe abiotic stress that causes huge reduction in biomass production. In total land of world, around 6% is affected with different salts. This land is totally dry land which is about 800 Mha (FAO, 2008). Out of 230 million hectares of irrigated area affected by different abiotic stresses, 45 million hectares is affected by salinity in whole world (Ashraf, 2010). In another estimation, Internationaly, different salts affected 831 x 10⁶ hectares area (Beltran and Manzur, 2005). According to other estimation, half of the total irrigated area (about 2.5 x 10⁸ ha) is affected with different salts (Rhoades and Loveday, 1990). Till 2050, salts will degrade approximately half of the arable land (Manchanda and Garg, 2008). Saboora et al. (2006) said, around 10% of land is being degraded per year globally. Dried areas of land are severely affected by salts due to short of rainfall, to much heat and evapo-transpiration (Neto et al., 2006). Salinity problem is increasing abruptly all over the world mainly due to accumulation of soluble salts in root area as low quality irrigation is under practice.

2.4. Scenario of salinity in Pakistan

Agriculture sector is deffinitly most important as Pakistan is an agricultural country. Out of total 79.61 Mha areas (Khan et al., 2004), canal water is irrigating approximately 50 Mha which is 62400 kilometer long. Salinity, flodding, drought, sodacity, climate change and heat are threatenig agriculture farming in Pakistan. Out of these all stresses, major threats are salinity and sodicity (Khan, 2006).

Soil potential in Pakistan is reduced for agricultural farming due to salinity. Inappropriate soil management and mishandaling of resources erode soil which is now unfit fot crop production. Out of total irrigated land of Pakistan, 25% (1.4 Mha) is now not fit for crop production (World Bank, 2006a). Crop production is severely limited due to salinity beneth the soil in our country (Dang et al., 2006). Naturly the soils of Pakistan are calcareous and alkaline with low organic matter (Sillanpaa, 1982 and Khattak, 1991). It is estimated, out of total arable land, around, 0.2 to 0.4% is being unfit for crop production each year due to
accumulation of salts and water (Qureshi, 1978). Regarding area of agricultural farming, 6.8 million hectares (33%) are affected by salinity (Anonymous, 2008).

2.5. Mechanism of salt stress on plants

2.5.1. Osmotic effect

High salinity poses drastic stress on plant mainly due to high osmotic potential or increased highly toxic ions (Brady and Weil, 2002). In scarcity of water, water potential reduced due to soluble salts result in unavailability of free water to uptake in plants which limit growth ultimately. Shortage of water is either by salinity or drought, difficult to judge (Nawaz et al., 2010). Development of new leaves depends upon the water potential. Increased soluble salts are transported to vacuoles of newly growing cells which remained helpful for new leaves to continue their growth without any interruption (Munns, 2005). Shortage of water has more drastic impacts on shoot and root than toxic ion effect during initial stress (Munns, 2002). Shoot growth is more affected than root growth even at little shortage of water (Hsiao and Xu, 2000). Different factors like varieties, duration of stress, types of cells and how stress applied governed drastic effects of scarcity of water on plants.

2.5.2. Specific ion effect

Uptake of Na\(^+\), Cl\(^-\) and SO\(_4\)\(^2-\) ions in plants increased in saline environment which causes ion cytotoxicity. Crops are affected right from emergence to physiological maturity. Crops fail especially when specific ions affect at lateral growth stages. Regarding tolerance against salt stress, different crops have different levels of responses. Mostly higher plants and crops are susceptible to salinity (Abrol et al., 1988). Under saline or sodic environments, increased amount of Na\(^+\) and Cl\(^-\) ions and decreased amount of K\(^+\) ions was reported in wheat varieties (Maas et al., 1986). Older leaves accumulate more salts which eventually cause death of leaves. In this condition high amount of salts are gathered in cytoplasm where they hinder enzyme activity. In other situation, gathering of too much salt in cell wall results in cell dehydration (Munns, 2005). To cope with these situations, plants start their defense mechanism in which they try to stop uptake of salts or transport salt to vacuole to minimize the amount of salt in cytoplasm. Range of concentration of Na\(^+\) in root cells is from 10-30 mM (Tester and Davenport, 2003). Fresh weights of root and shoot are decreased up to 50% increased level of sodium and chloride ions in leaf sap (Parveen and Qureshi, 1992).
2.5.3. Nutritional imbalance

Maximum transport of sodium and chloride ions to plants in saline environment leads to reduce the uptake of essential minerals like calcium, potassium and manganese (Karimi et al., 2005). Normal functioning of enzymes and metabolic activities of plants disturbed by high Na\(^+\): K\(^+\) (Booth and Beardall, 1991; Lacerda et al., 2003). Increased gathering of soluble salts in plants hinders the uptake of water and essential nutrients. Interaction of salt and nutrients is reduced and causes imbalance of essential nutrients (McCue and Hanson, 1990). Potassium deficiency symptoms are reported due to decreased transport of potassium in plants under saline environment (Gopal and Dube, 2003). Calcium concentration in plants is important trait to study the salinity tolerance in plants under saline environment (Soussi et al., 2001). Potassium plays main role in photosynthesis, formation of protein, osmoregulation and maintenance of cell turgor (Ashraf, 2004). Reduction in uptake of K\(^+\) due to high concentration of sodium and chloride ions was also reported (Marcar et al., 1991). K\(^+\) and Ca\(^{2+}\) play main role in membrane functioning. The plants having high K\(^+/Na^+\) are observed with increased tolerance to salinity (Saqib et al., 2005). Higher uptake of K\(^+\) in plants and compartmentation of Na\(^+\) to shoots is very important for enough availability of K\(^+\) in plants (Munns et al., 2000).

2.5.4. Oxidative stress

Salt stress produces ROS (reactive oxygen species) hydrogen peroxide (H\(_2\)O\(_2\)), hydroxyl radicals (OH\(^-\)) and superoxide (O\(_2^-\)). Proteins, nucleic acids and lipids are damaged due to oxidation by ROS which disturb the cellular metabolism (Imlay, 2003). ROS are produced by oxygen reduction that disturbs metabolism (Asada, 1999). Normaly ROS are produced at little level (Polle, 2001); but in stress, abrupt increase takes place in ROS production (Laloi et al., 2004). Stomata opening are hindered due to osmotic effect which reduces the supply of CO\(_2\) for photosynthesis leads to super oxides gathering in chloroplast. This super oxides gathering endorses the photoinhibition and photooxidation in cells (Ashraf, 2009). There is distinctive mechanism like antioxidative pathway to salvage the ROS (Smirnoff, 2005).

2.6. Effect of salinity on plant growth

2.6.1. Germination stage

Glycophytes and halophytes are severely affected by salinity particularly at germination stage. Germination plays vital role in development of vigorous seedlings.
Germination stage is more sensitive than other stages (Khan and Unger, 1997; Ashraf and Wahid, 2000). Accumulated toxic ions cause imbalancing in essential minerals in plants under salinity. Physiological activities are disturbed due to reduced essential ions in plants. Generally, salinity shows more drastic effects in pulses due to their susceptibility. Process of seed germination is retarded due to high salinity whereas low salinity results in seed dormancy (Khan and Weber, 2008). Seed maintains reduced water potential to overcome the limitation of nutrients (Allen et al., 1994), or start mechanism of salinity tolerance against toxicity of salts (Rumbaugh et al., 1993).

There are many different ways in which germination is affected by salinity. Soil osmotic potential is reduced which results in reduction of imbibition of water by seed (Khan and Weber, 2008) and causes toxicity of ions which leads to modify enzymes activity important for metabolic activity. Metabolic activity of protein is also altered during seed germination due to salinity stress (Rasheed, 2009).

Close relationship between seed and soil makes seed more sensitive to salinity (Dodd et al., 1999). Seed germination is reduced by stress of Na\(^+\) and Cl\(^-\) ions in higher concentration of salts. Salinity decreases the water potential results in reduced uptake of water into seed ultimately poses drastic effect in growing embryo, which eventually hinders the process of germination (Khan and Ungar, 1984).

Strength of stress and genotypes govern the time required for seed germination. Germination is reduced with increased salinity (Ditommaso, 2004). Salinity has drastic impact on the rate of germination, 50% germination, germination index, germination percentage and vigor index. According to Carpici et al. (2009) germination index of corn plants was reduced under saline environment. Salinity reduced germination index and as well as chickpea seed size (Kaya et al., 2008). Higher and lower germination is seen in small and large sized seeds respectively. In case of citrus, time to 50% germination is delayed under salinity (Zerki, 1993). According to Farooq et al. (2006), seeds of rice treated with ethanol reduced the toxicity and time to 50% germination. Under high salinity, vigour index is negatively affected (Djanaguiraman et al., 2003). According to Bordi (2010) reduction in rate of germination, germination percentage, and germination speed was seen under salinity. The 32%, 80%, 78% and 95% decrease was reported in rate of germination, length of root, length of plumule, length of shoot and seed size of corn respectively (Khodarahmpour et al., 2012).
2.6.2. Vegetative stage
2.6.2.1. Plant physiology

Higher salinity in soil causes reduction in crop production due hindering biochemical and physiological processes in plants. According to Epstein (1980), transport of assential nutrients in plants is stopped which stunts growth due to disturbance in rate of metabolism. Highly saline environment alters the relationship between plant and water. To overcome the problem of salinity, there should be decrease in water potential. Turgor pressure of plants decreased due to reduced water uptake in plants. Low water uptake reduces cell division and regulation of stomata aperture which ultimately lead to low photosynthesis and finally tissues died (Marschner, 1995; Munns et al., 2012). Stomata are closed due to loss in turgor pressure which disturbe gaseous exchange (Munns, 1993; Munns and Tester, 2008). Embedded proteins in membrane are also destabled due to hinderance in permeability of membrane lead to reduce photosynthesis (Kao et al., 2003; Ashraf and Shahbaz, 2003; Sayed, 2003). Lowering of enzymes and different pigments also reduce photosynthesis. In mungbean investigation under salinity, plant growth reduced due to drastic effects of reactive oxygen species caused by extra gathering of soluble salts in leaves (Nazar et al., 2011). Biochemical, physiological, photosynthesis (Hayat et al., 2010), water uptake (Perez-Perez et al., 2009), transpiration (Cambrolle et al., 2011), total soluble sugars (Noreen and Ashraf, 2009), water use efficiency (Grewal, 2010), protein, osmolytes, relation between soil and water are reduced under salinity. Crop yield is reduced due to disturbance in mentioned processes.

2.6.2.2. Plant anatomy

Plant anatomy is significantly affected by salinity. Under salinity, plants start mechanism of stress tolerance to overcome the effect of stress. Mesophyll to leaf area is increased under salinity. Thickness of epidermis, cuticles, cell wall and leaves (Waisel, 1991) is enhanced under high salinity. Mesophyll layers and size of cells increased under high salinity (Zekri and Parsons, 1990) because of extensive cell wall due to increased turgor in plants (Munns and Termaat, 1986). Xylem vessels of salt affected plants are large while narrow in normal soil media (Walker et al., 1985). Number of palisade and epidermal cells are increased in unit area under high concentration of salts (Raafat et al., 1991) along with elevation of palisade and spongy tissues (Hussein et al., 2012); but total cells in a leaf reduced. Stomata (Cavisoglu et al., 2007) on epidermis, leaf area, (Awang et al., 1993), relative rate of leaf plastochron index and expansion (Bray and Reid, 2002) are also declined under increased salinity. Salinity also decreases the length of vascular bundle; rows of xylem
and total vessels (Hussein et al., 2012). Hypodermis and endoderm of roots are gathered with suberin under highly saline environment (Walker et al., 1985).

Development of vascular bundle particularly width is disturbed in case of mungbean under highly saline conditions (Beida and Ho, 1993; Rashid et al., 2004). Diameter of stem in case of rice is also decreased (Pimmongkol et al., 2002). According to findings of Junghans et al. (2006) high salinity hinders the cambial activity of Populus euphratica. Increased salt concentration decreases the thickness of mesophyll, lamina and mid vein in case of kallar (Ola et al., 2012). Size of cell, thickness of epidermal, cortex diameter, central cylinder, apical meristem and diameter of cortex of leaf are reduced under high concentration of salts. Exodermis and endodermis become thick under increased salinity and enhanced growth of sclerenchymatous (Javed et al., 2001). In other research, high amount of salts lignify the intercellular spaces of endodermis and cortex in case of Vracbiaria decumbens (Gomes et al., 2011).

### 2.6.2.3. Plant morphology

Establishment of crop is major goal after seed germination. Plant growth is affected severely by high salt concentration (Eschaie et al., 2002). Establishment of crop is declined by high salinity due to stunting of growth of internodes; shoot and leaf lead to leaf abscission (Ziska et al., 1990; Zekri, 1991). Decreased length and fresh weights of shoot ultimately lead to reduce biomass production under the stress of salinogenic salts (Dolatabadian et al., 2011). In case of Suaeda salsa, according to Guan et al. (2011), number of branches, shoot length and diameter were decreased due to abrupt increased in sodium and chloride ions. Three important aspects like osmotic stress, ion cytotoxicity and nutrient imbalance are accelerated under highly saline environment which lead to stunt growth and consequently crop failure. However, salinity treats differently with stages such as seed germination, vegetative growth and reproductive growth.

Plant morphology is disturbed in many ways by salinity, depending upon the concentration of salinity, time period of stress application and type of variety used (Munns and James, 2003). Toxicity due to different ions caused leave burning, necrosis, chlorosis. The plants affected by salinity have dark green and thick leaves. Volume and leaf area is also reduced (Bray and Reid, 2002). Germination, shoot growth and establishment of seedling are badly affected in saline area (Wahid et al., 1999). Leaves become succulent and yellow (Lutts et al., 1996; Wahid et al., 1997; Curtis and Lauchli, 1987). Plants start some defensing
mechanism like reduction of leaf area and highly dense root system to overcome the osmotic stress.

Dry and fresh weights of shoot and root, stem width and plant height were badly reduced in *Agropyron elongatum* under saline environment (Sanadgol, 2002). Dry weight of stem and leaf length in corn plants are declined under high salt concentration (Azaizeth and Steudl, 1991; Evlagon *et al.*, 1992). Increased concentration of NaCl decreases the dry weight of shoot and root (Ashrafuzzaman *et al.*, 2002). Growth and rate of assimilation is also reduced (Khan, 2001; Ahmad, 2010). According to Ashraf and Bhatti (2000), leaf area and biomass was reduced in rice under saline soil. Even in reduced salinity, growth and expansion of leaf were reduced in case of sugar beet (Terry and Waldren, 1984).

2.6.3. Reproductive stage

Internationally around 50% crop production is declined due to salt stress. According to Isla *et al.* (1998), 65% productivity of barley is decreased leads to enhance ash content under high salt concentration. Findings of Ahmad *et al.* (1995) reported that drastic impact of soluble salts decreased seed cotton yield. Khan *et al.* (1999) described that 69% grain yield and 64% straw yield is reduced in case of different wheat cultivars in salinity stress.

Reddy and Vora (1986) explained the disturbance in plant metabolism which causes reduction in yield components. Number of spiklets and tillers, seed weight, grain yield, seed growth and dry weight is reduced in wheat and barley under high salinity.

2.7. Mechanism of salt tolerance in plants

2.7.1. Osmotic adjustment

Osmoregulation is a considerable adaptation started by plants under high salt concentration and drought. High growth of plants is observed due to remarkable osmotic adjustment by improving turgor and cell volume (Munns, 1988). Toxic effects of salts are minimized by osmoregulation which helps cell to reduce its osmotic potential by gathering compatible solutes (Hasegawa *et al.*, 2000). Toxic ions of salts in root zone cause water stress (Flowers and Colmer, 2008). Solvent moves from lower to higher concentration in osmosis. There is increase solution of organic compounds in roots than in soil. Water transported from membrane towards root cells. Concentration of solute in soil is increased which leads to disturb the balance of solute ultimately causes reduction in movement of water towards plants. Various osmolytes like sugar and organic compounds are gathered by plants to overcome the salt solutes outside the root. In different amino acids, proline decreases water
potential in cell for osmotic adjustment (Zhao and Harris, 1992). Energy is prerequisite for this process which can be available only to cut its supply to metabolism process which leads to stunt plant growth (Hanson et al., 1999). Uptake of essential minerals towards plants is decreased due to water stress results in imbalance. It is only due to competition between toxic and essential nutrients in soil and plant. Enzyme and metabolic activity are also badly impacted by soluble salts (Lacerda et al., 2003).

2.7.2. Synthesis of compatible solutes

Gathering of metabolites as compatible solutes is also important to overcome salinity. Solutes with decreased molecular weight are produced by plants to overcome toxicity of saline ions are termed as compatible solutes (Hasegawa et al., 2000). Even under highly saline environment, metabolism of plants is not disturbed due to these osmolytes (Rhodes and Hanson, 1993). Integrity of membrane, functioning of enzymes and assembly of macromolecules are stabilized by their increased concentration of these osmolytes. Osmolytes serve as stored nitrogen, maintain pH, overcome problem of ROS, detoxify detrimental chemicals (Mansour et al., 2000) and guard cells from drastic impact of drought and salinity (Genard et al., 1991; Krishnamurthy, 1991).

Metabolites betains, polyols (Sakamoto and Murata, 2000) and soluble sugars (Wahid, 2004) are used as a compatible solutes. In these solutes, amino acids play vital role in adjusting osmotic potential (Bohnert, 1992). Now days it is confirm that solute potential between cell and surrounding is maintained by polyols, polyamines (Pollard and Wyn Jones, 1979).

2.7.3. Ionic compartmentalization

Inside the cell, compartmentalization is well known phenomenon of plants to overcome salinity (Carlos et al., 2009). Imbalance of essential minerals is happened due to salinity which stunt growth. Due to ionic stress Na+, Cl− ions increased and K+ ions decreased. Plants are badly impacted by this imbalance (Abdel Kader et al., 2011). Level of Ca²⁺, K⁺, Mg²⁺ reduced in cytosol due to abrupt increase in Na⁺ ions. Increased level of Na⁺ destabilize membrane, hinders function of protein, reduces cell division and cell expansion, decreases rate of metabolism and change homeostasis of essential nutrients (Munns and Tester, 2008). The competition between increased amount of Na⁺ and potassium disturb the cellular uptake (Niu et al., 1995). Metabolism of plants is disturbed due more than 100mM sodium ions in cytosol (Serrano et al., 1999). Balance of electrolytes and K⁺/Na⁺ ratio is
disturbed ultimately reduces K+ concentration due to increased amount of Na+ ions (Shabala and Cuin, 2008). Ionic homeostasis is maintained by controlling the sodium ions uptake in plant cell and its compartmentalization towards vacoule (Zhu, 2003). This approach is helpful in glycophytes as well as in halophytes to reduce the sodium and chloride concentration in cell and increase growth.

2.7.4. Synthesis of antioxidant

Disrupted cellular homeostasis due to drought, salinity and cold produces reactive oxygen species (ROS) (Dubey, 2011). These ROS are by-product (free radicals) of metabolism in plants or generated in process of electron transport by escaping of an electron in mitochondria and chloroplast (Joseph and Jini, 2010; Rishi and Sneha, 2013). These radicals include singlet oxygen O2^(-), O^2, OH and hydrogen peroxide H2O2 (Herandez et al., 2000).

Several mechanisms are activated in cell to cope with ROS like generation of enzymatic antioxidants such as superoxide, peroxidase, catalase, dismutase, ascorbate, monodehydroascorbate, reductase, glutathione reductase and dehydroascorbate reductase. Non-enzymatic antioxidants are glutathione, GSH, proline, ascorbate, tocopherols and carotenoids. Both types of antioxidant system help plants to overcome ROS stress (Alscher et al., 2002).

2.8. Management of salinity stress

Utilization of salinity tolerant genotypes with adoption of proper production technology is important to maintain maize production in saline environment. Study of genetic variability for salinity tolerance and marker assisted selection play major role to find out salt tolerant genotypes. Transgenic maize developed by the progress in genomics, biotechnology and conventional breeding perform well in the saline soils. Moreover, arbuscular mycorrhizal fungi also support plants to cope with salinity by improving uptake of macronutrients and micronutrients from saline soil.

2.8.1. Breeding approaches to enhance salinity tolerance in plants

2.8.1.1 Evaluation and selection of available germplasm

Several methods have been devised by scientists to overcome the salinity issue. One of them is to way is to study the genomes of existing maize germplasm for variation to sort out salt tolerant genotype for improving yield under saline area (Ashraf et al., 2006). For this purpose it is need to devise an appropriate selection criterion (Francois and mass, 1994).
Different species are categorized differently with respect to their salt tolerance (Francois and Mass, 1994). Several screening methods have been reported by different scientists e.g. for corn (Khan et al., 2003), wheat (Ali et al., 2002) and rice (Shannon, 1998).

Considerable tolerance is shown by some plants against salinity which is indication of existence of genetic potential to cope with toxicity of ions that is good indicator for selection in breeding program against salinity (Mahmood et al., 2000). Gathering of salts by plants is dependent on their capability to tolerate salts. Plants which exclude maximum Na$^+$ ions from their cells are known as salt tolerant and plants which accumulate maximum Na$^+$ ions are known as salt sensitive (Schachtman and Munns, 1992). Consequently, salt tolerant plants gather more K$^+$ ions and less Na$^+$ ions than salt sensitive plants (Tipirdamaz and Cakirlar, 1989). However, according to Gene et al. (2007), in case of wheat the situation was different because no considerable relation was seen in exclusion of Na$^+$ ions and tissue tolerance in wheat; so crops behave differently with respect to these both traits. Screening at seedling stage has much reliability, require less labour, time and cost (Dasgan et al., 2002). According to Moreno et al. (2000) seedlings of Phaseolus vulgaris L contain remarkable variations against salinity tolerance. They reported about the increase in root growth and essential elements of bean cultivars. Giaveno et al. (2007) confirmed the availability of genetic variability for salinity tolerance at germination and zero association between early seedlings and germination in tropical maize. In case of screening of maize at seedling stage, seedling health related parameters like weight, growth and photochemical efficiency of seedlings are noted as best selection criteria for breeding program under salinity. Akram et al. (2010) conducted a hydroponic experiment for screening of maize hybrids to study genetic variation. They reported the reduction of vegetative traits of some hybrids. Increased in vegetative traits and K$^+$/Na$^+$ ratio was observed in Pioneer 30Y87 and Pioneer 32B33 hybrids by their results.

2.9. Genetic variability for salt tolerance

To develop salinity tolerant plants, considerable genetic variation for salt tolerance should available in gene pool. Variability with respect to tolerance to salinity increases in a sequence like variety to species to genus to family. Though species having tolerance to salinity is available in many plant families, but some families contain more tolerant species. For example, there are many species having salt tolerance in family Chenopodiaceae like Salicornia and Atriplex to Beta vulgaris. Sugarcane (Saccharum officinarum), wild Spartina species, tall wheatgrass (Elytrigia pontica), barley (Hordeum vulgare) and bermudagrass (Cynodon dactylon) are representative salt tolerant species of Gramineae family. Regarding
intergeneric differences of salinity tolerance (Shani and Dudley, 2001), different crops have varied potential of salinity tolerance for selection in salinity tolerance breeding programs (Volkmar et al., 1998). Important thing is, many species have different salt tolerance potential at the intraspecific level like sorghum (Azhar and McNeilly, 2001), barley (Hussain et al., 1997), rice (Shannon et al., 1998) and soybean (Kamal et al., 2003).

Though, Noble and Rogers (1992) explained that some species were reported with zero variation of salinity tolerance as those species contained narrow genetic base. Many scientists confirmed plant to plant variation within varieties in species for tolerance to high salinity mostly within cross-pollinated like alfalfa (Al-Khatib et al., 1993). Ashraf (2002) confirmed that F₃ population developed by crossing of LU26S and cv. Kharchia performed well even at S₂₄₅₃m⁻¹ and S₉₆₅₃m⁻¹. This achievement was due to heritability of the trait and selection criterion followed during screening the segregating generations under salinity. Still we are deficient with exact knowledge about genetics of salinity tolerance, even though it is confirm that it is complex trait. As plants are versatile for salinity tolerance through their whole life cycle, it is important to define environment of experiment along with other stresses such as fertility, temperature, pest, disease and, in specifically, waterlogging. Due to these all, breeding for salinity tolerance becomes difficult as reported by Shannon and Noble (1990). Yet despite a lot of research has been done on this issue, there is very little genetic information of salinity tolerance has been gathered.

The potential of selection and breeding of salt tolerant plants may be well if information regarding genetic variation is known. This information would help the breeder in two different manners; firstly, to design suitable selection methods for evaluation of tolerant plant and their progenies, and secondly, it tells about heritability of trait, by which progress can be predicted through selection. In case of sorghum, it was demonstrated by genetic variation that salinity tolerance was controlled by additive and dominance genetic effects (Ashraf et al., 1987). Adetimirin et al., 2001 reported high interaction of epistatic effects with environment rather than additive and dominance gene effects. Revilla et al., 2000 revealed the role of additive and dominance × dominance gene action to govern most of the traits in control condition studies. Some other researches available on corn (Rao and McNeilly, 1999), rice (Shannon et al., 1998), wheat (Xing et al., 2002), Aegilops ovala (Farooq, 2002), cotton (Noor et al., 2001) and lucerne (Al-Khatib et al., 1994) reported that selection and breeding improved these species. Although there is confirmed that variations of salinity tolerance are controlled by genetics, there are only few crops that have been reported with improved
salinity tolerance. Only few varieties are bred and have been reported with high salinity tolerance (Shannon and Noble, 1990).

2.10 Marker-assisted selection

Salinity tolerant proteins in maize can be identified by proteomic approach. These proteins are used to give markers which can be used in breeding program for the development of salinity tolerant maize genotypes. Zorb et al. (2004) reported in maize that differential regulation of 31% shoot and 45% root protein was observed under 25 mM salinity whereas under high salinity (100 mM), 80% total proteins showed different regulation. Results of de Azevedo Neto et al. (2004) confirmed about the genotype BR5033 as a tolerant and genotype BR5011 as a sensitive on the basis of some vegetative traits. Likewise, there is no any clear association of different traits like shoot dry weight to root dry weight ratio, sodium organic solute concentration in leaf with salt tolerance but gathering of their concentration in root play important role in salt tolerance. Thus, their root gathering plays role as physiological markers in screening of maize germplasm under salinity stress.

Finally, molecular and physiological markers play vital role in selection of salinity tolerant maize genotypes. Traits such as sodium concentration in leaf, root gathering of organic solutes and proteins expression play major role in selection of salinity tolerant genotypes.

2.11 Role of biotechnology and functional genomics

Gene transferring from one to other species for incitation of desired characters is termed as transgenic technique. This is more robust than breeding and transfer required genes only. Salinity tolerant genes can be recognized by the use of genomics and biotechnology to produce transgenic salt tolerant plants by transgenic techniques. Maize plants are escaped from dangerous effects of toxic ions by transferring sodium in apoplasts or vacuole. ZmNHX transcription increased during salt stress which enhanced tonoplast sodium/hydrogen antiporters in salt tolerant corn hybrids leaves by transferring sodium to avoid its toxicity (Pitann et al. 2013). Increased exchange of sodium/hydrogen in tonoplast transgenic plants make their growth better in saline soils. Expression profiles are well studied by complementary DNA (cDNA) macroarray which helps to assess similarities and differences of different expression patterns in highly saline soils. A cDNA macroarray contained 190 corn expressed sequence tags due to drought stress. Corn tags were exposed to salinity, abscisic acid and low temperature stress. 48 tags were upregulated in leaves and 111
in roots by abscisic acid while due to salinity, 36 tags in leaves and 41 in roots were upregulated (Zheng et al. 2006). Maize transformed with O. sativa sodium/hydrogen antiporter (OsNHX1) gene performed well even at 200 mM. In transgenic maize, leaves showed increased Na\(^+\) and K\(^+\) concentration and decreased osmotic potential under highly saline environment. YieldGard 2 corn hybrid had some Bt transformed lines performed better at 0, 50, 100, and 150 mM NaCl due to increased chlorophyll contents and its stability index (Beltagi 2008). Transformed maize with AtNHX1 gene survived 83 and 50% at 5-6 leaf stage at 0.4 % NaCl whereas wild type maize showed 50% germination only. Furthermore, transformed maize performed well till 30 days at 0.6 or 0.8 % NaCl but wild type maize don’t reached even at five-leaf stage (Li et al. 2010). Likewise, high grain yield was shown by transformed corn than wild type corn due to increased grain per row under highly saline environment.

Transformed corn showed increased salt tolerance due to overexpression of AtNHX1. Transformed maize with rice OsNHX1 gathered increased biomass at 200 mM NaCl (Chen et al. 2007). Finally, transgenic technique plays vital role to enhance salt tolerance in maize. Transferred genes produce betaine aldehyde dehydrogenase and vacuolar Na\(^+\)/H\(^+\) antiporter which remained helpful for plants to perform well even under highly saline environment.

**2.12. Role of arbuscular mycorrhizal fungi**

Arbuscular mycorrhizal fungi pierce in roots of vascular plants and produce a peculiar type of structures known as arbuscules, and vesicles. These fungi aid plants to take micronutrients and macronutrients from the soil. Abundance of organic solutes is altered due to colonization of these fungi around roots (Sheng et al. 2011). Colonization of these fungi helps plants to tolerate high salinity. High concentration of soluble salts decreased this colony by hindering the establishment of arbuscular mycorrhiza (Sheng et al. 2008).

Plants with colony of these types of fungi show well growth under salinity. This is only due to improved nutrition and osmotic adjustment of plant with this colony. Water use efficiency and efficiency of photosynthesis is also improved by these fungi. Regulation of expression of genes that plays important role in proline biosynthesis, encoding aquaporins and involve in late embryogenesis with chaperone activity increased with this symbiosis under high salinity (Porcel et al. 2012). Approximately 30 or more aquaporin genes are present in maize, their regulation increases osmotic adjustment under this symbiosis. Pattern of gene
expression reveals that plants with this type of symbiosis are less strained under salinity (Porcel et al. 2012).

It is concluded that, salinity tolerance in maize is improved by this symbiosis due to increased potassium/sodium ratios, improvement in nutrients uptake and enhanced osmotic potential.
CHAPTER 3
MATERIALS AND METHODS

Current research was carried out in the screenhouse and research area of the department of PBG, UAF, Pakistan for the period of 2011-2014. The research area lies in the North East region of Punjab, Pakistan (latitude; 31° 25’N, longitude 73°, 90’E) with an elevation of about 184 meters from sea level.

3.1. Collection of Genetic Materials

Maize genetic materials used in the present study comprised of 40 genotypes of genetically distant origin are given in table 3.1. These genotypes were derived from open pollinated populations collected from PGRI, NARC, Islamabad.

Table 3.1. Maize genetic materials used in the present study.

<table>
<thead>
<tr>
<th>Sr. No</th>
<th>Genotypes</th>
<th>Sources/Origins</th>
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Origin of genotypes is UAF. Accessions were collected from PGRI, NARC and these genotypes were derived from those open pollinated varieties by selfing in UAF.
3.2. Screening Phase

The collected germplasm was screened at different salinity concentrations against different evaluating standards. Sowing was done following triplicated split plot design under completely randomized design (CRD). Screening phase comprised of two experiments:

I) Screenhouse experiment (hydroponic conditions)
II) Field experiment (under natural field salinity)

3.2.1. Experiment-I

Screening was conducted in the screenhouse equipped with air conditioner, heaters, humidifier, humidity, thermo-sensors and thermostat to control temperature and humidity. Maize genotypes were planted in germination trays filled by sand sieved and washed with distilled water. After fifteen days of planting, uniform maize seedlings were transferred to Hogland’s nutrient solution. Solution culture comprised of polystyrene sheet placed on Hoagland’s solution of half strength properly aerated (Hoagland and Arnon, 1950). After couple of days, full strength of solution was applied. Seedlings were permitted to stabilize in hydroponic medium for three days. After stability, stress was imposed with ¾ applications of NaCl as S_{0.8 \text{ dSm}^{-1}} (T_1; \text{Control}), S_{4 \text{ dSm}^{-1}} (T_2), S_{6 \text{ dSm}^{-1}} (T_3) and S_{10 \text{ dSm}^{-1}} (T_4). Experiment was carried out with completely randomized design (CRD) following split plot fashion. NaOH and HCl were used to maintain pH of aqua solution at 6.0±0.5 daily. The stress was applied three days after transplantation up to 40 days. In experiment-1 following were the standards on the basis of which maize genotypes were screened.

3.2.1.1. Morphological standards

3.2.1.1.1. Root length (RL)

Seedlings were obtained by picking seedlings gently from aqueous solution. Total 10 seedlings from each entry were taken and root lengths were calculated in centimeters (cm) by a measuring tape and its average was computed.

3.2.1.1.2. Shoot length (SL)

Seedlings already used for root length were used for the measurement of shoot length. Length of total 10 shoots were recorded in centimeters (cm) using a measuring tape and averaged.

3.2.1.1.3. Root and shoot fresh weight (RFW, SFW)

Fresh samples of roots and shoots were taken from 10 randomly selected seedlings of
each entry and washed with distill water. These samples were dried with tissue paper and weighed by using electric balance (OHAUS-GT4000, USA). Finally the average weights were computed in (g).

3.2.1.4. Root and shoot dry weight (RDW, SDW)

The seedling samples used to measure fresh root and shoot weights were dried by heating at 65±5 °C by oven. Then weight of root and shoot samples were determined by using electric balance (OHAUS-GT4000, USA) and average was calculated in (g).

3.2.1.2. Physiological Standards

3.2.1.2.1. Sodium and potassium concentrations in leaf sap (Na\(^+\), K\(^+\))

SE (0.42g) and LiSO\(_4\).2H\(_2\)O (15g) were putted in 350 ml of H\(_2\)O\(_2\). During placing this mixture in ice bath, concentrated H\(_2\)SO\(_4\) (420ml) was placed down slowly. For digestion this final solution was preserved at 4°C. 0.1 g dried ground leaves were moved to each tube; each tube was added with 0.5ml of digestion mixture and kept overnight. Then tubes were poured with 0.5ml perchloric and placed at 220°C on hot plate for one hour till fumes production. After the coolness of tubes till room temperature, the same process was repeated until mixture became colorless. The final volume must be setted up to 50ml in a flask. Sodium and potassium concentrations were measured in (mole m\(^{-3}\)) by flame photometer. Its model was Jenway, PFP-7 (Wolf, 1980).

3.2.1.2.2. Chloride concentration in leaf sap (Cl\(^-\))

Chloride determination was carried out by water extraction method. 0.1 gram dried leaf was taken in tube filled with distilled water upto 10 ml. Then tubes were kept at 85°C for 6 hours in a digestion block and add distilled water again up to 10ml. Chloride contents were determined in (mole m\(^{-3}\)) by using chloride Analyzer (Sherwood Scientific Ltd., UK).

3.2.1.2.3. Total Proline contents (PRO)

This trait was estimated with way of Bates et al., (1973). 5g leaves were mashed and mixed in 5ml of (3%) aqueous sulfosalicylic acid with mortar and pestle. Supernatent (2ml) and glacial acetic acid ninhydrin (2ml) were added. This blend kept in water bath to boil at 100°C for half an hour. Then reaction transferred in an ice bath following the addition of toluene (4ml) and then shifted in a separate funnel to mix it. Then chromophore and toluene were isolated and absorbance was noted on pectrophotometer (spectronic 21 D. Milton Roy) at 520 nm wavelength contrary to blank toluene. Standard curve was used to identify
concentration of Proline. Amount of free proline was calculated in (µ mol g⁻¹) using formula below:

\[
\text{µmoles proline/g fresh weight} = \frac{[(\mu g \text{ proline} / \text{ml} \times \text{ml toluene})]}{((115.5 \mu g / \mu mole) / [(g \text{ sample }/5)])}
\]

3.2.1.2.4. Sodium potassium ratio (Na⁺/K⁺)

The data recorded for Na⁺ and K⁺ concentration was used to calculate Na⁺/K⁺ ratio by following the formula proposed by Noiur et al. (1978).

\[
\text{Na⁺/K⁺ ratio} = \frac{\text{Na⁺ concentration}}{\text{K⁺ concentration}}.
\]

3.2.2. Experiment-II

This experiment was conducted under natural saline field conditions in Saline Soil Research Institute (SSRI), Pindi Bhatian at different salinity concentrations i.e. S₀.89 dSm⁻¹ (T₁; Control), S₅.2 dSm⁻¹ (T₂), S₆.7 dSm⁻¹ (T₃) and S₁₁ dsm⁻¹ (T₄). Sowing was done in triplicated split plot fashion under randomized complete block design (RCBD). Crop raised under suggested agronomic and plant protection measures. Data for the following traits was recorded in this experiment.

3.2.2.1. Physiological standards

3.2.2.1.1. Chlorophyll contents (Chl a, b)

Plant leaf samples were collected from 10 tagged plants per entry. One gram fresh plant leaves were ground in 80% acetone then run at 3000 rpm/10 minutes. The upper layer was isolated carefully using pipette. Total 3ml of supernatant was used to note the absorbance at 663nm, 645nm, 505nm and 453nm wavelengths using spectrophotometer (Spectronic 21 D. Milton Roy).

The Chlorophyll a and b contents were measured in (mg/g f.wt) by following Nagata and Yamashita, (1992). Calculations were made by using the following formulas in unit (mg/100ml):

\[
\text{Chl- } a = 0.999A663-0.0989A645
\]
\[
\text{Chl- } b = 0.328A663+1.77A645
\]
3.2.2.1.2. Relative water contents (RWC)

Leaf RWC was identified with methodology devised by Jones and Turner (1978). Healthy leaves were removed and weighted. In order to get complete saturation, all samples of leaves were kept in distilled water at room temperature for 10 hours and weight of turgid leaves was noted. Leaves were heated at 70 °C to dry till 2 days and weight was noted. RWC was then recorded in (%) using formula:

\[
\text{RWC (%)} = \frac{\text{Leaf fresh wt} - \text{Leaf dry wt} \times 100}{\text{Leaf turgid wt} - \text{Leaf dry wt}}
\]

3.2.2.1.3. Water potential (\(\Psi_w\))

To determine (\(\Psi_w\)), from top, mature leaf was picked up. Leaf water potential was taken with Scholander pressure chamber in (-Mpa) (Scholander et al., 1965) made by company Arimad-2-Japan.

3.2.2.1.4. Protein contents (PROT)

Total protein contents were identified with methodology devised by Lowery et al. (1951). Seeds (0.2g) were ground in five ml of 0.2 molar phosphate buffer with neutral pH. Two glass tubes having grain extract (first comprising 0.5 ml) and (2\textsuperscript{nd} comprising 1.0 ml) were arranged to assess protein contents. Standard Bovine Serum Albumin solution of 0.5, 0.1, 0.2, 0.4, 0.6 and 1.0 ml were concurrently used in current experiment. One (ml) purified water was added in blank and each tube. Each tube was added with 1 ml of copper reagents solution. Proper mixed reagents in tubes were permitted to remain at room temperature for ten minutes. Then these tubes were added with (1:1 diluted) Folin-phenol reagent (0.5 ml) and placed for half an hour at room temperature. The protein contents were measured in (\(\mu\) mol g\(^{-1}\)) by taking optical density (OD) on spectrophotometer at 620 nm wavelength.

3.2.2.1.5. Total soluble sugar (TSS)

Soluble sugars were identified with method of Yemm and Willis (1954). 0.1 gram proper ground grain material was extracted using ethanol solution (80%). Sample was shaken at 60°C for six hours. Extract was subjected to assess the amount of TSS. 25 ml tubes were filled with 100µl plant axtract and 6 ml anthrone, heated in water bath for 10 minutes. Tubes were incubated at 25°C for twenty minutes. OD of this blend and blank was noted at 625 nm wavelength. TSS were estimated in (%) from a glucose standard curve.
3.2.2.2. Growth and yield related standards

3.2.2.2.1. Leaf fresh weight (LFW)

At early vegetative stage, second last leaf from all the selected ten plants was taken carefully. The samples were weighed by using electric balance (OHAUS-GT4000, USA) and average was computed in (g).

3.2.2.2.2. Leaf Area (LA)

The top most physiologically mature leaf was taken from selected ten plants and area was calculated with leaf area meter (LI-3000C) then average was computed in (cm²).

3.2.2.2.3. Photosynthetic, transpiration rates and stomata conductance (A, E, Gs)

Physiological responses of maize plants like photosynthetic rate (mmolH₂O m⁻² sec⁻¹), transpiration rate (umolCO₂ m⁻¹ s⁻¹ mmol m⁻² sec⁻¹) and stomata conductance (mmol m⁻² sec⁻¹) of healthy youngest leaves of all the entries were estimated by portable IRGA (infrared gas analyzer).

3.2.2.2.4. Plant height (PH)

Total five developed plants per entry were selected and this trait was noted with meter rod from the start of stem to start of tassel. The average was computed in (cm) to have single figure data.

3.2.2.2.5. Number of grains per cob (GPC)

At harvesting, each cob from selected ten plants was subjected to harvesting and threshing. GPC of all the cobs per entry were counted and average was calculated.

3.2.2.2.6. 100 grain weight (100GW)

Total 10 samples of 100 healthy and vigorous representative grains from each genotype were picked from threshed cobs and weighed using electric balance (OHAUS-GT4000, USA). The average was computed in (g) from all the data collected.

3.2.2.2.7. Grain yield per plant (GYPP)

At crop maturity, cobs harvested from each plant per entry were threshed separately and grains were bulked. Total five samples of bulked seed from each entry were weighed using electric balance (OHAUS-GT4000, USA) and average was computed in (g).
3.3. Statistical analysis

The ANOVA of mean data of all the parameters was done (Steel et al., 1997) for the identification of differences in genotypes. Biplot analysis based on principal component analysis (PCA) was made using statistical package (XLSTAT) to select tolerant and susceptible genotype based on all traits including yield. Most tolerant and sensitive genotypes were selected to study breeding and inheritance.

3.4. Hybridization

On the basis of genotypic performance in both the experiments i.e. under hydroponic conditions against different saline treatments and under variable natural saline conditions in the field, two genotypes (most tolerant and most susceptible) were chosen as parents. The seeds of each chosen genotype were sown in 4 meter long three rows. In each single hole, 2 seed were sown keeping line to line and plant to plant distances 75cm and 25cm respectively. Later on thinning was done and one seedling retained. Crop was raised following all agronomic practices. The most tolerant and sensitive genotypes were nominated as female and male parent respectively in hybridization program. Foreign contamination was avoided to get the desired hybrids by covering female inflorescence of female parent and male inflorescence of male parent with butter paper bags and kraft paper bags respectively. The female parent was detasseled and pollinated manually to ensure enough seed setting in all crosses. The tolerant and susceptible genotypes were mated to develop F₁, F₂, BC₁ and BC₂ generations.

3.5. Evaluation phase

3.5.1. Experiment-III

Experiment was carried out to evaluate parents and generations in the greenhouse of the department of PBG, UAF, Pakistan. Experiment was carried out with same methodology as followed in experiment-I.

3.5.2. Experiment-IV

This experiment was performed in natural saline field conditions in Saline Soil Research Institute, Pindi Bhatian against different salinity concentrations for evaluation of parents along with all the generations developed with similar methodologies followed in experiment-II. Data was noted similarly as in experiment- II for the same traits. Addition to those traits data for the following traits was recorded in this experiment.
3.5.2.1 Germination related standards

The germination was counted daily from sowing date to last germinated seed. Following were the germination related morphological standards which were studied to assess the performance of genotypes at different saline concentrations.

3.5.2.1.1. Time to start germination (TSG)

The day when first seed was germinated separately in each entry was recorded on the basis of daily field visits.

3.5.2.1.2. Time to 50% germination (T_{50})

Emerged seedlings were counted on daily basis. T_{50} was calculated by formula given below (Coolbear et al., 1984).

\[
T_{50} = t_i + \left[ \frac{N/2 - n_i}{n_j - n_i} \right] (t_j - t_i)
\]

Where,

N = finally germinated seeds
ni, nj = germinated seeds at respective days ti and tj,

when, ni < (N+1)/2 < nj.

3.5.2.1.3. Mean germination time (MGT)

The data taken right from start to final germination was subjected to estimate the mean germination time (MGT) following Ellis and Roberts (1981) as given below:

\[
MGT = \frac{\sum Dn}{\sum n}
\]

Where,

n = Seeds emerged on day D
D = Total days from first germination

3.5.2.1.4. Energy of germination (GE)

It was noted at 4th day after planting seed. It is % of germinated seeds to total seeds
after four days of sowing (Farooq et al., 2006).

3.5.2.1.5. Germination index (GI)

It was computed by using following formulae:

\[
GI = \frac{\text{No. of germinated seeds}}{\text{Days of first count}} + \frac{-}{-} + \frac{\text{No. of germinated seeds}}{\text{Days of final count}}
\]

3.5.2.1.6. Final germination percentage (FGP)

It was noted when germination was completed. It is % of germinated seeds to total seeds sown.

3.5.2.1.7. Coefficient of uniformity of germination (CUG)

It was estimated with formulae of Bewley and Black (1994):

\[
CUE = \sum n / \sum \left[ (\hat{t} - t)^2 \right] \cdot n
\]

Where,

\( t \) = time (days) from planting
\( n \) = Seeds germinated on day \( t \)
\( \hat{t} \) = MGT.

3.6. Biometrical approaches

3.6.1. Analysis of variance

ANOVA of data was done with method described by Steel et al. (1997). Association studies were carried out following Kwon and Tirrie (1964). Generation means analysis was executed by method of Mather and Jinks (1982).

3.6.2. Genetic analysis

Each parameter was subjected to genetic analysis using generation mean analysis (GMA) devised by Mather and Jinks, 1982. A computer program devised by Dr. H. S. Poni was used to calculate genetic analysis. Initially, goodness of fit was tested by using model with one parameter. If model with one parameter (m) rejected, model with two parameters
(m,d) was tested. If both models did not fit then a model was included with dominance parameter. If there was any parameter come out as a non-significant then next parameter was tried. The parent with high value was all the time taken as P₁ for each trait in model fitting. If the tested parameter remained significant then model was selected. Theoretical genetic components of GMA are given in the table 3.2.

Table 3.2. Coefficients of the genetic effects for the weighed least square analysis of generation means.

<table>
<thead>
<tr>
<th>Generation</th>
<th>Components of genetic effects</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>M</td>
</tr>
<tr>
<td>P₁</td>
<td>1</td>
</tr>
<tr>
<td>P₂</td>
<td>1</td>
</tr>
<tr>
<td>F₁</td>
<td>1</td>
</tr>
<tr>
<td>F₂</td>
<td>1</td>
</tr>
<tr>
<td>BC₁</td>
<td>1</td>
</tr>
<tr>
<td>BC₂</td>
<td>1</td>
</tr>
</tbody>
</table>

3.6.3. Correlations

The association on the basis of phenotype and genotype between couples of plant traits was estimated from data of F₂ populations.

3.6.3.1. Phenotypic Correlations

The association on the basis of phenotype (rp) between two x and y traits were estimated with formula given below.

\[
rp = \frac{PCOV(x,y)}{(PVx \cdot PVy)^{1/2}}
\]

Where,

\[
PCOV(x,y) = \text{mean phenotypic covariance of x and y traits.}
\]
PVx and PVy = phenotypic variance of the same traits respectively.

### 3.6.3.2. Genotypic Correlations

The correlation on the basis of genotype (rg) between x and y traits was computed by formula given below,

\[ rg = \frac{GCOV(x,y)}{GVx \cdot GVy}^{1/2} \]

Where,

\[ GCOV(x,y) = COV(x,y) F_2 - COV(x,y)E \]
\[ COV(x,y)E = \left(\frac{1}{4}\right)[COV(x,y)P_1 + COV(x,y)P_2 + 2COV(x,y)F_1] \]

GCOV(x,y), COV(x,y)E, COV(x,y)P_1, COV(x,y)P_2, COV(x,y)F_1 and COV(x,y) F_2 are covariances of x and y related with genetic effects, non-genetic effects, P_1, P_2, F_1 and F_2 generations respectively and GV (x) and GV (y) are genetic variances of x and y traits respectively by Kwon and Torrie (1964).
CHAPTER 4

RESULTS

A set of 40 maize genotypes were screened on the basis of different standards against different salinity concentrations i.e. S_{0.8} dSm^{-1} (T_1; Control), S_{4} dSm^{-1} (T_2), S_{6} dSm^{-1} (T_3) and S_{10} dSm^{-1} (T_4) following triplicated split plot arrangement under completely randomized design (CRD) in the screenhouse of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan. In screenhouse experiment, genotypes were grown and screened under normal and variable saline conditions developed in aqua culture simultaneously. Same set of genotypes was also screened under natural saline field conditions in research area of Saline Soil Research Institute (SSRI) Pindi Bhattian against different salinity concentrations i.e. S_{0.89} dSm^{-1} (T_1; Control), S_{5.2} dSm^{-1} (T_2), S_{6.7} dSm^{-1} (T_3) and S_{11} dSm^{-1} (T_4) based on different standards.

4.1. Screening Phase

Split plot analysis of variance was conducted for data of studied standards in screenhouse and naturally developed saline field with CRD and RCBD respectively. Treatment, genotypic and treatment × genotypic interaction effects were found significant (P<0.05) for all the studied traits in screenhouse (Table 4.1). In this part, data were recorded on several important morphological and physiological standards which include root length, shoot length, root fresh weight, root dry weight, shoot fresh weight, shoot dry weight, sodium concentration, potassium concentration, chloride concentration, proline contents and sodium potassium ratio. Similar results were found in field study under natural saline conditions which also depicted the significant effects of genotypes, treatments and genotype × treatment interaction (Table 4.2). Data were recorded on various important physiological standards i.e. chlorophyll contents, relative water contents, water potential, protein contents, total soluble sugar and growth and yield related parameters like leaf fresh weight, leaf area, photosynthetic rate, plant height, stomata conductance, transpiration rate, number of grains per cob, 100 grain weight and grain yield per plant. Significant genetic variation was observed among genotypes based on all the standards in both studies.

4.1.1. Morphological and physiological standards

Salinity stress adversely affected the morphological and physiological parameters of genotypes in screenhouse and field studies which was confirmed on the basis of significant
(P<0.05) genetic variability among genotypes. Genotypes were sorted out as tolerant and susceptible on the basis of means of standards for salinity stress. UAC-0020 remained best performing (tolerant) in screenhouse as well as in field conditions due to having high mean value for set of standards (shoot length, shoot dry weight and proline contents) and low mean value for set of standards (sodium and chloride concentrations in leaf sap) at high salinity concentration in screenhouse conditions. Even high salinity level $S_{10 \text{ dsm}^{-1}}$ had no effect or had very least effect on morphology of UAC-0020. Reduced mean value of UAC-0028 for standards like potassium concentration in leaf sap, proline contents and high mean value of standards like sodium and chloride concentrations in leaf sap was indicator of its low performance (susceptible) even at least salinity stress level i.e. $S_{0.8 \text{ dsm}^{-1}}$ and $S_{4 \text{ dsm}^{-1}}$ in screenhouse conditions.

Results of field experiment also proved genotype UAC-0020 as tolerant and genotype UAC-0028 as sensitive with high and low means of different standards against different salinity concentrations. UAC-0020 had comparatively high mean values of standards like chlorophyll-a, chlorophyll-b, relative water contents and total soluble sugar even at high salinity level $S_{11 \text{ dsm}^{-1}}$. UAC-0028 had low mean values of standards like total soluble sugar at $S_{5.2 \text{ dsm}^{-1}}$, of water potential and relative water contents at $S_{6.7 \text{ dsm}^{-1}}$. Salinity affected its physiological standards badly due to its high sensitivity even towards low salt concentration. There was abundant variation also in field results. In 40 genotypes, many genotypes showed varied results when compared with screenhouse results.

4.1.2. Growth and yield related standards

Salts affected growth and yield related standards of genotypes drastically in field conditions. This was true indication of significance (P<0.05) of standards which explained high genetic variability among genotypes. Tolerant and sensitive genotypes were selected on the basis of low and high mean values against different salt concentration. UAC-0020 was identified as best genotypes regarding leaf area, leaf fresh weight, photosynthetic rate, transpiration rate and 100 grain weight at high salinity level $S_{11 \text{ dsm}^{-1}}$. UAC-28 proved to be a sensitive to salts on the basis of standards like transpiration rate, stomata conductance, 100 grain weight, plant height, leaf area, leaf fresh weight, No of grains per cob and grain yield per plant even at concentrations $S_{5.2 \text{ dsm}^{-1}}$. 

33
Table 4.1. Mean sum of squares with respective levels of significance for all of studied traits in maize at different salinity levels in screenhouse condition.

<table>
<thead>
<tr>
<th>SOV</th>
<th>DF</th>
<th>SL</th>
<th>RL</th>
<th>SFW</th>
<th>SDW</th>
<th>RFW</th>
<th>RDW</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>2</td>
<td>0.4</td>
<td>0.5</td>
<td>1.05</td>
<td>0.13</td>
<td>0.1</td>
<td>0.01</td>
</tr>
<tr>
<td>Treatment</td>
<td>3</td>
<td>2704.14*</td>
<td>3026.9*</td>
<td>594.9*</td>
<td>22.25*</td>
<td>34*</td>
<td>6.01*</td>
</tr>
<tr>
<td>Error Replication*Treatment</td>
<td>6</td>
<td>5</td>
<td>1.8</td>
<td>2.6</td>
<td>0.3</td>
<td>0.4</td>
<td>0.04</td>
</tr>
<tr>
<td>Genotype</td>
<td>39</td>
<td>186.16*</td>
<td>65.8*</td>
<td>12.55*</td>
<td>1.2*</td>
<td>1.8*</td>
<td>0.1*</td>
</tr>
<tr>
<td>Treatment*Genotype</td>
<td>117</td>
<td>55.7*</td>
<td>17.3*</td>
<td>3.35*</td>
<td>0.3*</td>
<td>0.7*</td>
<td>0.03*</td>
</tr>
<tr>
<td>Error Replication<em>Treatment</em>Genotype</td>
<td>312</td>
<td>327.1</td>
<td>191.5</td>
<td>104.06</td>
<td>8.6</td>
<td>14.6</td>
<td>3.5</td>
</tr>
<tr>
<td>Total</td>
<td>479</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SOV</th>
<th>DF</th>
<th>Na+</th>
<th>K+</th>
<th>Cl-</th>
<th>PRO</th>
<th>Na+/K+</th>
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</thead>
<tbody>
<tr>
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<td>2</td>
<td>0.2</td>
<td>2.3</td>
<td>0.09</td>
<td>0.1</td>
<td>0.0008</td>
</tr>
<tr>
<td>Treatment</td>
<td>3</td>
<td>11685.5*</td>
<td>4829.6*</td>
<td>4766.7*</td>
<td>60.3*</td>
<td>18.3*</td>
</tr>
<tr>
<td>Error Replication*Treatment</td>
<td>6</td>
<td>3.4</td>
<td>18.1</td>
<td>8</td>
<td>0.16</td>
<td>0.008</td>
</tr>
<tr>
<td>Genotype</td>
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<td>145.55*</td>
<td>69*</td>
<td>1.8*</td>
<td>0.8*</td>
</tr>
<tr>
<td>Treatment*Genotype</td>
<td>117</td>
<td>101.7*</td>
<td>56.2*</td>
<td>27.6*</td>
<td>0.9*</td>
<td>0.3*</td>
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<tr>
<td>Error Replication<em>Treatment</em>Genotype</td>
<td>312</td>
<td>169.2</td>
<td>278.2</td>
<td>398.3</td>
<td>13.7</td>
<td>0.3</td>
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<tr>
<td>Total</td>
<td>479</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* denotes highly significant differences (P<0.05)

Abbreviations: SL; shoot length, RL; root length, SFW; shoot fresh weight, SDW; shoot dry weight, RFW; Root fresh weight, RDW; root dry weight, Na+; sodium concentration, K+; potassium concentration, Cl-; chloride concentration, PRO; proline contents, Na+/K+; sodium/potassium ratio.
Table 4.2. Mean sum of squares with respective levels of significance for all of studied traits in maize at different salinity levels in field condition.

<table>
<thead>
<tr>
<th>SOV</th>
<th>DF</th>
<th>PH</th>
<th>LA</th>
<th>LFW</th>
<th>A</th>
<th>E</th>
<th>Ψw</th>
<th>RWC</th>
<th>Chl a</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
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<td>238</td>
<td>0.03</td>
<td>3.2</td>
<td>0.03</td>
<td>0.01</td>
<td>12.9</td>
<td>0.002</td>
</tr>
<tr>
<td>Treatment</td>
<td>3</td>
<td>70055.8*</td>
<td>296513*</td>
<td>116.4*</td>
<td>7236.3*</td>
<td>20*</td>
<td>2.28*</td>
<td>34745.5*</td>
<td>1.8*</td>
</tr>
<tr>
<td>Error Replication*Treatment</td>
<td>6</td>
<td>100</td>
<td>842</td>
<td>0.15</td>
<td>26</td>
<td>0.15</td>
<td>0.005</td>
<td>60</td>
<td>0.02</td>
</tr>
<tr>
<td>Genotype</td>
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<td>2516.7*</td>
<td>6873*</td>
<td>3*</td>
<td>135.1*</td>
<td>0.5*</td>
<td>0.08*</td>
<td>725*</td>
<td>0.03*</td>
</tr>
<tr>
<td>Treatment*Genotype</td>
<td>117</td>
<td>762*</td>
<td>2877*</td>
<td>1.1*</td>
<td>49.4*</td>
<td>0.3*</td>
<td>0.03*</td>
<td>291*</td>
<td>0.01*</td>
</tr>
<tr>
<td>Error Replication<em>Treatment</em>Genotype</td>
<td>312</td>
<td>7110</td>
<td>28158</td>
<td>5.5</td>
<td>675</td>
<td>5.6</td>
<td>0.003</td>
<td>1729</td>
<td>1.05</td>
</tr>
<tr>
<td>Total</td>
<td></td>
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<td></td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>Replication</td>
<td>2</td>
<td>0.004</td>
<td>0.06</td>
<td>0.03</td>
<td>71</td>
<td>68</td>
<td>6.5</td>
<td>4</td>
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</tr>
<tr>
<td>Treatment</td>
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<td>1.4*</td>
<td>176*</td>
<td>18.1*</td>
<td>245532*</td>
<td>630901*</td>
<td>10132.3*</td>
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</tr>
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<td>Error Replication*Treatment</td>
<td>6</td>
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<td>202</td>
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<td>2.15*</td>
<td>0.3*</td>
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<td>12243*</td>
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<tr>
<td>Treatment*Genotype</td>
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<td>0.1009*</td>
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<td>54.2*</td>
<td>776*</td>
<td></td>
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<tr>
<td>Error Replication<em>Treatment</em>Genotype</td>
<td>312</td>
<td>0.4</td>
<td>5.04</td>
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<td>668.2</td>
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<td>Total</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* denotes highly significant differences (P<0.05)

**Abbreviations:** PH; plant height, LA; leaf area, LFW; leaf fresh weight, A; photosynthetic rate, E; transpiration rate, Ψw; water potential, RWC; relative water contents, Chl a; chlorophyll-a contents, Chl b; chlorophyll-b contents, Prot; protein contents, TSS; total soluble salts, Gs; stomata conductance, GPC; No. of grains per cob, 100GW; 100 grain weight, GYPP; grain yield per plant
4.2. Bi-plot analysis

Bi-plot analysis based principal component analysis (Fig. 4.2 and 4.4) indicated presence of genetic variability among studied genotypes under both normal and stress conditions. Bi-plot displayed through principal component analysis technique was divided into four components. Genotype farther away from origin was good performer relative to the genotypes nearer to the origin. In screenhouse conditions, response of all genotypes was identified by plotting four PCA biplots in four different saline environments. In biplot S0.8 dsm\(^{-1}\), all genotypes depicted high dispersion which was prove of positive response for genetic variability for all studied standards (Fig. 4.1). Genotype UAC-0020 was identified as salinity tolerant, genetically most variable and adapted genotype, as it was located apart from the origin in positive direction with high mean and located in negative direction for standards like Na\(^+\) and Cl\(^-\) in all saline environments like S4 dsm\(^{-1}\) (Fig. 4.2), S6 dsm\(^{-1}\) (Fig. 4.3) and S10 dsm\(^{-1}\) (Fig. 4.4); Na\(^+\) and Cl\(^-\) concentration is inversely proportional to tolerance level. UAC-0028 was found susceptible and genetically least variable and least adapted genotype as positioned in a negative quadrant and opposite sides of environment vectors for different standards and in positive direction for standards like Na\(^+\) and Cl\(^-\) which showed comparative poor adaptability on biplot graph in stress treatments like S4 dsm\(^{-1}\) (Fig. 4.2), S6 dsm\(^{-1}\) (Fig. 4.3) and S10 dsm\(^{-1}\) (Fig. 4.4).

In biplot for S4 dsm\(^{-1}\) treatment, 1\(^{st}\) two components sorted out the genotypes under saline stress contributing 71.90% variation where PC\(_1\) contributed 62.86% and PC\(_2\) contributed 9.04% variation (Fig. 4.2). Bi-plot for treatment S6 dsm\(^{-1}\) presented that 1\(^{st}\) two components collectively classified genotypes by exploiting 74.56% variation (Fig. 4.3) where contribution of PC\(_1\) and PC\(_2\) towards variation was 66.18% and 8.37% respectively. PCA biplot analysis for S10 dsm\(^{-1}\) treatment explained that 1\(^{st}\) two components collectively had 71.77% interaction to show variability in genotypes where PC\(_1\) contributed 63.83% and PC\(_2\) contributed 7.95% variation.

In field conditions most of the genotypes gave variable response on biplot graph when compared with biplots of screenhouse data but there was consistency in the response of UAC-0020 and UAC-0028. PCA biplots of 40 genotypes were plotted for four salinity treatments, (S0.89 dsm\(^{-1}\), S5.2 dsm\(^{-1}\), S6.7 dsm\(^{-1}\) and S11 dsm\(^{-1}\)) with all studied standards. All graphs were plotted in PC\(_1\) & PC\(_2\) components of biplot. In biplot S0.89 dsm\(^{-1}\), all genotypes showed high dispersion which was indication of positive response towards genetic variability for all standards (Fig. 4.5). In biplot S5.2 dsm\(^{-1}\), UAC-0020 scattered away from origin of biplot in positive direction which showed that it was tolerant in S5.2 dsm\(^{-1}\) salinity level with respect to all standards (Fig.
Position of UAC-0028 away from origin of graph in negative portion confirmed that it was susceptible at $S_{5.2 \text{ dsm}^{-1}}$ with respect to all standards (Fig. 4.6). At $S_{5.2 \text{ dsm}^{-1}}$, biplot, PC$_1$ and PC$_2$ components collectively contributed 64.37% variation to sort out best and worst genotypes where PC$_1$ contributed 56.08% and PC$_2$ contributed 8.30% variation (Fig. 4.6). In biplot $S_{6.7 \text{ dsm}^{-1}}$, UAC-0020 found in positive region with high genetic variability and adaptability while UAC-0028 was present in negative region of graph showing sensitive response with low genetic variability (Fig. 4.7). Collective contribution of variation of PC$_1$ and PC$_2$ in this biplot was 64.31% where 57.43% and 6.89% variations were contributed by PC$_1$ and PC$_2$ respectively (Fig. 4.7). UAC-0020 and UAC-0028 showed same response in case of high salinity $S_{11 \text{ dsm}^{-1}}$ biplot. UAC-0020 scattered toward positive region while UAC-0028 scattered in negative region showing tolerant and sensitive response respectively (Fig. 4.8). PC$_1$ and PC$_2$ of $S_{11 \text{ dsm}^{-1}}$ biplot collectively depicted 65.53% contribution of variation to sort out tolerant and sensitive genotypes where PC$_1$ contributed 57.96% and PC$_2$ contributed 7.57% variation (Fig. 4.8).
Figure 4.1. Biplot based on principal components analysis (PCA) of maize genotypes under normal treatment $S_{0.8 \text{ ds m}^{-1}}$ in screenhouse condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.2. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment $S_4$ in screenhouse condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.3. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment $S_6\,dsm^{-1}$ in screenhouse condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.4. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment S$_{10}$ dsu$^{-1}$ in screenhouse condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.5. Biplot based on principal components analysis (PCA) of maize genotypes under normal treatment S0.89 dsm⁻¹ in field condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.6. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment S5.2 dsm⁻¹ in field condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.7. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment $S_{6.7 \text{ dsm}^{-1}}$ in field condition.

Blue dots representing maize genotypes while red lines with dots representing traits
Figure 4.8. Biplot based on principal components analysis (PCA) of maize genotypes under stress treatment $S_{11}$ in field condition.

Blue dots representing maize genotypes while red lines with dots representing traits.
4.3. Conclusions

The goal of present study was to find out a most tolerant and most susceptible maize genotypes for salinity stress and to assess the extent of genetic variability present among maize genotypes in different saline environments. Identification of tolerant genotypes was contradictory if based on a single standard. After screening maize genotypes under controlled salinity stress and natural field conditions, each genotype was subjected to biplot analysis with all standards. Biplot analysis was used to find out most tolerant and most susceptible genotypes against salinity stress. On the basis of relative performance, genotype UAC-0020 was found as most tolerant one to salinity stress under screenhouse and natural field stress conditions while genotype UAF-0028 was identified as most susceptible to salinity stress. Selection of one most tolerant and one most susceptible genotypes as parent were made because high level of genetic distance is required for heterosis in hybrid development program. Therefore representation of two extremes (most tolerant and least tolerant) was hybridized to ensure the chances of heterosis.

4.4. Correlation study

Correlation is degree of association among the standards. To breed a high yielding cultivar, breeder has to tailor a plant with combination of number of desirable standards. The estimates of association among standards are helpful for planning a breeding program to synthesize a genotype with desirable standards. Two large F₂ populations (one under normal and one under field stress conditions; 150 plants from each population) involving parents with contrasting standards were used in correlation studies. Alleles of parental standards in F₂ population are recombined, so the correlations among the standards indicate linkage relationships. Correlation matrix among the standards is given in tables 4.3, 4.4, 4.5 & 4.6.

Chlorophyll-α contents had positive association with grain yield per plant at genotypic level under normal condition $S_{0.89}$ dsm$^{-1}$. Significant positive correlation of chlorophyll-α contents was observed with all standards under study like chlorophyll-β contents, 100 grain weight, leaf fresh weight, plant height, number of grains per cob, grain yield per plant, protein contents, total soluble sugar, stomata conductance, transpiration rate, relative water contents, leaf area, photosynthetic rate and water potential studied in present study under all stress conditions $S_{5.2}$ dsm$^{-1}$, $S_{6.7}$ dsm$^{-1}$ and $S_{11}$ dsm$^{-1}$ at genotypic level. Significant negative association of chlorophyll-α contents was exhibited with plant height, transpiration rate and water potential at genotypic level under normal condition $S_{0.89}$ dsm$^{-1}$. Response of chlorophyll-α contents towards 100 grain weight remained similar under normal condition $S_{0.89}$ dsm$^{-1}$ and
all stress conditions like $S_{5.2\,\text{dsm}^{-1}}$, $S_{6.7\,\text{dsm}^{-1}}$ and $S_{11\,\text{dsm}^{-1}}$ at genotypic level as it showed significant negative correlation under all conditions.

Chlorophyll-\textit{b} contents were linked significantly and positively with 100 grain weight at genotypic level at normal condition $S_{0.89\,\text{dsm}^{-1}}$ while at $S_{5.2\,\text{dsm}^{-1}}$ it was significantly and positively associated with chlorophyll-\textit{a} contents, plant height, protein contents, total soluble sugar, stomata conductance, photosynthetic rate and water potential at genotypic level. Similar results were revealed at both $S_{0.89\,\text{dsm}^{-1}}$ and $S_{5.2\,\text{dsm}^{-1}}$ as chlorophyll-\textit{b} contents revealed significant positive association with leaf fresh weight, number of grains per cob, grain yield per plant, transpiration rate, relative water contents and leaf area at genotypic level. Significant positive association of chlorophyll-\textit{b} contents was noted with sets of standards (stomata conductance, transpiration rate and relative water contents) and (chlorophyll-\textit{a} contents, plant height, number of grains per cob and grain yield per plant) at $S_{0.89\,\text{dsm}^{-1}}$ and $S_{5.2\,\text{dsm}^{-1}}$ respectively. Chlorophyll-\textit{b} contents depicted significant positive linkage with leaf fresh weight, protein contents, leaf area, photosynthetic rate and water potential at genotypic level under $S_{6.7\,\text{dsm}^{-1}}$ and $S_{11\,\text{dsm}^{-1}}$ conditions. Significant negative association of chlorophyll \textit{b} contents was found with total soluble sugar at $S_{0.89\,\text{dsm}^{-1}}$ while with 100 grain weight it had significant positive correlation at both $S_{5.2\,\text{dsm}^{-1}}$ and $S_{6.7\,\text{dsm}^{-1}}$ conditions at genotypic level.

Leaf fresh weight had significant positive association with protein contents, total soluble sugar, relative water contents and leaf area at genotypic level at $S_{0.89\,\text{dsm}^{-1}}$ and $S_{5.2\,\text{dsm}^{-1}}$ levels. Significant positive correlation was observed with plant height, number of grains per cob, grain yield per plant, stomata conductance, transpiration rate, photosynthetic rate and water potential at genotypic level under stress level $S_{5.2\,\text{dsm}^{-1}}$. Leaf fresh weight depicted significant positive association with protein contents, transpiration rate and relative water contents at both $S_{5.2\,\text{dsm}^{-1}}$ and $S_{6.7\,\text{dsm}^{-1}}$ levels while at only $S_{6.7\,\text{dsm}^{-1}}$ stress level significant positive correlation of leaf fresh weight was found with chlorophyll-\textit{a} contents, number of grains per cob, total soluble sugar, stomata conductance, leaf area and water potential at genotypic level. At maximum stress condition $S_{11\,\text{dsm}^{-1}}$, leaf fresh weight had significant positive association with only few standards like plant height and grain yield per plant at genotypic level. Significant negative association of leaf fresh weight was shown with plant height at genotypic level under normal condition $S_{0.89\,\text{dsm}^{-1}}$ and with 100 grain weight at all stress conditions ($S_{5.2\,\text{dsm}^{-1}}$, $S_{6.7\,\text{dsm}^{-1}}$ and $S_{11\,\text{dsm}^{-1}}$) at genotypic level.

Plant height had significant positive association with number of grains per cob, grain yield per plant, protein contents, total soluble sugar, stomata conductance, transpiration rate, relative water contents, leaf area, photosynthetic rate and water potential at genotypic level.
under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$ while at maximum stress condition ($S_{11 \text{ dsm}^{-1}}$) plant height exposed significant positive association with only few standards like no of grains per cob, transpiration rate, photosynthetic rate and water potential at genotypic level. Significant negative association of plant height was disclosed with relative water content at the genotypic level under stress level $S_{0.89 \text{ dsm}^{-1}}$ and with 100 grain weight at both stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$ at genotypic level.

Number of grains per cob had significant positive association with protein contents and total soluble sugar at genotypic level under normal condition ($S_{0.89 \text{ dsm}^{-1}}$) and stress level $S_{5.2 \text{ dsm}^{-1}}$; it had significant positive association with some other standards like grain yield per plant, relative water contents, leaf area, photosynthetic rate and water potential at genotypic level under stress condition $S_{5.2 \text{ dsm}^{-1}}$. As number of grains per cob was noted with significant positive correlation with grain yield per plant, total soluble sugar, transpiration rate and leaf area at both stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ at genotypic level while some other standards were also observed with same results such as protein contents, stomata conductance, relative water contents and water potential at genotypic level of stress condition $S_{6.7 \text{ dsm}^{-1}}$. Significant positive association of number of grains with photosynthetic rate was also shown at genotypic level under stress condition $S_{11 \text{ dsm}^{-1}}$. Number of grains per cob was significantly and negatively correlated with leaf area, photosynthetic rate and water potential at genotypic level under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and with 100 grain weight at genotypic level under all the stress ($S_{5.2 \text{ dsm}^{-1}}, S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$) conditions.

100 grain weight displayed significant positive linkage with protein contents, total soluble sugar, stomata conductance and photosynthetic rate under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and with protein contents under stress condition $S_{5.2 \text{ dsm}^{-1}}$ at genotypic level. Significant negative association was presented with grain yield per plant, protein contents, total soluble sugar, stomata conductance, transpiration rate, relative water contents, leaf area and water potential at genotypic level under stress levels $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Significant negative association between 100 grain weight and photosynthetic rate was result of stress condition $S_{6.7 \text{ dsm}^{-1}}$ at genotypic level and at high stress condition ($S_{11 \text{ dsm}^{-1}}$), 100 grain weight had significant negative correlation with protein contents, transpiration rate and leaf area at genotypic level.

Grain yield per plant had significant positive association with protein contents and total soluble sugar at genotypic level under $S_{0.89 \text{ dsm}^{-1}}$ and stress $S_{5.2 \text{ dsm}^{-1}}$ levels of stress. Significant positive linkage of grain yield per plant was exhibited with protein contents, total soluble sugar, stomata conductance, transpiration rate, relative water contents, leaf area,
photosynthetic rate and water potential at genotypic level under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Grain yield per plant had significant positive correlation with chlorophyll-$a$ contents at stress level $S_{6.7 \text{ dsm}^{-1}}$ and with chlorophyll-$b$ contents, transpiration rate, photosynthetic rate and water potential under stress level $S_{11 \text{ dsm}^{-1}}$ at genotypic level. Significant negative association of grain yield per plant was observed with transpiration rate and water potential at genotypic level under stress level $S_{0.89 \text{ dsm}^{-1}}$.

At genotypic level, significant positive correlation of protein content with transpiration rate, relative water contents and leaf area at stress level $S_{0.89 \text{ dsm}^{-1}}$ and $S_{5.2 \text{ dsm}^{-1}}$ was observed whereas some standards like total soluble sugar, stomata conductance, photosynthetic rate and water potential showed same result under both stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$.

At $S_{6.7 \text{ dsm}^{-1}}$, protein contents exhibited significant positive correlation only with leaf area while at maximum stress $S_{11 \text{ dsm}^{-1}}$ same results were observed with total soluble sugar, transpiration rate and relative water contents at genotypic level. Similar behavior was depicted by total soluble sugar with some standards like stomata conductance, relative water contents and leaf area under normal ($S_{0.89 \text{ dsm}^{-1}}$) and stress ($S_{5.2 \text{ dsm}^{-1}}$) conditions; it behaved differently with some standards like transpiration rate, photosynthetic rate and water potential as these standards were exhibiting significant positive interaction only under stress condition $S_{5.2 \text{ dsm}^{-1}}$ at genotypic level. Same findings were recorded regarding total soluble sugar with some standards like transpiration rate, relative water contents, leaf area and photosynthetic rate on both maximum stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ but its behavior in term of stomata conductance and water potential was different as it revealed significant positive association at stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ at genotypic level respectively.

Stomata conductance elucidated significant positive association with water potential at genotypic level under normal condition ($S_{0.89 \text{ dsm}^{-1}}$). Significant positive correlation of stomata conductance with transpiration rate, relative water contents, leaf area and water potential was noted under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$; similar results were exhibited with photosynthetic rate and relative water contents under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ respectively at genotypic level.

At genotypic level, transpiration rate had positive association with leaf area and water potential under treatment levels $S_{0.89 \text{ dsm}^{-1}}$, $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Significant positive interaction of transpiration rate with relative water contents and photosynthetic rate was result of stress condition $S_{5.2 \text{ dsm}^{-1}}$ at genotypic level. At maximum stress condition ($S_{11 \text{ dsm}^{-1}}$) transpiration rate revealed significant positive correlation with only photosynthetic rate.
Significant positive linkage was observed between relative water contents and leaf area. Similar results were displayed in terms of water potential under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$; relative water contents showed significant positive correlation with water potential at genotypic level. The response of relative water contents towards photosynthetic rate was also similar on both stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$ as it interacted significantly and positively with photosynthetic rate.

Significant positive association of leaf area was perceived with photosynthetic rate and water potential under stress condition $S_{5.2 \text{ dsm}^{-1}}$ at genotypic level. Significant negative interaction of photosynthetic rate with water potential was detected under normal ($S_{0.89 \text{ dsm}^{-1}}$) and stress ($S_{5.2 \text{ dsm}^{-1}}$) conditions at genotypic level.
Table 4.3. Phenotypic (Lower diagonal) and genotypic correlation (Upper diagonal) matrix for traits under normal S 0.89 m⁻¹ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chl a</th>
<th>Chl b</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
<th>PROT</th>
<th>TSS</th>
<th>Gs</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>Ψw</th>
</tr>
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<tbody>
<tr>
<td>Chl a</td>
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<td></td>
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<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
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<td></td>
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<td>0.06</td>
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<td>-0.007</td>
<td>0.18*</td>
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<td>0.55**</td>
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<td>0.02</td>
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<td>0.16**</td>
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<td>-0.09</td>
<td>-0.10</td>
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<td>0.001</td>
<td>-0.26**</td>
<td>0.15</td>
<td>0.14</td>
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<td>0.33**</td>
<td>0.03</td>
<td>-0.11</td>
<td>0.25**</td>
<td>0.15</td>
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<td>E</td>
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<td>0.2</td>
<td>0.03</td>
<td>-0.19</td>
<td>0.09*</td>
<td>0.5</td>
<td>-0.34**</td>
<td>0.55**</td>
<td>0.22</td>
<td>-0.24</td>
<td>-0.06</td>
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<td>-0.44*</td>
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</tr>
<tr>
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<td>0.2**</td>
<td>-0.05**</td>
<td>0.1**</td>
<td>0.11</td>
<td>0.12</td>
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<td>LA</td>
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<td>0.13</td>
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<tr>
<td>A</td>
<td>-0.04</td>
<td>0.03</td>
<td>0.05</td>
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<td>0.04</td>
<td>0.11</td>
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* = P < 0.05, ** = P < 0.01
Chl a= Chlorophyll-a (mg/g f.wt)
Chl b= Chlorophyll-b (mg/g f.wt)
LFW= Leaf fresh weight (g)
PH= Plant height (cm)
GPC= Number of grains per cob
100GW= 100 grain weight (g)
GYPP= Grain yield per plant (g)
PROT= Protein contents (µ mol g⁻¹)
TSS= Total soluble sugars (%)
GS= Stomata conductance (mmol m⁻² sec⁻¹)
E= Transpiration rate (mmol H₂O m⁻² sec⁻¹)
RWC= Relative water contents (%)
LA= Leaf area (cm²)
A= Photosynthetic rate (umolCO₂ m⁻¹ s⁻¹ mmol m⁻² sec⁻¹)
Ψw= Water potential (-Mpa)
Table 4.4. Phenotypic (Lower diagonal) and genotypic correlation (Upper diagonal) matrix for traits under stress S5.2 dsm\(^{-1}\) field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chl (a)</th>
<th>Chl (b)</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
<th>PROT</th>
<th>TSS</th>
<th>(G_s)</th>
<th>(E)</th>
<th>RWC</th>
<th>LA</th>
<th>(A)</th>
<th>(\Psi_w)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chl (a)</td>
<td>0.91**</td>
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<td>0.78**</td>
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<td>0.66**</td>
<td>0.70**</td>
<td>0.72**</td>
<td>0.61**</td>
<td>0.65**</td>
<td>0.61**</td>
<td>0.34**</td>
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<td>Chl (b)</td>
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<td>0.93**</td>
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<td>0.72**</td>
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<tr>
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<td>0.74**</td>
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<td>0.64**</td>
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<td>0.59**</td>
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<tr>
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<td>0.65**</td>
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<td>GPC</td>
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<td>0.11**</td>
<td>-0.19*</td>
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<td>0.53**</td>
<td>0.56**</td>
<td>0.16</td>
<td>0.15</td>
<td>0.14*</td>
<td>0.21*</td>
<td>0.26*</td>
<td>0.19*</td>
<td></td>
</tr>
<tr>
<td>100GW</td>
<td>-0.24*</td>
<td>-0.33*</td>
<td>0.45</td>
<td>-0.28**</td>
<td>0.27**</td>
<td>-0.29**</td>
<td>0.04**</td>
<td>-0.22*</td>
<td>-0.20*</td>
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</tr>
<tr>
<td>GYPP</td>
<td>0.66</td>
<td>0.52</td>
<td>0.55</td>
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<td>0.45*</td>
<td>0.50**</td>
<td>0.47*</td>
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<td>-0.28</td>
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<tr>
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<td>0.54</td>
<td>0.48**</td>
<td>0.11*</td>
<td>-0.29</td>
<td>0.77</td>
<td>0.38**</td>
<td>0.37</td>
<td>0.48**</td>
<td>0.63**</td>
<td>0.43**</td>
<td>0.43**</td>
<td>0.42**</td>
<td></td>
</tr>
<tr>
<td>(E)</td>
<td>0.55*</td>
<td>0.42**</td>
<td>0.44**</td>
<td>0.54</td>
<td>0.11**</td>
<td>0.41</td>
<td>0.43</td>
<td>0.38</td>
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<td>0.34**</td>
<td>0.51**</td>
<td>0.52**</td>
<td>0.39**</td>
<td>0.52**</td>
<td></td>
</tr>
<tr>
<td>RWC</td>
<td>0.45**</td>
<td>0.49</td>
<td>0.34**</td>
<td>0.35</td>
<td>0.11*</td>
<td>-0.39</td>
<td>-0.44</td>
<td>0.33**</td>
<td>0.40**</td>
<td>0.45**</td>
<td>0.47**</td>
<td>0.52**</td>
<td>0.22**</td>
<td>0.53**</td>
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</tr>
<tr>
<td>LA</td>
<td>0.49</td>
<td>0.51*</td>
<td>0.46</td>
<td>0.64**</td>
<td>0.27**</td>
<td>-0.19</td>
<td>0.79</td>
<td>0.40</td>
<td>0.46</td>
<td>0.49**</td>
<td>0.36**</td>
<td>0.40**</td>
<td>0.20**</td>
<td>0.60**</td>
<td></td>
</tr>
<tr>
<td>(A)</td>
<td>0.33**</td>
<td>0.21*</td>
<td>0.35**</td>
<td>0.32**</td>
<td>0.21**</td>
<td>0.19</td>
<td>0.62</td>
<td>0.46</td>
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<td>0.31**</td>
<td>0.26</td>
<td>0.17**</td>
<td>0.11*</td>
<td></td>
</tr>
<tr>
<td>(\Psi_w)</td>
<td>0.44*</td>
<td>0.54*</td>
<td>0.45*</td>
<td>0.67**</td>
<td>0.21*</td>
<td>-0.28</td>
<td>0.49*</td>
<td>0.46**</td>
<td>0.48</td>
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<td>0.48*</td>
<td>0.41</td>
<td>0.56**</td>
<td>0.14*</td>
<td></td>
</tr>
</tbody>
</table>

\* \(P < 0.05\), ** \(P < 0.01\)

Chl \(a\) = Chlorophyll-\(a\) (mg/g f.wt)
Chl \(b\) = Chlorophyll-\(b\) (mg/g f.wt)
LFW = Leaf fresh weight (g)
PH = Plant height (cm)
GPC = Number of grains per cob
GYPP = Grain yield per plant (g)
PROT = Protein contents (µ mol g\(^{-1}\))
TSS = Total soluble sugars (%)
100GW = 100 grain weight (g)
RWC = Relative water contents (%)
LA = Leaf area (cm\(^2\))
\(A\) = Photosynthetic rate (umolCO\(_2\)m\(^{-2}\)s\(^{-1}\))
\(\Psi_w\) = Water potential (Mpa)

Chl = Chlorophyll (mg/g f.wt)
LFW = Leaf fresh weight (g)
PH = Plant height (cm)
GPC = Number of grains per cob
GYPP = Grain yield per plant (g)
PROT = Protein contents (µ mol g\(^{-1}\))
TSS = Total soluble sugars (%)
100GW = 100 grain weight (g)
RWC = Relative water contents (%)
LA = Leaf area (cm\(^2\))
\(A\) = Photosynthetic rate (umolCO\(_2\)m\(^{-2}\)s\(^{-1}\))
\(\Psi_w\) = Water potential (Mpa)
Table 4.5. Phenotypic (Lower diagonal) and genotypic correlation (Upper diagonal) matrix for traits under stress S6.7 dsm⁻¹ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chl a</th>
<th>Chl b</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
<th>PROT</th>
<th>TSS</th>
<th>Gs</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>Ψw</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chl a</td>
<td>0.45**</td>
<td>0.67*</td>
<td>0.54**</td>
<td>0.61</td>
<td>-0.45**</td>
<td>0.70**</td>
<td>0.49**</td>
<td>0.47**</td>
<td>0.54**</td>
<td>0.47**</td>
<td>0.71*</td>
<td>0.79*</td>
<td>0.67**</td>
<td>0.65*</td>
<td>0.47*</td>
</tr>
<tr>
<td>Chl b</td>
<td>0.33</td>
<td>0.47**</td>
<td>0.52</td>
<td>0.49</td>
<td>-0.46*</td>
<td>0.57</td>
<td>0.45*</td>
<td>0.67</td>
<td>0.40*</td>
<td>0.55*</td>
<td>0.56**</td>
<td>0.62*</td>
<td>0.42**</td>
<td>0.38**</td>
<td></td>
</tr>
<tr>
<td>LFW</td>
<td>0.45**</td>
<td>0.46</td>
<td>0.48</td>
<td>0.44**</td>
<td>-0.59*</td>
<td>0.50</td>
<td>0.37*</td>
<td>0.43**</td>
<td>0.50**</td>
<td>0.55*</td>
<td>0.65*</td>
<td>0.56**</td>
<td>0.53</td>
<td>0.36*</td>
<td></td>
</tr>
<tr>
<td>PH</td>
<td>0.38**</td>
<td>0.49**</td>
<td>0.41**</td>
<td>0.53**</td>
<td>-0.37*</td>
<td>0.61**</td>
<td>0.50*</td>
<td>0.53**</td>
<td>0.32**</td>
<td>0.58**</td>
<td>0.68*</td>
<td>0.60**</td>
<td>0.67**</td>
<td>0.40**</td>
<td></td>
</tr>
<tr>
<td>GPC</td>
<td>0.48**</td>
<td>0.46</td>
<td>0.33</td>
<td>0.55</td>
<td>-0.52*</td>
<td>0.64**</td>
<td>0.61**</td>
<td>0.59*</td>
<td>0.55**</td>
<td>0.67*</td>
<td>0.60**</td>
<td>0.65*</td>
<td>0.57</td>
<td>0.32*</td>
<td></td>
</tr>
<tr>
<td>100GW</td>
<td>-0.55</td>
<td>-0.50**</td>
<td>-0.60</td>
<td>-0.40**</td>
<td>-0.32</td>
<td>-0.61*</td>
<td>-0.25**</td>
<td>-0.53**</td>
<td>-0.69*</td>
<td>-0.59*</td>
<td>-0.54*</td>
<td>-0.63*</td>
<td>-0.55**</td>
<td>-0.49*</td>
<td></td>
</tr>
<tr>
<td>GYPP</td>
<td>0.58**</td>
<td>0.51</td>
<td>0.41</td>
<td>0.45*</td>
<td>0.57</td>
<td>-0.45**</td>
<td>0.75*</td>
<td>0.70*</td>
<td>0.50**</td>
<td>0.69*</td>
<td>0.76**</td>
<td>0.77*</td>
<td>0.70**</td>
<td>0.59**</td>
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</tr>
<tr>
<td>PROT</td>
<td>0.38</td>
<td>0.39</td>
<td>0.27**</td>
<td>0.34</td>
<td>0.50</td>
<td>-0.27</td>
<td>0.55**</td>
<td>0.46*</td>
<td>0.45*</td>
<td>0.81</td>
<td>0.56</td>
<td>0.56**</td>
<td>0.38</td>
<td>0.42**</td>
<td></td>
</tr>
<tr>
<td>TSS</td>
<td>0.41</td>
<td>0.45</td>
<td>0.27**</td>
<td>0.41</td>
<td>0.47**</td>
<td>0.60</td>
<td>0.59</td>
<td>0.32**</td>
<td>0.55**</td>
<td>0.56*</td>
<td>0.54**</td>
<td>0.52*</td>
<td>0.58**</td>
<td>0.44**</td>
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</tr>
<tr>
<td>Gs</td>
<td>0.41**</td>
<td>0.33**</td>
<td>0.38</td>
<td>0.35</td>
<td>0.41</td>
<td>-0.78**</td>
<td>0.41</td>
<td>0.31**</td>
<td>0.59</td>
<td>0.53**</td>
<td>0.52**</td>
<td>0.44**</td>
<td>0.37</td>
<td>0.52*</td>
<td></td>
</tr>
<tr>
<td>E</td>
<td>0.64</td>
<td>0.47**</td>
<td>0.41**</td>
<td>0.42</td>
<td>0.53</td>
<td>-0.71</td>
<td>0.41</td>
<td>0.44**</td>
<td>0.41</td>
<td>0.39</td>
<td>0.67</td>
<td>0.75**</td>
<td>0.58</td>
<td>0.54**</td>
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</tr>
<tr>
<td>RWC</td>
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<td>0.38</td>
<td>0.44</td>
<td>0.48**</td>
<td>0.39</td>
<td>0.60**</td>
<td>0.56</td>
<td>0.42</td>
<td>0.67</td>
<td>0.37**</td>
<td>0.45</td>
<td>0.72**</td>
<td>0.74**</td>
<td>0.49</td>
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<tr>
<td>LA</td>
<td>0.47</td>
<td>0.51**</td>
<td>0.42</td>
<td>0.52</td>
<td>0.47</td>
<td>-0.77</td>
<td>0.99</td>
<td>0.41**</td>
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<td>0.24</td>
<td>0.57</td>
<td>0.61</td>
<td>0.68</td>
<td>0.48</td>
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<tr>
<td>A</td>
<td>0.53</td>
<td>0.22</td>
<td>0.39</td>
<td>0.51</td>
<td>0.39</td>
<td>0.67</td>
<td>0.49**</td>
<td>0.24</td>
<td>0.66</td>
<td>0.27</td>
<td>0.44</td>
<td>0.99**</td>
<td>0.36</td>
<td>0.44</td>
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</tr>
<tr>
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<td>0.22**</td>
<td>0.25</td>
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<td>0.22</td>
<td>-0.58</td>
<td>0.41**</td>
<td>0.56</td>
<td>0.38**</td>
<td>0.33**</td>
<td>0.72</td>
<td>0.37</td>
<td>0.32</td>
<td>0.29</td>
<td></td>
</tr>
</tbody>
</table>

* = P < 0.05, ** = P < 0.01

Chl a= Chlorophyll-a (mg/g f.wt)
Chl b= Chlorophyll-b (mg/g f.wt)
LFW= Leaf fresh weight (g)
PH= Plant height (cm)
GPC= Number of grains per cob
100GW= 100 grain weight (g)
GYPP= Grain yield per plant (g)
PROT= Protein contents (µ mol g⁻¹)
TSS= Total soluble sugars (%)
Gs= Stomata conductance (mmolm⁻²sec⁻¹)
E= Transpiration rate (mmolH₂Om⁻²sec⁻¹)
RWC= Relative water contents (%)
LA= Leaf area (cm²)
A= Photosynthetic rate (umolco₂m⁻²s⁻¹mmolm⁻²sec⁻¹)
Ψw= Water potential (Mpa)
Table 4.6. Phenotypic (Lower diagonal) and genotypic correlation (Upper diagonal) matrix for traits under stress $S_{11}$ dom⁻¹ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chl $a$</th>
<th>Chl $b$</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
<th>PROT</th>
<th>TSS</th>
<th>Gs</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>$\Psi_w$</th>
</tr>
</thead>
<tbody>
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<td>Chl $a$</td>
<td>0.53*</td>
<td>0.64**</td>
<td>0.56</td>
<td>0.63</td>
<td>-0.71</td>
<td>0.47**</td>
<td>0.64*</td>
<td>0.39**</td>
<td>0.73</td>
<td>0.64*</td>
<td>0.68</td>
<td>0.79</td>
<td>0.31*</td>
<td>0.59</td>
<td></td>
</tr>
<tr>
<td>Chl $b$</td>
<td>0.34**</td>
<td>0.62**</td>
<td>0.35**</td>
<td>0.49**</td>
<td>-0.71</td>
<td>0.50**</td>
<td>0.52*</td>
<td>0.58</td>
<td>0.65</td>
<td>0.73</td>
<td>0.53</td>
<td>0.52**</td>
<td>0.45**</td>
<td>0.66**</td>
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</tr>
<tr>
<td>LFW</td>
<td>0.47</td>
<td>0.48</td>
<td>0.57**</td>
<td>0.54</td>
<td>-0.69**</td>
<td>0.36**</td>
<td>0.68**</td>
<td>0.47</td>
<td>0.64</td>
<td>0.66**</td>
<td>0.63**</td>
<td>0.66**</td>
<td>0.60</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>PH</td>
<td>0.39</td>
<td>0.22**</td>
<td>0.44**</td>
<td>0.46*</td>
<td>-0.67</td>
<td>0.33</td>
<td>0.64</td>
<td>0.42</td>
<td>0.44</td>
<td>0.47**</td>
<td>0.47</td>
<td>0.46</td>
<td>0.50**</td>
<td>0.52**</td>
<td></td>
</tr>
<tr>
<td>GPC</td>
<td>0.44**</td>
<td>0.37</td>
<td>0.38**</td>
<td>0.52</td>
<td>-0.48**</td>
<td>0.51*</td>
<td>0.60</td>
<td>0.52**</td>
<td>0.65</td>
<td>0.54**</td>
<td>0.63</td>
<td>0.63**</td>
<td>0.42**</td>
<td>0.45</td>
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</tr>
<tr>
<td>100GW</td>
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<td>-0.68**</td>
<td>-0.92</td>
<td>-0.77**</td>
<td>-0.49*</td>
<td>-0.41</td>
<td>-0.57**</td>
<td>-0.52</td>
<td>-0.60</td>
<td>-0.57**</td>
<td>-0.55</td>
<td>-0.60**</td>
<td>-0.57</td>
<td>-0.72</td>
<td></td>
</tr>
<tr>
<td>GYPP</td>
<td>0.57**</td>
<td>0.38*</td>
<td>-0.49*</td>
<td>0.22**</td>
<td>0.41**</td>
<td>-0.55</td>
<td>0.33</td>
<td>0.31</td>
<td>0.48</td>
<td>0.68**</td>
<td>0.54</td>
<td>0.52</td>
<td>0.31*</td>
<td>0.48**</td>
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<tr>
<td>PROT</td>
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<td>0.55**</td>
<td>0.50**</td>
<td>0.45</td>
<td>-0.77*</td>
<td>0.44</td>
<td>0.51**</td>
<td>0.67</td>
<td>0.67*</td>
<td>0.65*</td>
<td>0.59</td>
<td>0.50</td>
<td>0.72</td>
<td></td>
</tr>
<tr>
<td>TSS</td>
<td>0.23</td>
<td>0.41</td>
<td>0.43</td>
<td>0.37*</td>
<td>0.45</td>
<td>-0.77*</td>
<td>0.27</td>
<td>0.41</td>
<td>0.69</td>
<td>0.54**</td>
<td>0.43</td>
<td>0.40**</td>
<td>0.43**</td>
<td>0.58</td>
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</tr>
<tr>
<td>Gs</td>
<td>0.69*</td>
<td>0.64</td>
<td>0.42**</td>
<td>0.32</td>
<td>0.59*</td>
<td>-0.77</td>
<td>0.32</td>
<td>0.77</td>
<td>0.32*</td>
<td>0.63</td>
<td>0.65*</td>
<td>0.74</td>
<td>0.37</td>
<td>0.63</td>
<td></td>
</tr>
<tr>
<td>E</td>
<td>0.56</td>
<td>0.63</td>
<td>0.61*</td>
<td>0.45</td>
<td>0.53**</td>
<td>-0.38</td>
<td>0.44**</td>
<td>0.42*</td>
<td>0.40</td>
<td>0.59</td>
<td>0.66</td>
<td>0.58</td>
<td>0.31*</td>
<td>0.58</td>
<td></td>
</tr>
<tr>
<td>RWC</td>
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<td>0.55</td>
<td>-0.77**</td>
<td>0.93*</td>
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<td>0.64*</td>
<td>0.61**</td>
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<td>0.40</td>
<td>0.65**</td>
<td></td>
</tr>
<tr>
<td>LA</td>
<td>0.55</td>
<td>0.43</td>
<td>0.45</td>
<td>0.33</td>
<td>0.43</td>
<td>-0.88*</td>
<td>0.67</td>
<td>0.48</td>
<td>0.23*</td>
<td>0.54</td>
<td>0.48*</td>
<td>0.34</td>
<td>0.23</td>
<td>0.62</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>0.19</td>
<td>0.31</td>
<td>0.28</td>
<td>0.78*</td>
<td>0.31</td>
<td>-0.67</td>
<td>0.55*</td>
<td>0.39</td>
<td>0.38**</td>
<td>0.27</td>
<td>0.21</td>
<td>0.51**</td>
<td>0.20</td>
<td>0.44</td>
<td></td>
</tr>
<tr>
<td>$\Psi_w$</td>
<td>0.41*</td>
<td>0.78**</td>
<td>0.43</td>
<td>0.39*</td>
<td>0.31</td>
<td>-0.89</td>
<td>0.32</td>
<td>0.60*</td>
<td>0.55</td>
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<td>0.39</td>
<td>0.43*</td>
<td>0.51</td>
<td>0.40</td>
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</tr>
</tbody>
</table>

* = $P < 0.05$, ** = $P < 0.01$

Chl $a$ = Chlorophyll-$a$ (mg/g f.wt)
Chl $b$ = Chlorophyll-$b$ (mg/g f.wt)
LFW = Leaf fresh weight (g)
PH = Plant height (cm)
GPC = Number of grains per cob
100GW = 100 grain weight (g)
GYPP = Grain yield per plant (g)
PROT = Protein contents ($\mu$mol g$^{-1}$)
TSS = Total soluble sugars (%)
GS = Stomata conductance (mmol m$^{-2}$ s$^{-1}$)
E = Transpiration rate (mmol H$_2$O m$^{-2}$ s$^{-1}$)
RWC = Relative water contents (%)
LA = Leaf area (cm$^2$)
A = Photosynthetic rate (umol CO$_2$ m$^{-2}$ s$^{-1}$)
$\Psi_w$ = Water potential (-Mpa)
4.5. Generation Mean Analysis

In quantitative parameters, gene action is described as additive, dominance and epistatic effects (additive x additive, additive x dominance and dominance x dominance). Additive effect is normally the average effect of genes from both parents; dominance is the interaction of allelic genes and epistasis is the interaction of non-allelic genes affecting a particular parameter. Gene action is estimated using diallel crosses or by using generation means and variance of different populations (parents, segregating and backcross populations).

The cross was evaluated under normal and salinity stress in screenhouse and field conditions. The data of P₁, P₂, F₁, F₂ and backcross populations (BC₁ and BC₂) grown under normal and salinity stress conditions were recorded for various important parameters such as root length, shoot length, root fresh weight, root dry weight, shoot fresh weight, shoot dry weight, sodium concentration, potassium concentration, chloride concentration, proline contents and sodium potassium ratio. Under field condition, various important physiological parameters like chlorophyll contents, relative water contents, water potential, protein contents, total soluble sugar and some growth and yield related parameters like leaf fresh weight, leaf area, photosynthetic rate, plant height, stomata conductance, transpiration rate, no of grains per cob, 100 grain weight and grain yield per plant were measured. Addition to those parameters data for the following parameters such as time to 50% germination, germination index, mean germination time, final germination percentage, time to start germination, energy of germination and coefficient of uniformity of germination were also recorded.

The results of generation mean analysis are given in tables (4.7-4.22).

4.5.1. Root length (RL)

Better parent P₁ had maximum root length as compared to generations P₂, F₁, F₂, BC₁ and BC₂ under normal condition S₀.₈ dsm⁻¹ and stress conditions S₄ dsm⁻¹, S₆ dsm⁻¹ and S₁₀ dsm⁻¹ in screenhouse. Minimum root length of BC₂ generation was observed under normal S₀.₈ dsm⁻¹ and stress condition S₆ dsm⁻¹ in screenhouse. Least root length of P₂ and F₁ generations were observed under stress condition S₄ dsm⁻¹ and S₁₀ dsm⁻¹ in screenhouse. Five parameters models [mdhil] was found best fitted to data for root length under normal conditions S₀.₈ dsm⁻¹, stress conditions S₆ dsm⁻¹ and S₁₀ dsm⁻¹ in screenhouse. In mentioned conditions, dominance effect was greater than additive effect indicating the preponderance of dominant genes controlling the parameter. Negative sign of ‘h’ indicated that F₁ skewed towards P₂ that was, parent with low root length was dominant over parent with high root length. Interacting genes were
dispersed in parents as shown by negative sign of ‘i’. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’. Five parameters model \([mhij]\) was best fitted to the data under stress conditions \(S_4\,ds^{-1}\) in screenhouse. Dominance effect was higher than additive effect. Positive sign of ‘h’ narrated the dominance of \(P_1\) over \(P_2\). Additive genes showing interaction were associated in parents that was, increasing alleles were in one parent while decreasing alleles were in another parent. Epistasis was of complementary type as shown by same signs of ‘h’ and ‘l’.

4.5.2. Shoot length (SL)

Maximum shoot length was found for \(F_1\) generation as compared to \(P_1, P_2, F_2, BC_1\) and \(BC_2\) under normal conditions \(S_{0.8\,ds^{-1}}\) in screenhouse. Maximum shoot length was found for \(P_1\) generation as compared to \(P_2, F_1, F_2, BC_1\) and \(BC_2\) under \(S_{0.8\,ds^{-1}}\) normal as well as stress conditions \(S_{4\,ds^{-1}}, S_{6\,ds^{-1}}\) and \(S_{10\,ds^{-1}}\) in screenhouse. Minimum shoot length was found in \(F_1\) under normal condition \(S_{0.8\,ds^{-1}}\). \(P_2\) had minimum shoot length under stress condition in \(S_{4\,ds^{-1}}\) and \(S_{6\,ds^{-1}}\) in screenhouse while \(F_1\) had minimum shoot length under stress condition \(S_{10\,ds^{-1}}\) in screenhouse. Under normal \(S_{0.8\,ds^{-1}}\) and stress conditions \(S_{4\,ds^{-1}}\) in screenhouse, four parameters models \([mhij]\) and \([mdhi]\) were found best fitted to data respectively. In mentioned conditions, additive genes contributed less than dominance effect and direction of dominance was toward less shoot length. Negative sign of ‘i’ implied that genes showing interaction were dispersed in parents. Negative sigh of ‘h’ revealed that parent with low shoot length was dominant over parent with high shoot length. Two parameters model \([md]\) under stress conditions \(S_{6\,ds^{-1}}\) was observed best fitted to data with significant deviation of parameters from zero. It informed that shoot length was controlled by additive genes and there was no involvement of epistasis or dominance. Under stress conditions \(S_{10\,ds^{-1}}\) in screenhouse, three parameters model \([mdi]\) was found good fitted to data for shoot length. It confirmed that additive genes were prevailing for controlling shoot length. Alleles increasing the shoot length were present in one parent while decreasing alleles were present in another parent as indicated by positive sign of ‘i’.

4.5.3. Root fresh weight (RFW)

Higher root fresh weight value was found for \(P_1\) generation as compared to \(P_2, F_1, F_2, BC_1\) and \(BC_2\) under normal conditions \(S_{0.8\,ds^{-1}}\) in screenhouse. Under stress conditions \(S_{4\,ds^{-1}}\) and \(S_{10\,ds^{-1}}\) of screenhouse, \(P_1\) generation had higher root fresh weight as compared to other generations. \(F_2\) generation had maximum root fresh weight under stress condition \(S_{6\,ds^{-1}}\) in
screenhouse. BC₂ generation has minimum value under normal condition \( S_{0.8 \text{ dsm}^{-1}} \) in screenhouse. Under stress condition \( S_{4 \text{ dsm}^{-1}} \) and \( S_{10 \text{ dsm}^{-1}} \) in screenhouse, P₂ generation had lower root fresh weight while F₁ has minimum value of root fresh weight under stress condition \( S_{6 \text{ dsm}^{-1}} \) in screenhouse. One parameter model \([m]\) was proved good fitted to data under normal condition \( S_{0.8 \text{ dsm}^{-1}} \) in screenhouse and two parameters model \([md]\) was found best fitted to data for stress conditions \( S_{4 \text{ dsm}^{-1}} \) and \( S_{10 \text{ dsm}^{-1}} \) in screenhouse. It explained that root fresh weight was controlled by additive genes. There was no any role of epistasis. Under stress conditions \( S_{6 \text{ dsm}^{-1}} \) in screenhouse, four parameters model \([mhij]\) was observed good fitted to data. It governed that root fresh weight was controlled by dominant genes. Dominance effect was higher than additive effect representing the dominance of dominant genes controlling the parameter. Negative sign of ‘\(h\)’ specified that F₁ skewed towards P₂ that was, parent with low root length was dominant over parent with high root length. Alleles increasing the root length were recessive to alleles decreasing the root length. Interacting genes dispersed in parents as shown by negative sign of ‘\(i\)’. Epistasis was of complimentary type as shown by same signs of ‘\(h\)’ and ‘\(l\)’.

4.5.4. Root dry weight (RDW)

Generation P₁ was found with highest value of root dry weight as compared to F₁, P₂, F₂, BC₁ and BC₂ under normal conditions \( S_{0.8 \text{ dsm}^{-1}} \) and stress condition \( S_{6 \text{ dsm}^{-1}} \) in screenhouse. Under stress conditions \( S_{4 \text{ dsm}^{-1}} \) in screenhouse, F₂ generation had higher root dry weight as compared to rest of the generations. F₂ generation had higher value under stress condition \( S_{10 \text{ dsm}^{-1}} \) in screenhouse. BC₂ generation was observed with minimum value under normal condition \( S_{0.8 \text{ dsm}^{-1}} \) in screenhouse. Under stress conditions \( S_{4 \text{ dsm}^{-1}} \), \( S_{6 \text{ dsm}^{-1}} \) and \( S_{10 \text{ dsm}^{-1}} \), P₂ had minimum root dry weight in screenhouse. For root dry weight, two parameters model \([md]\) under normal condition \( S_{0.8 \text{ dsm}^{-1}} \) and five parameters model \([mdhil]\) under stress conditions \( S_{4 \text{ dsm}^{-1}} \) was proved satisfactory fitted to data in screenhouse. Under normal condition \( S_{0.8 \text{ dsm}^{-1}} \), root dry weight was controlled by additive genes. There was no any involvement of epistasis. Under stress condition \( S_{4 \text{ dsm}^{-1}} \), dominance effect was prominent than additive effect showing the majority of dominant genes controlling the parameter. Negative sign of ‘\(h\)’ showed that alleles increasing the root dry weight were recessive to alleles decreasing the root dry weight. Interacting genes were in dispersion phase in parents as shown by negative sign of ‘\(i\)’. Three parameters model \([mdh]\) under stress conditions \( S_{6 \text{ dsm}^{-1}} \) and two parameters model \([mi]\) under stress condition \( S_{10 \text{ dsm}^{-1}} \) were found best fitted to data in screenhouse. Under stress condition \( S_{6 \text{ dsm}^{-1}} \), additive dominance model was adequate.
Additive component was higher than dominance indicating additive nature of the parameter. Direction of dominance was towards $P_2$ that was, alleles increasing root dry weight were recessive to alleles reducing the parameter. Under maximum stress condition $S_{10 \text{ dsm}^{-1}}$, additive genes played role to control root dry weight. Interacting genes dispersed in parents as shown by negative sign of ‘$i$’.

4.5.5. Shoot fresh weight (SFW)

Maximum shoot fresh weight value was found for $P_1$ generation as compared to $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ under normal condition $S_{0.8 \text{ dsm}^{-1}}$ and stress condition $S_{4 \text{ dsm}^{-1}}$ in screenhouse. Maximum shoot fresh weight was observed for $F_1$ and $F_2$ in stress conditions $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse respectively. $BC_2$ generation had minimum value for shoot fresh weight under normal condition $S_{0.8 \text{ dsm}^{-1}}$ in screenhouse. Generation $P_2$ was found with minimum value for shoot fresh weight under stress conditions $S_{4 \text{ dsm}^{-1}}$ and $S_{6 \text{ dsm}^{-1}}$ in screenhouse. Minimum shoot fresh weight was found for $F_1$ generation under stress condition $S_{10 \text{ dsm}^{-1}}$ in screenhouse. For shoot fresh weight, three parameters models $[\text{mdi}]$ and $[\text{mdh}]$ were proved good fitted to data under normal condition $S_{0.8 \text{ dsm}^{-1}}$ and stress condition $S_{6 \text{ dsm}^{-1}}$ in screenhouse respectively. Under normal condition $S_{0.8 \text{ dsm}^{-1}}$, additive model was observed important than dominance model. Shoot fresh weight was controlled by additive genes. Positive sign of ‘$i$’ showed that additive genes showing interaction were associated in parents. In case of stress condition $S_{6 \text{ dsm}^{-1}}$, additive model was observed remarkable than dominance model. Shoot fresh weight was controlled by additive genes. Positive sign of ‘$i$’ showed that additive genes showing interaction were associated in parents. Under stress condition $S_{4 \text{ dsm}^{-1}}$, two parameters model $[\text{md}]$ was found best fitted to data. Shoot fresh weight was controlled by additive genes. There was no role of dominant genes and epistasis. Under stress condition $S_{10 \text{ dsm}^{-1}}$ four parameters model $[\text{mdhi}]$ was found best fitted to data. Dominance effect had greater impact over additive effect representing the majority of dominant genes controlling the parameter. Negative sign of ‘$h$’ specified that $F_1$ skewed towards parent with decreased shoot fresh weight. Interacting genes were in repulsion fashion in parents as shown by negative sign of ‘$i$’.

4.5.6. Shoot dry weight (SDW)

Under normal conditions $S_{0.8 \text{ dsm}^{-1}}$ and stress condition $S_{6 \text{ dsm}^{-1}}$ in screenhouse, $P_1$ had higher shoot dry weight as compared to $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ generations. Highest value for shoot dry weight was recorded in case of $F_2$ generation as compared to rest of the
generations under stress conditions $S_4 \text{ dsm}^{-1}$ in screenhouse. BC$_2$ generation was observed with high value of shoot dry weight under stress condition $S_{10} \text{ dsm}^{-1}$ in screenhouse. BC$_2$ was found with minimum value under normal condition $S_{0.8} \text{ dsm}^{-1}$ in screenhouse. Under stress conditions $S_4 \text{ dsm}^{-1}$, $S_6 \text{ dsm}^{-1}$ and $S_{10} \text{ dsm}^{-1}$ in screenhouse, P$_2$ has minimum value for shoot dry weight. For this parameter, two parameters model [md] was found good fitted to data under normal conditions $S_{0.8} \text{ dsm}^{-1}$ and stress condition $S_{6} \text{ dsm}^{-1}$ in screenhouse. In mentioned condition, shoot dry weight was controlled by additive genes. Four parameters model [mdil] was found best fitted to data under stress condition $S_4 \text{ dsm}^{-1}$ in screenhouse. In this condition, additive gene action was higher than dominance gene action. Interacting genes were dispersed in parents as shown by negative sign of ‘i’. Three parameters model [mij] was found best fitted to data under stress condition $S_{10} \text{ dsm}^{-1}$ in screenhouse. It explained that additive gene effect was higher than dominant gene effect. Negative sign of ‘i’ indicated that interacting genes were dispersed in parents. Epistasis was involved in development of shoot dry weight.

4.5.7. Proline contents (PRO)

Generation P$_1$ had higher proline contents as compared to F$_1$, P$_2$, F$_2$, BC$_1$ and BC$_2$ generations under normal condition $S_{0.8} \text{ dsm}^{-1}$, stress conditions $S_6 \text{ dsm}^{-1}$ and $S_{10} \text{ dsm}^{-1}$ in screenhouse. F$_2$ generation had higher proline contents under stress condition $S_4 \text{ dsm}^{-1}$ in screenhouse as compared to P$_1$, P$_2$, F$_1$, BC$_1$ and BC$_2$ generations. Generation P$_2$ had minimum value of proline contents under normal condition $S_{0.8} \text{ dsm}^{-1}$ and stress condition $S_{10} \text{ dsm}^{-1}$ in screenhouse. F$_1$ generation was found with minimum value of proline contents under stress conditions $S_4 \text{ dsm}^{-1}$ and $S_6 \text{ dsm}^{-1}$ in screenhouse. On the basis of proline contents, significant differences among the generations were observed. For proline contents, two parameters model [md] was found good fitted to data under normal conditions $S_{0.8} \text{ dsm}^{-1}$ and stress condition $S_{10} \text{ dsm}^{-1}$ in screenhouse. It revealed that additive genes were involved in development of proline contents. Three parameters model [mhi] was proved good fitted to data under stress condition $S_4 \text{ dsm}^{-1}$ in screenhouse while under stress condition $S_6 \text{ dsm}^{-1}$, model with five parameters [mdhil] was proved good fitted to data. It narrated that development of proline contents was more dependent on dominant gene rather additive genes. Negative sign of ‘h’ specified that alleles decreasing the proline contents were dominant to alleles increasing the proline contents. Interacting genes were remote away from each other in parents as shown by negative sign of ‘i’. Opposite sign of ‘h’ and ‘l’ revealed that epistasis was of duplicate type under stress conditions $S_6 \text{ dsm}^{-1}$.
4.5.8. Sodium concentration (Na\(^+\))

P\(_1\) generation had higher sodium concentration under normal condition S\(_{0.8\ dsm^{-1}}\) and stress condition S\(_{6\ dsm^{-1}}\) in screenhouse while in stress conditions S\(_{4\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\), BC\(_1\) and F\(_1\) generation contained high sodium concentration in screenhouse respectively. In normal condition S\(_{0.8\ dsm^{-1}}\) of screenhouse, BC\(_2\) was noted with least sodium concentration while in rest of all stress environments S\(_{4\ dsm^{-1}}\), S\(_{6\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\), P\(_2\) generation was depicted with decreased sodium concentration in screenhouse. Four [mdij] and two [md] parameters models were best fitted to data under normal condition S\(_{0.8\ dsm^{-1}}\) and stress condition S\(_{6\ dsm^{-1}}\) in screenhouse respectively. Under normal condition S\(_{0.8\ dsm^{-1}}\), additive genes were more prevalent for controlling sodium concentration. Increasing alleles were present in one parent while decreasing alleles were present in another parent as specified by positive sign of ‘i’. Under stress condition S\(_{0\ dsm^{-1}}\), sodium concentration was controlled by additive genes. Five parameters models [mdhil] and [mdhij] were found good fitted to data under stress conditions S\(_{4\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\) in screenhouse. Under said conditions, sodium concentration was primarily controlled by dominant genes. Positive sign of ‘h’ and ‘i’ reported the dominance of P\(_1\) over P\(_2\) and additive genes displaying interaction were associated in parents, that was increasing alleles were in one parent while decreasing alleles were in another parent. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’.

4.5.9. Potassium concentration (K\(^+\))

High level of potassium concentration was found for P\(_1\) generation as compared to P\(_2\), F\(_1\), F\(_2\), BC\(_1\) and BC\(_2\) generations under normal condition S\(_{0.8\ dsm^{-1}}\) and all stress conditions S\(_{4\ dsm^{-1}}\), S\(_{6\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\) in screenhouse. F\(_2\) and P\(_2\) generations had low potassium concentration under normal S\(_{0.8\ dsm^{-1}}\) and stress S\(_{4\ dsm^{-1}}\) conditions in screenhouse respectively while in stress conditions S\(_{6\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\), F\(_1\) generation contained low potassium concentration. Three parameters models [mij] and [mdh] were noted well fitted to data under normal S\(_{0.8\ dsm^{-1}}\) and stress condition S\(_{4\ dsm^{-1}}\) in screenhouse. Additive genes were mainly involved to control potassium concentration under normal condition S\(_{0.8\ dsm^{-1}}\). Positive sign of ‘i’ indicated that additive genes were associative in parents. Dominant genes were responsible to control potassium concentration under stress condition S\(_{4\ dsm^{-1}}\). Negative sign of ‘h’ implied that alleles decreasing potassium concentration were dominant over the alleles increasing potassium concentration. Five [mdhij] and four [mdjl] parameters models were satisfactory fitted to data under stress conditions S\(_{6\ dsm^{-1}}\) and S\(_{10\ dsm^{-1}}\) in screenhouse. Under said conditions, potassium concentration was primarily controlled by dominant genes. Under
stress condition $S_{6 \text{ dsm}^{-1}}$, negative sign of ‘h’ and ‘i’ reported the dominance of $P_2$ over $P_1$ and additive genes displaying interaction were dispersed in parents.

4.5.10. Chloride concentration (Cl\(^{-}\))

$P_1$ generation had maximum chloride concentration in normal condition $S_{0.8 \text{ dsm}^{-1}}$ as well as in all stress conditions $S_{4 \text{ dsm}^{-1}}$, $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse. $P_2$ generation was reported with low chloride concentration under normal condition $S_{0.8 \text{ dsm}^{-1}}$ and all stress conditions $S_{4 \text{ dsm}^{-1}}$, $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse. Five [mdhil] and two [md] parameters models were best fitted to data under normal condition $S_{0.8 \text{ dsm}^{-1}}$ and stress condition $S_{6 \text{ dsm}^{-1}}$ in screenhouse respectively. It clarified that chloride concentration was mainly controlled by dominant genes. Positive sign of ‘h’ reported the dominance of better parent over poor parent. Additive genes displaying interaction were associated in parents, that was increasing alleles were in one parent while decreasing alleles were in another parent as shown by positive sign of ‘i’. Opposite signs of ‘h’ and ‘l’ proved that epistasis was of duplicate type. In case of stress condition $S_{6 \text{ dsm}^{-1}}$, it revealed that chloride concentration was under the control of additive genes. Three parameters models [mdl] and [mdh] were good fitted to data under stress conditions $S_{4 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse respectively. It described that dominance effect was higher than additive effect. Positive sign of ‘h’ narrated the dominance of $P_1$ over $P_2$.

4.5.11. Sodium potassium ratio (Na\(^{+}\)/K\(^{+}\))

Generations $P_1$ and $F_1$ had more sodium potassium ratio under normal $S_{0.8 \text{ dsm}^{-1}}$ condition and stress condition $S_{6 \text{ dsm}^{-1}}$ in screenhouse. Generation $BC_1$ had high sodium potassium ratio under stress conditions $S_{4 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse. $BC_2$ generation was found with low sodium potassium ratio under normal condition $S_{0.8 \text{ dsm}^{-1}}$ in screenhouse while $P_2$ generation had low sodium potassium ratio in all stress conditions $S_{4 \text{ dsm}^{-1}}$, $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse. Two parameters [md] and one parameter [m] models were best fitted to data under normal condition $S_{0.8 \text{ dsm}^{-1}}$ and stress condition $S_{4 \text{ dsm}^{-1}}$ in screenhouse. It proved the main role of additive genes to control sodium potassium ratio. Five parameters model [mdhij] was best fitted to data under stress conditions $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ in screenhouse. Results of stress conditions $S_{6 \text{ dsm}^{-1}}$ and $S_{10 \text{ dsm}^{-1}}$ confirmed that dominance effect was greater than additive effect representing the majority of dominant genes controlling the parameter. Positive sign of ‘h’ and ‘i’ proved the dominance of better parent over poor parent.
and additive genes displaying interaction was associative in parents, that was increasing alleles were in one parent while decreasing alleles were in another parent.

4.5.12. Time to 50% germination (T50)

Lower value of time to 50% germination was found for parent P2 as compared to P1, F1, F2, BC1 and BC2 under normal condition S0.89 dsm⁻¹ and stress condition S11 dsm⁻¹ in field while BC2 and BC1 had lower value in stress conditions S5.2 dsm⁻¹ and S6.7 dsm⁻¹ respectively. Maximum time to 50% germination was found for P1 parent as compared to P2, F1, F2, BC1 and BC2 under normal condition S0.89 dsm⁻¹ as well as all stress conditions S5.2 dsm⁻¹, S6.7 dsm⁻¹ and S11 dsm⁻¹ in field. Five parameters model [mdhil] was found best fitted for normal field condition S0.89 dsm⁻¹. Four parameters model [mdhi] was proved best fitted for stress condition S5.2 dsm⁻¹ in field. Four and three parameter models [mdij] and [mdj] were proved best fitted for time to 50% germination in stress conditions S6.7 dsm⁻¹ and S11 dsm⁻¹ respectively. Under normal condition S0.89 dsm⁻¹ and stress condition S6.7 dsm⁻¹, time to 50% germination was principally controlled by dominant genes. Positive sign of ‘h’ stated the dominance of better parent over poor parent while positive sign of ‘i’ implied that additive genes showing interaction were associative in parents that increasing alleles were in one parent while decreasing alleles were in another parent. Under stress conditions S5.2 dsm⁻¹ and S11 dsm⁻¹, additive genes controlled time to 50% germination.

4.5.13. Germination index (GI)

Higher germination index value was found for BC2 generation as compared to P1, P2, F1, F2, and BC1 under normal conditions in field. Higher germination index was found for P1, F1 and BC1 under stress conditions S5.2 dsm⁻¹, S6.7 dsm⁻¹ and S11 dsm⁻¹ respectively in field. Lower germination index was noted for P2 in normal S0.89 dsm⁻¹ as well as in all stress conditions S5.2 dsm⁻¹, S6.7 dsm⁻¹ and S11 dsm⁻¹. In germination index, model with three parameters [mhj] was proved best fitted to data under normal field condition S0.89 dsm⁻¹ which was indication that germination index was impacted by dominance effect not additive effect. Positive sign of ‘h’ denoted dominance of better parent over poor parent while under stress conditions S5.2 dsm⁻¹ of field, five parameters model [mdhil] was proved best fitted to data. It reported that dominance effect was higher than additive effect. Negative sign of ‘h’ and ‘i’ reported the dominance of P2 over P1. Additive genes displaying interaction were dispersed in parents. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’. Four parameters models [mdhl] and [mdij] were proved best fitted for stress conditions S6.7 dsm⁻¹ and S11 dsm⁻¹ respectively. Under
stress condition $S_{6.7\ \text{dsm}^{-1}}$, dominance effect remained more reliable than additive effect. Positive sign of ‘h’ proved dominance of $P_1$ over $P_2$. Duplicate type of epistasis was confirmed due to opposite sign of ‘h’ and ‘l’. Additive genes were prevailing for controlling germination index under maximum stress condition $S_{11\ \text{dsm}^{-1}}$. Alleles revealed dispersed fashion in parents as indicated by negative sign of ‘i’.

4.5.14. Final germination percentage (FGP)

Higher final germination percentage was found for $P_1$ generation as compared to $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ under normal conditions $S_{0.89\ \text{dsm}^{-1}}$ as well as for all stress conditions $S_{5.2\ \text{dsm}^{-1}}$, $S_{6.7\ \text{dsm}^{-1}}$ and $S_{11\ \text{dsm}^{-1}}$ in field. Lower final germination percentage was recorded with respect to $BC_2$ in normal condition $S_{0.89\ \text{dsm}^{-1}}$ while in stress condition $S_{5.2\ \text{dsm}^{-1}}$, $F_2$ had lower value. Decreased value of $P_2$ as compared to $P_1$, $F_1$, $F_2$, $BC_1$ and $BC_2$ in stress conditions $S_{6.7\ \text{dsm}^{-1}}$ and $S_{11\ \text{dsm}^{-1}}$ proved minimum final germination percentage in concerned stress environments. For final germination percentage, the model with four parameters [mdjl] under normal conditions $S_{0.89\ \text{dsm}^{-1}}$ and model with five parameters [mdhil] under stress condition $S_{5.2\ \text{dsm}^{-1}}$ were found good fitted to data in field. Under said conditions, dominance effect was higher than additive effect. Positive sign of ‘h’ narrated the dominance of $P_1$ over $P_2$. Additive genes showing interaction were associated in parents, that was increasing alleles were in one parent while decreasing alleles are in another parent. Opposite sign of ‘h’ and ‘l’ under stress condition $S_{5.2\ \text{dsm}^{-1}}$ declared the dominance of duplicate epistasis. Three parameters model [mdh] and four parameters model [mdjl] were good fitted to data for field stress conditions $S_{6.7\ \text{dsm}^{-1}}$ and $S_{11\ \text{dsm}^{-1}}$ respectively. It enlightened that dominance effect was important than additive effect. Negative sign of ‘h’ confirmed that $P_2$ was dominant over $P_1$.

4.5.15. Mean germination time (MGT)

High mean germination time was found for $F_2$ generation as compared to $P_1$, $P_2$, $F_2$, $BC_1$ and $BC_2$ under normal condition $S_{0.89\ \text{dsm}^{-1}}$ of field. Maximum mean germination time was found for $P_1$ in all stress conditions $S_{5.2\ \text{dsm}^{-1}}$, $S_{6.7\ \text{dsm}^{-1}}$ and $S_{11\ \text{dsm}^{-1}}$ in field. Minimum mean germination time was noted for $BC_1$, $BC_2$, $F_1$ and $P_2$ in normal field condition $S_{0.89\ \text{dsm}^{-1}}$, stress conditions $S_{5.2\ \text{dsm}^{-1}}$, $S_{6.7\ \text{dsm}^{-1}}$ and $S_{11\ \text{dsm}^{-1}}$ respectively. For mean germination time, four parameters models [mhil], [mdhl] and [mdij] were best fitted to data under normal condition $S_{0.89\ \text{dsm}^{-1}}$, stress conditions $S_{5.2\ \text{dsm}^{-1}}$ and $S_{6.7\ \text{dsm}^{-1}}$ in field respectively. Three parameters model [mdj] was proved best fitted to data under field stress condition $S_{11\ \text{dsm}^{-1}}$. Results of normal condition $S_{0.89\ \text{dsm}^{-1}}$ and stress condition $S_{5.2\ \text{dsm}^{-1}}$ reported that dominance effect was
higher than additive effect. Negative sign of ‘h’ and ‘i’ expressed the dominance of P₂ over P₁ and additive genes showing interaction were dispersed in parents. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’. Results of normal condition S_{6.7 \, \text{dsm}^{-1}} and stress condition S_{11 \, \text{dsm}^{-1}} reported that additive genes were prevailing for controlling mean germination time. Positive sign of ‘i’ in case of stress condition S_{6.7 \, \text{dsm}^{-1}} was indicator of association of interacting additive genes in parents.

### 4.5.16. Water potential (Ψw)

Maximum water potential was found for P₁ under normal condition S_{0.89 \, \text{dsm}^{-1}} while in all stress conditions S_{5.2 \, \text{dsm}^{-1}}, S_{6.7 \, \text{dsm}^{-1}} and S_{11 \, \text{dsm}^{-1}} of field, P₁ was observed with high water potential. Regarding this parameter, least value for F₁ generation was noted under normal condition S_{0.89 \, \text{dsm}^{-1}}. Water potential of P₂ generation remained low in all stress conditions S_{5.2 \, \text{dsm}^{-1}}, S_{6.7 \, \text{dsm}^{-1}} and S_{11 \, \text{dsm}^{-1}} of field. For water potential four parameters models [mhil] was good fitted to data under normal condition S_{0.89 \, \text{dsm}^{-1}} and [mdij] was best fitted to data under stress conditions S_{6.7 \, \text{dsm}^{-1}} and S_{11 \, \text{dsm}^{-1}} in field. Dominance effect was prevalent over additive effect in control condition S_{0.89 \, \text{dsm}^{-1}}. Positive sign of ‘h’ and ‘i’ in case of [mhil] revealed the dominance of P₁ over P₂ and additive genes expressing interaction were associated in parents. Epistasis was of complementary type as displayed by same signs of ‘h’ and ‘l’. In stress conditions S_{6.7 \, \text{dsm}^{-1}} and S_{11 \, \text{dsm}^{-1}}, additive genes were responsible for controlling water potential. Additive genes were in dispersed fashion in parent as indicated by negative sign of ‘i’. Three parameters model [mdh] was noted as a best fitted to data under stress condition S_{5.2 \, \text{dsm}^{-1}} in field. It explained that additive component was greater than dominance component indicating additive nature of the parameter. As sign of ‘h’ was positive, direction of dominance was towards P₁ that was, alleles increasing water potential were dominant to alleles reducing the water potential.

### 4.5.17. Coefficient of uniformity of germination (CUG)

Highest value for coefficient of uniformity was recorded in case of F₁ and BC₁ generations under normal condition S_{0.89 \, \text{dsm}^{-1}} and stress condition S_{11 \, \text{dsm}^{-1}} in field respectively. P₁ was reported with high coefficient of uniformity under both the stress conditions S_{5.2 \, \text{dsm}^{-1}} and S_{6.7 \, \text{dsm}^{-1}} in field. Coefficient of uniformity for P₂ generation remained very low in normal S_{0.89 \, \text{dsm}^{-1}} as well as stress conditions S_{5.2 \, \text{dsm}^{-1}}, S_{6.7 \, \text{dsm}^{-1}} and S_{11 \, \text{dsm}^{-1}} in field. Four parameters models [mdhj] and [mdjl] were reported as best fitted to data under normal condition S_{0.89 \, \text{dsm}^{-1}} and stress condition S_{6.7 \, \text{dsm}^{-1}} in field respectively. In said
conditions, dominance effect was dominating over additive effect. Positive sign of ‘h’ in normal condition $S_{0.89 \text{ dsm}^{-1}}$ indicated that better parent was dominant over poor better. Two [md] and five [mdhil] parameters models were good fitted to data under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field respectively. In stress condition $S_{5.2 \text{ dsm}^{-1}}$, [md] model revealed the dominance of additive component. In maximum stress condition $S_{11 \text{ dsm}^{-1}}$, dominance effect was higher than additive effect. Positive sign of ‘h’ confirmed the dominance of $P_1$ over $P_2$ and positive sign of ‘i’ revealed that additive genes showing interaction were associated in parents, that was increasing alleles were in one parent while decreasing alleles were in another parent. Same sign of ‘h’ and ‘l’ was indication of complimentary epistasis.

### 4.5.18. Leaf fresh weight (LFW)

Maximum leaf fresh weight was found for $BC_1$ generation as compared to $P_1$, $P_2$, $F_1$, $F_2$ and $BC_2$ under normal conditions $S_{0.89 \text{ dsm}^{-1}}$ in field while under stress conditions $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$, $F_1$, $F_2$ and $P_1$ showed high leaf fresh weight correspondingly. Minimum leaf fresh weight was observed in $BC_1$ in normal field condition $S_{0.89 \text{ dsm}^{-1}}$ while in stress conditions $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field, $P_2$ generation was found with decreased leaf fresh weight as compared to $P_1$, $F_1$, $F_2$, $BC_1$ and $BC_2$. For leaf fresh weight, four parameters model [mhil] was found best fitted to data under normal condition $S_{0.89 \text{ dsm}^{-1}}$ in field whereas in stress conditions of field $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$, three parameters [mdi], four parameters [mdjl] and three parameters [mdl] models were observed good fitted to data respectively. In normal condition $S_{0.89 \text{ dsm}^{-1}}$, dominance phenomenon remained remarkable than additive phenomenon to govern leaf fresh weight. Positive sign of ‘h’ and ‘i’ explained the dominance of $P_1$ over $P_2$ and additive genes showing interaction were associated in parents, that was increasing alleles were in one parent while decreasing alleles were in another parent. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’. Under stress condition $S_{5.2 \text{ dsm}^{-1}}$, concerned parameter was control by additive genes which were dispersed in parent due to negative sign of ‘i’. Leaf fresh weight was more impacted by dominance effect rather than additive effect in maximum stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$.

### 4.5.19. Chlorophyll-a contents (Chl a)

Among all the generations, $BC_2$ generation under normal field conditions $S_{0.89 \text{ dsm}^{-1}}$ and $F_1$ generation under field stress condition $S_{5.2 \text{ dsm}^{-1}}$ possessed highest chlorophyll-a contents. Highest chlorophyll-a contents for $F_2$ and $P_1$ generations were observed under field
stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ respectively. Models with four parameters [mdhil] and [mdhil] were found good fitted to data in normal $S_{0.89 \text{ dsm}^{-1}}$ and stress $S_{5.2 \text{ dsm}^{-1}}$ field conditions respectively. In mentioned conditions, dominance effect was higher than additive effect. Three parameters [mhl] and four parameters [mhil] models were recorded best fitted to data under stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ respectively. In case of normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress conditions ($S_{5.2 \text{ dsm}^{-1}}$ & $S_{6.7 \text{ dsm}^{-1}}$), positive sign of ‘h’ narrated the dominance of $P_1$ over $P_2$. Additive genes showing interaction were associated in parents, meaning, increasing alleles were in one parent while decreasing alleles in another parent. In stress condition $S_{5.2 \text{ dsm}^{-1}}$, opposite sign of ‘h’ and ‘l’ revealed that duplicate epistasis played vital role in chlorophyll-\textit{a} contents development. In stress condition $S_{11 \text{ dsm}^{-1}}$, negative sign of ‘h’ specified that $F_1$ skewed towards poor parent. Interacting genes were dispersed in parents as shown by negative sign of ‘i’. Epistasis was of duplicate type as shown by different signs of ‘h’ and ‘l’.

4.5.20. Chlorophyll-\textit{b} contents (Chl \textit{b})

Under normal field conditions $S_{0.89 \text{ dsm}^{-1}}$, high chlorophyll-\textit{b} contents were found for BC$_2$ generation as compared to $P_1$, $P_2$, $F_1$, $F_2$ and BC$_1$. Generations $F_1$, BC$_1$ and $P_1$ had high value for chlorophyll-\textit{b} contents in field stress conditions $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ respectively. Chlorophyll-\textit{b} contents for $F_1$ generation were very low in normal field condition $S_{0.89 \text{ dsm}^{-1}}$. $P_2$ generation was observed with low chlorophyll-\textit{b} contents in field stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Chlorophyll-\textit{b} contents in BC$_2$ were also in low quantity in maximum field stress condition $S_{11 \text{ dsm}^{-1}}$. For chlorophyll-\textit{b} contents, models with four parameters [mijl] under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and with three parameters [mdh] under field stress conditions ($S_{5.2 \text{ dsm}^{-1}}$ & $S_{6.7 \text{ dsm}^{-1}}$) were good fitted to data. Under field stress condition $S_{11 \text{ dsm}^{-1}}$, four parameters model [mhil] was proved best fitted to data. Dominant phenomenon was higher than additive phenomenon in normal condition $S_{0.89 \text{ dsm}^{-1}}$ and maximum stress condition $S_{11 \text{ dsm}^{-1}}$. Negative sign of ‘h’ and ‘i’ showed the dominance of $P_2$ over $P_1$ and additive genes expressing interaction were dispersed in parents. Epistasis was of duplicate type as showed by different signs of ‘h’ and ‘i’. In stress condition $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$, additive gene action had higher magnitude than dominance effect. Positive sign of ‘h’ revealed that $P_1$ was dominant over $P_2$. 

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4.5.21. Plant height (PH)

BC\textsubscript{1} generation possessed highest plant height value as compared to P\textsubscript{1}, P\textsubscript{2}, F\textsubscript{1}, F\textsubscript{2} and BC\textsubscript{2} under normal and as well as in stress conditions S\textsubscript{5.2 dsm\textsuperscript{-1}} and S\textsubscript{6.7 dsm\textsuperscript{-1}} of field. P\textsubscript{1} generation remained high for plant height in maximum stress condition S\textsubscript{11 dsm\textsuperscript{-1}}. Decreased plant height was observed in BC\textsubscript{2} in normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} while in stress conditions S\textsubscript{5.2 dsm\textsuperscript{-1}}, S\textsubscript{6.7 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}}, P\textsubscript{2} reported with least plant height. In the present generation means analysis four parameters model [mdhj] was found good fitted to the data under normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} and stress condition S\textsubscript{5.2 dsm\textsuperscript{-1}} in field. Four parameters model [mdhi] and [mdjl] were proved good fitted to data under stress conditions S\textsubscript{6.7 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}} respectively. Dominance effect played vital role to govern plant height rather than additive effect in all mentioned conditions. Better parent remained dominant over poor parent as sign of ‘h’ was positive in case of normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} and stress condition S\textsubscript{5.2 dsm\textsuperscript{-1}}. P\textsubscript{2} was better than P\textsubscript{1} as indicated by positive sign of ‘h’ and genes were dispersed in parents as indicated by negative sign of ‘i’ in case of stress condition S\textsubscript{6.7 dsm\textsuperscript{-1}}.

4.5.22. Protein contents (PROT)

Highest protein contents were found for F\textsubscript{2} generation as compared to P\textsubscript{1}, P\textsubscript{2}, F\textsubscript{1}, BC\textsubscript{1} and BC\textsubscript{2} under normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} and stress condition S\textsubscript{5.2 dsm\textsuperscript{-1}} in field while P\textsubscript{1} had highest protein contents under stress conditions S\textsubscript{6.7 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}} in field. Least protein contents were observed in P\textsubscript{2} in normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} as well as in stress conditions S\textsubscript{5.2 dsm\textsuperscript{-1}}, S\textsubscript{6.7 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}} in field. In the present study, generation means analysis for protein contents with four parameters model [mdij] was best fitted to data in normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} as well as in stress condition S\textsubscript{6.7 dsm\textsuperscript{-1}}. Five parameters model [mdhil] and four parameters model [mdhj] were good fitted to data in stress conditions S\textsubscript{5.2 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}} respectively. Under normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}} and stress condition S\textsubscript{6.7 dsm\textsuperscript{-1}}, additive genes were prevailing for controlling protein. Additive genes scattered in parents as indicated by positive sign of ‘i’ in case of normal condition S\textsubscript{0.89 dsm\textsuperscript{-1}}. Dominance mode of gene action was greater than additive gene action under stress conditions S\textsubscript{5.2 dsm\textsuperscript{-1}} and S\textsubscript{11 dsm\textsuperscript{-1}}. In case of stress condition S\textsubscript{5.2 dsm\textsuperscript{-1}}, negative sign of ‘h’ indicated that alleles enhancing the protein contents were recessive to alleles reducing the protein contents. Interacting genes were dispersed in parents as shown by negative sign of ‘i’. Epistasis was of duplicated type as shown by different signs of ‘h’ and ‘l’. Under maximum stress S\textsubscript{11 dsm\textsuperscript{-1}}, dominance effect was higher than additive effect. Positive sign of ‘h’ confirmed the dominance of better parent over poor parent. Additive genes showing interaction were linked in parents, that was increasing...
alleles were in one parent while reducing alleles were in another parent as shown by positive sign of ‘i’. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’.

4.5.23. Time to start germination (TSG)

P₁ had higher time to start germination under all conditions S₀.₈₉ dsm⁻¹, S₅.₂ dsm⁻¹, S₆.₇ dsm⁻¹ and S₁₁ dsm⁻¹ in field. Least F₂ generation regarding time to start germination was found under normal condition S₀.₈₉ dsm⁻¹ and stress condition S₆.₇ dsm⁻¹ in field. Time to start germination for F₂ and P₂ generations remained very low under stress conditions S₅.₂ dsm⁻¹ and S₁₁ dsm⁻¹ in field. Four parameters models [mdjl], [mdij], [mdjl] and [mdij] were good fitted to data under normal S₀.₈₉ dsm⁻¹ as well as in stress conditions (S₅.₂ dsm⁻¹, S₆.₇ dsm⁻¹ & S₁₁ dsm⁻¹) in field. Time to start germination was mainly impacted by dominance effect rather than additive effect in normal condition S₀.₈₉ dsm⁻¹ and stress condition S₆.₇ dsm⁻¹ in field while in case of stress conditions S₅.₂ dsm⁻¹ and S₁₁ dsm⁻¹, additive effect was higher than dominance effect. Positive sign of ‘i’ represented associative interaction of interacting genes in parent.

4.5.24. Stomata conductance (Gs)

High level of stomata conductance was found for F₂ and F₁ generations under normal S₀.₈₉ dsm⁻¹ and stress S₅.₂ dsm⁻¹ conditions in field respectively while in high stress conditions S₆.₇ dsm⁻¹ and S₁₁ dsm⁻¹, P₁ had high value. Least stomata conductance was noted in P₂ in normal S₀.₈₉ dsm⁻¹ as well as in stress conditions (S₅.₂ dsm⁻¹, S₆.₇ dsm⁻¹ & S₁₁ dsm⁻¹) in field. In stomata conductance, five parameters model [mdhij] and four parameters model [mdjl] were satisfactory fitted to data under normal S₀.₈₉ dsm⁻¹ and stress S₆.₇ dsm⁻¹ conditions respectively in field. Stomata conductance was developed by dominance gene action under normal S₀.₈₉ dsm⁻¹ and stress S₆.₇ dsm⁻¹ conditions. In case of normal condition S₀.₈₉ dsm⁻¹, Negative sign of ‘h’ reported that parent with lower stomata conductance was dominant over parent with higher stomata conductance. Positive sign of ‘i’ narrated that interacting genes were associated in parents. Four parameters model [mdij] was proved best fitted to data under stress conditions S₅.₂ dsm⁻¹ and S₁₁ dsm⁻¹. In those conditions, stomata conductance was highly impacted by additive effect rather than dominance effect. Positive sign of ‘i’ expressed that interacting genes were associated in parents under stress condition S₅.₂ dsm⁻¹. Negative sign of ‘i’ confirmed dispersal pattern of interacting genes in parents under maximum stress condition S₁₁ dsm⁻¹.
4.5.25. Energy of germination (GE)

Under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress condition $S_{5.2 \text{ dsm}^{-1}}$ in field, $F_1$ and $F_2$ generations had higher energy of germination as compared to all other generations respectively while under stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field, $P_1$ generation had higher energy of germination as compared to $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ generations. Reduced energy of germination was observed for $P_2$ generation under all conditions $S_{0.89 \text{ dsm}^{-1}}$, $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field. For energy of germination, five parameters model [mdhil] was found better fitted under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress condition $S_{5.2 \text{ dsm}^{-1}}$ in field. Under high stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field, four parameters models [mdhl] and [mdhj] were best fitted to data respectively. Dominance effect was greater than additive effect indicating the preponderance of dominant genes controlling the parameter in mentioned conditions. Negative sign of ‘h’ and ‘i’ confirmed the dominancy of poor parent over better parent and dispersion of interacting additive genes in parents respectively. In case of stress condition $S_{5.2 \text{ dsm}^{-1}}$, positive sign of ‘i’ revealed coupling pattern of interacting additive genes in parents. Epistasis was of duplicate type as shown by opposite signs of ‘h’ and ‘l’. Under stress condition $S_{6.7 \text{ dsm}^{-1}}$, negative sign of ‘h’ showed that $P_2$ was dominant over $P_1$ and opposite sign of ‘h’ and ‘l’ confirmed duplicate epistasis. Positive sign of ‘h’ showed that $P_1$ was dominant over $P_2$ under maximum stress condition $S_{11 \text{ dsm}^{-1}}$.

4.5.26. Total soluble sugars (TSS)

Highest value for total soluble sugars was found for $F_1$ generation under normal field condition $S_{0.89 \text{ dsm}^{-1}}$ and maximum field stress condition $S_{11 \text{ dsm}^{-1}}$. Maximum total soluble sugars were observed in $F_1$ and $F_2$ generations in stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$ respectively. Least total soluble sugars were noted in $BC_2$ generation under normal condition $S_{0.89 \text{ dsm}^{-1}}$ in field. Minimum total soluble sugars was found in $P_2$ generation in all stress conditions $(S_{5.2 \text{ dsm}^{-1}}, S_{6.7 \text{ dsm}^{-1}}$ & $S_{11 \text{ dsm}^{-1}}$) in field. Generation means analysis for total soluble sugars showed that model with two parameters [md] was found best fitted to data under normal $S_{0.89 \text{ dsm}^{-1}}$ as well as under stress condition $S_{5.2 \text{ dsm}^{-1}}$ in field. Additive genes were controlling development of total soluble sugar in those conditions. Five parameters model [mdhil] and four parameters model [mhil] were good fitted to data under stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field. Dominance effect was higher than additive effect under high stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$. In those conditions, negative signs of ‘h’ and ‘i’ implied that parent with low soluble sugars was dominant over parent with higher levels of soluble sugars.
and additive interacting genes were dispersed in parents. Epistasis was of duplicate type as shown by contrasting signs of ‘h’ and ‘l’.

4.5.27. Transpiration rate (E)

Generations F₂ had greater transpiration rate under normal S₀.₈₉ dsm⁻¹ and stress condition S₅.₂ dsm⁻¹ in field. Generation P₁ had greater transpiration rate under stress conditions S₆.₇ dsm⁻¹ and S₁₁ dsm⁻¹ in field. Generation P₂ reported with high transpiration rate in normal condition S₀.₈₉ dsm⁻¹ and stress conditions (S₆.₇ dsm⁻¹ & S₁₁ dsm⁻¹) in field. Generation BC₂ had least value of transpiration rate under stress condition S₅.₂ dsm⁻¹ in field. Four parameters models [mdij], [mdhi] and [mdhj] were good fitted to data under normal condition S₀.₈₉ dsm⁻¹ and stress conditions (S₅.₂ dsm⁻¹ & S₁₁ dsm⁻¹) in field respectively. Five parameters model [mdhil] was best fitted to data under stress condition S₆.₇ dsm⁻¹ in field. In case of normal condition S₀.₈₉ dsm⁻¹ and stress condition S₅.₂ dsm⁻¹, transpiration rate was controlled by additive genes. Under stress conditions S₆.₇ dsm⁻¹ and S₁₁ dsm⁻¹, dominant genes controlled transpiration rate as dominance effect was higher than additive effect. Negative signs of ‘h’ and ‘i’ was indication of dominancy of P₂ over P₁ and dispersion of additive interacting genes in parents under stress condition (S₆.₇ dsm⁻¹). Different sign of ‘h’ and ‘l’ was confirmation of duplicate type of epistasis in mentioned condition. Negative sign of ‘h’ explained the dominancy of P₂ over P₁ under maximum stress condition S₁₁ dsm⁻¹.

4.5.28. Photosynthetic rate (A)

Under normal condition of field for photosynthetic rate, F₂ generation showed more photosynthetic rate as compared to P₁, P₂, F₁, BC₁ and BC₂ generations while under stress conditions (S₅.₂ dsm⁻¹ & S₆.₇ dsm⁻¹), P₁ generation was found with high photosynthetic rate. In maximum field stress condition S₁₁ dsm⁻¹, P₂ generation showed high photosynthetic rate. Decreased photosynthetic rate was noted in P₂ generation under normal S₀.₈₉ dsm⁻¹ and stress condition S₆.₇ dsm⁻¹ in field. Reduced level of photosynthetic rate was recorded in F₂ and BC₂ under stress conditions (S₅.₂ dsm⁻¹ & S₁₁ dsm⁻¹) in field. Five parameters model [mdhil] was best fitted to data under normal condition S₀.₈₉ dsm⁻¹ and stress conditions (S₅.₂ dsm⁻¹ & S₆.₇ dsm⁻¹) in field. Four parameters model [mdjl] was best fitted to data under maximum stress condition S₁₁ dsm⁻¹ in field. Dominance effect was higher than additive effect as photosynthetic rate was governed by dominant genes under all mentioned conditions. Negative signs of ‘h’ and ‘i’ were exhibiting dominancy of poor parent over better parent and dispersion of additive interacting genes in parents under normal condition S₀.₈₉ dsm⁻¹ and stress condition S₆.₇ dsm⁻¹.
Duplicate epistasis was observed due to contrasting signs of ‘h’ and ‘l’ under mentioned conditions. Under stress condition $S_{5.2 \text{ dsm}^{-1}}$, positive signs of ‘h’ and ‘i’ were explaining dominancy of better parent over poor parent and association of additive interacting genes in parents respectively. Duplicate epistasis was observed due to opposite sign of ‘h’ and ‘l’ under mentioned condition.

4.5.29. Leaf area (LA)

Generation $F_2$ had higher leaf area as compared to rest of the generations under normal field condition $S_{0.89 \text{ dsm}^{-1}}$ and stress field condition $S_{5.2 \text{ dsm}^{-1}}$ while in stress field conditions ($S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$), $P_1$ generation was found with higher leaf area as compared to $P_2$, $F_1$, $F_2$, $BC_1$ and $BC_2$ generations. $P_2$ generation was observed with decreased leaf area under normal $S_{0.89 \text{ dsm}^{-1}}$ as well as in all stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$) in field. Four parameters models [mhil], [mdhi], [mdhl] and [mdhj] were reported as best fitted to data under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$) in field respectively. Leaf area was developed by dominance gene action in normal $S_{0.89 \text{ dsm}^{-1}}$ as well as stress conditions ($S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$) in field. Complementary epistasis was resultant of similar signs of ‘h’ and ‘l’ and positive sign of ‘h’ was signal of dominancy of $P_1$ over $P_2$ under normal condition $S_{0.89 \text{ dsm}^{-1}}$ while under stress condition $S_{6.7 \text{ dsm}^{-1}}$, negative sign of ‘h’ confirmed the dominancy of $P_2$ over $P_1$ and opposite sign of ‘h’ and ‘l’ clearly explained the role of duplicate epistasis in leaf area development. Additive genes were responsible to develop leaf area was clear from model [mdhi] under stress condition $S_{5.2 \text{ dsm}^{-1}}$ where positive sign of ‘h’ and ‘i’ implied that better parent was dominant over poor parent and additive interacting genes were in associative pattern in parents.

4.5.30. Relative water contents (RWC)

$F_2$, $F_1$, $P_1$ and $BC_1$ generations showed higher relative water contents in normal $S_{0.89 \text{ dsm}^{-1}}$ and stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$) in field respectively. Least relative water contents were noted in $P_2$ generation under normal condition $S_{0.89 \text{ dsm}^{-1}}$ as well as under stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}} \& S_{11 \text{ dsm}^{-1}}$) in field. Five parameters model [mdhil] and four parameters model [mdjl] were good fitted to data under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress condition $S_{6.7 \text{ dsm}^{-1}}$ in field. Dominance effect remained dominant over additive effect in mentioned conditions. Negative sign of ‘h’ explained that parent with low relative water contents was dominant over parent with high relative water contents while said parameter showed associative fashion of additive genes in parents due to positive sign of ‘i’ under
normal condition $S_{0.89 \text{ dsm}^{-1}}$. Duplicate epistasis was the phenomenon which was responsible to govern trait under discussion due to contrasting sign of ‘h’ and ‘l’. Three parameters models [mil] and [mdi] were satisfactory fitted to data under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ in field. Additive component was dominant over dominant component under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$ where negative and positive signs of ‘i’ were clearly explaining the dispersion and association of additive interacting genes in parents respectively.

**4.5.31. Number of grains per cob (GPC)**

Maximum number of grains per cob was recorded in generation $P_1$ in all field conditions as compared to $P_2$, $F_1$, $F_2$, $B_1$, and $B_2$ generations. Minimum number of grains per cob was noted in $B_1$ under normal field condition $S_{0.89 \text{ dsm}^{-1}}$ while in stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$, & $S_{11 \text{ dsm}^{-1}}$), $P_2$ generation was observed with least number of grains per cob. For number of grains per cob, four parameters model [mdjl] was best fitted to data under normal condition in field $S_{0.89 \text{ dsm}^{-1}}$. Three parameters model [mdh] was good fitted to data under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Four parameters model [mdij] was best fitted to data under maximum stress condition $S_{11 \text{ dsm}^{-1}}$ in field. Dominance effect was higher rather than additive effect under normal condition $S_{0.89 \text{ dsm}^{-1}}$. Number of grains per cob was increased by dominant genes in said condition. Additive effect was seemed to be dominant over dominance effect under all stress condition $S_{5.2 \text{ dsm}^{-1}}$, $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$. Better parent was dominant over poor parent as indicated by positive sign of ‘h’ under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$. Additive interacting genes were scattered in parents due to negative sign of ‘i’.

**4.5.32. 100 grain weight (100GW)**

$F_1$ generation had greater 100 grain weight as compared to rest of the generations under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress condition $S_{5.2 \text{ dsm}^{-1}}$ in field while in stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$, $F_2$ and $P_1$ generations contained high 100 grain weight respectively. Least 100 grain weight was observed in $P_2$ generation in normal $S_{0.89 \text{ dsm}^{-1}}$ as well as all stress conditions ($S_{5.2 \text{ dsm}^{-1}}$, $S_{5.2 \text{ dsm}^{-1}}$ & $S_{6.7 \text{ dsm}^{-1}}$). Four parameters models [mihil] and [mdjl] were best fitted to data under normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress condition $S_{11 \text{ dsm}^{-1}}$ in field. Five parameters model [mihil] and three parameters model [mdj] were good fitted to data under stress conditions $S_{5.2 \text{ dsm}^{-1}}$ and $S_{6.7 \text{ dsm}^{-1}}$ respectively. In normal condition $S_{0.89 \text{ dsm}^{-1}}$ and stress conditions ($S_{5.2 \text{ dsm}^{-1}}$ & $S_{11 \text{ dsm}^{-1}}$), dominance effect was higher than additive effect which implied that parent with low 100 grain weight was dominant over
parent with high 100 grain weight due to negative sign of ‘h’ while positive sign of ‘i’ revealed the association of additive interacting genes in parent. Contrasting signs of ‘h’ and ‘l’ declared the duplicate epistasis. Additive genes controlled 100 grain weight under stress condition $S_{6.7\text{ dsm}^{-1}}$.

4.5.33. Grain yield per plant (GYPP)

$F_1$ generation had highest grain yield per plant under normal $S_{0.89\text{ dsm}^{-1}}$ and stress condition $S_{5.2\text{ dsm}^{-1}}$ in field as compared to $P_1$, $P_2$, $F_2$, $BC_1$ and $BC_2$ generations whereas under stress conditions $S_{6.7\text{ dsm}^{-1}}$ and $S_{11\text{ dsm}^{-1}}$ in field, generation $F_2$ and $P_1$ were found high for grain yield per plant respectively. Minimum grain yield per plant was recorded for $P_2$ under normal $S_{0.89\text{ dsm}^{-1}}$ and stress conditions ($S_{5.2\text{ dsm}^{-1}}$, $S_{6.7\text{ dsm}^{-1}}$ & $S_{11\text{ dsm}^{-1}}$) as compared to $P_1$, $F_1$, $F_2$, $BC_1$ and $BC_2$ generations. For grain yield per plant, four parameters model [mdjl] was proved to be satisfactory fitted to data under normal condition $S_{0.89\text{ dsm}^{-1}}$ and as well as for maximum stress condition $S_{11\text{ dsm}^{-1}}$ in field. Five parameters models [mdhjl] and [mdjl] were best fitted to data under stress conditions $S_{5.2\text{ dsm}^{-1}}$ and $S_{6.7\text{ dsm}^{-1}}$ in field respectively. Under all conditions, dominant genes were prevalent over additive genes as dominant effect was higher than additive effect. Under stress condition $S_{5.2\text{ dsm}^{-1}}$, positive sign of ‘h’ indicated that $P_1$ was dominant over $P_2$ and similar signs of ‘h’ and ‘l’ confirmed the complementary epistasis in case of grain yield per plant.
Table 4.7. Generation means for traits under normal $S_{0.8 \text{ dsm}^{-1}}$ screenhouse conditions.

<table>
<thead>
<tr>
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<tbody>
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<td>P2</td>
<td>F1</td>
<td>F2</td>
<td>BC1</td>
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<td>29.30</td>
<td>29.41</td>
<td>30.15</td>
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</tr>
<tr>
<td>SL</td>
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<td>37.22</td>
<td>35.78</td>
<td>37.7</td>
<td>36.2</td>
</tr>
<tr>
<td>RFW</td>
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<td>5.01</td>
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<td>5</td>
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<tr>
<td>SFW</td>
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<td>11.5</td>
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<td>2.75</td>
<td>2.84</td>
<td>2.7</td>
<td>2.8</td>
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<td>1.28</td>
<td>1.32</td>
<td>1.37</td>
</tr>
<tr>
<td>Na⁺</td>
<td>22.5</td>
<td>18.41</td>
<td>19</td>
<td>19.39</td>
<td>21.4</td>
</tr>
<tr>
<td>K⁺</td>
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<td>50.00</td>
<td>48.79</td>
<td>48</td>
<td>49.15</td>
</tr>
<tr>
<td>Cl⁻</td>
<td>20.56</td>
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<td>20.18</td>
<td>18.25</td>
<td>20.32</td>
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<td>9</td>
<td>9</td>
<td>9.8</td>
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<tr>
<td>Na⁺/K⁺</td>
<td>0.42</td>
<td>0.31</td>
<td>0.36</td>
<td>0.30</td>
<td>0.39</td>
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</table>

RL= Root length (cm)  
SL= Shoot length (cm)  
RFW= Root fresh weight (g)  
RDW= Root dry weight (g)  
SFW= Shoot fresh weight (g)  
SDW= Shoot dry weight (g)  
Na⁺= Sodium concentration (mole m⁻³)  
K⁺= Potassium concentration (mole m⁻³)  
Cl⁻= Chloride concentration (mole m⁻³)  
PRO= Proline contents (µ mol g⁻¹)  
Na⁺/K⁺= Sodium potassium ratio
Table 4.8. Generation means for traits under stress $S_4$ dm$^{-1}$ screenhouse conditions.

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<tr>
<td>RFW</td>
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</tr>
<tr>
<td>SFW</td>
<td>12.2</td>
</tr>
<tr>
<td>SDW</td>
<td>2.46</td>
</tr>
<tr>
<td>RDW</td>
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</tr>
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<td>Na$^+$</td>
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</tr>
<tr>
<td>K$^+$</td>
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</tr>
<tr>
<td>Cl$^-$</td>
<td>22.8</td>
</tr>
<tr>
<td>PRO</td>
<td>4.99</td>
</tr>
<tr>
<td>Na$^+$/K$^+$</td>
<td>0.42</td>
</tr>
</tbody>
</table>

RL = Root length (cm)  \hspace{1cm} Na$^+$ = Sodium concentration (mole m$^{-3}$)
SL = Shoot length (cm) \hspace{1cm} K$^+$ = Potassium concentration (mole m$^{-3}$)
RFW = Root fresh weight (g) \hspace{1cm} Cl$^-$ = Chloride concentration (mole m$^{-3}$)
RDW = Root dry weight (g) \hspace{1cm} PRO = Proline contents ($\mu$ mol g$^{-1}$)
SFW = Shoot fresh weight (g) \hspace{1cm} Na$^+$/K$^+$ = Sodium potassium ratio
SDW = Shoot dry weight (g)
Table 4.9. Generation means for traits under stress $S_{6 \text{dsm}^{-1}}$ greenhouse conditions.

<table>
<thead>
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<th>Generations</th>
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<th></th>
</tr>
</thead>
<tbody>
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<td>F₁</td>
<td>F₂</td>
<td>BC₁</td>
</tr>
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<td>32.81</td>
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<td>SFW</td>
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<td>6.77</td>
<td>8.15</td>
<td>8.14</td>
<td>8.05</td>
</tr>
<tr>
<td>SDW</td>
<td>2.2</td>
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<td>1.73</td>
<td>1.73</td>
<td>1.93</td>
</tr>
<tr>
<td>RDW</td>
<td>1.2</td>
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<td>1.15</td>
<td>1.069</td>
<td>1.11</td>
</tr>
<tr>
<td>Na⁺</td>
<td>21.5</td>
<td>18.1</td>
<td>19.6</td>
<td>19.89</td>
<td>20.69</td>
</tr>
<tr>
<td>K⁺</td>
<td>36.15</td>
<td>35.96</td>
<td>21.20</td>
<td>29.81</td>
<td>28.40</td>
</tr>
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<td>Cl⁻</td>
<td>25.53</td>
<td>23.00</td>
<td>24.05</td>
<td>24.2</td>
<td>24.7</td>
</tr>
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<td>PRO</td>
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<td>3.50</td>
<td>3.22</td>
<td>4.20</td>
<td>3.37</td>
</tr>
<tr>
<td>Na⁺/K⁺</td>
<td>0.81</td>
<td>0.42</td>
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RL= Root length (cm)  
SL= Shoot length (cm)  
RFW= Root fresh weight (g)  
RDW= Root dry weight (g)  
SFW= Shoot fresh weight (g)  
SDW= Shoot dry weight (g)  
Na⁺= Sodium concentration (mole m⁻³)  
K⁺= Potassium concentration (mole m⁻³)  
Cl⁻= Chloride concentration (mole m⁻³)  
PRO= Proline contents (µ mol g⁻¹)  
Na⁺/K⁺= Sodium potassium ratio
Table 4.10. Generation means for traits under stress $S_{10 \text{ dsm}^{-1}}$ screenhouse conditions.

<table>
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<td>RFW</td>
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<tr>
<td>SFW</td>
<td>5</td>
</tr>
<tr>
<td>SDW</td>
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<td>Na⁺</td>
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<td>K⁺</td>
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<td>PRO</td>
<td>3.35</td>
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<tr>
<td>Na⁺/K⁺</td>
<td>1.02</td>
</tr>
</tbody>
</table>

RL= Root length (cm)  
SL= Shoot length (cm)  
RFW= Root fresh weight (g)  
RDW= Root dry weight (g)  
SFW= Shoot fresh weight (g)  
SDW= Shoot dry weight (g)  
Na⁺= Sodium concentration (mole m⁻³)  
K⁺= Potassium concentration (mole m⁻³)  
Cl⁻= Chloride concentration (mole m⁻³)  
PRO= Proline contents (µ mol g⁻¹)  
Na⁺/K⁺= Sodium potassium ratio
Table 4.11. Estimates of the best fit model for traits under normal S_{0.8 \ dm}^{-1} screenhouse conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Genetic Effects</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>[m]</td>
<td>[d]</td>
</tr>
<tr>
<td>RL</td>
<td>36.25±0.71</td>
<td>1.19±0.11</td>
</tr>
<tr>
<td>SL</td>
<td>38.87±0.63</td>
<td>-3.22±0.81</td>
</tr>
<tr>
<td>RFW</td>
<td>4.91±0.11</td>
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</tr>
<tr>
<td>SFW</td>
<td>10.44±0.22</td>
<td>1.59±0.08</td>
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<tr>
<td>SDW</td>
<td>2.81±0.15</td>
<td>0.12±0.03</td>
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<tr>
<td>RDW</td>
<td>1.29±0.01</td>
<td>0.092±0.01</td>
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<tr>
<td>Na$^+$</td>
<td>19.33±0.34</td>
<td>2.02±0.02</td>
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<tr>
<td>K$^+$</td>
<td>48.66±0.77</td>
<td>-</td>
</tr>
<tr>
<td>Cl$^-$</td>
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<td>0.98±0.03</td>
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<tr>
<td>PRO</td>
<td>9.02±0.11</td>
<td>1.04±0.07</td>
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<tr>
<td>Na$^+$/K$^+$</td>
<td>0.35±0.2</td>
<td>0.06±0.3</td>
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</table>

RL= Root length (cm)  Na$^+$ = Sodium concentration (mole m$^{-3}$)
SL= Shoot length (cm)  K$^+$ = Potassium concentration (mole m$^{-3}$)
RFW= Root fresh weight (g)  Cl$^-$ = Chloride concentration (mole m$^{-3}$)
RDW= Root dry weight (g)  PRO= Proline contents (µ mol g$^{-1}$)
SFW= Shoot fresh weight (g)  Na$^+$/K$^+$= Sodium potassium ratio
SDW= Shoot dry weight (g)
Table 4.12. Estimates of the best fit model for traits under stress $S_4$ dm$^{-1}$ screenhouse conditions.

<table>
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<th>Traits</th>
<th>Genetic Effects</th>
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<tbody>
<tr>
<td></td>
<td>[m]</td>
<td>[d]</td>
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<tr>
<td>RL</td>
<td>22.17±0.36</td>
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</tr>
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<td>SL</td>
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<td>SFW</td>
<td>10.93±0.06</td>
<td>1.30±0.09</td>
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<tr>
<td>SDW</td>
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<td>0.11±0.03</td>
</tr>
<tr>
<td>RDW</td>
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<td>0.10±0.01</td>
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<td>Na$^+$</td>
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<tr>
<td>K$^+$</td>
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<td>2.32±0.16</td>
</tr>
<tr>
<td>Cl$^-$</td>
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<td>1.77±0.17</td>
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<tr>
<td>Na$^+$/K$^+$</td>
<td>0.44±0.03</td>
<td>-</td>
</tr>
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</table>

RL= Root length (cm)  Na$^+$= Sodium concentration (mole m$^{-3}$)
SL= Shoot length (cm)  K$^+$= Potassium concentration (mole m$^{-3}$)
RFW= Root fresh weight (g)  Cl$^-$= Chloride concentration (mole m$^{-3}$)
RDW= Root dry weight (g)  PRO= Proline contents (µ mol g$^{-1}$)
SFW= Shoot fresh weight (g)  Na$^+$/K$^+$= Sodium potassium ratio
SDW= Shoot dry weight (g)
Table 4.13. Estimates of the best fit model for traits under stress $S_0$ dm$^{-1}$ screenhouse conditions.

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</tr>
<tr>
<td>RFW</td>
<td>4.31±0.09</td>
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</tr>
<tr>
<td>SFW</td>
<td>8.12±0.06</td>
<td>0.56±0.12</td>
</tr>
<tr>
<td>SDW</td>
<td>1.73±0.01</td>
<td>0.44±0.03</td>
</tr>
<tr>
<td>RDW</td>
<td>1.02±0.27</td>
<td>0.13±0.28</td>
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<tr>
<td>Na$^+$</td>
<td>19.82±0.08</td>
<td>1.70±0.13</td>
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<tr>
<td>K$^+$</td>
<td>38.43±1.24</td>
<td>-0.70±0.38</td>
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<td>Cl$^-$</td>
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<td>PRO</td>
<td>6.62±0.23</td>
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<tr>
<td>Na$^+$/K$^+$</td>
<td>0.25±0.03</td>
<td>0.16±0.06</td>
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RL= Root length (cm)  
SL= Shoot length (cm)  
RFW= Root fresh weight (g)  
RDW= Root dry weight (g)  
SFW= Shoot fresh weight (g)  
SDW= Shoot dry weight (g)  
Na$^+$= Sodium concentration (mole m$^{-3}$)  
K$^+$= Potassium concentration (mole m$^{-3}$)  
Cl$^-$= Chloride concentration (mole m$^{-3}$)  
PRO= Proline contents ($\mu$ mol g$^{-1}$)  
Na$^+$/K$^+$= Sodium potassium ratio
Table 4.14. Estimates of the best fit model for traits under stress $S_{10, \text{dsm}^{-1}}$ screenhouse conditions.

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<td>[d]</td>
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<td>RFW</td>
<td>2.495±0.02</td>
<td>0.64±0.05</td>
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<td>SFW</td>
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<td>0.30±0.14</td>
</tr>
<tr>
<td>SDW</td>
<td>1.83±0.02</td>
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</tr>
<tr>
<td>RDW</td>
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</tr>
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<td>Na$^+$</td>
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<td>K$^+$</td>
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<td>8.53±0.33</td>
</tr>
<tr>
<td>Cl$^-$</td>
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<td>5.46±0.15</td>
</tr>
<tr>
<td>PRO</td>
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<td>0.38±0.05</td>
</tr>
<tr>
<td>Na$^+$/K$^+$</td>
<td>0.21±0.04</td>
<td>0.22±0.01</td>
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</tbody>
</table>

RL= Root length (cm)  
SL= Shoot length (cm)  
RFW= Root fresh weight (g)  
RDW= Root dry weight (g)  
SFW= Shoot fresh weight (g)  
SDW= Shoot dry weight (g)  
Na$^+$= Sodium concentration (mole m$^{-3}$)  
K$^+$= Potassium concentration (mole m$^{-3}$)  
Cl$^-$= Chloride concentration (mole m$^{-3}$)  
PRO= Proline contents (µ mol g$^{-1}$)  
Na$^+$/K$^+$= Sodium potassium ratio
Table 4.15. Generation means for traits under normal S0.89 dm⁻¹ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl &lt;i&gt;a&lt;/i&gt;</th>
<th>Chl &lt;i&gt;b&lt;/i&gt;</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
</tr>
</thead>
<tbody>
<tr>
<td>P₁</td>
<td>5</td>
<td>17.15</td>
<td>91.18</td>
<td>3.69</td>
<td>0.58</td>
<td>0.52</td>
<td>5.74</td>
<td>146.04</td>
<td>376.6</td>
<td>34.53</td>
<td>132.36</td>
</tr>
<tr>
<td>P₂</td>
<td>4.1</td>
<td>16.53</td>
<td>86</td>
<td>3.64</td>
<td>0.52</td>
<td>0.5</td>
<td>5.28</td>
<td>140.75</td>
<td>366.86</td>
<td>32.8</td>
<td>124.66</td>
</tr>
<tr>
<td>F₁</td>
<td>4.56</td>
<td>19.26</td>
<td>88.59</td>
<td>3.61</td>
<td>0.72</td>
<td>0.5</td>
<td>6.58</td>
<td>155.99</td>
<td>375.5</td>
<td>41</td>
<td>143.33</td>
</tr>
<tr>
<td>F₂</td>
<td>4.2</td>
<td>20.81</td>
<td>88.59</td>
<td>4.21</td>
<td>0.64</td>
<td>0.63</td>
<td>5.31</td>
<td>151.31</td>
<td>370.14</td>
<td>38.28</td>
<td>132.65</td>
</tr>
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<td>4.72</td>
<td>19.35</td>
<td>89.88</td>
<td>3.48</td>
<td>0.73</td>
<td>0.5</td>
<td>6.24</td>
<td>158.7</td>
<td>364.9</td>
<td>33.93</td>
<td>126.3</td>
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<tr>
<td>BC₂</td>
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<td>21.07</td>
<td>84.4</td>
<td>3.48</td>
<td>0.75</td>
<td>0.7</td>
<td>6.61</td>
<td>138.9</td>
<td>376.5</td>
<td>33.86</td>
<td>134.23</td>
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</table>

<table>
<thead>
<tr>
<th>Traits</th>
<th>PROT</th>
<th>TSS</th>
<th>Gₛ</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>TSG</th>
<th>GE</th>
<th>CUG</th>
<th>Ψₜw</th>
</tr>
</thead>
<tbody>
<tr>
<td>P₁</td>
<td>5.27</td>
<td>1.42</td>
<td>196</td>
<td>2.2</td>
<td>82.56</td>
<td>282.2</td>
<td>35.94</td>
<td>4.96</td>
<td>76.28</td>
<td>82.16</td>
<td>-0.35</td>
</tr>
<tr>
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<td>4.7</td>
<td>1.26</td>
<td>186.33</td>
<td>1.95</td>
<td>77.36</td>
<td>280.83</td>
<td>32.39</td>
<td>3.76</td>
<td>65.39</td>
<td>77.51</td>
<td>-0.35</td>
</tr>
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<td>F₁</td>
<td>5.29</td>
<td>1.29</td>
<td>208.53</td>
<td>2.29</td>
<td>88.26</td>
<td>291.56</td>
<td>40.4</td>
<td>3.63</td>
<td>82</td>
<td>89.65</td>
<td>-0.72</td>
</tr>
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<td>1.37</td>
<td>213.6</td>
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<td>89.34</td>
<td>295.33</td>
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<td>80</td>
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<td>1.27</td>
<td>205.36</td>
<td>2.17</td>
<td>85.3</td>
<td>283</td>
<td>36.86</td>
<td>3.8</td>
<td>79.57</td>
<td>85.2</td>
<td>-0.38</td>
</tr>
<tr>
<td>BC₂</td>
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<td>1.17</td>
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<td>4.46</td>
<td>75.36</td>
<td>85.45</td>
<td>-0.36</td>
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</table>

T50= Time to 50% germination (days)  
GI= Germination index (%)  
FGP= Final germination percentage (%)  
MGT= Mean germination time (days)  
Chl <i>a</i>= Chlorophyll-<i>a</i> (mg/g f.wt)  
Chl <i>b</i>= Chlorophyll-<i>b</i> (mg/g f.wt)  
LFW= Leaf fresh weight (g)  
PH= Plant height (cm)  
GPC= Number of grains per cob  
100GW= 100 grain weight (g)  
LA= Leaf area (cm²)  
A= Photosynthetic rate (umolCO₂m⁻¹s⁻¹)  
TSG= Time to start germination (days)  
PROT= Grain yield per plant (g)  
GYP= Protein contents (µ mol g⁻¹)  
GE= Energy of germination (%)  
TSS= Total soluble sugars (%)  
CUG = Coefficient of uniformity of germination  
Ψₜw= Water potential (-Mpa)  
RWC= Relative water contents (%)
Table 4.16. Generation means for traits under stress S5.2 dsm⁻¹ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl a</th>
<th>Chl b</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
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</thead>
<tbody>
<tr>
<td>P1</td>
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<td>15.41</td>
<td>79.76</td>
<td>5.81</td>
<td>0.51</td>
<td>0.46</td>
<td>6.42</td>
<td>138.25</td>
<td>364.07</td>
<td>31.69</td>
<td>130.03</td>
</tr>
<tr>
<td>P2</td>
<td>5.27</td>
<td>14.19</td>
<td>73.37</td>
<td>4.38</td>
<td>0.4</td>
<td>0.39</td>
<td>5.2</td>
<td>124.22</td>
<td>339.74</td>
<td>28.43</td>
<td>110.55</td>
</tr>
<tr>
<td>F1</td>
<td>4.98</td>
<td>20.03</td>
<td>79.13</td>
<td>4.12</td>
<td>0.7</td>
<td>0.68</td>
<td>6.5</td>
<td>149.9</td>
<td>362.95</td>
<td>37.99</td>
<td>139.18</td>
</tr>
<tr>
<td>F2</td>
<td>4.91</td>
<td>19.35</td>
<td>64.93</td>
<td>3.88</td>
<td>0.57</td>
<td>0.57</td>
<td>6.44</td>
<td>141.26</td>
<td>353.87</td>
<td>35.17</td>
<td>129.98</td>
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<td>5.59</td>
<td>17.91</td>
<td>79.68</td>
<td>3.6</td>
<td>0.67</td>
<td>0.44</td>
<td>5.96</td>
<td>150.79</td>
<td>360.9</td>
<td>31.29</td>
<td>129.58</td>
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<td>77.63</td>
<td>3.56</td>
<td>0.66</td>
<td>0.43</td>
<td>5.87</td>
<td>129.83</td>
<td>349.49</td>
<td>30.79</td>
<td>121.22</td>
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</table>

<table>
<thead>
<tr>
<th>Traits</th>
<th>PROT</th>
<th>TSS</th>
<th>Gs</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>TSG</th>
<th>GE</th>
<th>CUG</th>
<th>Ψw</th>
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<tbody>
<tr>
<td>P1</td>
<td>5.2</td>
<td>1.38</td>
<td>194.21</td>
<td>2.3</td>
<td>76</td>
<td>282.6</td>
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<td>76</td>
<td>81.27</td>
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<td>0.96</td>
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<td>2.11</td>
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<td>236.07</td>
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<td>4.2</td>
<td>58</td>
<td>70.06</td>
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</tr>
<tr>
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<td>1.14</td>
<td>207.12</td>
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<td>72.46</td>
<td>75.17</td>
<td>-0.39</td>
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<td>197.61</td>
<td>2.14</td>
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<td>78.9</td>
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<td>4.33</td>
<td>61.47</td>
<td>73.05</td>
<td>-0.36</td>
</tr>
</tbody>
</table>

T50= Time to 50% germination (days)
GI= Germination index (%)
FGP= Final germination percentage (%)
MGT= Mean germination time (days)
Chl a= Chlorophyll-a (mg/g f.wt)
Chl b= Chlorophyll-b (mg/g f.wt)
LFW= Leaf fresh weight (g)
PH= Plant height (cm)
GPC= Number of grains per cob
100GW= 100 grain weight (g)
PROT= Protein contents (µ mol g⁻¹)
TSS= Total soluble sugars (%)
Gs= Stomata conductance (mmolm⁻²sec⁻¹)
E= Transpiration rate (mmolH₂Omol⁻²sec⁻¹)
RWC= Relative water contents (%)
LA= Leaf area (cm²)
A= Photosynthetic rate (umolco₂m⁻²s⁻¹mmolm⁻²sec⁻¹)
100GW= 100 grain weight (g)
TSG= Time to start germination (days)
GE= Energy of germination (%)
CUG = Coefficient of uniformity of germination
Ψw= Water potential (-Mpa)
### Table 4.17. Generation means for traits under stress $S_{6.7\text{ dsm}^{-1}}$ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl $a$</th>
<th>Chl $b$</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
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<tr>
<td>$P_1$</td>
<td>8.32</td>
<td>15.21</td>
<td>75.92</td>
<td>7.24</td>
<td>0.31</td>
<td>0.35</td>
<td>5.32</td>
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<td>26.59</td>
<td>116.86</td>
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<td>9.13</td>
<td>60</td>
<td>4.51</td>
<td>0.3</td>
<td>0.26</td>
<td>3.29</td>
<td>103.11</td>
<td>291.05</td>
<td>17.94</td>
<td>84.33</td>
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<td>$F_1$</td>
<td>5.6</td>
<td>14.2</td>
<td>66.4</td>
<td>4.4</td>
<td>0.35</td>
<td>0.36</td>
<td>4.44</td>
<td>124.29</td>
<td>330</td>
<td>22.99</td>
<td>110.23</td>
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<td>66.4</td>
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<td>320.13</td>
<td>27.06</td>
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<td>71.16</td>
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<td>0.37</td>
<td>4.19</td>
<td>126.97</td>
<td>332.03</td>
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<td>106.47</td>
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<td>0.32</td>
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<td>48.74</td>
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<td>250.03</td>
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<td>5.43</td>
<td>45</td>
<td>57</td>
<td>-0.63</td>
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</tbody>
</table>

- **T50**= Time to 50% germination (days)
- **GI**= Germination index (%)
- **FGP**= Final germination percentage (%)
- **MGT**= Mean germination time (days)
- **Chl $a$**= Chlorophyll-$a$ (mg/g f.wt)
- **Chl $b$**= Chlorophyll-$b$ (mg/g f.wt)
- **LFW**= Leaf fresh weight (g)
- **PH**= Plant height (cm)
- **GPC**= Number of grains per cob
- **100GW**= 100 grain weight (g)
- **GYPP**= Grain yield per plant (g)
- **PROT**= Protein contents (µ mol g$^{-1}$)
- **TSS**= Total soluble sugars (%)
- **Gs**= Stomata conductance (mmol m$^{-2}$ s$^{-1}$)
- **E**= Transpiration rate (mmol H$_2$O m$^{-2}$ s$^{-1}$)
- **RWC**= Relative water contents (%)
- **LA**= Leaf area (cm$^2$)
- **A**= Photosynthetic rate (µmol CO$_2$ m$^{-2}$ s$^{-1}$)
- **TSG**= Time to start germination (days)
- **GE**= Energy of germination (%)
- **CUG**= Coefficient of uniformity of germination
- **Ψ$w$**= Water potential (-Mpa)
Table 4.18. Generation means for traits under stress S11 dm$^{-1}$ field conditions.

<table>
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<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl a</th>
<th>Chl b</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
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<tbody>
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<tr>
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<td>9.1</td>
<td>15.55</td>
<td>66.27</td>
<td>7.66</td>
<td>0.43</td>
<td>0.35</td>
<td>4.82</td>
<td>125.72</td>
<td>330.35</td>
<td>26.57</td>
<td>116.86</td>
</tr>
<tr>
<td>P2</td>
<td>5.61</td>
<td>6.73</td>
<td>30.35</td>
<td>4.52</td>
<td>0.34</td>
<td>0.35</td>
<td>1.39</td>
<td>26.7</td>
<td>105.34</td>
<td>11.04</td>
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<td>0.32</td>
<td>0.31</td>
<td>3.48</td>
<td>86</td>
<td>310.09</td>
<td>21.1</td>
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<td>6.61</td>
<td>12.38</td>
<td>52.8</td>
<td>5.41</td>
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<td>0.21</td>
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<td>LA</td>
<td>A</td>
<td>TSG</td>
<td>GE</td>
<td>CUG</td>
<td>Ψw</td>
</tr>
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<td>29.47</td>
<td>0.23</td>
<td>14.99</td>
<td>83.93</td>
<td>7.8</td>
<td>5.59</td>
<td>15.94</td>
<td>21.92</td>
<td>-1.03</td>
</tr>
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<td>1.36</td>
<td>160</td>
<td>1.14</td>
<td>60.99</td>
<td>237.07</td>
<td>27.07</td>
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<td>61.57</td>
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<td>1.25</td>
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<td>69.32</td>
<td>215.15</td>
<td>23.46</td>
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</tr>
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<td>42.88</td>
<td>194.75</td>
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<td>6.44</td>
<td>48.65</td>
<td>50</td>
<td>-0.64</td>
</tr>
</tbody>
</table>

T50= Time to 50% germination (days)  
GI= Germination index (%)  
FGP= Final germination percentage (%)  
MGT= Mean germination time (days)  
Chl a= Chlorophyll-α (mg/g f.wt)  
Chl b= Chlorophyll-β (mg/g f.wt)  
LFW= Leaf fresh weight (g)  
PH= Plant height (cm)  
GPC= Number of grains per cob  
100GW= 100 grain weight (g)  
GYPP= Grain yield per plant (g)  
PROT= Protein contents (µ mol g$^{-1}$)  
TSS= Total soluble sugars (%)  
Gs= Stomata conductance (mmolm$^{-2}$sec$^{-1}$)  
E= Transpiration rate (mmolH$_2$Om$^{-2}$sec$^{-1}$)  
RWC= Relative water contents (%)  
LA= Leaf area (cm$^2$)  
A= Photosynthetic rate (umolco$_2$m$^{-2}$s$^{-1}$)  
TSG= Time to start germination (days)  
GE= Energy of germination (%)  
CUG = Coefficient of uniformity of germination  
Ψw= Water potential (-Mpa)
Table 4.19. Estimates of the best fit model for traits under normal S0.89_dsm field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl a</th>
<th>Chl b</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
</tr>
</thead>
<tbody>
<tr>
<td>[m]</td>
<td>3.46±0.32</td>
<td>16.74±0.21</td>
<td>87.55±0.46</td>
<td>6.59±0.33</td>
<td>0.15±0.06</td>
<td>0.68±0.01</td>
<td>1.09±0.71</td>
<td>143.29±0.64</td>
<td>370.33±0.82</td>
<td>51.35±4.15</td>
<td>128.53±0.62</td>
</tr>
<tr>
<td>[d]</td>
<td>0.44±0.04</td>
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<td>2.69±0.79</td>
<td>-</td>
<td>0.01±0.01</td>
<td>-</td>
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<td>3.85±0.68</td>
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<tr>
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<td>1.36±0.16</td>
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<td>12.45±1.24</td>
<td>-</td>
<td>-41.9±4.09</td>
<td>-</td>
</tr>
<tr>
<td>[i]</td>
<td>1.08±0.31</td>
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<td>-2.9±0.58</td>
<td>0.40±0.06</td>
<td>-0.16±0.01</td>
<td>4.45±1.32</td>
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<td>-17.5±7.46</td>
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</tr>
<tr>
<td>[j]</td>
<td>-</td>
<td>-0.82±</td>
<td>4.48±0.34</td>
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<td>-0.42±0.01</td>
<td>-</td>
<td>34.56±0.77</td>
<td>-33.22±0.09</td>
<td>-</td>
<td>-16.1±0.088</td>
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</tr>
<tr>
<td>[l]</td>
<td>-0.7±0.07</td>
<td>-11.33±</td>
<td>0.74±0.08</td>
<td>3.54±0.65</td>
<td>-0.79±0.055</td>
<td>-5.90±0.33</td>
<td>-</td>
<td>3.53±0.84</td>
<td>31.59±0.44</td>
<td>14.80±0.23</td>
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</tr>
</tbody>
</table>

| χ²(df) | 0.25(1)  | 1.89(2)  | 4.57(2)  | 0.26(2)  | 2.1(1)    | 2.8(2)    | 4(2)     | 1.75(2)  | 3.7(2)   | 1.5(2)   | 0.53(2)  |

<table>
<thead>
<tr>
<th>Traits</th>
<th>PROT</th>
<th>TSS</th>
<th>Gs</th>
<th>E</th>
<th>RWC</th>
<th>LA</th>
<th>A</th>
<th>TSG</th>
<th>GE</th>
<th>CUG</th>
<th>Ψw</th>
</tr>
</thead>
<tbody>
<tr>
<td>[m]</td>
<td>5.39±0.06</td>
<td>1.38±0.05</td>
<td>218.74±2.81</td>
<td>2.30±0.01</td>
<td>102.27±2.20</td>
<td>322.96±2.47</td>
<td>68.43±2.10</td>
<td>4.33±0.06</td>
<td>80.55±2.02</td>
<td>80.29±0.34</td>
<td>-0.57±0.02</td>
</tr>
<tr>
<td>[d]</td>
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<td>0.43±0.10</td>
<td>3.01±1.22</td>
<td>0.13±0.02</td>
<td>2.79±0.34</td>
<td>-</td>
<td>1.30±0.35</td>
<td>0.60±0.09</td>
<td>4.91±0.39</td>
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<td>-</td>
</tr>
<tr>
<td>[h]</td>
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<td>-</td>
<td>-37.71±5.75</td>
<td>-109.1±2.36</td>
<td>-67.6±5.71</td>
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<td>-3.64±5.43</td>
<td>9.59±0.57</td>
<td>0.71±0.02</td>
<td>-</td>
</tr>
<tr>
<td>[i]</td>
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<td>-27.71±3.12</td>
<td>-0.2±0.10</td>
<td>-22.34±2.17</td>
<td>-51.09±4.54</td>
<td>-34.3±2.07</td>
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<td>-9.92±2.00</td>
<td>-</td>
<td>0.21±0.36</td>
<td>-</td>
</tr>
<tr>
<td>[j]</td>
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<td>-14.09±7.49</td>
<td>-0.4±0.06</td>
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<td>-2.52±0.39</td>
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<td>-4.92±0.06</td>
<td>-</td>
<td>-</td>
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<td>-</td>
</tr>
<tr>
<td>[l]</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>23.71±1.98</td>
<td>67.72±3.98</td>
<td>39.56±2.43</td>
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<td>5.10±2.11</td>
<td>-</td>
<td>0.86±0.87</td>
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</tbody>
</table>

| χ²(df) | 2.43(2)  | 3.8(4)   | 2.3(1)   | 2.1(4)   | 0.4(1)   | 1.21(2)  | 1.69(1)  | 0.22(2)  | 2.09(1)  | 2.13(2)   | 3.03(2)  |

T50= Time to 50% germination (days)
GI= Germination index (%)
FGP= Final germination percentage (%)
MGT= Mean germination time (days)
Chl a= Chlorophyll-a (mg/g f.wt)
Chl b= Chlorophyll-b (mg/g f.wt)
LFW= Leaf fresh weight (g)
PH= Plant height (cm)
GPC= Number of grains per cob
100GW= 100 grain weight (g)
GYPP= Grain yield per plant (g)
PROT= Protein contents (µ mol g⁻¹)
TSS= Total soluble sugars (%)
Gs= Stomata conductance (mmolm⁻²sec⁻¹)
E= Transpiration rate (mmolH₂Omm⁻²sec⁻¹)
RWC= Relative water contents (%)
Table 4.20. Estimates of the best fit model for traits under stress $S_{5.2 \, \text{dm}^{-1}}$ field conditions.

<table>
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<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl $a$</th>
<th>Chl $b$</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
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<tr>
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<td>6.37±0.03</td>
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</tr>
<tr>
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<td>0.64±0.03</td>
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<td>350.25±1.46</td>
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<tr>
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<td>[l]</td>
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<tr>
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<td>1.40±0.05</td>
<td>78.05±0.43</td>
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<td>3.54±0.04</td>
<td>96.72±2.95</td>
<td>76.28±0.09</td>
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<td>13.67±1.79</td>
<td>0.19±0.01</td>
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<td>19.79±1.19</td>
<td>3.98±0.20</td>
<td>0.60±0.06</td>
<td>8.58±0.40</td>
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<td>14.39±3.28</td>
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<td>0.13±0.01</td>
</tr>
<tr>
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<td>-2.68±0.22</td>
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<td>-1.66±0.05</td>
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<td>47.28±0.023</td>
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<th>$G_s$</th>
<th>$E$</th>
<th>RWC</th>
<th>LA</th>
<th>$A$</th>
<th>TSG</th>
<th>GE</th>
<th>CUG</th>
<th>$\Psi_w$</th>
</tr>
</thead>
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<td>1.16±0.01</td>
<td>205.10±1.08</td>
<td>1.40±0.05</td>
<td>78.05±0.43</td>
<td>248.31±2.31</td>
<td>22.94±1.27</td>
<td>3.54±0.04</td>
<td>96.72±2.95</td>
<td>76.28±0.09</td>
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<td>13.67±1.79</td>
<td>0.19±0.01</td>
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<td>19.79±1.19</td>
<td>3.98±0.20</td>
<td>0.60±0.06</td>
<td>8.58±0.40</td>
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<td>14.39±3.28</td>
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<tr>
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<td>-24.27±8.11</td>
<td>0.70±0.05</td>
<td>-2.25±0.49</td>
<td>8.73±2.66</td>
<td>12.27±1.25</td>
<td>1.28±0.36</td>
<td>-29.97±2.93</td>
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<tr>
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<td>[j]</td>
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<td>-</td>
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<td>-2.68±0.22</td>
<td>-</td>
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<td>-</td>
</tr>
<tr>
<td></td>
<td>[l]</td>
<td>3.49±0.35</td>
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<td>-</td>
<td>4.61±0.74</td>
<td>-</td>
<td>-1.66±0.05</td>
<td>-</td>
<td>47.28±0.023</td>
<td>-</td>
</tr>
</tbody>
</table>

| $\chi^2$(df) | 3.1(2) | 1.4(1) | 0.561 | 3.44(2) | 2.3(1) | 1.1(3) | 0.5(3) | 1.22(2) | 4.2(3) | 0.72(1) | 1.11(1) |
| $\chi^2$(df) | 1.8(1) | 2.68(4) | 0.77(2) | 4.1(2) | 1.5(3) | 3.39(2) | 0.7(1) | 2.8(2) | 1.6(1) | 0.77(4) | 1.89(3) |

**Notes:**
- T50= Time to 50% germination (days)
- GI= Germination index (%)
- FGP= Final germination percentage (%)
- MGT= Mean germination time (days)
- Chl $a$= Chlorophyll-$a$ (mg/g f.wt)
- Chl $b$= Chlorophyll-$b$ (mg/g f.wt)
- LFW= Leaf fresh weight (g)
- PH= Plant height (cm)
- GPC= Number of grains per cob
- 100GW= 100 grain weight (g)
- GYPP= Grain yield per plant (g)
- PROT= Protein contents ($\mu$ mol g$^{-1}$)
- TSS= Total soluble sugars (%)
- Gs= Stomata conductance (mmol m$^{-2}$ s$^{-1}$)
- $E$= Transpiration rate (mmol H$\text{2}$O m$^{-2}$ s$^{-1}$)
- $A$= Photosynthetic rate (umol CO$\text{2}$ m$^{-2}$ s$^{-1}$)
- TSG= Time to start germination (days)
- GE= Energy of germination (%)
- CUG = Coefficient of uniformity of germination
- $\Psi_w$= Water potential (-Mpa)

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Table 4.21. Estimates of the best fit model for traits under stress $S_6.7dm^{-1}$ field conditions.

<table>
<thead>
<tr>
<th>Traits</th>
<th>T50</th>
<th>GI</th>
<th>FGP</th>
<th>MGT</th>
<th>Chl $a$</th>
<th>Chl $b$</th>
<th>LFW</th>
<th>PH</th>
<th>GPC</th>
<th>100GW</th>
<th>GYPP</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>[m]</td>
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<td>[d]</td>
<td>[h]</td>
<td>[i]</td>
<td>[j]</td>
<td>[l]</td>
<td>[m]</td>
<td>[d]</td>
<td>[h]</td>
<td>[i]</td>
</tr>
<tr>
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T50= Time to 50% germination (days)  
GI= Germination index (%)  
FGP= Final germination percentage (%)  
MGT= Mean germination time (days)  
Chl $a$= Chlorophyll- $a$ (mg/g f.wt)  
Chl $b$= Chlorophyll- $b$ (mg/g f.wt)  
LFW= Leaf fresh weight (g)  
PH= Plant height (cm)  
GPC= Number of grains per cob  
100GW= 100 grain weight (g)  
GYPP= Grain yield per plant (g)  
PROT= Protein contents (µ mol $g^{-1}$)  
TSS= Total soluble sugars (%)  
$G_s$= Stomata conductance (mmolm$^{-2}$sec$^{-1}$)  
$E$= Transpiration rate (mmolH$2$Om$^{-2}$sec$^{-1}$)  
RWC= Relative water contents (%)  
LA= Leaf area ($cm^2$)  
$A$= Photosynthetic rate (umolcm$^{-1}$s$^{-1}$mmolm$^{-2}$sec$^{-1}$)  
TSG= Time to start germination (days)  
GE= Energy of germination (%)  
CUG = Coefficient of uniformity of germination  
$\Psi_w$ = Water potential (-Mpa)
Table 4.22. Estimates of the best fit model for traits under stress S11 dm⁻² field conditions.

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RWC= Relative water contents (%)
LA= Leaf area (cm²)
Ψw= Water potential (-Mpa)
CHAPTER 5

DISCUSSION

The present studies were carried out in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad (Pakistan) and research area of Saline Soil Research Institute (SSRI) Pindi Bhattian against different salinity concentrations based on different standards in order to evaluate the genetic potential in maize for improving its salinity tolerance. For this purpose seeds of 40 genotypes differing for their genetic makeup were collected from NARC, Islamabad. The objectives of the present investigations was to identify salt tolerant and salt sensitive genotypes, to assess genetic diversity based on salinity tolerance levels and to determine genetic inheritance and association of different physiological, morphological, growth and yield related parameters.

In the current study, pattern of variability was examined in 30 days old seedlings of diverse maize germplasm grown in different saline solutions under the hydroponic culture system for salinity tolerance. Validation of the practice in providing primary assessment derives from the data of Qureshi et al. (1990) and Khan et al. (2003). All the scientists who are keen to improve salinity tolerance in plants have highlighted the importance of variability. Since the modern cultivars such as maize, rice, barley and wheat have intentionally been bred for favorable environments, quite possible that salt tolerance genes or the potential to develop salt tolerance within them may be inadequate (Richards, 1983). The variability found in most of genotypes against high salinity in the rooting medium specified difference in abilities to grow in salt solutions, and variability within these genotypes.

Maize screening against variable salinity was carried out in the current investigation to sort out salinity tolerant and sensitive genotypes among under study germplasm. The efficacy of screening method has been inspected in many studies as an key regarding the response of salt stress. For example, this practice was utilized for screening different genotypes of groundnut against iron-deficiency chlorosis (Samdur et al., 2000) and tissue tolerance for high Na+ concentration (Munns and James, 2003). In current study treatment, genotypic and treatment × genotypic interaction effects were found significant (P<0.05) for all the studied standards against salinity in hydroponic as well as in field conditions. Decrease was observed in physiological, morphological, growth and yield related standards of genotypes under four different saline concentrations and a series of responses was discovered from highly tolerant to highly susceptible. On the behalf of studied standards from this plant material, genotypes UAC-0024 and UAC-0020 were found as comparatively tolerant and
UAC-0028 and UAC-0048 were found to be comparatively susceptible. The potential of these two tolerant genotypes was found due to low accumulation of Na$^+$ and low Na$^+$/K$^+$ ratio whereas high accumulation of Na$^+$ and high Na$^+$/K$^+$ ratio was observed in susceptible genotypes. Significant reduction in growth of susceptible genotypes was due ion cytotoxicity, low external osmotic potential and nutrients deficiencies under saline environment. These results are in accordance of so many scientists.

Salt stress affects plant physiology at whole plant as well as cellular levels through osmotic and ionic stress (Hasegawa et al., 2000; Muranaka et al., 2002a, b, Ranjbarfordoei et al., 2002; Murphy et al., 2003). Despite causing osmotic and ionic stress, salinity causes ionic imbalances that may impair the selectivity of root membranes and induce potassium deficiency (Gadallah, 2000). The accumulation of high amounts of toxic salts in the leaf apoplasm leads to dehydration and turgor loss, and eventually death of leaf cells and tissues (Marschner, 1995). Ion cytotoxicity caused by the replacement of K$^+$ with Na$^+$ in biochemical reactions which causes conformational changes and loss of function of proteins as Na$^+$ and Cl$^-$ ions penetrated the hydration shells and interfere with non-covalent interaction between their amino acids. Dionisiose and Tobita (2000) reported that increased concentration of Na$^+$ under saline conditions suppressed the leaf gas exchange and PS II photochemical activity and consequently hampered the growth and development of plants.

An ionic imbalance occurs in the cells due to excessive accumulation of Na$^+$ and Cl$^-$ and reduced uptake of other mineral nutrients, such as K$^+$, Ca$^{2+}$, and Mn$^{2+}$ (Karimi et al., 2005). Excess Na$^+$ and Cl$^-$ concentrations inhibit the uptake of K$^+$ and its deficiency initially leads to chlorosis and then necrosis (Gopal and Dube, 2003). These results of different researchers clearly explained the reduction of K$^+$ concentration of susceptible genotypes in our study. The role of K$^+$ is necessary for osmoregulation and protein synthesis, maintaining cell turgor and stimulating photosynthesis (Freitas et al., 2001; Ashraf, 2004). Both K$^+$ and Ca$^{2+}$ are required to maintain the integrity and functioning of cell membranes (Wenxue et al., 2003). This indicated that tolerant genotype managed to restrict the entry of Na$^+$ and Cl$^-$ in to the roots and maintain higher contents of K$^+$ and decreased Na$^+$/K$^+$ ratio in the leaf sap. The enhanced contents of these nutrients appeared to buffer the toxicity of Na$^+$ and Cl$^-$, and enabled the tolerant genotype to exhibit better growth.

Salt stress has considerable effect on root length (Gulzar et al., 2003). It is reported that root growth is sensitive to high salt concentrations and rapidly reduced by salinity (Ashraf et al., 2005). Similar results were observed in pearl millet by Hussain et al. (2008).
Low salinity concentration in culture medium showed low level of effect on shoot length but this may vary with plant species or genotype. In present study lesser shoot length of sensitive genotypes and higher shoot length of tolerant genotypes were observed in variable salinity stresses. Pessarakli & Kopec (2009) found that shoot length decreased with the increase in salt concentrations. Similar results were reported by Mohammad et al., (1998) in tomato and by Gill & Singh (1989) in rice. The reduction in shoot length is due to excessive accumulation of salts in cell wall and reduces elasticity. Further, secondary cells appear sooner and walls become rigid, consequently the turgor pressure efficiency in cell enlargement decreases.

Many researchers’ reports claimed that fresh weight of root was one of the most adversely affected characters with increased salt stress level (Hameed et al., 2008). With the increase in salinity concentration there was a significant decrease in biomass production along with root fresh weight in black seeds (Hussain et al., 2009). Higher amount of sodium in plant tissues decreased growth significantly, which was reported in our findings. The Na\(^+\) with high concentration in leaves become poisonous and lead to saline injury (Saqib et al., 2005). Salt tolerance was linked with low concentration of Na\(^+\) in shoot (Munns et al., 2006). High NaCl concentration brought a progressive absorption of sodium and chloride ions in plant, supportive with Turan et al., (2007a). Increased amount of Na\(^+\) ions in the plant tissue hampers nutrient balance, osmotic regulation and causes toxicity (Bernstein, 1963). It is proved in previous studies that salinity tolerance of plant is associated to lower Na\(^+\) concentration and hence protects leaf tissues (Munns and Tester, 2008). Akram et al., (2007) reported that root dry weight of all corn hybrids showed a decline towards increase in salinity level.

Less shoot fresh weight was due to higher accretion of Na\(^+\) in leaves with least K\(^+\) concentration and K\(^+\)/Na\(^+\). Under saline environment, the prime cause of decline in plant growth seemed might either be due to osmotic drop in water availability or too much accretion of ions (Chinnusamy et al., 2005). The metabolic imbalances, fundamental alterations and disturbance in functions of proteins were consequents of ion cytotoxicity which was prompted by the transposition of K\(^+\) by N\(^+\) in biochemical reactions. A drop in the rates of net photosynthesis happens due to contrary effects on CO\(_2\) assimilation, which cause diminution in nutrient uptake and ultimately cause decline in growth of plants (Cha-Um and Kirdmanee, 2009). In our study minimum shoot fresh weight was observed in case of UAC-0028 and UAC-0048 at highest salinity level S\(_{10}\) dsm\(^{-1}\) and S\(_{6}\) dsm\(^{-1}\) respectively, while
maximum shoot fresh weight was observed by UAC-0024 and UAC-0020 in $S_{0.8\text{ dsm}^{-1}}$ and $S_{4\text{ dsm}^{-1}}$ saline environments.

Due to varied selectivity response for K$^+$ over Na$^+$ different genotypes contained different extent of reduction in dry matter production (Ashraf, 2002). The significant decline in plant growth and dry-matter accretion in saline environments has been written in many important legumes (Tejera et al., 2006). In our study least and high shoot dry weight was observed in susceptible and tolerant genotypes. Hussain et al., (2007) reported that a negative relationship was detected between vegetative growth and increasing salt concentration.

Accumulation of solutes especially proline, glycine-betaine and sugars is a common observation under stress condition (Qasim et al., 2003). Leaf proline content in salt stressed plants increased as observed in maize by Carpici et al. (2010) and Moussa (2006). Proline accumulation in salt stressed plants is a primary defense response to maintain the osmotic pressure in a cell. It is also reported by Ashraf et al. (1998) that proline is an important osmolyte to adjust the plant under drought/saline conditions. Several other reports show a significant role of proline in osmotic adjustment, protecting cell structure and its function in plants in salt-tolerant and salt-sensitive cultivars of many crops (Koca et al., 2007; Turan et al., 2007a). The present findings are in accordance with the results of other researchers which explain that high salt treatments $S_{10\text{ dsm}^{-1}}$, $S_{6\text{ dsm}^{-1}}$ and $S_{4\text{ dsm}^{-1}}$ induced an increase in proline concentration of UAC-0020, UAC-0036 and UAC-0024 maize genotypes. Similar results have been reported by Cha-Um and Kirdmanee, 2009 and Ashraf and Foolad, 2005.

High concentration of sodium in plant tissues reduced growth significantly; susceptible genotypes contained maximum Na$^+$ concentration and created less dry matter. In contrast, elevation of production of shoot fresh weight was found in case of tolerant genotypes as these genotypes were least with respect to Na$^+$ concentration in leaf. The toxicity of leaves enhanced due to high Na$^+$ concentration which lead to severe salt injury (Saqib et al., 2005). Salt tolerant genotypes accumulated low amount of Na$^+$ in the present study. Na$^+$ concentration in shoot correlates with salt tolerance; increasing levels of NaCl induced a progressive absorption of Na$^+$ and Cl$^-$ in plants (Turan et al., 2007a, b). Excessive Na$^+$ concentration in the plant tissue hinders nutrient balance, osmotic regulation and causes toxicity (Bernstein, 1963). It is evident from the literature that plant tolerance to salinity is linked to lower Na$^+$ uptake and a subsequent reduction in Na$^+$ accumulation protects leaf tissues (Tester and Davenport, 2003; Flowers, 2004; Munns and Tester, 2008).

The findings showed that K$^+$ concentration in UAC-0024 and UAC-0036 was high in least saline environment while low K$^+$ contents were reported in UAC-0041 and UAC-0033
in high saline treatment. Reduction of K\(^+\) was due to ion cytotoxicity instigated by the translocation of K\(^+\) with Na\(^+\). The decreased K\(^+\) uptake was due to Na\(^+\) uptakes through same Na\(^+\)-K\(^+\) co-transporters (Tammam et al., 2008). The reduction in uptake of K\(^+\), Ca\(^{2+}\), and Mn\(^{2+}\) was result of ionic imbalance in the cells (Karimi et al., 2005). The K\(^+\) plays vital role for osmoregulation, protein synthesis, cell turgor maintenance and photosynthesis stimulation (Ashraf, 2004). The integrity and function of cell membranes were maintained by K\(^+\) and Ca\(^{2+}\) (Wenxue et al., 2003).

The tolerant genotypes had lowest shoot Cl\(^-\) concentration in leaf sap under S\(_4\) dsm\(^{-1}\) and S\(_6\) dsm\(^{-1}\) salinity levels and sensitive genotypes had high Cl\(^-\) in leaf sap under S\(_6\) dsm\(^{-1}\) and S\(_{10}\) dsm\(^{-1}\) respectively. Higher concentrations of external Cl\(^-\) during NaCl stress might have disturbed the osmotic balance consequently inducing effect of water deficiency. Salt injury was reported due to toxicity of leaves with increased concentrations of Cl\(^-\) (Serrano et al., 1999). Salt injury of plant leaves and stems is result of maximum inflow of Cl\(^-\) associated with drop of K\(^+\) uptake (Sharma, 1995).

Decreased Na\(^+\)/K\(^+\) ratio in tolerant and increased Na\(^+\)/K\(^+\) ratio in sensitive genotypes were observed in present study. Raised level of Na\(^+\) in soil solution leads to reduce uptake of K\(^+\) in plants as well as water, essential nutrients (P, K, Fe, Cu, and Zn) and soil bacteria resultantly increases Na\(^+\)/K\(^+\) ratio (Barea et al., 2005). Presently the tolerant genotypes UAC-0024 and UAC-0036 were expressing the least Na\(^+\)/K\(^+\) ratio due to high K\(^+\) uptake while susceptible genotypes were showing high Na\(^+\)/K\(^+\) ratio due to reduction in uptake of K\(^+\). Increased Na\(^+\)/K\(^+\) ratio badly impacts growth of plants. Disruption of various metabolic processes such as protein synthesis in the cytoplasm results in plants growth with high Na\(^+\)/K\(^+\) ratio (Tester and Davenport, 2003).

In the present investigation, salinity affected the sensitive genotypes badly. Least amount of chlorophyll-a, chlorophyll-b and protein contents were present in UAC-0028 and UAC-0048 under stress condition S\(_{5.2}\) dsm\(^{-1}\). Tolerant genotypes UAC-0020 and UAC-0024 survived well with high chlorophyll-a, chlorophyll-b and protein contents under stress condition S\(_{6.7}\) dsm\(^{-1}\). Findings regarding chlorophyll-a and chlorophyll-b contents were in accordance with the finding of Dogan et al., 2010; they narrated that salinity reduces the chlorophyll-a, chlorophyll-b contents and degree of reduction in total chlorophyll contents depends on salt tolerance of plant species. Mittler (2002) reported that stress induced cellular accumulation of damaging active oxygen species. Active oxygen species can damage membrane lipids, proteins and nucleic acids.
Presently it is found that sensitive genotypes were impacted adversely by salinity but tolerant genotypes survived even in highly saline environments. Decreased amount of relative water contents, proline contents and sugar contents were observed in sensitive genotypes. These findings confirmed the results of number of scientist like Ahmad and John (2005) who reported that salinity stress caused significant reduction in relative water contents, potassium concentration, nitrate reductase activity and chlorophyll contents in pea plants. Sairam et al., (2002) confirmed the reduction of relative water contents under salinity stress in plants. Cicek and Cakirlar (2002) observed the effect of salinity on physiological attributes of maize cultivars and reported that salinity caused a marked decrease in shoot length, fresh and dry weight, leaf area and relative water contents of maize plants.

Salt tolerant genotypes have ability to overcome the salinity stress by osmoregulation. It is now well evident that photosynthetic activity is one of the major factors controlling growth (Shannon, 1998). Photosynthesis leads to the production of organic osmotica, which play an important role in osmoregulation. Osmoregulation (i.e. maintenance of turgor) is considered to be an important adaptation to drought (Morgan, 1984) and salinity stress (Ashraf and Foolad, 2005). It is thus, expected that the rate of photosynthesis in salt tolerant species is inhibited less than that in salt sensitive ones (Mansour et al., 2005). The production of organic solutes like total soluble sugars, proteins and free proline are closely related to the well-functioning of all the activities related with growth under saline medium (Ashraf and Foolad, 2007; Ashraf and Bashir, 2003). A large number of plant species accumulate glycinebetaine and proline in response to salinity stress and their accumulation may play a role in combating salinity stress (Mansour, 2000; Ashraf and Harris, 2004). Same findings were reported in our study as increased amount of protein, proline and sugar contents were reported in tolerant genotypes UAC-0020 and UAC-0024 even under high salinity concentration $S_{11dm^{-1}}$. Osmotic adjustment or accumulation of solutes by cells is a process by which water potential of a cell can be decreased without an accompanying decrease in cell turgor. It is a net increase in solute contents per cell that is independent of the volume change that results from loss of water (Taiz and Zeiger, 2002). Osmotic adjustment in plants subjected to salt stress can occur by the accumulation of high concentrations of their inorganic ions or organic solutes (or both). Proline accumulates in larger amounts than other amino acids in salt stressed plants (Abraham et al., 2003). Although both organic and inorganic solutes play a crucial role in osmo-regulation of higher plants subjected to saline conditions, their relative contribution varies among species, among cultivars and even between different compartments within the same plants (Ashraf and Bashir, 2003).
The most observable effect of salinity on maize plant growth is the reduction of leaf water potential. Low osmotic potentials in the soil solution induced water deficit in plant tissues. As a consequence, the turgor in plants may decrease, resulting from faster decrease in water potential than in osmotic potential. Salt tolerance of maize genotypes may also vary with their leaf water relations. Munns (1993) proposed that water deficit in plants occur before the plants suffer from ionic effect (ion toxicity and ion imbalance). These results are confirmed in the findings of current study that genotypes UAC-0024 and UAC0036 (Tolerant ones) were depicted with high water potential while genotypes UAC-0028 and UAC-0041 (susceptible ones) were mentioned with least water potential under stress condition S6.7 dsm⁻¹.

According to findings of present study, under maximum stress condition S11 dsm⁻¹, tolerant genotypes UAC-0020 and UAC-0024 were reported with high plant height and leaf area while sensitive genotypes UAC-0028 and UAC-0033 were noted with least which was reviewed in the findings of Hajer et al. (2006) as they reported that salinity caused significant reduction in plant height and leaf area. The inhibitory effects of salinity on plant growth are attributed to specific ion cytotoxicity, low external osmotic potential and nutrients deficiencies (Parida and Das, 2005). High salinity decreases the rate of leaf expansion which may result in reduction of total leaf area. The decrease in leaf area in salt sensitive genotypes is due to non-effective exclusion of toxic ions from transpiration stream which leads to high buildup of these toxic ions in the leaves, resulting in death of older leaves and succulence of new leaves (Munns and James, 2003).

Salinity is not only responsible for ion toxicity and imbalance, but also indirectly leads to low photosynthesis in plants and photosynthesis is directly related to stomata conductance, transpiration, chlorophyll contents and water potential. At low or moderate soil salinity, decreased growth is primarily associated with a reduction in photosynthetic area rather than a reduction in photosynthesis per unit leaf area (Munns, 1993). At high salinity, however, leaf photosynthesis can be reduced by lowered stomata conductance as result of water imbalance (Brugnoli and Lauteri, 1991) or by non-stomata factors that may be caused by toxic ions. Evidence in support of this comes from strong negative correlations between ions and photosynthetic activity, where Na⁺ and Cl⁻ has been implicated primarily in crop species such as rice (Yeo et al., 1985) and wheat (Rawson, 1986) and Cl⁻ in woody perennials such as citrus (Walker et al., 1993) and grapevine (Walker et al., 1981). Previous studies showed that the stomata conductance was linearly correlated with maximum net photosynthesis in plants like in soybean (Ma et al., 1995), rice (Laza et al., 1996), and wheat (Gutierrez-Rodriguez et al., 2000). While performing experiment on 34 canola genotypes,
Ulfat et al. (2007) found that increasing salinity caused reduction in stomata conductance and photosynthetic capacity which resulted in reduced growth. In tomato, salinity causes accumulation of toxic ions in root, stem and leaves that result in reduction in photosynthesis (Dogan et al., 2010). Salt stress decreased the assimilate supply to the growing shoot by inhibiting photosynthesis and by lowering the rate of transport of assimilates to the growing points in maize plants. This decrease of assimilate supply could be responsible for shoot growth inhibition during first phase of salt stress; in addition, its role in controlling growth, assimilate supply influence the plant capacity to maintain turgor through osmotic adjustment (Yang and Lu, 2005). Munns and Tester, 2008 reported that reduction in leaf area due to salinity means that photosynthesis per plant is reduced. Findings of present study were also in line with of results reported by these scientists as tolerant genotypes showed maximum stomata conductance and photosynthetic rate while sensitive genotypes showed minimum stomata conductance and photosynthetic rate.

It seems that transpiration rate as a screening criterion may be more important for drought stress than salt stress. Because one of the stresses caused by salinity is osmotic stress or water deficit, the trait of leaf transpiration in salt tolerant genotypes should be improved in order to further increase their salt tolerance under saline conditions. However many scientists (Storey and Walker, 1999) confirmed the importance of transpiration rate to control the accumulation of salt ions in shoot. In present study low transpiration rate was observed in sensitive genotypes UAC-0028 and UAC-0033 while high transpiration rate was observed in tolerant genotypes UAC-0020 and UAC-0024 under stress condition S6.7 dsm⁻¹.

Significant reduction in yield related traits were observed in sensitive genotypes UAC-0028 and UAC-0048 while tolerant genotypes UAC-0020 and UAC-0024 were nominated with high yield. The study conducted by Akhtar (2000) supported our findings that at a salinity level of S12 dsm⁻¹, reduction was observed in yield and yield contributing standards of sugarcane genotypes; this could be attributed to reduced photosynthetic efficiency under salt stress. Francois et al., (1994) demonstrated that the time or stage of salinity stress had a significant effect on grain weight.

Significant differences among genotypes with respect to all standards indicated that the breeding material had genetic variability and this variability may be exploited in future breeding programs for the improvement of yield and its related traits. When such a potential plant material is available for exploitation through selection and breeding, the adoption of a biometric method which could partition the genetic variation into different components is important. The generation means analysis which uses the segregating and non-segregating
generations provides information on genetic effects i.e. additive and dominance. Significance ($\chi^2$) indicated the inadequacy of additive-dominance model and suggests the breeders to grow further generations of the cross to study the inheritance mechanism of abiotic stress tolerance in maize (*Zea mays* L.), as has been suggested by Adetimirin et al., 2001. The present genetic investigation revealed that additive and dominance × dominance interactions majorly influenced the number of traits. Sodium concentration, sodium potassium ratio, chlorophyll-a, plant height, photosynthetic rate and grain yield per plant influenced by dominance × dominance interactions under maximum stress conditions $S_{6.7 \text{ dsm}^{-1}}$ and $S_{11 \text{ dsm}^{-1}}$. These results supported by the previous studies of McConnell and Gardner (1976). They mentioned in their studies that dominance genetic effects influenced yield under abiotic stress conditions. The dominant genetic effects were also found for various traits studied under both normal and salinity stress conditions. Shoot length, T50%, proline contents, number of grain per cob and 100 grain weight were controlled by additive genes. Selection on the basis of dominant genetic effects indicated that hybrid seed production program may be helpful to improve the traits under salinity stress conditions. The presence of additive gene effect has been suggested as being of major importance in plant characters which are less complex in inheritance (Ali et al., 2007). Generation means analysis revealed additive, non-additive and dominance gene effects (Tables 4.10-4.13) and (Tables 4.18-4.21). The genetic analysis of data at plant maturity indicated that mostly additive [d] and non-additive [h] types of inheritances were followed by the characters under normal and salinity conditions. The presence of epistatic component suggests that fixation of additive alleles is possible in later generation (Singh et al., 2000; Ali et al., 2007). The positive sign of [i] shows the effect of increasing alleles for salinity tolerance and vice versa. Genetic mechanism controlling salinity tolerance appeared to be complicated by additive × dominance [j] and dominance × dominance [l] interactions and these epistatic components warns the breeders to be careful while looking for salinity tolerant plants in segregating generations. This showed that the trait may not be simple in inheritance; epistatic effects interact more strongly with the environment than additive and dominance gene effects have been reported for maize by Adetimirin et al., 2001. The involvement of gene interactions for quantitative characteristics in maize has been reported previously (Eta-Ndu and Openshaw, 1999). Successful genetic studies of tolerance related traits under field salinity stress majorly depends on weather conditions (Gardner, 1986). In screenhouse studies, additive and dominance × dominance action appeared to be controlling the most of the traits (Revilla et al., 2000). Frascaroli and Landi (2013) used diallel scheme
for their experiments and find the variations among crosses mainly by additive genetic effects under abiotic stress.

Positive association of grain yield with plant height under stress condition $S_{6.7\, \text{dsm}^{-1}}$ indicated that selection for taller plants will simultaneously improve potential grain yield and accumulate the desirable gene combinations. Moreover, based on its positive association with grain yield, the taller plants would be good selection criteria for maize improvement. Several researchers in the past have reported similar pattern of positive association between plant height and grain yield (Lorenzana and Bernado, 2008). Shakoor et al. (2007) reported highly significant genotypic correlation coefficient of plant height with grain yield per plant under abiotic studies. Therefore, selection for these traits will simultaneously improve potential grain yield and accumulate the desirable genes. On the other hand Rather et al. (1999) published that plant height had no association with grain yield per plant. Plant height was found to be positively correlated with number of grains per cob and 100 grain weight while negative correlation of (chlorophyll-a contents with 100 grain weight), (100 grain weight with stomata conductance) was observed under stress condition $S_{5.2\, \text{dsm}^{-1}}$ at genotypic levels. These results were in accordance with Sadek et al., 2006; Saleem et al. (2007)

Number of grains per cob was found to be positively correlated with 100 grain weight and grain yield per plant under stress condition $S_{11\, \text{dsm}^{-1}}$ at genotypic level. 100 grain weight showed higher positive correlation with grain yield per plant at genotypic levels under stress condition $S_{6.7\, \text{dsm}^{-1}}$. Similar reports were published by Abdelmula and Sabiel (2007).

The previous information on genetic progress regarding salinity tolerance in maize had many reports in literature. Tolerance in maize for salinity stress can be regulated by using additive and epistatic effects. In this study, genotypes UAC-0020, UAC-0024 and UAC-36 showed tolerance against salinity stress and could be used as tolerant source for any breeding program. The better performing combinations can be utilized to develop high yielding maize hybrids as well as for exploiting hybrid vigor. Moreover, the traits like emergence (emergence percentage, mean emergence time, time to 50% emergence and emergence index), root length, shoot length, $\text{Na}^+$ concentration, $\text{Cl}^-$ concentration, proline contents, leaf area, number of grain per cob, 100 grain weight and grain yield per plant are very good parameters to screen the germplasm against stress. Present study showed correlation among different traits while screening the germplasm at both phases of stresses (screenhouse stress and natural field stress). For future program, these promising genotypes UAC-0020, UAC-0024 and UAC-36 could be used for development of salinity stress tolerant hybrids. From the foregoing discussion it is concluded that studied traits may help in development of salinity
tolerance. The knowledge obtained here about the genetic controlling system of salinity tolerance may be of value to the maize breeders working in the maize belt of Pakistan.

**Future Research**

- Information demonstrates that on the basis of inheritance studies, marker assisted selection technique could be used for gene discovery related to salinity stress in maize.
- Maize hybrid with high yield would be developed for salinity stress conditions.
- Correlation analysis would be studied for other physiological and biochemical traits.
- Additive gene action would be expected to be more reliable as compared to the non-additive type of gene action.
CHAPTER 6

SUMMARY

A set of 40 maize genotypes collected from NARC, Islamabad were screened following triplicated completely randomized design (CRD) in screenhouse of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad (Pakistan) and randomized complete block design (RCBD) under natural field conditions in the research area of the Soil Salinity Research Institute Pindi Bhattian following split plot arrangement. In both experiment, the genotype es were evaluated under normal and salinity stress conditions. The seedlings were uprooted to study various important traits which includes shoot length, root length, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, sodium concentration, potassium concentration, chloride concentration, proline contents and sodium potassium ratio to screen out tolerant and susceptible genotypes under both normal and stress conditions of screenhouse. Under field conditions, in addition to all above traits, data were recorded for the traits like chlorophyll contents, relative water contents, water potential, protein contents, total soluble sugar and some growth and yield related traits like leaf fresh weight, leaf area, photosynthetic rate, plant height, stomata conductance, transpiration rate, no of grains per cob, 100 grain weight and grain yield per plant. Biplot analysis was used for the selection of most tolerant (P₁) and most susceptible (P₂) genotype for hybridization program. Two parents (P₁ and P₂) were selected to make cross combinations. The parents (P₁, P₂), F₁, F₂ and backcross (BC₁, BC₂) generations of cross were studied in screenhouse and field under saline and normal conditions to find gene action of salinity stress related traits. One hundred and fifty plants from each of the F₂ populations were used to find correlation of the traits. Generation means analysis revealed all three kinds of gene effects (additive, dominance and interactions) contributed in the inheritance of traits. The present genetic investigation revealed that additive and dominance × dominance interactions majorly influenced most of the traits. The dominant genetic effects were also found for different traits studied under both normal and salinity stress conditions. Selection on the basis of dominant genetic effects indicated that hybrid seed production program may be helpful to improve the traits under salinity stress conditions.

The genetic analysis of data at plant maturity indicated that mostly additive [d] and dominance × dominance [l] types of inheritances were present in the characters under normal and salinity stress conditions. The presence of additive × additive [i] interaction was observed
in the inheritance of almost all the characters. The results showed that traits studied may not be simple in inheritance under salinity stress conditions.

Generally, correlations were consistent among the population for pair of traits. Strong positive genotypic correlation for grain yield per plant was found with the leaf fresh weight, plant height, stomata conductance, transpiration rate, number of grains per cob and 100 grain weight under salinity stress conditions. 100 grain weight showed positive correlation with leaf fresh weight, stomata conductance and number of grains per cob at genotypic level. The findings of the present study on the basis of genetic diversity present among maize germplasm, correlation among different salinity stress tolerance related traits and genetic effects involved in the control of different traits, explained the presence of potential to breed for salinity stress tolerance maize. This is recommended that tolerance in maize for salinity stress can be regulated by using additive and epistatic effects. In this study, genotypes UAC-0020 showed tolerance against salinity stress and could be used as tolerance source for any breeding program. According to findings of this study, selection of maize plants for salinity tolerance would be suitable in later generations. Objective of any plant maize breeder is to drag efficiently introgression of targeted genomic regions with minimal linkage. Therefore, there is need to estimate other tolerance sources which are prone to different stress environments. From this study, information demonstrates that there is need to exploit marker assisted selection technique for gene discovery related to salinity stress. All this can be achieved by using the advances in genomics, proteomics and bioinformatics.


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