IJCRT.ORG ISSN : 2320-2882

INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

# Brininess Tolerance Of Crops

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Abstract : **S**oil salinity is a major constraint to agriculture. To improve salinity tolerance of crops, various traits can be incorporated, including ion exclusion, osmotic tolerance and tissue tolerance. We review the roles of a range of genes involved in salt toleran cetraits. Different tissues and cells are adapted for specific and often diverse function, so it is important to express the genes inspecific cell-types and to pyramid a range of traits. Modern biotechnology (marker-assisted selection or genetic engineering) needs to be increasingly used to introduce the correct combination of genes into elite crop cultivars. Importantly, the effects of introduced genes need to be evaluated in the field to determine their effect on salinity tolerance and yield improvement. Soil salinity reduces crop yield. The extent and severity of salt-affected agricultural land is predicted to worsen as a result of inadequate drainage of irrigated land, rising water tables and global warming. The growth and yield of most plant species are adversely affected by soil salinity, but varied adaptations can allow some crop cultivars to continue to grow and produce a harvestable yield under moderate soil salinity. Significant costs are associated with saline soils: the economic costs to the farming community and the energy costs of plant adaptations. We briefly consider mechanisms of adaptation and highlight recent research examples through a lens of their applicability to improving the energy efficiency of crops under saline field conditions.

IndexTerms – **Salinity, KSE-100 index, Photosynthesis, Salt tolerance, Reactive oxygen species (ROS), Davidson and MacKinnon, Posterior Odds Ratio**

## I. INTRODUCTION

Soil salinity can reduce crop, horticulture and forage production in arid and semiarid regions. Salt may arise naturally in the subsoil or be introduced by brackish irrigation waters. Salinity is becoming more extensive as a result of land clearing and unsustainable irrigation practices and through pressures for bringing marginal land into production. Agronomic and engineering solutions are being exhausted, so to minimize the impact of saline land on global food production the way forward is to breed greater salt tolerance into present crops and to introduce new species for cultivation.

In this article we focus on the costs of soil salinity. One cost, relevant to farmers, is the economic cost of reduced yield (Box 1). The second cost – and the cause of the reduced yield that underpins the economic loss to the farmer – is the energy cost incurred by the plant when exposed to soil salinity. We briefly consider these two costs and highlight recent research with the potential to improve crop salinity tolerance.

The economic cost of salinity

The major economic cost of salinity is the reduced income to farmers caused by the reduced yield. Areas where salinity occurs are always arid or semiarid, and so crops are always limited by water, but they can also be limited by the salt concentration in the soil, especially when rainfall is below average.

The economic costs differ from one country to another and are influenced largely by the cost of farmer inputs vs the profit they can make in the seasons with average rainfall. In broad-acre dryland farming, the inputs to the crop (including off-farm subsidies) may cost as much as $300 ha−1. The water-limited yield may be 3 tonnes ha−1, and at a good market price (say $200 tonne–1), the crop will return a gross income of $600 ha−1 with a net return of 300 ha−1. If the yield is reduced by salinity to 2 tonnes ha−1, the gross income drops to $400 ha−1 and the net return is only $100 ha−1. Consistent losses to salinity as a result of climate change or rising water tables may mean that cropping is impossible, and the land usage reverts to pasture production, using salt-tolerant grasses or other species, including halophytes. This usually brings a much lower return to farmers, but the inputs are fewer, so farming may still be viable. Farmers have many other expenses on the farm and are always living close to the margin of profit or loss, and a small decrease in yield or an enforced change in land use may have devastating economic consequences.

Soil salinity affects the growth, productivity, physiology, and nutritional values of a number of plant species, blue panicum in particular [23]. For a better understanding of the yield variation of blue panicum as affected by soil salinity, it is necessary to understand the physiological mechanisms for salinity tolerance [24-27]. This crop is an ideal fodder grass that can optimally produce fresh biomass up to 60 t ha−1 year−1 at moderate salinity (10–15 dS·m−1 ) [11]. Up to 12.5 dS·m−1 salinity, biomass production of blue panicum is not affected due to its coping physiological mechanisms such as improved gas exchange and water use efficiency [24]. The growth and yield of blue panicum are correlated with net CO2 assimilation and stomatal conductance rates [26].

## II. MECHANISMS OF PLANT ADAPTATION TO SALINE SOIL AND POTENTIAL ENERGY COSTS

The majority of energy acquired by photosynthesis and fixed into carbon (C) compounds is used by plants in general maintenance (Amthor, 2000; Jacoby et al., 2011). Only a small proportion (10–40%) is used directly for biomass accumulation even under optimal conditions (Fig. 1). Stress can be defined in terms of energy costs; we consider stress to be occurring when the amount of energy acquired by plants is reduced (because of a reduction in photosynthesis rate or leaf area) and/or when energy is redistributed from growth into stress defence (Fig. 1). By improving the energy efficiency of plant metabolism and physiology, especially during floral development and grain fill, more fixed C could be allocated to grain, improving yield. When crops are exposed to stress, the less energy plants need to use in tolerating salt, the more will be available for grain yield (Fig. 1).

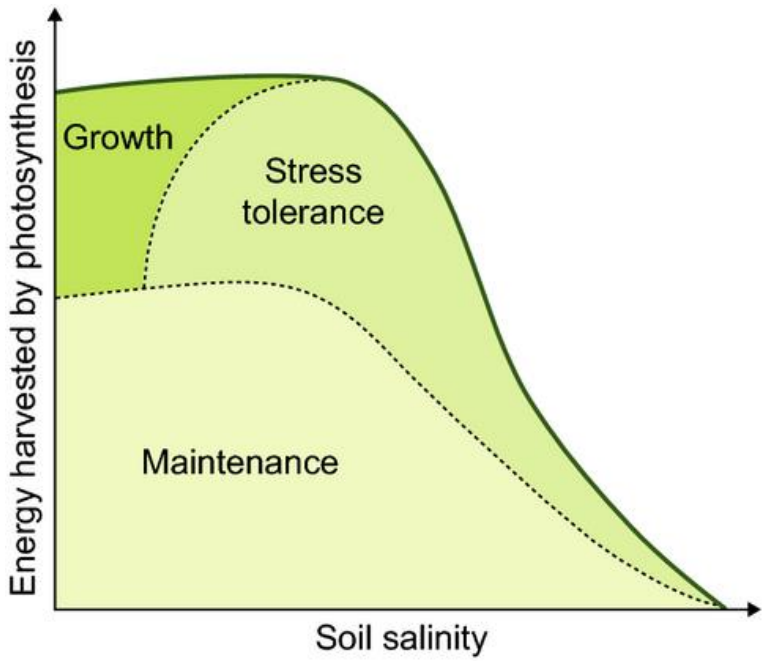


**Figure 1**

Open in figure viewerPowerPoint

Schematic of energy gain and use of a crop plant under salinity stress. At any given time, there is a finite amount of energy that can be harvested by the plant through photosynthesis. Plants use the majority of this energy in processes necessary for maintenance of biomass, including protein turnover, synthesis of lipids and carbohydrates, maintaining ion gradients, gaining nutrients and source to sink transfer. Growth also requires the investment of energy in these processes; whether this is biomass accumulation or grain yield depends on the developmental stage of the plant. The proportion of energy used in maintenance, growth and stress defence is portrayed under the dotted lines. The relative proportions will change depending on the developmental stage of the plant – maintenance costs will be greater when plants are larger. Total energy gain will decrease with greater salinity by decreasing photosynthetic rate following induced closure of stomata and damage to cellular and photosynthetic machinery. Stress tolerance mechanisms represent additional costs to the plant required to deal with the salt load in the soil (for example, but not limited to, greater costs in ion exclusion or compartmentation, and reactive oxygen species (ROS) detoxification). At high salinity there will be zero growth, as the total costs to the plant equal energy gain; when costs exceed energy gained, then tissue will senesce. Adapted from a concept by A. H. Millar and H. Lambers, based on data and reasoning of Amthor (2000) and Van der Werf et al. (1988).

Plants deploy a variety of traits to combat salt in soil solution. The most essential trait is osmotic adjustment – all cells must accumulate sufficient solutes to balance extra osmotic pressure in the soil solution to maintain turgor. To achieve this, plants use two strategies to varying degrees: excluding $Na^+$ and $Cl^-$, particularly from leaves, and relying on organic solutes for osmotic adjustment (‘ion exclusion’); or accumulating sufficient $Na^+$ and $Cl^-$ to balance those in the soil solution but having strict ionic regulation in various cell compartments (‘tissue tolerance’).

In general, salt-tolerant species have high $Na^+$ and $Cl^-$ concentrations in leaves – higher than the external solution. This is particularly true for halophytes and the more salt-tolerant nonhalophytes, such as barley, where the trait of tissue tolerance is clearly evident. Such plants must compartmentalize most of the leaf $Na^+$ and $Cl^-$ in vacuoles to keep the cytosolic and organellar concentrations below toxic values, and use organic osmolytes (and $K^+$) to balance the osmotic pressure in these cytoplasmic compartments (Shabala, 2013). The concentration where $Na^+$ (or $Cl^-$) becomes toxic in the cytoplasm is unclear, and is a priority area for research; cytosolic estimates are c. 30 mM $Na^+$ (Munns & Tester, 2008; Conn & Gilliham, 2010), whereas chloroplasts and mitochondria appear to tolerate 100–200 mM $Na^+$ and $Cl^-$ (Flowers et al., 2015). Estimates of osmotic adjustment costs using organic molecules vs $Na^+$ and $Cl^-$ (Greenway & Munns, 1983; Yeo, 1983; Raven, 1985) indicate that the energy demands are significant and could restrict growth rates at high salinity, either in the diversion of C or N compounds from growth to storage pools, or in costs of controlling $Na^+$ and $Cl^-$ transport across membranes. Table 1 indicates that 200 mM NaCl is the limit of growth for species that have low $Na^+$ and $Cl^-$ concentrations in leaves and that rely on organic solutes for osmotic adjustment.

Table 1. Demand for organic solutes (in hexose units) vs Na+ and Cl− for osmotic adjustment (OA)

| | | Hexose for OA | | NaCl for OA | |
|---|---|---|---|---|---|
| NaCl ext (mM) | Leaf H2O/DW (g g−1) | (g l−1 H2O) | (g g−1 DW) | (g l−1 H2O) | (g g−1 DW) |
| 50 | 6 | 18 | 0.102 | 3 | 0.018 |
| 100 | 5.5 | 36 | 0.198 | 6 | 0.033 |
| 200 | 5 | 72 | 0.360 | 12 | 0.060 |
| 300 | 4.5 | 108 | 0.486 | 18 | 0.072 |

The contribution of osmotica to the DW is calculated from the concentration needed to balance the osmotic pressure of the external solution and the water content of a typical cereal leaf. (Note that 1 mole of NaCl is equivalent in osmolarity to 2 moles of hexose, and the molecular weights of hexose and NaCl are 180 and 60, respectively.) Most plants accumulate sucrose as the preferred organic osmotica, which has twice the mass of hexose; thus, setting 200 mM NaCl as an upper limit for growth in saline soil as it would comprise 70% of the DW.

The more sensitive species tend to have low Na+ concentrations in leaves, lower than in the external solution, that is they rely on 'ion exclusion' as the major adaptive trait. Within any species where there is significant genotypic variation in Na+ accumulation in leaves, there is a correlation between salt tolerance and Na+ exclusion. This is true for sensitive species like rice and durum wheat (reviewed in Munns, 2005), but it may also be true for the more salt-tolerant species like barley (e.g. Chen et al., 2005). This presents a paradox that seemingly contradicts the notion that 'tissue tolerance' is the most cost-efficient strategy; it indicates that there are significant costs of compartmentation of Na+ and/or Cl− in leaf cells, and that reducing the salt load on a leaf confers a benefit. This presumably becomes important over time when the initial osmotic adjustment has occurred and salt toxicity threatens as ions continue to be transported to leaves.

Future work is needed to quantify the costs of the different traits for salt tolerance to test the limits of each strategy and to provide new ideas for research approaches to increase the salt tolerance of crops.

## III. NEW INSIGHTS INTO SALINITY TOLERANCE MECHANISMS

Salinity research is predominantly performed on model systems. Very few fundamental research findings relevant to salinity tolerance have been applied to crop plants. An exception is the application of AtNHX1 (Na+/H+ antiporter 1 proteins) to improve salt compartmentation in the vacuoles of tomato vegetative tissue, which improved yield without increasing salt in the tomato fruit (cited in Bassil & Blumwald, 2014). More recently, AtCIPK16, an SNF1-related kinase/CBL-interacting protein kinase underlying a quantitative trait locus for Na+ exclusion in the Arabidopsis thaliana Bay-0 × Shahadara mapping population, was expressed in barley and found to improve Na+ exclusion and biomass in a saline field (Roy et al., 2013). Here, we discuss recent research that has the potential to improve salt tolerance in the field, which is also summarized at both the cellular and organ levels in Fig. 2.

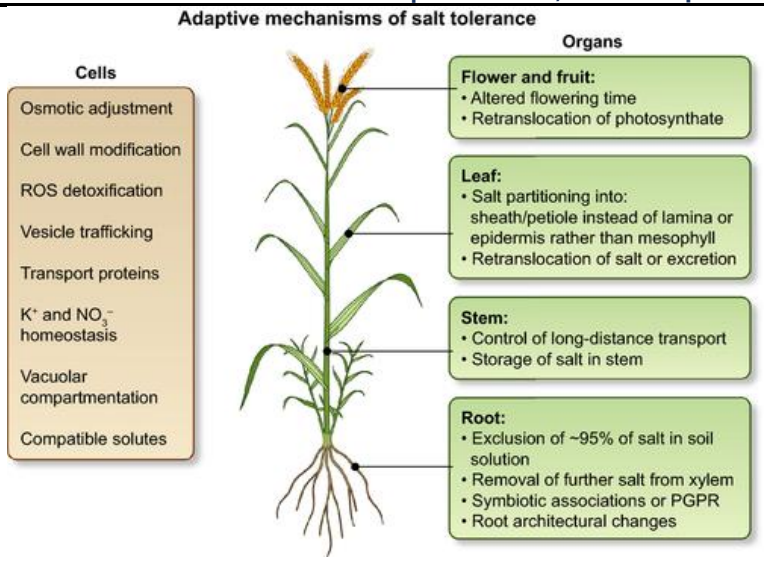


**Figure 2**

Adaptive mechanisms of salt tolerance. On the left are listed the cellular functions that would apply to all cells within the plant. On the right are the functions of specific tissues or organs. Exclusion of at least 95% (19/20) of salt in the soil solution is needed as plants transpire 20 times more water than they retain (Munns, 2005). Most of these functions are explained in the text. Omitted for space, and lack of recent advances, is the limitation that Cl− can impose on growth through its antagonistic accumulation against the nitrogen form NO3− (NO3− homeostasis) (Henderson et al., 2014) and the differential capacity and sensitivity of different cell types and tissues to accumulate Na+ and Cl−; for example, NaCl accumulation within photosynthetic cells incurs a larger cost than accumulation in root cortical cells (Conn & Gilliham, 2010). ROS, reactive oxygen species; PGPR, plant growth-promoting rhizobacteria.

## CELLULAR MECHANISMS OF SALT TOLERANCE

Reactive oxygen species (ROS) act as a signal during salt stress but can also damage plant root and shoot tissue during salinity stress by perturbing enzyme, cell wall and membrane function. Several genes involved in ROS detoxification have been cloned from SR3 wheat, which is a hybrid with a high degree of salinity tolerance (e.g. Dong et al., 2013). Overexpression of genes involved in ROS scavenging has resulted in lower cellular damage, the maintenance of photosynthetic energy capture, and an improvement in shoot and root growth under saline conditions (Roy et al., 2014). Many of these transgenics have reduced growth under nonsaline conditions so the energetics of ROS detoxification is important to quantify, as are the implications of ROS detoxification on final grain yield.

Ion transport can account for the majority of respiratory costs in plants (Van der Werf et al., 1988). Ion transporters (e.g. Osakabe et al., 2014) and their localization in key cell types underpin plant salinity tolerance. Root xylem parenchyma cells represent ‘gatekeeper’ cell types for shoot NaCl exclusion as they have a physical location and unique protein circuitry primed for this role (Henderson & Gilliham, 2015). TaHKT1;5-D is responsible for maintaining high cytosolic K+/Na+ ratios in bread wheat shoots; it underpins the Kna1 locus, resides on the plasma membrane (PM) of root xylem parenchyma cells and reduces Na+ load in the xylem before entering the shoot (Byrt et al., 2014). Orthologous proteins in sequence and function are found in Arabidopsis, durum wheat and rice (Henderson & Gilliham, 2015). Introgression of the Triticum monococcum HKT1;5-A into durum wheat improved shoot Na+ exclusion and improved grain yield in the field by 25% (Munns et al., 2012). Other salt tolerance factors expressed in the root stele include the salt overly sensitive (SOS) pathway genes and AtCIPK16 (Roy et al., 2013). Root stelar cells also confer control shoot Cl− accumulation, which can induce salinity toxicity in crops; however, we know little about the proteins involved (Henderson et al., 2014).

Aquaporin proteins, members of a large multigenic family that regulates a large proportion of water transport across membranes, are rapidly influenced both transcriptionally and post-translationally by salt (Chaumont & Tyerman, 2014). Overexpression of a PM intrinsic protein in soybean increased shoot Na+ exclusion and increased seed yield from a saline field (Zhou et al., 2014). Wheat TIP2;2 is regulated by methylation following salt treatment (Xu et al., 2013), as is HKT1 in Arabidopsis (Sani et al., 2013). The role of methylation and aquaporins in salt tolerance is worth further exploration.

## THE EMERGING ROLE OF THE ENDOMEMBRANES AND ENDOSOMES

In salt-acclimated tobacco BY2 cells, Garcia de la Garma et al. (2015) reported extensive vesicle trafficking of Na+ between the PM and the Na+-rich vacuolar compartment. This novel mechanism of salt deposition presumably avoids raising cytosolic Na+, so its application is worth further exploration. The role of RAB6 GTPase ARA6 and VAMP727-mediated endocytotic machinery in salt tolerance was also shown in Arabidopsis roots; when ARA6 was overexpressed it improved salt tolerance, whereas ara6/vamp727 knockout plants were salt-hypersensitive (Ebine et al., 2011).

The CPA1 family of Na+/H+ antiporters, NHX1 (tonoplast-localized) and NHX7/SOS1 (PM-localized) are often reported to confer Na+ compartmentation or exclusion under high salt loads, but their role is less clear under moderate salinities. Double knockouts of nhx1/nhx2 are not sensitive to moderate external Na+ concentrations, whereas they are sensitive to moderate external K+ concentrations (reviewed in Bassil & Blumwald, 2014). By contrast, the trans-Golgi network-localized NHX double knockouts, nhx5/nhx6, are hypersensitive to moderate salinity and disrupt vesicle trafficking to the vacuole (Bassil & Blumwald, 2014). Another CPA family member, a cation/H+ exchanger (CHX), GmSALT3, improves shoot Na+ exclusion and salt tolerance in soybean (Guan et al., 2014). CHX proteins, including GmSALT3, have frequently been localized to the endoplasmic reticulum using fluorescent protein fusions. If these membrane localizations are to be trusted, this is further evidence to suggest that endosomal-localized transport proteins have crucial roles in salt tolerance – possibly in endosomal pH or cation homeostasis, or vesicle trafficking, but their exact roles are still to be determined.

## CAN WE BETTER EXPLOIT BENEFICIAL SOIL MICROORGANISMS TO IMPROVE SALINITY TOLERANCE?

Rhizospheric fungi and plant growth-promoting rhizobacteria (PGPR) can increase plant yield under stressed and nonstressed conditions (De-la-Pena & Loyola-Vargas, 2014; Nadeem et al., 2014). Salt-tolerant PGPR populations can reduce Na+ content of shoots, increase the expression of stress-responsive transcription factors, induce greater proline synthesis, enhance ROS scavenging and improve plant biomass under salinity stress (De-la-Pena & Loyola-Vargas, 2014; Nadeem et al., 2014). Arbuscular mycorrhizal fungal colonization of roots can improve plant salt tolerance by increasing water acquisition and shoot K+ whilst decreasing shoot Na+ concentration (Auge et al., 2014). Therefore, treatment with rhizospheric organisms is an attractive option to improve crop yields under saline conditions, so the quantification of their costs and expansion of trials to the field should be encouraged.

## HOW DOES ROOT SYSTEM ARCHITECTURE INFLUENCE SALINITY TOLERANCE OF CEREALS?

Root systems are key to improving crop salt tolerance through their potential for improving access to water and nutrients and limiting salt acquisition (Jung & McCouch, 2013). Salt, reportedly through its osmotic effects, decreases root epidermal cell division and elongation rates, reducing primary root growth but initiating lateral root development in Arabidopsis and wheat (Rahnama et al., 2011; Jung & McCouch, 2013). This would assist plants to mine nonsaline areas for water and minerals until exploitation of saline areas is necessary. In the field, soil salinity is always heterogeneous and usually increases with depth. A complex set of intersecting hormone-mediated pathways control root system architecture in Arabidopsis (Jung & McCouch, 2013), with the mechanisms little explored in crops (Rogers & Benfey, 2015). Arabidopsis roots exposed to a band of high NaCl in sterile culture exhibit negative halotropism, that is they grow away from salt. This asymmetric root growth response is initiated by an external Na+ gradient and is mediated by clathrin-mediated endocytosis of the PIN-FORMED 2 (PIN2) auxin efflux carrier, which actively redistributes the auxin gradient to the side of the root facing the salt (Galvan-Ampudia et al., 2013). Whether halotropism exists in crops, rather than root growth being inhibited purely by decreased water potential of the soil, is yet to be reported and the costs of changing root architecture are unexplored.

## IV. BETTER YIELD UNDER NONSALINE CONDITIONS EQUALS BETTER SALT TOLERANCE?

Elite cultivars that perform particularly well under optimal conditions are also often best yielding under water-limited conditions (Richards et al., 2014), and this principle may apply to saline conditions as long as the enhanced yields are a result of energy-efficient processes. Overexpression of the Arabidopsis vacuolar proton pumping pyrophosphatase (H+-PPase) improves the salinity tolerance of various crop species under controlled conditions, and was shown by Schilling et al. (2014) to increase growth and yield of transgenic barley under saline conditions in both glasshouse and field conditions. Notably, the AtAVP1 overexpressing barley also produced greater shoot biomass and grain yield under nonsaline conditions. The mechanism for these improvements was unclear and is the subject of further research (Schilling et al., 2014). The transgenic manipulation of a crop to improve yield under both control and saline conditions is an exciting development and warrants further exploration.

In semiarid regions, phenology is a primary factor determining grain yield. Worryingly, climate change models predict increased temperature and decreased rainfall in certain semiarid regions (Anwar et al., 2015). This may leave crops susceptible to terminal droughts, and very high salt concentrations in the soil during grain filling, which reduces grain size. Planting and flowering time is therefore crucial to maximize opportunities for photosynthetic capture and translocation of photosynthate to grain. Salinity affects flowering time and can delay or advance it according to species and degree of salinity (Munns & Rawson, 1999; Kim et al., 2013). Research that has recently highlighted novel genes that have an impact on this salinity–flowering time interaction is summarized in Supporting Information Notes S1. Further understanding of the molecular controls of flowering time and their interaction with soil salinity is needed to explain and exploit the difference in the salt-induced phenology responses between genotypes and species.

Whilst the salinity tolerance of many cereals remains poor, breeders are still producing annual incremental improvements in grain yield. It has been suggested that the narrowing crop genetic diversity following domestication and intensive breeding has reduced the potential for large gains in stress tolerance (Munns et al., 2012). Useful natural variation clearly exists in ‘exotic’ cereals; for instance, many Tibetan wild barley lines show higher than normal amounts of salt tolerance in terms of biomass accumulation (Wu et al., 2011). Exploiting such germplasm has great potential for improving crop salt tolerance.

## V. WHAT DOES THE FUTURE HOLD FOR STRESS TOLERANCE RESEARCH?

This insight has highlighted mechanisms with potential for improving crop stress tolerance. It has also highlighted the fact that we lack basic information on the energy costs of salinity tolerance. There is a rationale for revisiting questions posed over 30 yr ago and quantifying the costs of salt to plants (i.e. Greenway & Munns, 1983; Yeo, 1983).). The challenge is to gain quantitative data for the role of specific salt tolerance mechanisms at the genetic level through to single cells and whole plants, so we can develop models that predict which pathways lead to energy gains. The desired outcome will be the informed selection of crops with lower energy costs and greater yields. A rigorous understanding of the plant economy when faced with salt, and the natural variation that exists in this economy will provide a foundation for a targeted approach to crop breeding for stressful environments that has not yet been possible.

A role of prebreeding is to provide germplasm to breeders that produces significant increases in yield in stressful environments (e.g. Schroeder et al., 2013). Fundamental research on Arabidopsis has led to interesting insights into salt tolerance mechanisms, but how much of this can be applied to crop plants in the field (Fig. 2)? Affordable next-generation sequencing and novel transformation techniques now allow fundamental research to be performed on crops. The greater available natural variation within crops, and their more complex genomes, will probably lead to greater yield improvements than has been possible with model plants, providing tangible research impacts towards food security targets.

## VI. RESEARCH METHODOLOGY

The methodology section outline the plan and method that how the study is conducted. This includes Universe of the study, sample of the study,Data and Sources of Data, study's variables and analytical framework. The detailsare as follows;

**Population and Sample**

KSE-100 index is an index of 100 companies selected from 580 companies on the basis of sector leading and market capitalization. It represents almost 80% weight of the total market capitalization of KSE. It reflects different sector company's performance and productivity. It is the performance indicator or benchmark of all listed companies of KSE. So it can be regarded as universe of the study.Non-financial firms listed at KSE-100 Index (74 companies according to the page of KSE visited on 20.5.2015) are treated as universe of the study and the study have selected sample from these companies.

The study comprised of non-financial companies listed at KSE-100 Index and 30 actively traded companies are selected on the bases of market capitalization.And 2015 is taken as base year for KSE-100 index.

**Data and Sources of Data**

For this study secondary data has been collected. From the website of KSE the monthly stock prices for the sample firms are obtained from Jan 2010 to Dec 2014. And from the website of SBP the data for the macroeconomic variables are collected for the period of five years. The time series monthly data is collected on stock prices for sample firmsand relative macroeconomic variables for the period of 5 years. The data collection period is ranging from January 2010 to Dec 2014. Monthly prices of KSE -100 Index is taken from yahoo finance.

**Theoretical framework**

Variables of the study contains dependent and independent variable. The study used pre-specified method for the selection ofvariables. The study used the Stock returns are as dependent variable. From the share price of the firm the Stock returns are calculated. Rate of a stock salable at stock market is known as stock price.

Systematic risk is the only independent variable for the CAPM and inflation, interest rate, oil prices and exchange rate are the independent variables for APT model.

Consumer Price Index (CPI) is used as a proxy in this study for inflation rate. CPI is a wide basic measure to computeusualvariation in prices of goods and services throughout a particular time period. It is assumed that arise in inflation is inversely associated to security prices because Inflation is at lastturned into nominal interest rate andchange in nominal interest rates caused change in discount rate so discount rate increase due to increase in inflation rate and increase in discount rateleadstodecreasethe cash flow's present value (Jecheche, 2010). The purchasing power of money decreased due to inflation, and due to which the investors demand high rate of return, and the prices decreased with increase in required rate of return (Iqbal et al, 2010).

Exchange rate is a rate at which one currency exchanged with another currency. Nominal effective exchange rate (Pak Rupee/U.S.D) is taken in this study.This is assumed that decrease in the home currency is inverselyassociated to share prices (Jecheche,2010). Pan et al. (2007) studied exchange rate and its dynamic relationship with share prices in seven East Asian Countries and concludethatrelationshipof exchange rate and share prices varies across economies of different countries. So there may be both possibility of either exchange rate directly or inverselyrelated with stock prices.Oil prices are positively related with share prices if oil prices increase stock prices also increase (Iqbal et al, 1012).Ataullah (2001) suggested that oil prices cause positive change in the movement of stock prices. The oil price has no significant effect on stock prices (Dash &Rishika, 2011).Six month T-bills rate is used as proxy of interest rate. As investors arevery sensitive about profit and where the signals turn into red they definitely sell the shares. And this sensitivity of the investors towards profit effects the relationship of the stock prices and interest rate, so the more volatility will be there in the market if the behaviors of the investors are more sensitive. Plethora (2002)has tested interest rate sensitivity to stock market returns, and concluded an inverse relationship between interest rate and stock returns. Nguyen (2010) studies Thailand market and found thatInterest rate has aninverse relationship with stock prices.

KSE-100 index is used as proxy of market risk. KSE-100 index contains top 100 firms which are selected on the bases of their market capitalization. Beta is the measure of systematic risk and has alinear relationship with return (Horn, 1993). High risk is associated with high return (Basu, 1977, Reiganum, 1981 and Gibbons, 1982). Fama and MacBeth (1973) suggested the existence of a significant linear positive relation between realized return and systematic risk as measured by β. But on the other side some empirical results showed that high risk is not associated with high return (Michailidis et al. 2006, Hanif, 2009). Mollah and Jamil (2003) suggested thatrisk-return relationship is notlinear perhaps due to high volatility.

**Statistical tools and econometric models**

This section elaborates the proper statistical/econometric/financial models which are being used to forward the study from data towards inferences. The detail of methodology is given as follows.

**Descriptive Statistics**

Descriptive Statics has been used to find the maximum, minimum, standard deviation, mean and normally distribution of the data of all the variables of the study. Normal distribution of data shows the sensitivity of the variables towards the periodic changes and speculation. When the data is not normally distributed it means that the data is sensitive towards periodic changes and speculations which create the chances of arbitrage and the investors have the chance to earn above the normal profit. But the assumption of the APT is that there should not be arbitrage in the market and the investors can earn only normal profit. Jarquebera test is used to test the normality of data.

**Model for CAPM**

In first pass the linear regression is used to estimate beta which is the systematic risk.

$$R_i - R_f = (R_m - R_f)\beta \qquad (1.1)$$

Where $R_i$ is Monthly return of thesecurity, $R_f$ is Monthly risk free rate, $R_m$ is Monthly return of market and βis systematic risk (market risk).

The excess returns $R_i$ - $R_f$ of each security is estimated from a time series share prices of KSE-100 index listed shares for each period under consideration. And for the same period the market Premium $R_m$ - $R_f$ also estimated. After that regress the excess returns $R_i$ - $R_f$ on the market premium $R_m$ - $R_f$ to find the beta coefficient (systematic risk).

Then a cross sectional regression or second pass regression is used on average excess returns of the shares and estimated betas.

$$\hat{R}_i = \gamma_0 + \gamma_1\beta_1 + \epsilon \qquad (1.2)$$

Where $\lambda_0$= intercept, $\hat{R}_I$is average excess returns of security i,$\beta_I$ is estimated be coefficient of security I and Є is error term.

**Model for APT**

In first pass the betas coefficients are computed by using regression.

$$R_i - R_f = \beta_i f_1 + \beta_{i2} f_2 + \beta_{i3} f_3 + \beta_{i4} f_4 + \epsilon \qquad (1.3)$$

Where Ri is the monthly return of stock i,$R_f$ is risk free rate, $\beta_i$is the sensitivity of stock i with factors and ϵ is the error term.

Then a cross sectional regression or second pass regression is used on average excess returns of the shares on the factor scores.

$$\hat{R} = \gamma_0 + \gamma_1\beta_1 + \gamma_2\beta_2 + \gamma_3\beta_3 + \gamma_4\beta_4 + \epsilon_i \qquad (1.4)$$

Where$\hat{R}$ is average monthly excess return of stock I, $\lambda$ = risk premium, $\beta_1$ to $\beta_4$ are the factors scores and $\varepsilon_i$ is the error term.

**Comparison of the Models**

The next step of the study is to compare these competing models to evaluate that which one of these models is more supported by data.This study follows the methods used by Chen (1983), the Davidson and Mackinnon equation (1981) and the posterior odds ratio (Zellner, 1979) for comparison of these Models.

**Davidson and MacKinnon Equation**

CAPM is considered the particular or strictly case of APT. These two models are non-nested because by imposing a set of linear restrictions on the parameters the APT cannot be reduced to CAPM. In other words the models do not have any common variable. Davidson and MacKinnon (1981) suggested the

method to compare non-nested models. The study used the Davidson and MacKinnon equation (1981) to compare CAPM and APT.

This equation is as follows;

$$R_i = \alpha R_{APT} + (1-\alpha) R_{CAPM} + e_i \qquad (1.5)$$

Where$R_{i=}$ the average monthly excess returns of the stock i, $R_{APT=}$ expected excess returns estimated by APT, $R_{CAPM=}$ expected excess returns estimated by CAPM and α measure the effectiveness of the models. The APT is the accurate model to forecast the returns of the stocks as compare to CAPMif α is close to 1.

**Posterior Odds Ratio**

A standard assumption in theoretical and empirical research in finance is that relevant variables (e.g stock returns) have multivariate normal distributions (Richardson and smith, 1993). Given the assumption that the residuals of the cross-sectional regression of the CAPM and the APT satisfy the IID (Independently and identically distribution) multivariate normal assumption (Campbell, Lo and MacKinlay, 1997), it is possible to calculate the posterior odds ratio between the two models. In general the posterior odds ratio is a more formal technique as compare to DM equation and has sounder theoretical grounds (Aggelidis and Maditinos, 2006).

The second comparison is done using posterior odd radio. The formula for posterior odds is given by Zellner (1979) in favor of model 0 over model 1.

The formula has the following form;

$$R = [ESS_0/ESS_1]^{N/2} N^{K_0 - K_1/2} \qquad (1.6)$$

Where$ESS_0$iserror sum of squares of APT, $ESS_1$iserror sum of squares of CAPM, N is number of observations, $K_0$is number of independent variables of the APT and $K_1$ is number of independent variables of the CAPM.As according to the ratio when;

R> 1 means CAPM is more strongly supported by data under consideration than APT.

R < 1 means APT is more strongly supported by data under consideration than CAPM.

## VII. RESULTS AND DISCUSSION

**Results of Descriptive Statics of Study Variables**

Table 1.1: Descriptive Statics

| Variable | Minimum | Maximum | Mean | Std. Deviation | Jarque-Bera test | Sig |
|---|---|---|---|---|---|---|
| KSE-100 Index | -0.11 | 0.14 | 0.020 | 0.047 | 5.558 | 0.062 |
| Inflation | -0.01 | 0.02 | 0.007 | 0.008 | 1.345 | 0.510 |
| Exchange rate | -0.07 | 0.04 | 0.003 | 0.013 | 1.517 | 0.467 |
| Oil Prices | -0.24 | 0.11 | 0.041 | 0.060 | 2.474 | 0.290 |
| Interest rate | -0.13 | 0.05 | 0.047 | 0.029 | 1.745 | 0.418 |

Table 1.1 displayed mean, standard deviation, maximum minimum and jarque-bera test and its p value of the macroeconomic variables of the study. The descriptive statistics indicated that the mean values of variables (index, INF, EX, OilP and INT) were 0.020, 0.007, 0.003, 0.041 and 0.047 respectively. The maximum values of the variables between the study periods were 0.14, 0.02, 0.04, 0.41, 0.11 and 0.05 for the KSE- 100 Index, inflation, exchange rate, oil prices and interest rate.

The standard deviations for each variable indicated that data were widely spread around their respective means.

Column 6 in table 1.1 shows jarque-bera test which is used to check the normality of data. The hypotheses of the normal distribution are given;

$H_0$ : The data is normally distributed.

$H_1$ : The data is not normally distributed.

Table 1.1 shows that at 5 % level of confidence, the null hypothesis of normality cannot be rejected. KSE-100 index and macroeconomic variables inflation, exchange rate, oil prices and interest rate are normally distributed.

The descriptive statistics from Table 4.1 showed that the values were normally distributed about their mean and variance. This indicated that aggregate stock prices on the KSE and the macroeconomic factors, inflation rate, oil prices, exchange rate, and interest rate are all not too much sensitive to periodic changes and speculation. To interpret, this study found that an individual investor could not earn higher rate of profit from the KSE. Additionally, individual investors and corporations could not earn higher profits and interest rates from the economy and foreign companies could not earn considerably higher returns in terms of exchange rate. The investor could only earn a normal profit from KSE.

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