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Under Abiotic Stress Conditions

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# Biotechnological Interventions to Enhance Food Security Under Abiotic Stress Conditions

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## Abstract

The human population is increasing and the total arable land is decreasing all over the world. Therefore, it is very important to enhance world food production to feed this ever increasing population. Abiotic stresses add yet another challenge to global food security and malnutrition. Biotechnological advances hold a great promise to fulfill the food demand and quality of increasing population. Many genes for different stresses have been cloned and characterized in some crop plants, with limited success. Engineering crop plant with improved stress tolerance is in its early stage but realization of its full potential will help to get food security in near future.

**Key word:** Biotechnology, drought, high temperature, salinity.

## Introduction

At the start of the new millennium, the world's population was estimated to be just more than 7 billion. It is growing by about 73 million people per year and expected to reach 9.2 billion by 2050. For our concern, India, China, Pakistan, Nigeria, Bangladesh, Indonesia, the Democratic Republic of Congo and USA will account for half of this growth. According to FAO, there is an urgent need to enhance food production by 70% by 2050 to feed this expected population<sup>3</sup>. Beside quantity, it is also important to think for addition of certain nutrients with stable food to fortify the needs of undernourished population. With the success of the green revolution and biotechnological advances, the global food production has kept pace with population growth over the past 40 years, still one million people worldwide-most of who live in developing world- remain undernourished (Fig 1).

The global arable area has reached to its plateau and is now decreasing slowly due to increasing

urbanization. Thus, enhancement of crop yield for assuring food supply can be achieved by increased cropping intensity through biotechnological interventions. Nobel Peace Laureate, Norman Borlaug quoted that biotechnology and plant genetic engineering complemented with conventional plant breeding is needed to boost crop yield to feed the increasing population of the world<sup>4</sup>. Twenty years ago plant biotechnology comprised few applications like tissue culture, recombinant DNA technology and monoclonal antibodies. Today, its applications have extended to genetic transformation, marker-aided selection, molecular breeding and development of genetically modified (GM) crops. The new DNA manipulation technique provides opportunity for transferring genes from any organism into plant overcoming the limitation of crossing to plant breeders. The commercial applications of biotechnology include Bt- cotton, insect - resistant maize, rice and potato crops, virus-resistant papaya, squash and potatoes, and herbicide tolerant crops such as wheat, maize, sugarcane, rice, onion and beets that allow more effective weed management. Recent biotechnological tools have helped to modify the genetic make-up of many crops. The first GM /Biotech crop was

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commercialized in 1996 with mere 1.7 million ha area in six countries of the world. This area has extended to 125 million ha in 2008 in 25 countries as presented<sup>6</sup> (Fig2). GM maize and soybean are covering sizeable area in the world. In Indian context, *Bt* cotton has provided large industrial benefits and there are more technologies in pipeline for other biotech crops in India. The environmental risk, especially pollen-mediated transgene flow and unintended genetic and epigenetic effects of the first generation of GM crops produced *via* nuclear transformation, has restricted its public perception in many countries. The problem of transgene escape from GM crops to their wild relatives or other cultivated species is due to the presence of the transgene in pollen, which is a consequence of nuclear transformation<sup>5</sup>. Thus, the modification of important crops must be implemented in more sustainable approach to accelerate crop production in an environmentally friendly manner. The global temperature is predicted to increase by 2.5-4.3°C by the end of this century which will certainly affect the food production in malnutrition in the world<sup>9</sup>. Drought and salinity are the other major abiotic stresses which in combination with high temperature reduce average yield of major crops by more than 50 per cent. To survive under these conditions, plants have evolved intricate mechanisms to perceive external signals, allowing optimal response to environmental condition (Fig. 3). These mechanisms are based on the manipulation of genes that protect and maintain the function and structure of cellular components. However, the plant responses to the abiotic stresses are genetically complex (polygenic) and are very difficult to control and engineer. Scientific efforts to improve plant stress tolerance by gene transformation have resulted in significant achievements but the nature of the genetically complex mechanisms of abiotic stress tolerance and the potential detrimental side effects have made this task extremely difficult. In this review, we are summarizing the work done related to genetic manipulation of major abiotic stresses in higher plants.

## High Temperature

Temperature of the earth is increasing linearly due to global climate change and greenhouse effects. According to a report of the Intergovernmental Panel on Climatic Change (IPCC), global mean temperature will rise 0.3°C per decade reaching to approximately 1 and 3°C above the present value by years 2025 and 2100, respectively<sup>9,18</sup>. This increasing temperature causes various metabolic changes in plants, leading to sharp reduction in growth and yield. Initial research on molecular manipulation to improve plant heat tolerance was focused on production of enzymes that detoxify reactive oxygen species (SOD, POX, CAT etc.). Induction of ROS in response to abiotic stresses is the common phenomenon in most of the plants<sup>1</sup>. Transgenic tomato plants with altered chloroplast membrane by silencing the gene encoding chloroplast omega-3 fatty acid desaturase have been produced. These plants produce less trienoic fatty acid and more dienoic fatty acid in their chloroplast as compared to wild type. Further, these plants exhibited greater photosynthesis and grow better than wild type plants under high temperature<sup>11</sup>. Development of transgenic plants capable of high glycine-betaine production with BADH gene has been demonstrated as an effective method to enhance heat tolerance in plants<sup>20</sup>. Sharkey *et al.*<sup>15</sup> reported that thermo-tolerance can be achieved in tobacco plants by transferring rubisco-activase gene which help to protect the photosynthetic apparatus. There is synthesis and accumulation of specific proteins during a rapid temperature stress which are known as heat shock proteins (HSPs). Genes responsible for inducing the synthesis of heat shock proteins have been identified and isolated in maize and tomato<sup>17</sup>. It has been determined that induction of many heat inducible genes is attributed to the conserved heat shock elements (HSEs), which are located in the TATA box proximal 5' flanking regions of heat shock genes. The HSEs are the binding sites for the transitive heat shock transcription factor (HSF). This HSF converts from monomeric to trimeric form under heat stress. It is believed that

interaction of HSF with HSPs results in the activation of HSFs *via* conformational changes involving monomer to trimer transition and nuclear targeting<sup>14</sup>. It has been observed that tomato MT-sHSP gene exhibits thermo-tolerance in transferred tobacco at the plant level<sup>13</sup>. The interaction among HSP, HSF and HSE regulates the short term induction of HSP gene transcription. Thus, the response to HSP gene transcription to heat shock is a fine-tuned process that opens up many possibilities for genetic engineering and induction of heat stress tolerance in plants.

### Salt Stress

Salt tolerance and yield stability are complex genetic traits that are difficult to establish in crop since salt stress may occur as a catastrophic episode, be imposed continuously or intermittently and become gradually more severe at any stage during development. Na<sup>+</sup> and other ions taken up by roots are transported to shoots in the transpiration stream where they accumulate overtime. The molecular biology research has provided new insights into the plant responses to salinity and identified genetic determinants that affect salt tolerance. In tolerant plants, Na<sup>+</sup> and Cl<sup>-</sup> ions are compartmentalized into the vacuole and used as osmotic solute. Beside ions, many compatible solutes also accumulate in the cytosol and vacuoles to act as osmo-protectant. These solutes consist of sugars (glucose, fructose, trehalose, etc.), sugar alcohols (glycerol and methylated inositol), amino acid derivatives (proline, glycine-betaine) and sulfonicum compounds (choline osulfate, dimethyl sulfonicum propionate). Genes for some of these osmolytes have been transferred successfully in model plant *Arabidopsis* and crop plants where they enhanced stress tolerance in transgene products<sup>22</sup>. These workers identified three genetically linked *Arabidopsis* loci (SOS1, SOS2 and SOS3) which are components of a stress signaling pathway that controls ion homeostasis and salt tolerance. It has been demonstrated that SOS signaling pathway regulates Na<sup>+</sup> and K<sup>+</sup> homeostasis and is Ca<sup>2+</sup> activated. Interaction of SOS3 with the SOS2 kinase and SOS2

activation is Ca<sup>2+</sup> dependent. HKT genes have been identified in rice varieties which helps in imparting salt tolerance by mediating either preferential Na<sup>+</sup> transport or Na<sup>+</sup>-K<sup>+</sup> symport<sup>12</sup>. In cereals, natural variation in the activity or expression of HKT transporters is a good genetic resource to enhance salt tolerance. Quantitative genetic analysis in wheat have also led to the identification of two loci, *Nax1* and *Nax2*, that reduced Na<sup>+</sup> accumulation in the leaf blade by excluding Na<sup>+</sup> from the xylem by two different mechanisms<sup>7</sup>. It has also been reported that the over-expression of AtNHX genes enhances plant salt tolerance, presumably by increasing vacuolar Na<sup>+</sup> compartmentalization that minimizes the toxic accumulation of ions in the cytosol and facilitates growth in saline environment. These genes have been cloned successfully in few crops including wheat and it is expected that soon we will have GM crops with salt tolerance characteristics<sup>10</sup>.

### Drought Stress

Drought, being the most important abiotic stress, severely impairs plant growth and development, limits plant production and the performance of crop plants, more than any other environmental stresses. It affects the growth, dry matter and harvesting yield in plants. Following drought, stomata close progressively with a parallel decline in net photosynthesis and water use efficiency. Recently, several transcriptional factors have been implicated in the regulation of stomatal movements in *Arabidopsis*<sup>12</sup>. Adaption to water deficit is often associated not only with stomatal control of water use but also with rooting depth. The HDG11 and HARDY proteins link both phenomena molecularly, suggesting that these proteins may have evolved as master switches directing the evolution of plant species better suited to survive drought. DDG11 gene has been cloned in tobacco and this transgenic tobacco recapitulated water stress tolerance associated with modified root architecture and reduced leaf stomatal density<sup>21</sup>. Scavenging of reactive oxygen species by enzymatic and non-enzymatic system, cell membrane stability, expression

of aquaporins and stress proteins are some other mechanisms of drought tolerance<sup>2</sup>. A mutant with improved resistance to water shortage and to oxidative stress enhanced drought tolerance 1 has been isolated in an *Arabidopsis* mutant. The mutant plants (*edt1*) showed an array of stress-related traits, including a more extensive root system with deeper primary roots and more lateral roots than the wild-type plants, and higher level of ABA, proline, and superoxide dismutase<sup>21</sup>. Several stress induced genes, such as *rd29A* have been induced in model plant. A cis-acting element has been identified in the promoter region of the *rd29A* gene which is responsible for dehydration and cold induced expression<sup>8</sup>. Xiao *et al.*<sup>19</sup> reported that the enhanced production of the signaling hormone abscisic acid by the over-expression of the *LOS5/ABA3* gene encoding a Mo cofactor sulfurase, required for ABA synthesis conferred enhanced drought tolerance in transgenic rice plants under field conditions. Quantitative trait loci (QTL) for drought tolerance have been found in several crops. After identifying markers associated with QTLs or genes for traits of interest, the candidate genes can be introgressed in elite lines through marker assisted backcrossing (MABS). With this approach, one major QTL for drought tolerance has been identified in rice<sup>16</sup>. Many transgenic crops have been engineered for drought tolerance; few of them (rice, maize and canola) have been tested under field stress conditions also. We expect that in near future we will have more genetically engineered/transgenic crops with drought tolerance mechanism.

## Conclusion

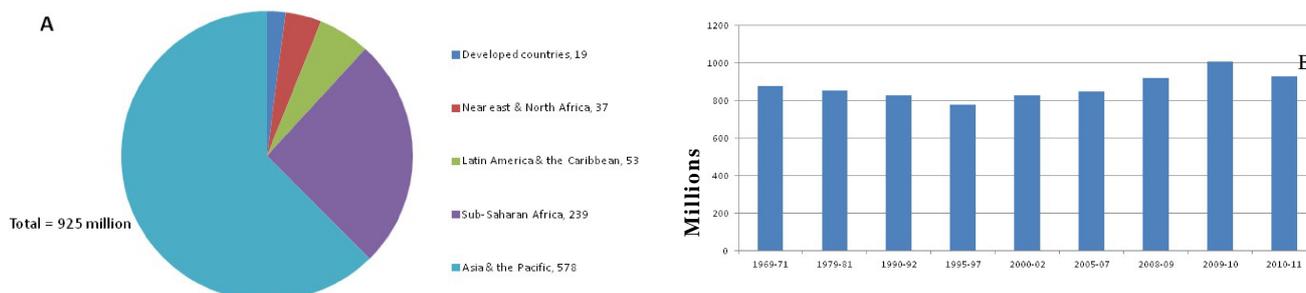
Biotechnology approaches have identified many genes for drought, salinity and high temperature tolerance; however, their successful deployment in the development of a superior cultivar is very limited. The vast majority of stress genes have been tested in model plants in highly controlled environmental conditions and the same have not been repeated successfully in crop plants except in few cases. Nevertheless, with current and fast emerging techniques in this field, the

future of biotechnology seems bright with respect to development of crops with improved tolerance to abiotic stresses.

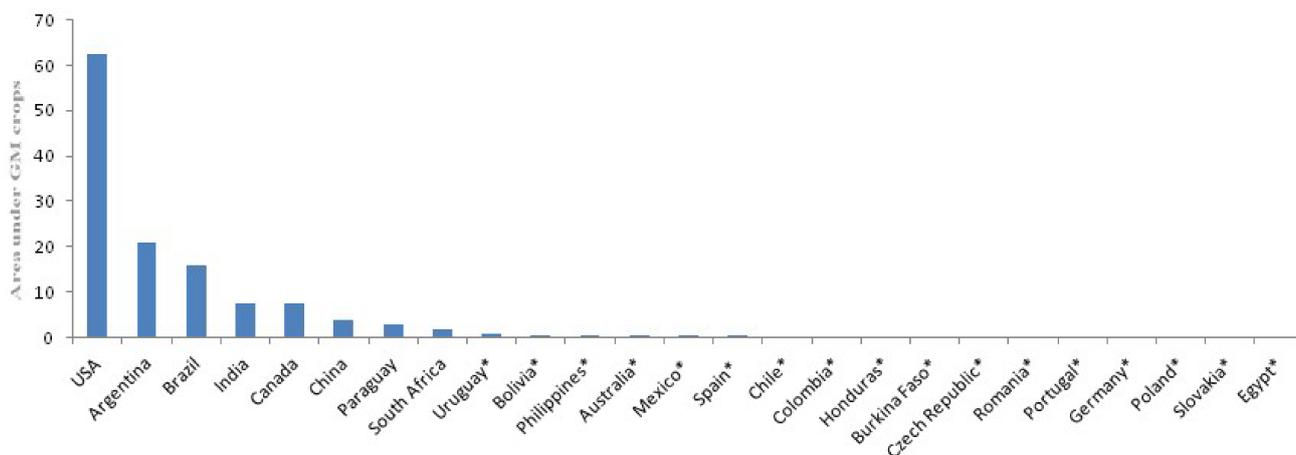
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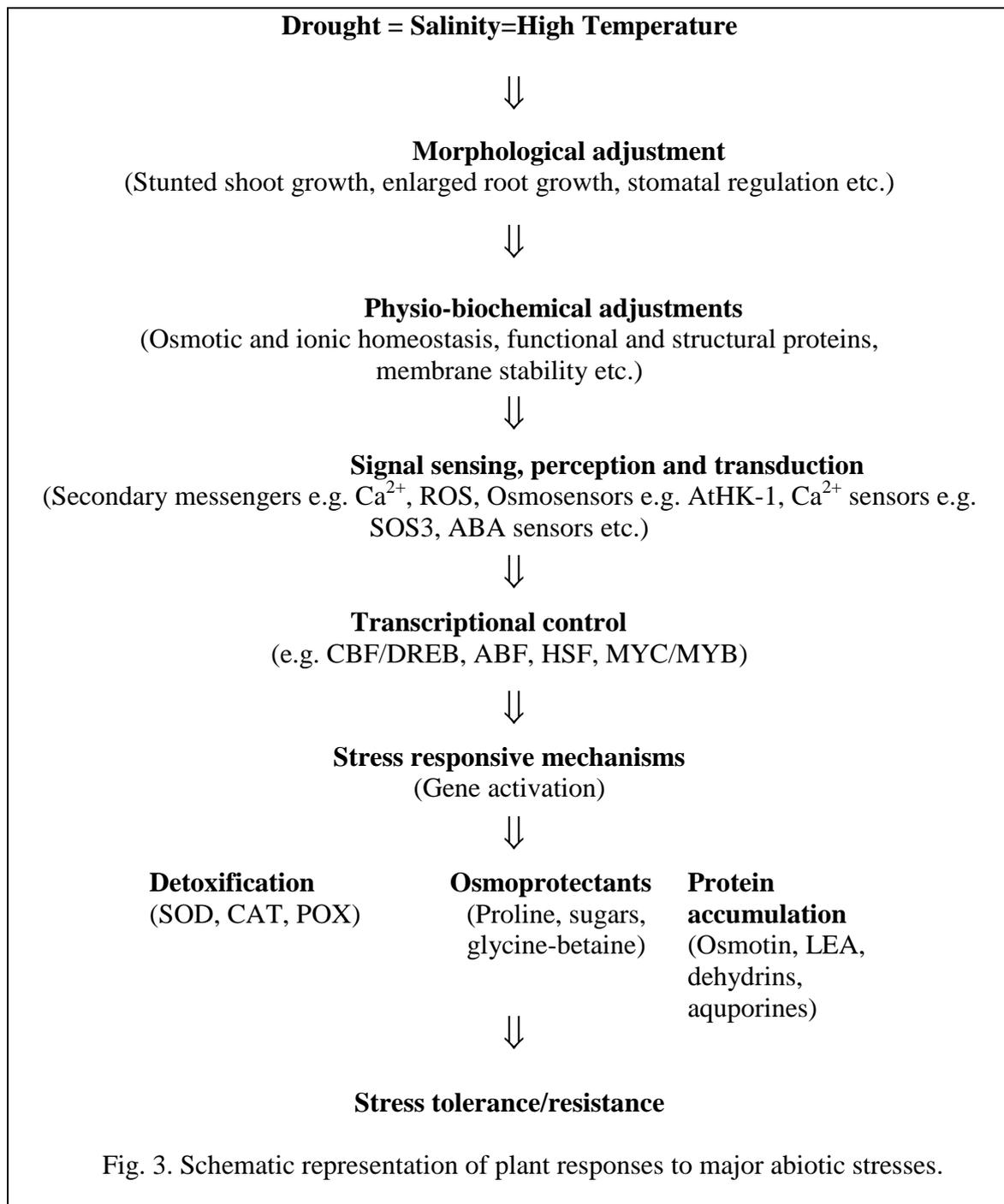
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**Fig. 1: Prevalence of undernourishment in 102 developing countries in the world (A) Undernourishment in 2010, by region (millions) and (B) Number of undernourishment in the world (Source: James, 2008)**



**Fig. 2: Area under GM crops in the world in 2008 (million ha). Note: the countries are ranked from left to right and countries tagged with '\*' are having area less than a million ha. (Source: James, 2008)**



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# CONTENTS

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## Review Articles

- 01 On Scientific Explanation of Consciousness  
(Syamala D Hari) 1-11
- 02 Impact and Strategies for Yield Improvement of Arid Legumes under Drought  
(S. P. Vyas) 12-19
- 03 Experimental Validation of Indigenous Knowledge for Managing Crop Diseases in  
Arid Rajasthan  
(Arun Kumar) 20-27
- 04 Integrated Farming System-Need of Today  
(L.N. Dashora and Hari Singh) 28-37
- 05 Biotechnological Interventions to Enhance Food Security Under Abiotic  
Stress Conditions  
(N.K. Gupta, V.P. Agarwal, S. Gupta, G. Singh and A.K. Purohit) 38-43

## Research Articles

- 06 Scanning Electron Microscopic Study Reveals Stomatal Malfunctioning in *In Vitro*  
Grown *Celastrus paniculatus* Willd.  
(Manohar Singh Rao, Dimple Suthar and Sunil Dutta Purohit) 44-50
- 07 Effect of Calcium and Potassium Supplementations on Shoot Necrosis and  
Recovery of Healthy Plantlets of *Jatropha curcas* L.  
(Vinod Saharan, M.A. Shah, B.R. Ranwah and Birchand Patel ) 51-57
- 08 Direct Use of Rock Phosphate along with Lignite on Cowpea  
(N.C. Aery and D.K. Rana) 58-61
- 09 Agronomic Efficiency of Rock Phosphate in Fine Size with Ammonium Sulphate and  
Ammonium Nitrate  
(Mahesh Ganesa Pillai, Sumedh Sudhir Bektalkar and Saket Sanjay Kashettiwar) 62-65
- 10 Application of Low Grade Phosphate Rock as Fertilizer with Urea and  
Urea along with Organic Manure in Alkaline Soil: A Preliminary Study  
(Shashank Bahri, Satyawati Sharma and Sreedevi Upadhyayula) 66-69
- 11 High frequency Multiplication of *Jasminum sambac* (L.) Aiton using Plant Growth  
Hormone Solutions on Stem Cuttings  
(Surya Prakash Sharma and R.S. Brar) 70-73

### **Short Communications**

- 12 Nitro PROM using Wool Waste: A Preliminary Study  
(Praveen Purohit and G. Prabhulingaiah) 74-76
- 13 Eshidiya Phosphate Deposit-Jordan  
(G. Prabhulingaiah, Hanna Qutami and Yasser Dassin) 77-78
- 14 Lignite in PROM A Preliminary Study  
(D.S. Xanthate, Zeba Rashid, P.K. Mathur and G. Prabhulingaiah) 79-80
- 15 Marine Phosphate Deposit - Namibia  
(Hans Hückstedt and DMR Sekhar) 81-82
- 16 The "Twins" Paradox  
(R. Rapparini) 83-86
- 17 Direct Application of Phosphate Rock with Ammonium Sulphate  
(Raguram Sandeep Mutnuru and Ch. V. Ramachandra Murthy) 87-88

### **Opinion**

- 18 Evolution of Species  
(DMR Sekhar) 89-96

### **News and Views**

- 19 Life as a Phenomenon  
(Georgi Gladyshev) 97-98

### **Correspondence**

- 20 Future of Phosphatic Fertilizers  
(DMR Sekhar) 99-100