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Review Article

Potential of Different Plant Genes in Stress Conditions and Applications in Agriculture

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Abstract

Salinity is one of the major abiotic stress factors in plants that devastatingly affect the plants growth and reduce productivity. The major causes of soil salinity are dry climates and low precipitations, high evaporation rate, which adds salts to the ground surface; poor drainage or waterlogging. Tracking the genetic sequences and control of switching on/off of such transcriptional genes may help in mitigating influences of several biotic and abiotic stresses. PtSOS2, AtNHX1, and OsRab7 are the most important salt tolerant genes. Under drought treatments, induction of NAC and homeobox domain containing TFs illustrates their regulatory roles. Uptake of compatible solutes, synthesis of antifreeze proteins and antioxidants, and expression of cold responsive genes perform significant preventive roles against cold stress. Glucanase gene is one of the reflective examples of disease resistant enzyme. It catalyzes the synthesis of phytoalexins. Through this is strategy, the process involved in defensive mechanisms of plants contouring abiotic stress. Heat shock (HS) is often lethal to plants and exert negative impacts on the structural as well as functional profiles in many crops. It occurs by genetic modification in the Arabidopsis by viral DNA from recognition by the guide RNA.

Keywords: Plant genetics, biotic and abiotic stresses, drought treatments, cold responsive genes.

INTRODUCTION

The dynamic nature of the universe always tends to alter the physical and chemical systems but overall energy remains constant. Changes/entropy in biological systems may disrupt the structural or physiological arrays. Several biotic and abiotic factors contribute to the biochemical processes directly or indirectly [1, 4, and 7]. Salinity is one of the major abiotic stress factors in plants that devastatingly affect the plants growth and reduce productivity. It, most of the cases, interfere the essential metabolic reactions and exerts inhibitory properties. However, in response to such inhibitory circumstances, plants trigger their regulatory mechanisms i.e., activation of transcriptional genes which stimulate pronounced effects helping in overcoming stress conditions. Tracking the genetic sequences and control of switching on/off of such transcriptional genes may help in mitigating influences of several biotic and abiotic stresses. Genetic engineering is the advanced technique used in identifying the role of different genes expressed or suppressed during different stress conditions. Salinity can be controlled by over expression or silencing of the regulatory genes. PtSOS2, AtNHX1, and OsRab7 are the most important salt tolerant genes [1, 2].

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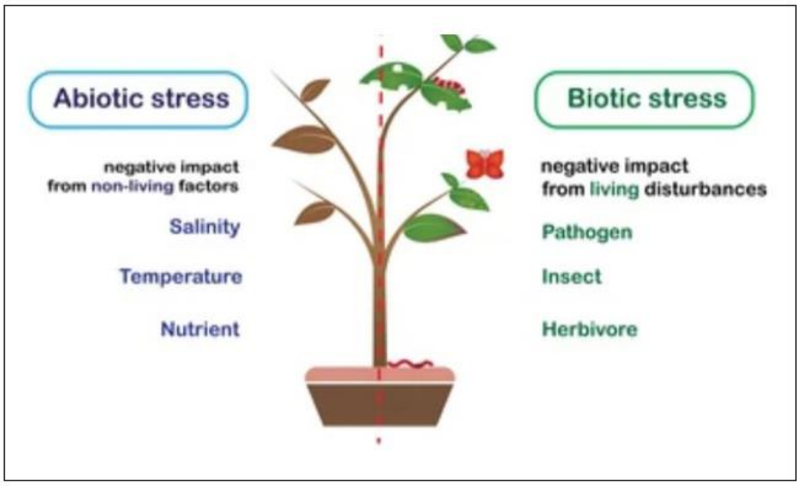

Figure 1: Shows the different stress conditions and applications

Transgenic plants have been developed to attain eugenic aims. The plant varieties retaining desirable traits with high competencies and resistant to several pathogens can now be developed through genetic engineering. Transfer of genes to the specialized parts of the plants reflects to obtaining optimum yields, high quality foods and enables plants to tolerate severe environmental stresses. Soil salinity is majorly caused by arid climate with very low precipitations accompanied by high evaporation and poor drainage system or waterlogging. Soil reclamation by developing salinity tolerant varieties through genetic tools has been adopted at broad scale in order to avoid soil loss in the major agricultural lands [2, 4].

Potential of Different Plant Genes in Stress Conditions and Applications

The control mechanism of regulatory genes can be categorized in four major functional groups: at transcriptional level, at signal transduction level, at cellular metabolic reactions level, and at protection of cellular structures and transport of metabolites across the cell membranes. Genetic control at transcriptional level (switching on or off the genes) is very effective strategy to contour different environmental stresses like salt stress and drought. A profound investigation on the *Arabidopsis thaliana* has been practiced and a number of regulatory genes involved during drought circumstances have been assayed [5, 6].

Six different classes of transcription factors (TFs) involved in expression or repression of different genes in water deficient conditions have been tagged. Under drought treatments, induction of NAC and homeobox domain containing TFs illustrates their regulatory roles. Proteins synthesized by the action of such factors promote adaptations to water-deficient stress. Late embryogenesis abundant (LEA) genes are one of the examples of the six TFs. These genes possess coding sequence for small hydrophilic proteins which protect membranes from chaperone-like functions, for instance, high performance of rice crops due to protection of cell membranes against the injury under abiotic stresses [7, 8].

Temperature below tolerance denatures the molecular framework of cellular compartments and hence reduces the biochemical and physiological processes. Modifications taking place during cold stress are very important for survival. Cold stress can profoundly be associated to short photoperiods often occurred in extreme latitudes (Polar Regions). All the essential biological processes such as water absorption, development and growth, photoperiods, energy metabolism are the most important phenomena effected by cold stress. Uptake of compatible solutes, synthesis of antifreeze proteins and antioxidants, and expression of cold responsive genes perform significant preventive roles against cold stress [9, 11].

Salinity is the major problem associated with crop productivity and has certain implications in the fields of agricultural sectors. The response of plants in abiotic stresses stimulates the activation of transcriptional genes. The expression of these genes may helpful for overcoming the different issues in agriculture land. Plant genetic engineering is the most versatile and dynamic for exploring the role of different genes induced in different stress conditions. It is mainly categorized the gene manipulation either through over expression or silencing of alien/native genes. While on the other hand, alt-tolerant plants; trees (including mangroves), shrubs, grasses and herbs. The salt tolerant plants induced the resistance against the inclusion salinity stress [1, 2].

Table 1: Shows the different factors and genes in plants

Factors/Gene	Function	Applications	Implications
PtSOS2, AtNHX1, and OsRab7	Salt tolerant genes	Soil salinity is majorly caused by arid climate with very low precipitations accompanied by high evaporation and poor drainage system or water logging. Salinity and other stresses can be controlled	Helpful for improving the agricultural land conditions
NAC	Molecular Factor	Expression or repression of different genes	Small hydrophilic proteins which protect membranes
Cold stress	Stress conditions	Short photoperiods often occurred in extreme latitudes	Water absorption, development and growth, photoperiods, energy metabolism
Heat shock	Functional proteins	Decrease net biomass due to reduced photosynthesis and enhanced respiration	Water uptake and its distribution to other organs
Tomato yellow leaf curl virus	Genetic modifications	Introduction of novel genes	This potential of resistance leads to increases the survival rate of plants in the drought and saline conditions.

Low temperature triggers the expression of many genes which code for a number of metabolically important proteins such as enzymes involved in metabolism of carbohydrates, lipids, phenylpropanoids, antioxidants and cellular respiration, and production of antifreeze proteins and chaperones. In addition, several other tolerance mechanisms are also prompted by an array of regulatory genes under cold-induced dehydration. Controlled switching on/off of these regulatory genes enhances the potential of plants to survive under severe chilling temperatures and yield also increases [12, 14].

Many researchers have been investigating since long times the patterns of defensive mechanisms in plants evolved under biotic and abiotic stress conditions. Direct or indirect role of different genes in inducing resistance to pathogenic infections have been identified in a diverse scientific studies. Glucanase gene is one of the reflective examples of disease resistant enzyme. It catalyzes the synthesis of phytoalexins (antifungal substances) which degrade the fungal cell walls and destabilize their integrity, and hence provide protection against their parasitic attack. Moreover, phenylalanine ammonia lyase is another plant defensive gene. It is induced by the glucanase. In transgenic potatoes, overexpression of soybean glucanase gene provides increased resistance against *Phytophthora infestans* [15, 18].

Functionality and expression mechanisms of genes in different tissues in different circumstances can be exploited with the help of comparison between transcriptome data. Through this strategy, the processes involved in defensive mechanisms of plants contouring abiotic stress can easily be investigated i.e. microarray and RNA sequence such as by expressed sequence tags (ESTs) [18, 20].

Temperature is another important factor in crop physiology. It affects plants development, growth, and yield. A subsequent rise of temperature above optimum range may denature the globular structure of proteins and restrict physiological processes, and hence reduce the net yield. Tolerance to temperature in different plants varies with the intensity, frequency, or duration of heat events. Heat shock (HS) is often lethal to plants and exert negative impacts on the structural as well as functional profiles in many crops. It may decrease net biomass due to reduced photosynthesis and enhanced respiration. In addition, HS also limits the root growth and ultimately water uptake and its distribution to other organs is checked [19, 22].

Food insecurity has been remained a parallel challenge with the rapidly flourishing population in the world. With the initiation of agriculture about 12,000 years ago, agriculturists have been trying to increase crop yield through various agronomic strategies. Selection and cultivation of high-yielding cultivars and adaptation of new tools and better land management practices are the traditional methods to access sufficient calories and nutrients to the people. Before nineteenth century, famine and hunger were common problems worldwide. However, during green revolution, advancement in technology and invention of new agricultural techniques has greatly contributed in mitigating this problem [23, 25].

There is another technique used for the gene transformation in plants with high genetic diversity. This technique can be applied for those cells growing in a culture medium are stripped of their protective walls. This wall happens to breakage through the action of biocatalysts such as cellulase, and hemicellulose. It depends upon on the two conditions such as low genetic update and high uptake of genetic material. Low uptake leads to the smaller or little resistance to the diseases occurs in the different plants of the pants while on the other hand, high uptake leads to the potential resistance to the diseases occurs in the different plants of the pants [26, 28].

One of the ideal examples of gene transformation is the genetic modification in the tomato yellow leaf curl virus (TYLCV). It is belongs to the single-stranded circular DNA genomes. Its genome is expressed through TYLCV conferred resistance. This potential of resistance leads to increases the survival rate of plants in the drought and saline conditions. While the other example is the genetic modification is the Arabidopsis by viral DNA from recognition by the guide RNA. The genetic alterations in the Arabidopsis helpful of resistance lead to increases the survival rate of plants saline conditions. The other genetic modification can occurs in plants through molecular cloning that address the introduction of novel genes into the different plant varieties for increases the resistance also helpful for the production of transgenic plants. It is also for predicting and assessing adverse health effects [29, 31].

There are different methods are used for the gene transformation such as Agrobacterium-mediated transformation system that are more reliable, high efficiency, reduce cost, environment friendly. This is type of genetic transformation helpful for oil bacterium that has the ability to infect plant cells and transfer a defined sequence of their DNA to the plant cell by infection. A while on the other hand, non-gene transformation that are not reliable, low efficiency, increase the cost, causes the environmental pollution. These genetic modifications strategies helpful for regulatory status of classic GMOs. In plants, cellular processes are often regulated by complex genetic networks, and the manipulation of agronomic traits depends on the precise engineering of complex metabolic pathways, which requires the concerted expression of multiple genes [32, 35].

CONCLUSION

Transgenic plants have been developed for crop improvement in order to achieve the desire traits characteristics with high potency of resistance against infections in different parts of plants. Transgenics in diverse crops have gained special importance in order to reflect the high quality of foods and yields at optimum concentrations. Different genes can be transferred to the potential parts of plants through genetic transformation that enable the plants to grow in severe environment. The major causes of soil salinity are dry climates and low precipitations, high evaporation rate, which adds salts to the ground surface; poor drainage or waterlogging. Many of genetic tools have been adopted for developing the engineering tolerance to salinity that overcomes the soil damage tenants to the main agricultural land.

Informed Consent Statement: Not applicable.
Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

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