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Original Article

Regulon: An overview of plant abiotic stress transcriptional regulatory system and role in transgenic plants

Regulon: Uma visão geral do sistema regulador da transcrição do estresse abiótico em plantas e papel nas plantas transgênica

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Abstract

Population growth is increasing rapidly around the world, in these consequences we need to produce more foods to full fill the demand of increased population. The world is facing global warming due to urbanizations and industrialization and in this concerns plants exposed continuously to abiotic stresses which is a major cause of crop hammering every year. Abiotic stresses consist of Drought, Salt, Heat, Cold, Oxidative and Metal toxicity which damage the crop yield continuously. Drought and salinity stress severally affected in similar manner to plant and the leading cause of reduction in crop yield. Plants respond to various stimuli under abiotic or biotic stress condition and express certain genes either structural or regulatory genes which maintain the plant integrity. The regulatory genes primarily the transcription factors that exert their activity by binding to certain cis DNA elements and consequently either up regulated or down regulate to target expression. These transcription factors are known as masters regulators because its single transcript regulate more than one gene, in this context the regulon word is fascinating more in compass of transcription factors. Progress has been made to better understand about effect of regulons (AREB/ABF, DREB, MYB, and NAC) under abiotic stresses and a number of regulons reported for stress responsive and used as a better transgenic tool of Arabidopsis and Rice.

Keywords: abiotic stress, drought and salt stress, transgenic approach, transcription factors, regulons.

Resumo

O crescimento populacional está aumentando rapidamente em todo o mundo, e para combater suas consequências precisamos produzir mais alimentos para suprir a demanda do aumento populacional. O mundo está enfrentando o aquecimento global devido à urbanização e industrialização e, nesse caso, plantas expostas continuamente a estresses abióticos, que é uma das principais causas do martelamento das safras todos os anos. Estresses abióticos consistem em seca, sal, calor, frio, oxidação e toxicidade de metais que prejudicam o rendimento da colheita continuamente. A seca e o estresse salino são afetados de maneira diversa pela planta e são a principal causa de redução da produtividade das culturas. As plantas respondem a vários estímulos sob condições de estresse abiótico ou biótico e expressam certos genes estruturais ou regulatórios que mantêm a integridade da planta. Os genes reguladores são principalmente os fatores de transcrição que exercem sua atividade ligando-se a certos elementos cis do DNA e, consequentemente, são regulados para cima ou para baixo para a expressão alvo. Esses fatores de transcrição são conhecidos como reguladores mestres porque sua única transcrição regula mais de um gene; nesse contexto, a palavra regulon é mais fascinante no âmbito dos fatores de transcrição. Progresso foi feito para entender melhor sobre o efeito dos regulons (AREB / ABF, DREB, MYB e NAC) sob estresses abióticos e uma série de regulons relatados como responsivos ao estresse e usados como uma melhor ferramenta transgênica de Arabidopsis e Rice.

Palavras-chave: estresse abiótico, estresse hídrico e salino, abordagem transgênica, fatores de transcrição, regulons.

1. Introduction

Abiotic stress is the key cause of crop hammering globally, reducing average yields of most of the major crop plants. Plants are being sessile in nature it can't move from one place to other places and contentiously exposed by extensive array of environmental stresses like as water deficit condition (drought), low temperature (cold), salt and high temperature (heat) etc. Tolerance and susceptibility for plant under stress condition are

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complex events in which stresses may affect the multiple stage of plant development. Under the influence of abiotic stress plant change their molecular and physiological fine tuning and try to cope up and maintain the molecular and physiological disturbance which obtained from stress environment. In this disturbance the maintenance involve the gene expression under the stress either in the form of structural gene or regulatory.

Plant stress including drought and salinity are widespread in various regions of the world, and existing constraints present at an agreed time. Plant/ crop productivity effected by the environmental strains such as water deficit condition (drought), Low temperature (cold), salt and High temperature (heat) these stresses disturb the signal transduction of gene regulatory systems of plants. Water deficit condition (drought), Low temperature (cold), salt and High temperature (heat) are the major troubles of agriculture because they stresses make an adverse environmental stress condition for crop development which reduce the crop productivity. Plant development and yield negatively affected by the abiotic stresses which disturb the integrity of plant molecular, physiological, biochemical morphological and developmental events. Raised salt stress interrupts homeostasis in water potential (osmotic homeostasis) and ion distribution (ionic homeostasis). This disturbance of homeostasis occurs at both the cellular level and entire plant levels. During stresses in plant molecular damage, stunting or retarted growth are common problems due to imbalance in ion and water homeostasis (Evelin et al., 2019). To accomplish salt tolerance, three organized characteristics of plant actions are important, first, prevent to injure, second, re-establish homeostatic in the stressful environment. Third, growth must restart, although at a reduced rate (Evelin et al., 2019). Heavy metal stress is also one of the major problems associated with abiotic stress in this concern irrigated water is one of the key sources of heavy metal toxicity in plants which comes due to industrial effluent containing heavy metals in revers and canals. Agriculture field irrigated with this water and the toxicity of heavy metals seize the growth of crops due to chlorosis, altered photosynthesis, retarted growth and senescence. Apart from this most of the agriculture soil contaminated with heavy metals naturally contains chromium, cadmium, arsenic, lead and many more. Plant under the expose of metals due to any consequences, plants always tries to cope up from this situation. Under this situation plants exert there mechanism for survival and at molecular level it express the metal stress responsive genes, antioxidants (CAT, MnSOD, ZnSOD, MnSOD, GR, DHA, GST, Alkyl hydroperoxide, Sulfite oxidase, Serine acetyltransferase), hormone mediated stress tolerance (Salicylic acid, Brassinosteroids, Gibberellic acid) and transcription factors (WRKY, AP2/EREF, bZIP, HSF, ZIP, b HLH, MYB) play an important role.

According to FAO (Food and Agriculture Organization of united nation) last 10 year (2005-2015) surprisingly loss of $96 billion due to environmental stresses including abiotic stress. In this total loss half of the loss ($48 billion) occurred in Asia (Matek Sarić et al., 2020). Data and evidence suggest that the central Europe effected from drought in recent 2018 the cause was low rain fall and under these consequences the yield of agriculture crop was low (Reinermann et al., 2019). Drought stress is a common problem word wide and the agriculture production/ yield is dramatically affected every year. Investigation suggested that the periods of drought in future will increase and the crop yield would be decrease (Karl et al., 2009). So this is important to understand how to increase the crop yield in the presence of environmental stress. We can't escape the crops under the exposer of stress and for food security we must have to generate high yielding stress tolerance crops. To achieve this goal there is two different methods one is traditional breeding method and another is transgenic approach. A traditional breeding method has very low probability of success while a transgenic approach is widely accepted to generate transgenic plants using genetic engineering methodology. Transgenic approaches follow the rules of gene regulatory system in which plant recognize the stress inducible genes under the influence of particular stress and induce the stress signal which help to initiate adaptive responses in transgenic crop.

Utilizing advance molecular tools, techniques and high throughput sequencing methods helps to identified & characterized several abiotic stress responsive genes. In light of the sequence based characterization of stress genes are divided in two categories first is functional gene and second one is regulatory gene. Functional gene consist mainly enzymes and metabolic proteins which protect the cell from damage while second one generate regulatory protein, transcription factors which involve in signal transduction under the influence of stress. More than a few genes are activated in answer to abiotic stresses at the transcriptional level, and their products are contemplated to provide stress tolerance by the production of very important metabolic proteins and also in regulating the downstream genes. A gene pools are induces in response to abiotic stresses at transcriptional level and there product help to gain stress tolerance by the production of metabolic protein which also help to regulate downstream gene. Several studies demonstrate that the functional gene/ single gene were not enough to maintain the integrity of plant under stress condition because single stress induces multiple genes. Evidence suggested that in the agriculture field condition crops expose under various stress and this situation plant regulon induces transcription factors and regulatory genes which regulate a large set of stress irresponsive genes. For food security we must have to generate high yielding abiotic tolerance crops in this context regulons and transcription factors is a good road map to derive a better stress tolerant crop (Wang et al., 2016). Transgenic crop containing regulatory gene/TF favor stress tolerance because network regulatory mechanism enhance stress signal which regulate various stress responsive genes (Chen et al., 2007). In context with molecular study of stress responsive genes of regulatory elements various transcription factors family DREB, AP2/ERF, MYB, and NAC has major contribution in plant stress. These regulatory elements have a potential to regulate various downstream genes and transcription factors. They transcription factors define on the basis of conserve binding protein. Among all family members of transcription factor only few of them has unique binding domain which function as a domain of stress binding protein (Joshi et al., 2016). The cis elements (DRE/CRT) where transcription factors bind DREB/CBF, AP2/ERF, NAC, MYB is considered as stress responsive regulons which involves in various gene expression under the influence of abiotic stress. Regulon be made up of of number of genes carrying a similar cis-acting element, thus these particular set of genes are induced by the same Transcription factors (Kimotho et al., 2019) or in simple word we can say genes regulated by cis element binding factors; AREB/CBF, DREB, NAC, MYB. Under drought/ salt stress condition DREB & NAC regulon regulate various drought stress responsive genes (Singh & Laxmi, 2015). Evidence suggested that regulons have important role not only in plant development but also in abiotic stress (Wang et al., 2016). Plant consist a large number of transcription factors in its own genome; for example, In *Arabidopsis* at least 1500 TFs is reported (Riechmann et al., 2000) while in *Oryza sativa* 2025 TF (Gao et al., 2006).

This review explains regulons and the transcriptional regulation of abiotic stress responsive genes particularly focus on AP2/ERF, DREB, MYB, NAC & bZIP and their role in abiotic stress in transgenic plants of *Arabidopsis thaliana* & *Oryza Sativa*. Among all plant transcription factors NAC (NAM, ATF, CUC) transcription factor has vital role in abiotic stress along with vegetative development. Evidence suggested that NAC regulate at wide array of abiotic stress in different plants like as SNAC express in rice under cold and drought stress, PbeNAC1 strongly express in *Pyrus betulifolia* under cold and drought condition (Jin et al., 2017). *Miscanthus lutarioriparius* is a bioenergy crop in which MINAC5, MINAC9, MINAC10 and MINAC12 express under abiotic stress condition (Yang et al., 2015; Zhao et al., 2016; He et al., 2019; Yang et al., 2018).

DREB regulon and its expressed transcription factor genes involves in abiotic stress (Drought, Salt and cold). After the isolation of first DREB from Arabidopsis using yeast one hybridized techniques since then many DREB gene have been isolated from various plant (Figure 5). Newly DREB have been isolated in various plants such as VuDREB2A isolated in cow pea (*Vigna unguiculata* L. Walp) expressed under drought stress condition (Sadhukhan et al., 2014) While in mung bean (*Vigna radiata*) VrDREB2A were expressed under abiotic stress and confer the stress tolerance in transgenic Arabidopsis (Chen et al., 2016). EsDREB2B were expressed under drought, salinity, cold, heat, heavy metal, mechanical wounding, oxidative stress in *E. songoricum* plant (Li et al., 2014a). In tomato (Solanum lycopersicum L) a novel SlDREB2 were expressed under salinity condition (Hichri et al., 2016) while under salt stress a woody plant *Broussonetia papyrifera* BpDREB2 were expressed which help to maintain the growth of economical trees in salty region (Sun et al., 2014). A novel BdDREB2 were identified & expressed in buffalo grass (*Buchloe dactyloides*) under drought and salt stress condition (Zhang et al., 2014). SlNAC1 were expressed in *Suaeda liaotungensis* K under drought, salt and cold and confer them in Transgenic Arabidopsis (Li et al., 2014b).

2. Stress Regulatory System

Mostly plants can't move from one place to another and it exposed continuously under the abiotic stresses. Due to continuous exposer of abiotic stress it evolves various mechanisms to cope up under stresses using cellular and molecular adaptation. In stress regulatory system signal transduction is very important step because it decides the fate of survival of plants under stress. First step in signal transduction the signal perceived by the receptor; hormones, receptor like kinases, G protein couple receptor. The ABA (abscisic acid) introduces in second signaling step and the second step is responsive to mediate the modulation of transcription factors (Gong et al., 2013). Signalling pathways comes in action due to the continuous exposer of ecological stresses. Several study demonstrate this pathway involve various component. Signalling pathway is a multifaceted network this is also known as signal transduction pathway/signal transduction network (Figure 1). Signal transduction has various unique junctions which explain its how it designs to solve the various stresses using single signal transduction pathway. Signal transduction pathways is complex, circuitry and multiple faceted pathway along with this it is tissue and cell specific to coordinate the fine tuning of gene network (Sewelam et al., 2016; Dombrowski, 2003). Plant answers to different stresses to exert their molecular and cellular changes for the sake of maintain the plant physiology for better survival. The stress induced genes are thought to function not only in stress tolerance but also in the regulation of gene expression and signal transduction (Shinozaki et al., 2003). Abscisic acid (ABA) a plant hormones have a great importance in terms of plant vegetative development or in abiotic stress condition. Along with all developmental support ABA mediates stress signals/switch on the genes to maintain the osmotic adjustment. Experimental validation suggested that ABA maintain water adjustment to prevent excess transpiration and maintain the wilting process. Evidence also suggests that ABA induces various stress responsive genes under drought stress condition or intersection in the expression of stress responsive genes under different abiotic stress condition (Drought, Salt, and Cold & Heat). However other

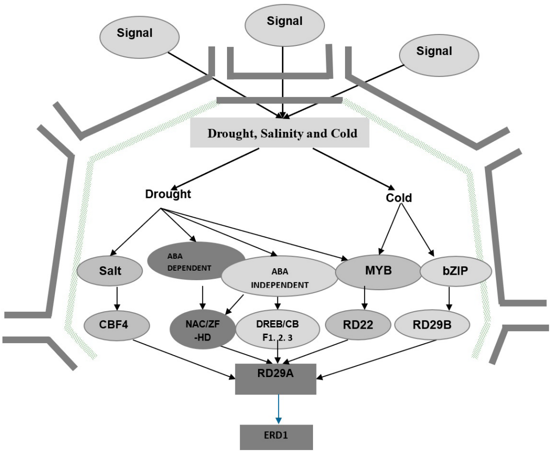

Figure 1. Abiotic stress Signal Transduction in Plant cell; Schematic representation of regulons (In plant cells) involves in abiotic stresses responses. Transcription factors and its stress inducible gene are showing in boxes.

evidence suggests that ABA doesn't accumulate under the cold stress condition. Abiotic stress condition signals perceived through ABA dependent and independent manner by plant. Microarray analysis suggested that various genes up and down regulated under the influence of drought or salt stress conditions. Stress responsive gene expressed when transcription factor (regulatory protein) binds to their promoter region. Transcription factor help to mediate the abiotic signal to cell response. Transcription factor has ability to modulate a large number of genes. Under the influence of abiotic stress plant induces their regulons either ABA dependent manner or ABA independent manner (Nakashima et al., 2009). Gene profiling is the best methods to know about the stress inducing genes in which in which genes product classified in to the two groups one is Functional protein and the second one is regulatory protein. The first group consists of osmolytes related protein, Proline, betaine and sugar etc. Under the effect of drought stress osmolytes accumulates along with proline, betaine and sugar they help in biosynthesis of osmolytes. Along with this aquaporin and LEA is also belongs to the first group which defend the plant cells from stresses. Now this is well known the function of functional protein. They are responsive to conduct the water across the cell; Aquaporin a water channel proteins involved in the movement of water through membranes, Osmoprotectants responsive enzymes (The enzymes required for the biosynthesis of various osmoprotectants (sugars, Proline, and Gly-betaine), proteins responsive to protect macromolecules/membranes (LEA protein, osmotin, antifreeze protein, chaperon, and mRNA binding proteins), Proteases for protein turnover (thiol proteases, Clp protease, and ubiquitin) and the enzyme responsive for detoxification (Glutathione S-transferase, soluble epoxide hydrolase, Catalase, Superoxide dismutase, and Ascorbate peroxidase).

In the second one is group of gene under stress are mostly regulatory proteins in which signalling component that regulate gene expression in response of stress including protein kinases and transcription factors (TFs; Regulatory proteins which involve in the regulation of signal transduction; DREB, MYB, MYC, bZIP, NAC etc) which considered as master regulators. Rabbani and his co-workers identified various regulatory genes which induced by cold, drought, and high salinity (Rabbani et al. 2003). In this review we summarized the abiotic stress responses mediated by regulons (Transcriptional network) and main focus is on role of regulons (Transcription factors) in abiotic stress responses and their role in transgenic plants. Genes induced during stress conditions are thought to function not only in protecting cells from water deficit by the production of important metabolic proteins but also in the regulation of genes for signal transduction in the water-stress response. Thus, these gene products are classified into two groups: group first consist of function protein and second is regulatory protein (Figure 2). The product of functional protein helps to maintain the cell damage while the transcription factors gene product mediate the signal transduction for the expression of stress responsive downstream genes.

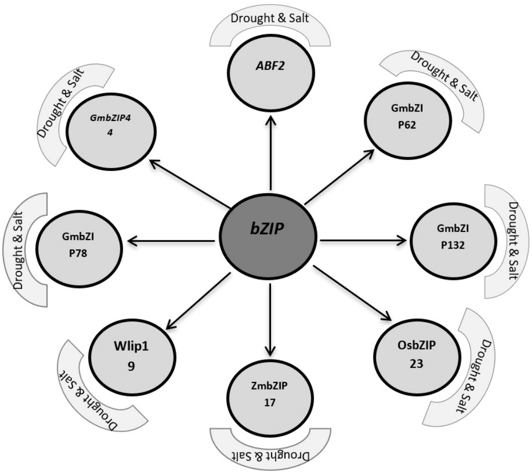

Figure 2. bZIP stress (drought and salt) inducible transcription factors in different plant. A family of bZIP induced the following genes under the influence of abiotic stress of drought and salt.ABF2 (Choi et al., 2000), GmbZIP44, GmbZIP62 & GmbZIP78 (Liao et al., 2008c), GmbZIP132 (Liao et al., 2008a), Wlip19 (Kobayashi et al., 2008), ZmbZIP17 (Jia et al., 2009) and OsbZIP23 (Park et al. 2015).

3.Transgenic Approaches to Improved Tolerance to Abiotic Stress

Abiotic stress is the major cause of crop damage word wide. Plants exposed continuously under abiotic stress condition and evolve/ express the gene against to them. Expressed genes under the abiotic stress condition can be used as tolerant genes to various plants. Every year various successful attempts have been made to utilizes these genes (functional or regulatory) as a tolerant gene in several plants. In this concern Regulons, Transcription factor, Osmolytes and ROS is fascinating tools to generate abiotic stress tolerance plant/crops (Wani et al., 2016). Transgenic approach is the best methods to counter abiotic stress using suitable stress tolerant gene from any vital source and ligated in any important agricultural crop (Bajaj and Mohanty, 2005). Various efforts have been made and varieties of tolerant plants have been generated after the field trial (Bajaj and Mohanty, 2005). Further constitutive expression of certain stress tolerance gene may effects the normal development of transgenic plant. Thus it is desirable to generate transgenic plant that generates high level of proteins only under stress condition. Many genes and their product have been identified when plant induced to various abiotic stresses. Some of these useful genes gene have been implicated in stress tolerance plant (Wani et al., 2016). Evidence suggested that the abiotic stress induced genes or protein with known function have been exploited for producing stress tolerant transgenic plants. In transgenic plants gene encodes reactive oxygen species or antioxidant, protective protein for cellular machinery, membrane protein or ion transporters, transcription factors and osmolytes.

Osmolytes is important organic compounds that maintain the integrity of cell fluid using ionic potential of biological fluid. It uses to produces transgenic to enhance tolerance to osmotic stresses in plants. Compatible solutes are small electrically neutral molecules that stabilize protein and membrane under the different stresses and accumulate in high level without disturbing intracellular biochemistry. They synthesized in response to osmotic stresses. Osmoprotectants differentiated on the basis of chemical composition; proline (amino acid), trehalose (Non-reducing sugar) and betaine (amino acid derivatives). Osmolytes behave as osmoprotectants and maintain the osmotic adjustment which prevent the cells damage under the abiotic stress (Mansour and Ali, 2017) Under stress condition conditions plant produces ROS (Reactive Oxygen Species). It accumulates during the abiotic stress condition and responsive to oxidative damage and death of cells. The production of ROS in plant have various function like as in signal transduction to, maintain the plant integrity during stress along with this function it is also responsive to produce toxic byproducts in metabolic pathway. The key member of ROS is super oxide, hydroxyl radical and hydrogen peroxide. Increase concentration of ROS to inhibit the ability to repair damage of photosynthesis (photo system II) and failure to recover the membrane and macromolecules (Huang et al., 2019). Plant has developed several antioxidant systems to scavenge these toxic compounds. Enhancement of antioxidants in plant increase tolerance to different stresses such as Catalase, superoxide dismutase (SOD), superoxide dismutase (SOD), Ascorbate peroxidase (APX), glutathione reductase (GR) and glutathione synthase. Recent evidence suggested that ROS is not only cell damage factors but also have various functioned to maintain the plant vegetative structure (Huang et al., 2019).

Plants express various genes which responsive to the build-up of stress related protein. Heat shock protein and late embryogenesis abundance accumulate under various abiotic stresses (Water, Salinity and extreme temperature). They stress inducing protein behave as a molecular chaperon, and function as a development and degradation cellular processes. LEA Protein (Late Embryogenesis Abundant) expresses in water deficit plants either it comes from drought, salt, cold and osmotic stresses. The over expression of heterogonous LEA gene Rab16A from rice enhance enhanced salinity stress tolerance in tobacco plant (Magwanga et al., 2018; Ganguly et al., 2012)

A key policy to achieving tolerance to abiotic stress is to help plants to maintenance and re-establish of cellular ion homeostasis during stress conditions. The membrane protein, water channel protein, and transport protein responsive to osmotic stress tolerance. Under drought and salt stress water channel protein maintain the cellular water transport. SOS1 and *GhSOS1* gene encode plasma membrane Na^+/H^+ antiporter which improve salt tolerance in transgenic Arabidopsis (Chen et al., 2017). In a transgenic approach a single gene encoding a single specific protein is not enough to maintain the molecular cellular disturbances to cope up from the stresses (Bohnert et al., 1995). The above facts designate to better transgenic to enhance multiple stress tolerance by a gene which transcribe a stress inducible transcript which encode a transcription factor that maintain the regulation of various stress inducible genes (Ganguly et al., 2012).

. In plants TFs have been employed to manipulate various type of metabolic developmental and stress responsive pathways. In plant various type of transcription factor that have great role in various stresses and tag into several large transcription families. Few transcription act as common player for different stresses it reveals that the stress responsive gene share transcription factors to maintain the physiological and molecular status of plants. This review emphasize that regulon be made up of number of genes carrying a similar cis-acting element (AREB/CBF, DREB, NAC, MYB) thus these particular set of genes are induced by the various abiotic stresses. (Kimotho et al., 2019).

4. Roles of Regulon in Abiotic Stress Responses

The words regulons principally associated with transcription factors in which a transcript regulate a group of gene or a group of gene is controlled by a certain transcription factors (TFs) that transcript is known as regulons (Saibo et al., 2009). TFs (Transcription factors) (TFs) are those proteins molecules which binds to specific sites on a DNA which leads to up regulate or down regulate the expression of certain genes. Various regulons discovered in plants having an important role in plant development as well as in abiotic stresses (Wang et al., 2016). Plant consist a large number of transcription factors in its own genome; for example, *Arabidopsis* and *Oryza sativa* were reported 1500 and 2025 transcription factors respectively (Riechmann et al., 2000; Gao et al., 2006). Under the abiotic stress condition various gene express either Functional or regulatory. Regulatory genes consist of transcription factors which bind to the promoters of *cis*-elements and decide the fate of stress inducible genes. Under the abiotic stress condition the set of genes regulated at transcriptional level by the signal cascade binding of transcription factors to upstream regions of genes is known as *cis*-regulatory elements (Javed et al., 2020). Evidence suggested that various abiotic stress responsive transcription factors and its binding motif have been characterized and identified in plants (Yoon et al., 2020). Abiotic stress signals in plants divided in to two pathway on the basis of cis regulatory elements; ABA dependent pathways and ABA independent pathways. Study of transcriptome in plants suggests that there are numerous pathways that autonomously respond to environmental stresses either on ABA dependent or independent manner this suggest that stress tolerance at transcriptional level is a highly multifaceted gene regulatory system (Fernando and Schroeder, 2016).

ABA dependent process defines by the accumulation of Phytohormones Abscisic Acid (ABA) under the abiotic stress conditions. The Phytohormones Abscisic Acid (ABA) has grate role in signal transduction in plant gene regulation either in development process or in stress condition. It is a messenger which maintains the fine tuning of adoptive responses (drought, salt and cold) of plants under the different abiotic stress condition the concentration of abscisic acid increases and initiate the signal transduction. The gene regulated by ABA contains ABRE: ABA responsive elements a five to six nucleotide sequence promoter region which have ability to bind transcription factors responsive to ABA regulated gene. Evidence suggested that in *Arabidopsis thaliana* rd22 drought responsive gene expressed under the situation of ABA dependent manner. The promoter region of rd22 gene has conserved motif of DNA binding protein. Under the drought condition increases the ABA in plants and triggers the stress responsive genes AB12, rab18 and rd29B (Saez et al., 2006; Kim et al., 2010). ABA independent process define the absence of accumulation of phytohormones Abscisic Acid (ABA) in these condition various abiotic stress genes induces apply the key rules of ABA independent signal transduction pathway. Evidence suggested this in *Arabidopsis* mutant's and prove that there is no need of ABA for their expression of rd29A, kin1, cor6.6 (kin2), and cor47 (rd17) under cold or drought stress conditions but do response to exogenous ABA (Shinozaki et al., 2003). The ABA independent responsive genes rd29A, kin1, cor6 and cor47 on promoter region contain DRE elements (Dehydration Responsive Elements) which recognized an alternative protein for regulation of abiotic stress genes or plant development responsive genes. Rd29A gene express under drought, salt and cold stress and research reveals that the promoter of this gene contains DRE element (Dehydration Responsive Elements) and it is not similar as ABRE; Abscisic Acid Responsive Element. Evidence suggested that Cor15 gene induced under the cold stress condition and the express gene contain promoter DRE elements (TGGCCGAC motif) which reveals the ABA independent signal transduction of expression of gene (Khan, 2011). Evidence suggested that various abiotic stress gene like as drought inducible gene not expressed in ABA or cold stress not follow the ABRE they are rd19 and rd21 (Nakashima et al., 1997). Both ABA dependent and independent pathway influence regulons using the key of transcriptional response under drought or salt stress condition (Nakashima et al., 2009). In the following section of review we will discuss brief about drought and salt responsive regulons.

4.1. AREB/ABF Regulon

Abscisic acid (ABA) acts as a key signal molecule under different abiotic stress conditions. When plants exposed under abiotic stresses sudden ABA content increased and it leads to expression of various genes using ABRE binding protein (ABA responsive element binding protein), AREB/ABF (ABRE Binding Factor) transcription factors. Evidence suggested that AREB/ABF regulons has vital role in ABA dependent regulations of genes (Yoshida et al., 2010). Exogenous use of ABA also stimulates a numerous of genes. AREB/ABF act as a regulon because regulate various gene under different abiotic stress condition using ABA dependent manner. All the ABA inducible genes contain a conserve *cis*-acting element of ABRE. Yamaguchi and his o workers demonstrate the Arabidopsis contain ABRE binding protein in bZIP type of transcription factor (Shinozaki et al., 2003). In Arabidopsis bZIP transcription factors were identified which reveals the protein of ABRE which involve in drought and salt stress (Figure 2) (Kim et al., 2011). This is to investigate that under the ABA and osmotic stress condition AREB1/ABF2, AREB2/ABF4, and ABF3 were showing the gene expression in vegetative tissues of plants (Fujita et al., 2007). In normal condition of plants tissue specific expression of AREB/ABF genes are redundant. Evidence suggested that in Transgenic Arabidopsis ABA inducible gene and AREB1 were expressed in stress condition (Furihata et al., 2006). Study reveals that AREB expressed tissue specifically at germination stage *ABI5* and *EEL* were expressed while *AREB1/ABF2*, *AREB2/ABF4*, and *ABF3* were mainly expressed in vegetative tissues (Yoshida et al., 2010; Zandkarimi et al., 2015). The role of ABFs has varies according to stresses such as ABF1 (Cold) ABF2 (Salt, drought and heat) ABF3 (Salt) and ABF4 (Cold, salt and drought) (Kim et al., 2004; Yoshida et al., 2010). The regulation of *OsABI5* enhances in the presence of ABA and salinity stress but down regulate under the condition of drought and cold stress (Nakashima at al., 2009). In rice TRAB1 were showing the homology with Arabidopsis AREB2/ABF4 it express during the regulation of ABA. Evidence suggested that the ABA insensitive, ABA-deficient & ABA hypersensitive mutant of Arabidopsis need to ABA for activation of respective transcription factors *abi1, aba2 & era1* respectively (Uno et al., 2000). The function of several abiotic stress-inducible bZIP-type TFs has been studied in transgenic Arabidopsis (Table 1) and rice (Table 2). Expression of Osb- ZIP23 was induced by drought, high salinity and ABA (Xiang et al. 2008) on this behalf the generation of transgenic rice using Osb-ZIP23 as a tool, exhibited improved tolerance towards drought and high-salinity stresses. Rice transcription factor ABI5 obtain from rice panicles was down-regulated by drought and cold stresses in rice seedlings. Transgenic rice plants over expressing OsABI5 showed high tolerant to salt stress (Zou et al., 2008).

4.2. NAC Regulon

NAC word originated from the three defined transcription factors in which N comes from NAM (No Apical Meristem), A indicate ATAF1-2 (Arabidopsis thaliana Activating factor) and C come from CUC2 (cup-shaped cotyledon). NAC TFs isolated at first from Arabidopsis. NAC is one of the largest TFs in Plant genome, with 163, 152, 151,117, 79 and 26 members in Poplar, Soybean, Rice, Arabidopsis, Grape and citrus respectively (Nuruzzaman et al., 2010). NAC gene protein contain C & N terminal domain where N represents the DNA binding region (Hu et al., 2008). Several workers examined that NAC TFs has a great importance not only in plant developmental programme but also in disease resistance and various environmental stresses. Investigation reveals that several NAC stress-inducible genes along with drought tolerance in the transgenic lines (Takasaki et al., 2010). In rice and Arabidopsis numerous NAC genes are reported to be induced by drought, high salinity, and cold stresses. ANAC055, and ANAC072 TFs regulate expression of a salt- and drought induced gene in Arabidopsis (Lu et al., 2018). In Arabidopsis ATAF1 and AtNAC2 encodes a type of transcription factor which is responsive for drought and salt respectively (Lu et al., 2007; He et al., 2016) while AtNAC19, AtNAC55 and AtNAC72 is responsive for drought and salt stress. We summarized some stress responsive NAC transcription factor is in Figure 2 which might a good player in drought and salt

Table 1. Transgenic Arabidopsis plant using different stress (Salt and Drought) inducible Transcription factors.

Transgenic plant	Transcription factor Family and gene in Transgenic approach		Stress tolerance	References
Arabidopsis	bZIP	ABF2	Drought	Kim et al. (2004); Lee et al. (2010)
		ABF3	Drought	Kang et al. (2002; Yoshida et al. (2010)
		ABF4	Drought	Kang et al. (2002); García et al. (2018)
		GmbZIP44	Salinity	Liao et al., 2008c); Cao et al. (2018)
		GmbZIP62	Salinity	Liao et al., 2008c; Alves et al. (2015)
		GmbZIP78	Salinity	Liao et al., 2008c); Wang et al. (2018)
		GmbZIP132	Salinity	Liao et al., 2008a); Hossain et al. (2015)
		AtbZIP60	Salinity	Fujita et al. (2007); Tang et al. (2012)
	MYB	MYB15	Drought, Salinity	Ding et al. (2009); Hou et al. (2018)
		OsMYB3R-2	Drought, Salinity	Dai et al. (2007); Yang et al. (2012)
		OsMYB4	Drought	Mattana et al. (2005); Raldugina et al. (2018)
	CBF/DREB	AtDREB1A	Drought	Liu et al. (1998); Oh et al. (2005)
		AtDREB1A	Drought	Rehman & Mahmood (2015)
		AtDREB2A	Drought	Rehman & Mahmood (2015)
		AtCBF1	Salinity	Ma et al. (2015)
		OsDREB1A	Drought, Salinity,	Dubouzet et al. (2003)
		OsDREB2B	Drought,	Matsukura et al. (2010); Joshi et al. (2016)
		OsDREB1F	Drought, Salinity,	Rehman & Mahmood (2015)
		ZmDREB2A	Drought	Qin et al. (2007)
		HvDREB1	Salinity	Xu et al. (2009)
	NAC	AtNAC2	Drought	Tran et al. (2004)
		AtNAC019	Drought	Tran et al. (2004)
		AtNAC055	Drought	Tran et al. (2004)
	WRKY	OsWRKY45	Drought, Salinity	Qiu and Yu (2009)
		GmWRKY54	Drought, Salinity	Tripathi et al. (2014)

tolerant stress. SNAC1 is the type of rice NAC regulon induces transcription factor which expressed only in guard cell under dehydration condition and is responsible for stomata closure (Hu et al., 2006; Tran et al., 2004). In the rice, NAC Regulon encode a kind of NAC transcription factor which responsive for multiple abiotic stress tolerance such as drought, salt and cold they are NAC6 and NAC2. We summarized NAC TFs having role in drought and salt in different plants (Figure 3). NAC regulon induced the following regulatory genes under the influence of abiotic stress of drought and salt. AtNAC019 (Tran et al., 2004), AtNAC055 (Tran et al., 2004), AtNAC072 (Tran et al.,

Table 2. Transgenic rice plant using different stress (Salt and Drought) inducible Transcription factors

Transgenic plant	Transcription factor Family and gene in Transgenic approach		Stress tolerance	References
Rice	bZIP	OsABI5	Salinity	Zou et al. (2008)
		OsbZIP23	Drought, Salinity	Xiang et al. (2008)
		OsAREB1	Drought	Jin et al. (2010)
	CBF/DREB	AtDREB1A	Drought, Salinity	Oh et al. (2005)
		OsDREB1F	Drought, Salinity,	Rehman & Mahmood (2015)
		OsDREB1G	Drought	Chen et al. (2008)
	NAC	SNAC1	Drought, Salinity	Hu et al. (2006)
		OsNAC6	Drought, Salinity	Nakashima et al. (2007)
		ONAC045	Drought, Salinity	Zheng et al. (2009)
	Others	HARDY	Drought, Salinity	Karaba et al. (2007); Guo et al. (2017)

2004), SiNAC (Puranik et al., 2011), GhNAC4 (Meng et al., 2009), SNAC1 (Hu et al., 2006), SNAC2 (Hu et al., 2008); Rachmat et al., 2014) (Figure 3).

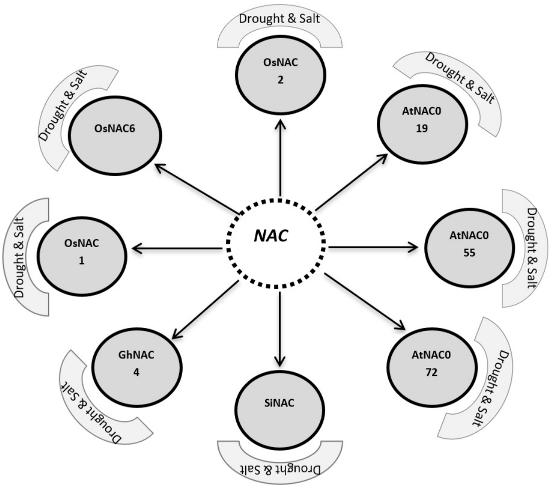

Figure 3. NAC gene family stress (drought and salt) inducible transcription factors in different plant. NAC regulon induced the following regulatory genes under the influence of abiotic stress of drought and salt. AtNAC019, AtNAC055 & AtNAC072 (Tran et al., 2004), SiNAC (Puranik et al., 2011), GhNAC4 (Meng et al., 2009), SNAC1 (Hu et al., 2006), SNAC2 (Hu et al., 2008), OsNAC6 (Nakahsima et al., 2007; Rachmat et al., 2014)

4.3. MYB Regulon

Regulon MYB/MYC found in both plant and animal. This is the largest TF found in plants consisting of approximately one-eighth of the TFs in Arabidopsis and one thirty six in rice. It belongs to ABA-dependent pathway group. The story of MYB begins first in avian myeloblastosis virus (AMV). The first report of plant MYB gene was in *Zea mays* as C1 which encode a c-MYB like TF that involved in Biosynthesis of anthocyanin (Paz-Ares et al., 1987). Plant MYB genes are more complex and diverse then the mammalian MYB genes and only a few of them exhibited constitutive and ubiquitous expression in Arabidopsis (Schmid et al., 2005). MYB TFs has various roles in plant development (seed, flower and meristem development) cell cycle, stress and in defense response (Ambawat et al., 2013). MYC and MYB TFs accumulate only after ABA accumulation. AtMYB2 and AtMYC2 are dehyhdrin and ABA responsive myb coding transcription factor which function as cooperatively as transcriptional activators and induced *rd22* (Abe et al., 2003). During the peptide sequence of MYB it was found that helix turn helix motif conformation intercalating in the major groove of the DNA (52 amino acid residue). Domain of MYB consists of one to three repeats. MYB family divided on the basis of number and position of MYB domain repeats it is a family of proteins that include the conserved MYB DNA-binding domain. Plants contain a MYB-protein subfamily that is characterized by the R2R3-type MYB domain (Stracke et al., 2001). On the basis of domain repeat MYB distinguish in following three groups; first R2R3-MYB second R1R2R3-MYB and third is MYB-related proteins (Stracke et al., 2001). It is evident that MYB is responsive for abiotic stress tolerance in different plant, MYB regulon encode MYB transcription factor which is drought and salt stress responsive in *Arabidopsis, Glycine max* and *Oryza sativa* (Figure 4) (Ambawat et al., 2013; Ding et al., 2009; Liao et al., 2008b; Dai et al., 2007). Transgenic Arabidopsis (Table 1) is also reported that using MYB15, OsMYB3R-2 and OsMYB4 (Zhang et al., 2018; Mattana et al. 2005).

4.4. DREB Regulon

Dehydration responsive element binding protein (DREB) which belongs to Ap2 transcription factor family that is responsive to induction of stress related genes. Dehydration responsive gene expressed when DREB related DNA binding protein binds on the *cis* elements of those genes

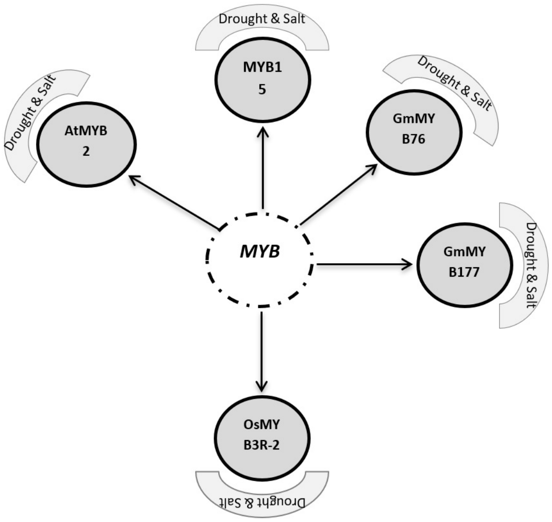

Figure 4. MYB stress (drought and salt) inducible transcription factors in different plant. MYB stress (drought and salt) inducible transcription factors in different plant.OsMYB3R-2 (Dai et al., 2007), AtMYB2 (Abe et al., 2003), GmMYB177 & GmMYB76 (Liao et al., 2008b) and MYB15 (Ding et al., 2009)

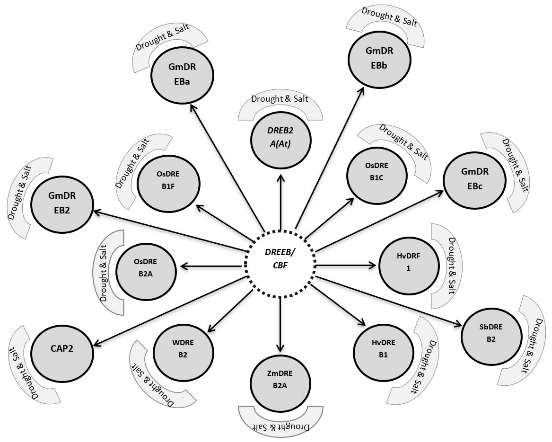

Figure 5. DREB gene family express under drought and sat stress condition in different plants. GmDREBa, GmDREBb, GmDREBc (Li et al., 2005), GmDREBa (Chen et al., 2007), CAP2 (Shukla et al., 2006), DREB2A (Liu et al., 1998), OsDREB1C & OsDREB2A (Dubouzet et al., 2003), OsDREB1F (Rehman & Mahmood, 2015), HvDRF1 (Xue and Loveridge, 2004), HvDREB1 (Xu et al., 2009), ZmDREB2A (Qin et al., 2007), SiDREB2 (Lata et al., 2011),

which contain DRE core sequence 5'-TACCGACAT-3' or A/GCCGAC. Basically the presence of these core sequences is responsible for abiotic stress and first report about these sequences was in *Arabidopsis* of rd29A a drought responsive gene (Yamaguchi-Shinozaki & Shinozaki 2005). Two different type of DREB is identified for different stress these are DREB1 and DREB2. DREB1A, DREB1B and DREB1C encode a protein which is responsive for cold inducible gene expression even itself these three DREBS expressed in cold stress. The responses of DREB2 is different from DREB1, researcher found that DREB2A and DREB2B expressed under drought and salt stress conditions as summarized in table 1. DREB gene family express under drought and sat stress condition in different plants (Figure 5) i.e. GmDREBa, GmDREBb, GmDREBc (Li et al., 2005), GmDREBa (Chen et al., 2007), CAP2 (Shukla et al., 2006), DREB2A (Liu et al., 1998), OsDREB1C & OsDREB2A (Dubouzet et al., 2003), HvDRF1 (Xue and Loveridge, 2004), HvDREB1 (Xu et al., 2009), ZmDREB2A (Qin et al., 2007), SiDREB2 (Lata et al., 2011).

In plant kingdom AP2 DNA binding domain conserve in DREB transcription factors. Domain conformation defines on the basis of alpha and b pleated sheets along with the Arg and Trp amino acid residue. In the DNA binding domain, two functional amino acid Valine and Glutamic acids founds which provides the place for the DNA binding of DREBS Domain consist of amino acid region act as a nuclear localization signal (NLS). Research report suggest that DREB transcript expressed tissue /organ specifically because when Arabidopsis plant exposed to salt it showed good expression in Root in place of leaves. In the table 1 & 2 we summarized stress responsive DREB transcription factor in various plants. Transgenic Arabidopsis is reported using DREB stress responsive regulon from different plant, these DREB transcription factor are: OsDREB1A, OsDREB2B, OsDREB1F, ZmDREB2A, HvDREB1, AtDREB1A, AtDREB1A, and AtDREB2A (Rehman & Mahmood 2015).

5. Other Regulons

The transcription factor involves in abiotic stress responses other than the above describe regulon. These include Homeodomain transcription factors: HOS9 and HOS10 responsive for cold stress, AP2/ERFs (AP37 and AP59) is responsive for drought tolerance and HDG11 which is responsive for dehydration in plants. C2H2 zinc fingers and WRKY are also important role in stress tolerance. HARDY transcription factor is responsive for salt tolerance in rice plant (karaba et al., 2007). C2H2 Zinc finger consist of ZFP252, ZFP245 and ZFP179 transcription factor gene reported about abiotic stress responses. Over expression of ZFP179 enhance salt tolerance which increases the levels of proline (Cheuk and Houde, 2016). WARKY is another important name in the list of stress associated transcription factor in which OsWARKY45 showed good expression under drought, salt and temperature (Qiu and Yu, 2009). Over expression of OsWRKY45-2 lead to increased salt stress tolerance. OsTIFY11 gene is responsive for multiple stresses: drought, salt and cold (Tao et al., 2011; Chini et al., 2017).

6. Conclusion and Future Perspectives

Plant is sessile in nature it can't move from one place to other for their defense that's why they evolve a mechanism to prevent from stress in which regulons has a great importance. When plant exposed to abiotic stresses: drought, salinity, cold, heat and mechanical so many transcripts up regulated and their product help to survive the plant under adverse condition. This review summarizes the role of regulons and plant TFs namely; ABRE, MYC/MYB, CBF/DREBs and NAC that regulate numerous trauma responsive gene expression. They show a vital role in tolerance to abiotic stresses. Population is growing rapidly although limited land of agriculture filed and abiotic stresses is major constrain in the field of crop production so we need to improve the crop productivity and the yield. Evidence suggested that regulons and transcription factors are better transgenic tools. These Regulons can be genetically engineered to produce transgenic with higher tolerance to drought, salinity, and other stresses.

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