

GENETIC RESPONSE OF GROWTH PHASES FOR ABIOTIC ENVIRONMENTAL STRESS TOLERANCE IN CEREAL CROP PLANTS

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The yield potential and quality of main cereals crop plants including maize, wheat, rice and barley have improved through breeding and introduction of transgenic crop plants from last three decades. There has been intensive research for the improvement of resistance against biotic and abiotic environmental conditions to safe the potential of cereal crop plants. Among abiotic stresses drought and heat are two most important abiotic factors which caused major loss in yield and quality of crop plants. The heat stress leads towards drought due to loss of water from soil and plant surfaces, therefore drought and heat caused combined adverse effects on plant morphological, physiological and yield traits which leads to reduce crop plant potential. There has been always an interaction among the environmental conditions and crop plants to produce grain and restore productivity. The drought and heat stress caused changes at cellular level, molecular changes and gene expression changes in cereals at various vegetative and reproductive stages/phases of crop growth and development. A large number of genes have indentified in cereals which switch up-regulated and down-regulated during drought and heat stress conditions. However, there is a need to improve resistance in cereals at gene level to maintain potential of yield and quality under abiotic stress conditions like drought, heat, salinity, and cold.

Keywords: drought, heat, maize, wheat, rice, reproductive phase, plant and environmental interactions

INTRODUCTION

From studding the crop plant evolution, it has been found that the reproduction and the survival of plants even under stressful conditions become possible because of the evolutionary changes in the crop plants. On the other side due to breeding efforts the yield rather than survival have been made into focal point of crop breeders, especially in cereal improvement. Yield safety attained

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more and more importance due to the pervasiveness of high yield giving cereal cultivars in agriculture. The productivity and growth of some main crops like cereals is inhibited somehow by some abiotic stressful conditions such as water scarcity and high temperature. Both stresses took place at the same time so the basic requirement of cereal breeding has been always the main objective to develop such cultivars that can endure or tolerate the both stress environmental conditions (TESTER and BACIC, 2005; HONG-BO, 2006; YOUNIS *et al.*, 2014). The grain development started with double fertilization of male and female gametes. However, it may be absolutely not vital to spotlight those processes that were concerned within the development of female and male gametes also those which ensure the fusion of both male and female gametes so that the development and growth of embryo and reproductive structure called endosperm has been remained uninterrupted (BOYER and WESTGATE, 2004; YANG and ZHANG, 2006). The abiotic stress has a negative impact on whole growth and developmental processes which caused the decrease in grain yield and also inhibit the growth of crop plants (MAHAJAN and TUTEJA, 2005; FAROOQ *et al.*, 2009; GILL and TUTEJA, 2010). The yield of modern cultivars has always been badly influenced due to the harsh environmental conditions which became the cause for breeding against specific environmental conditions or the life habitats. The ultimate yield is always qualitatively and quantitatively which always influenced by the grain filling process, the build-up of reserve plant nutrients to develop a mature grain as they are always highly terribly sensitive to setting conditions (YANG and ZHANG, 2006; MIR *et al.*, 2012; GUPTA and HUANG, 2014). Dependency of cereal reproduction and realization of yield potential of a given vascular plant is not solely depends on the strain sensitivity of procreative and grain-filling steps however conjointly the general plant growth and development. The formation of generative organs and final yield has been powerfully plagued by the economical chemical process and stem reserve accumulation throughout the vegetative section (BLUM, 1998; ARAUS *et al.*, 2002; CATTIVELLI *et al.*, 2008). Consequently the yield safety in cereals has been improved by deliberating the whole method (biological process) process, from grain to grain and appropriate conditions might target many organic process stages (TRIBOI and TRIBOI-BLONDEL, 2002; GOODING *et al.*, 2003; ERCOLI *et al.*, 2008).

Plant response for drought

The worldwide food production has been greatly restricted by the issues, heat and drought. The most important world concern has been to supply drought tolerant crop plant cultivars with higher water use efficient plant. The population rate has been increasing and water sources for crop production fail to satisfy the demand. During last few decades, short and extreme periods of drought severally have been seen within the productive agricultural regions (SHAO *et al.* 2008; ATKINSON and URWIN, 2012; SUZUKI *et al.*, 2014). The plants have created their survival and reproduction straightforward by evolving some appropriate mechanism changes for living under temporary water limitation conditions. Escape, turning away and tolerance methods were subdivisions of plants resistance to heat and drought (CHAVES *et al.*, 2003; CATTIVELLI *et al.*, 2008; CHAVES *et al.*, 2009; ASIF *et al.*, 2020). Escape methods could depends upon the successful reproduction before the start of severe environmental stress which means that the life cycle completed in short interval of time, the rate of crop plant growth or the economical storage in sense of grains and uses of reserves for grain production in plants. Dehydration turning away is

to take care of high plant water standing throughout stress that will ensue to reduced water loss from their body through various means (trichomes, caused by stomata closure, reduced leaf space and the senescence of all older plant leaves etc.) it may also be through increase water uptake by roots (by enlarged root length and increase root growth and development) (HASANUZZAMAN *et al.*, 2013b; REJEB *et al.*, 2014; SUZUKI *et al.*, 2014). Lastly, tolerance to low water and osmotic potential (to maintain physiological processes of plant at highly restricted water availability and/or the morphological and physiological recovery of crop plants under low water availabilities to continue growth and development of crop plants under stressful environmental conditions) could include diffusion and osmosis changes, however may additionally be the results of rigid plant cell walls with higher osmotic pressure. The short removal of reactive O₂ species or ROS created as a result of disturbed in metabolism could also be coupled with drought tolerance in plants (PETROV *et al.*, 2015; RAMEGOWDA and SENTHIL-KUMAR, 2015; SEWELAM *et al.*, 2016; NAZIR MI, 2020).

The plants respond to low water or drought stress conditions at the cellular, molecular, physiological and morphological levels (Figure 1). The crop plant response for drought always depends on the genotype and species with presence or absence of stress tolerance genes in crop plants (RAMPINO *et al.*, 2006; FALQUETO *et al.*, 2009; BOWNE *et al.*, 2012) along with the severity of stress (ARAUS *et al.*, 2002; FAROOQ *et al.*, 2009) and length of water deficit or drought stress conditions (BARTELS and SOUER, 2004; FUJITA *et al.*, 2011; SANCHEZ-BEL *et al.*, 2012), the crop plant age, growth and developmental stage of crop plant also showed response for drought (BORSANI *et al.*, 2005; ZHU *et al.*, 2005), it also depends upon the type of plant organ and cells which showed effects of drought (COMINELLI *et al.*, 2005; COMINELLI *et al.*, 2008; REJEB *et al.*, 2014) and the sub-cellular level compartments of cells (BATTAGLIA *et al.*, 2007; CAFFALL and MOHNEN, 2009; MEIR *et al.*, 2010). The figure 1 shows the reaction or response of plants organs to the limited water supply that highlights that hormone abscisic acid (ABA) is the major long term signal operating under drought stress (BRAY, 2002; VERSLUES *et al.*, 2006; ZHANG *et al.*, 2006). The increased root hydraulic conductivity and maintenance of root growth may be because of the high amount of ABA in roots which is produced due to soil drying. An enlargement of water shortage and increase in water uptake in plant shoots was postponed by these two processes (VERSLUES and BRAY, 2005; FUJII *et al.*, 2007; TUBEROSA, 2012). The dehydration of tissues of leaf was prevented by ABA which in turn delivered in xylem to crop plant shoot where it results in stomata closure and the leaf expansion decreases, mobilization of reserve nutrients under drought or water deficit conditions are because of the involvement of ABA (XIONG and YANG, 2003; YANG *et al.*, 2006; CHINNUSAMY *et al.*, 2008). Plant photosynthesis and water status during grain filling may be lessened because of stress that prompt the conversion of stem reserves or nutrients into soluble plant sugars and transfer or mobilization of plant sugars into the grains of crop plant (BLUM, 1998; WANG *et al.*, 2007). The development of plants is influenced by the regulation of genes expression which are involved in the control mechanism of carbohydrate or plant sugars metabolic enzymes activity and cell division under drought or water deficit environmental conditions and this was because of the transfer of xylem-borne abscisic acid to the reproductive structures of plant (LIU *et al.*, 2005; ZARGAR *et al.*, 2011; LITTELL *et al.*, 2016). Protein phosphatase/kinase cascade interacting with

Ca^{2+} was involved in the abscisic acid signal transduction pathway (BRAY 2002; VERSLUES and BRAY, 2005).

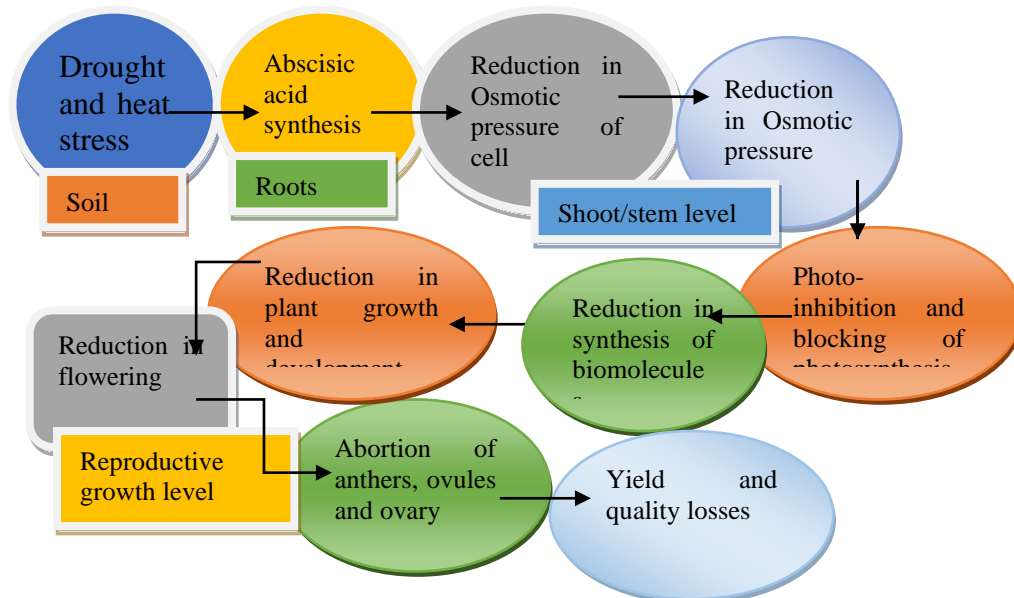


Figure 1. The response of plant under the of drought and heat stress

An environment signal such as drought is always triggered by the signal of specific receptor(s). The response of plants to drought may depends upon various processes or factors such as bound water, water status, hormones like ABA and cell turgor pressure, alteration in plant cell membranes, and stomata opening and closing etc. (VERSLUES and BRAY, 2005; CHAVES *et al.*, 2009; KRASENSKY and JONAK, 2012). The water loss in *Arabidopsis* found to be related by the potential 'osmosensor' that was produced by a transmembrane receptor called histidine kinase receptor (ATHK 1) and its related proteins (URAO *et al.*, 1999; TESTER and DAVENPORT, 2003; VANCE *et al.*, 2003). Plant cells can detect or sense water scarcity by various other processes and mechanisms that were still unknown (CHAVES *et al.*, 2003; NEVO and CHEN, 2010; TUBEROSA 2012; MUHAMMAD *et al.*, 2020). Different cellular signal transduction pathways were triggered if water loss was sensed or observed by the cells. In this way the conversion of physical stress can be done in to biological response. It was promising that the signaling of water loss was also a complicated phenomenon in plants and it was seen under the light of density of cellular, molecular and physiological reactions to drought. The figure 2 shows some of the most identified components of plant cellular adaptation to increase temperature and water loss. The signal transduction cascades involving proteins like dephosphorylation and phosphorylation which mediated by phosphatases and kinases up-regulated through water stress started through the stimulation of the osmosensor like proline or other drought sensing processes and mechanisms of

defense (BRAY, 2002; MISHRA *et al.*, 2006; URAJI *et al.*, 2012; MASOOD *et al.*, 2020). The integration of different signaling pathways may be mediated by the transition in the calcium concentration of cytoplasm (GUPTA and KAUR, 2005; MIAO *et al.*, 2006; VISHWAKARMA *et al.*, 2017). The water stress related signaling is related to different Ca²⁺ dependent protein kinases (KLIMECKA and MUSZYNSKA, 2007; CAMPO *et al.*, 2014). The drought activated kinase cascades used to conduct the phosphorylation (GUPTA and KAUR, 2005; KAUR *et al.*, 2005; SINGH *et al.*, 2012) and activation of transcriptional factors which regulate stress responsive genes expression under drought stress (NAKASHIMA and YAMAGUCHI-SHINOZAKI, 2006; KANCHISWAMY *et al.*, 2010). Hundreds of genes which encode transcription factors were suppressed or persuaded by genome-wide transcriptome analysis (CHEN and ZHU, 2004; ASHRAF *et al.*, 2008; DOWNS *et al.*, 2013). There are various genes which have been detected among the groups of genes for transcriptional factors regulated genes (1) specifically by the abiotic stress known as class I and (2) by both abiotic and biotic stresses group as class II in *Arabidopsis thaliana* have been discovered. Stress resistance and tolerance are regulated at the transcription level through extremely complicated genes expression and regulatory networks also the expressional patterns of these transcriptional factors are highly complicated (VANDERAUWERA *et al.*, 2005; JOURNOT-CATALINO *et al.*, 2006; SREENIVASULU *et al.*, 2007). Different induced genes by abiotic stresses including drought have been detected by experiments like micro-array technology and those genes were classified or categorized into two major groups of genes. The first group of genes encoded the products which directly protects crop plant organs and cells against the all types of stresses, while on the other hand the 2nd group regulates signal transduction and gene expression under all types of abiotic stresses and crop plant responses (SREENIVASULU *et al.*, 2007; MITTLER and BLUMWALD, 2010; HUANG *et al.*, 2012; MIR *et al.*, 2012).

The one of useful and effective method to detect downstream elements and gene interactions is to show the complex stress related transcription reactions in an accurate knockout mutants or transgenic plants. The stress responsive gene which coded for dehydration responsive element binding protein 1a (DREB1a) was expressed too much by transcriptome profiling (1300 genes) that detects or identifies 12 genes as drought inducible and cold target genes related or belonged to the DREB1 transcriptional factor family of genes (BEHNAM *et al.*, 2007; ZHAO *et al.*, 2007; LI *et al.*, 2011). It has been found from detection of just 8 genes which have been found in common while the 14 genes found which are probably the targets for DREB2a was done by the analysis of transgenic crop plants with over expressing DREB2 and DREB1 (ITO *et al.*, 2006; LATA and PRASAD, 2011; LICAUSI *et al.*, 2013). These factors finally consisted of at least 9 late embryogenesis abundant proteins (LEA proteins) that thought to deliberate dehydration tolerance in cereal crop plants. It was found that the abscisic acid resistant or insensitive mutant (*abi1-1*), the abscisic acid regulation was found about 84.5% and 6.9% of the identified responsive genes was lessened or highly declined, respectively; while 8.6% from all of the stress responsive genes remained rightly regulated (HOTH *et al.*, 2002; ASSELBERGH *et al.*, 2008), showing the involvement of both ABA independent and dependent regulatory systems for stress-responsive gene expression (CHOI *et al.*, 2005; CUTLER *et al.*, 2010; FUJITA *et al.*, 2011). The drought related transcriptional units may also be called as regulons which has been achieved through the collected information on genes and promoters which are being activated by them and the transcriptional factors (VANDERAUWERA *et al.*, 2005; HUANG *et al.*, 2012). The NAC, DREB2

and ZF-HD transcriptional factors regulons or the transcriptional units regulates the changes in abscisic acid independent genes expression in the response of drought stress, while the regulation of abscisic acid responsive genes was done by ABF/AREB, CBF4/DREB1, MYB and MYC under the same identical circumstances (ZHAO *et al.*, 2007; LATA and PRASAD, 2011).

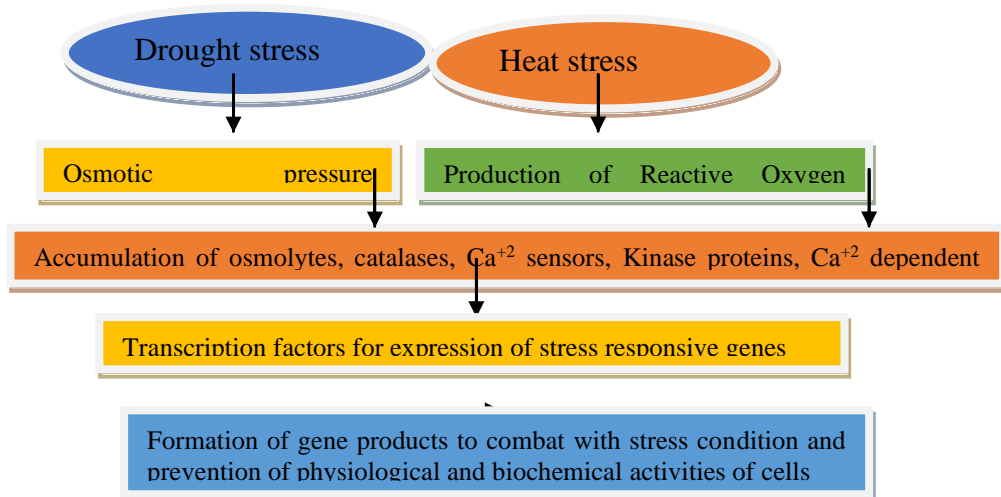


Figure 2. Response of plants cellular level under drought and heat stress

The processes which avoid water loss, repair damage involve the genes products which protect the cellular machinery are activated under drought stress (RAMEGOWDA and SENTHILKUMAR, 2015). Osmolytes are synthesized by the response of plant to water loss (KOYRO *et al.*, 2012; IQBAL *et al.*, 2015). Osmoregulation or water loss is avoided by ion channels, transport proteins and carriers (VALLIYODAN and NGUYEN, 2006; LI *et al.*, 2017b). Osmotic pressure under stressful circumstances is adjusted by sugar transporter that transported sugar through plasma membrane and tonoplast. Cellular water status results by water loss may be controlled by a family of membranous proteins that transport water called Aquaporins (ALEXANDERSSON *et al.*, 2005; FINKELSTEIN, 2013; NISHANTH *et al.*, 2018; WANI *et al.*, 2018). During desiccation tolerance development in the seeds, accumulation of various hydrophilic globular proteins occurs during the maturation phase. During time of water loss, vegetative organs may lack those late embryogenesis abundant (LEA) proteins (XIAO *et al.*, 2007; LYZENGA and STONE, 2011). During water loss, different proteins have been involved in limiting the removal and or damage of toxic organic and inorganic compounds is preferred. Cells are protected against water loss and low temperature conditions such as high salinity and drought stress conditions by a large number of dehydration responsive and cold stress regulated (COR) gene which encoded hydrophilic type of polypeptides (proteins) (FLOWERS and COLMER, 2008; LENKA *et al.*, 2011; SINHA *et al.*, 2011). Fenton reaction utilizing ferritin shield cells from all types of oxidative damages caused by stress through sequestering the intracellular ion involved in creating different reactive hydroxyl radicals (SEKI *et al.*, 2001; BHATNAGAR-MATHUR *et al.*, 2008). Physiological and environmental

oxidative stress may regulate the genes that encoded the plant catalase enzymes which plays a key role in antioxidant defense system (IWAMOTO *et al.*, 1999; KIM *et al.*, 2015; WAMBUGU *et al.*, 2015). Damage resulted by stress in membranes may be repaired by fatty acid metabolism related genes to regulate fluidity of the membrane and permeability to toxic ions (BRUCE *et al.*, 2002; YAMAGUCHI-SHINOZAKI and SHINOZAKI, 2006).

Plant Response against higher temperature

There are large number of factors which affect plant growth, among which temperature is the prominent factor to be considered which is mostly resulting due to higher sun radiation fall and mostly because of drought conditions of environment (BRUCE *et al.*, 2002; TAJI *et al.*, 2004). Changes in the worldwide weather, especially spatial and temporal patterns largely affect the plant growth (BUSHONG *et al.*, 2016; KUMAR *et al.*, 2017). The loss in yield because of heat stress in cereals is most importantly affected by shortening of development phases because of reduced light sensitivity, high temperature over the shortened plant life cycles and caused perturbation in the procedures related to the carbon usage (photosynthesis, respiration and transpiration). More carbon fixation is required for enhanced level of respiration to survive and maintain growth (ATKINSON and URWIN, 2012; BITA and GERATS, 2013). Temperature more than 35°C greatly diminish the activities of enzyme ribulose 1,5-biphosphate carboxylase or oxygenase (Rubisco), result in the limited level of photosynthesis in cereals crop plants. Under high temperature conditions, temperature at least 5°C more than optimal growing circumstances, higher plants show a characteristics set of metabolic and cellular responses necessary for the plant survival (HU *et al.*, 2010; AREND *et al.*, 2013; NAWAZ *et al.*, 2020). These effects decrease the normal protein synthesis and it increases the translation through transcription of genes responsive for the formation of heat shock proteins (HSPs) which is a group of stress tolerance inducing proteins (WAHID *et al.*, 2007; ANJUM *et al.*, 2011), antioxidants and alterations in the cellular structural organizations, the production and release of phytohormones, including cell organelles, change in the structure of organelles and cytoskeleton and functions of organelle and cell membranes (FAROOQ *et al.*, 2011; MCDOWELL, 2011).

During vegetative growth heat stress causes different metabolic and physiological alternations, including different changes in homeostasis through hormonal abnormalities. It has been found that there are few processes at organ, cell and whole of the plant level which are heat-induced can be hormone regulated; some other processes are may also be the result of heat and drought which caused formation of new hormones (LU and FEDOROFF, 2000; ARTECA, 2013; KHALIL *et al.*, 2020b). Abscisic acid formation is controlled through intracellular dehydration signaling pathways in the response of osmotic stress in plants (ALLAKHVERDIEV *et al.*, 2008). The induction of abscisic acid may also be an essential part of temperature tolerance where heat stress and water shortage frequently occurs in field conditions. Gibberellin effects opposite to ABA in high temperature tolerance conditions. The inherently heat resistant dwarf mutant of *Hordeum vulgare* showed lower synthesis of gibberellins which when treated with exogenous (foliar) application of gibberellins caused to change in more heat and drought, whereas the treatment with a gibberellins antagonist compound grant heat and drought tolerance in barley. However, still our knowledge of involvement of phytohormones under the heat and drought

tolerance in cereals crop plants is still too far from completion (YAMAGUCHI, 2008; COLEBROOK *et al.*, 2014).

One of the effects of raised temperature and drought in plants include oxidative damages occurs because of heat and drought induced unbalancing of respiration and photosynthesis. As detected by observation in maize, increased temperature may lessened or diminish the antioxidant enzymes activity (GONG *et al.*, 2001; SATO *et al.*, 2006; HASEEB *et al.*, 2020). Therefore, the ability to gain heat and drought tolerance are related with highest activities for superoxidase dismutase and catalase, less oxidative damage and higher ascorbic acid content in wheat germplasm. Raised temperature causes modifications in the function of membrane basically because of alternations in membranes fluidity (SINSAWAT *et al.*, 2004; HOSSAIN *et al.*, 2015; KHALIL *et al.*, 2020a). In the plant cells, the membrane based mechanisms are essential especially respiration and photosynthesis. Three normally used assays of drought and heat tolerance in cereal plants are related to the plasmalemma of cells through cell membrane stability (CMS) assay, the mitochondrial membranes through cell viability assay based on 2,3,5-triphenyltetrazolium chloride (TTC) reduction and the photosynthetic thylakoid membranes through chlorophyll fluorescence assay. The photochemical efficiency of the most sensitive component during photosynthesis that is the photosystem II (PSII) in chloroplast is lessened by drought and heat stress (HASANUZZAMAN *et al.*, 2012; WARAICH *et al.*, 2012; HASANUZZAMAN *et al.*, 2013a).

The effect of heat and drought stresses led to misfolding and degradation of all newly made proteins along with the denaturation or breaking of existing cell proteins. There is a specific group of cell proteins called as chaperons capable for helping other cell proteins for maintaining their integrity and functions in appropriate post-translational protein foldings as the proper post-translational folding is considered responsible for protein stability (HECKATHORN *et al.*, 1998; SAVICKA and ŠKUTE, 2010). Some other aspects of heat and drought stress responses or reactions of induced production of heat shock proteins (HSPs) from unicellular like bacteria to multicellular like humans are highly conserved in nature. The one of the key functions of HSPs are the chaperon functions, the refolding or the denaturation prevention of already denatured proteins. The importance of HSPs in temperature tolerance was first proposed on the basis of most of the correlative evidences; however the HSPs involvement in acquire heat and drought tolerance of *Arabidopsis* has been now fully demonstrated (HECKATHORN *et al.*, 1998; SUN *et al.*, 2001; VAN MONTFORT *et al.*, 2001). The higher molecular weighted heat shock proteins like HSP90, HSP70 and HSP101 which showed a higher level of sequence similarity inside the plant kingdom has been identified from various crop plants including cereals. However, the molecular diversities in groups or families of higher molecular weighted HSPs have shown or suggested that even the closely related HSPs may differ in their specified functions during drought and heat stress (MAESTRI *et al.*, 2002; FAHAD *et al.*, 2017). However, it has also been found that there are different functions shown by same group member proteins of heat shock protein groups or families in various compartments or organelles of cells; the heat shock protein, HSP101 showed an important and major role under heat and drought stress tolerance in *Arabidopsis thaliana*. The same homologous protein of HSP101 was cloned and studied in wheat plant while there is still not fully know function of HSP101 in sense of regulation and expression in cereal crop plants under drought and heat stress conditions (GUAN *et al.*, 2004; DANSANA *et al.*, 2014). Young and

his colleagues investigated the regulation and expression of heat shock protein type, HSP101 under drought and heat leading stresses in maize/corn and wheat. It was found that the highest amount of protein HSP101 was found in developing cob, silk and tassel of corn plants. A heat induced increasing amount of HSP101 protein through higher transcription level of corresponding genes was supplemented by a consequent raise in the amount of protein HSP101 production in the vegetative meristematic and floral regions, led to full expansion of foliar leaves, the roots and young ears. The HSP101 transcriptional factors were also increased in tassel during anthesis stage under drought and heat stress stress conditions without the similar increase in the amount of HSP101 protein formation in cells. Alternation in increasing the amount of mRNA and HSP101 protein levels during the growth and development of all other plant organs may also be detected (QU *et al.*, 2013; LI *et al.*, 2017a). These findings from studied observations led to the suggestions that the HSP101 protein expression is controlled under an organ specific level or ways during that development and growth of cells or organs, and also that the HSP101 protein accumulations is also controlled by the regulation carried out at the mRNA level from pre and post transcriptional levels. The lower molecular weighted HSPs proteins have also been found in various organelles, cell membranes and cytoskeleton in reaction to drought and heat stress which was found in *Pisum sativum* under abiotic stress environmental conditions; it was suggested that the HSPs proteins play an essential role during drought and heat stress to protect photosynthetic electron transport chain (TODAKA *et al.*, 2012; XIONG *et al.*, 2014).

The drought and heat stress tolerance is a complicated characteristic in plants most probably under control of more than one gene. The relative molecular biology analysis of heat tolerant and sensitive genes in *Festuca* has depicted that heat and drought tolerant genotype responded to abiotic stresses by raising the gene expression partaking in protein synthesis, protection of cell shape and structure, and the entire drought and heat tolerance related transcriptional factors. The heat stress responsive transcriptional factors (HSFs) are the terminal portions or components of signal transduction pathway controlling regulation and the activations of genes along with their own expression responsive genes for heat and drought stress tolerance (RABELLO *et al.*, 2008; LI *et al.*, 2017a; DANISH *et al.*, 2020). The genome sequencing of *Arabidopsis* has shown the sole complications of the cereal plants HSF groups or families, about 21 HSF members are belonging to 14 groups and 3 classes. Of the around 24,000 observed genes in *Arabidopsis*, about 11% have shown considerable effects in the case of heat and drought stress treatments. Most of these genes are found to be under the main control of families of HSF-1a/-1b controlled by regulatory genes through global gene transcriptional mutant knockout analysis (SWAMY and KUMAR, 2013; DANSANA *et al.*, 2014). Besides a lot of HSP genes along with other stress response related genes, the HSFA-1a/1b genes are regulated which has been found to be involved in a large of cell functions, which included protein biosynthesis and processing, metabolism, signaling and transport of organic and inorganic molecules in cells. Likewise, all of the steps involved in the pathways resulting during osmolyte accumulations have also been found to be regulated by HSF AND HSPs under drought and heat stress conditions. It has been found that there are much similar reactions in the cells, organelles and membranes of plant cell during heat, cold and drought stress conditions (PATTNAIK *et al.*, 2016; HAKIM, 2017). Therefore, it is more convenient study one of the stress on cereal plants to understand the effects of other

stresses like to study heat stress can give brief information about the effects of drought and cold tolerance process in crop plant cells. The possible manipulation and additional consideration of these processes in cereals crop plants, either through transgenic techniques or approaches or through molecular plant breeding, may also depend on the further progresses and achievements in proteomics, metabolic and genomics profiling (LIMA *et al.*, 2015; MOUMENI and KIKUCHI, 2016; DINGKUHN *et al.*, 2017).

Combine effects of drought and heat on crop plants

The farmers and plant breeders have been known from long period that the concurrent incidence of many abiotic environmental stresses, which rather than a fastidious stress conditions, that is the most lethal for field crop. The recent investigations have discovered that the metabolic and molecular reactions of the plants to a combine effect of diverse abiotic or environmental stresses is distinctive which cannot be directly induced from crop plant response for each of all the different heat, drought and cold stresses individually (KOTAK *et al.*, 2007; MILLER *et al.*, 2008). It has been found that the combine effect of heat and drought stresses gives an outstanding example of combine abiotic stress conditions which may occur in the crop field simultaneously under same conditions. However, it is not well known that how the combine stress of drought and heat affect crop plants in the field conditions (VINOCUR and ALTMAN, 2005; HIRAYAMA and SHINOZAKI, 2010). The climate throughout the glob is changing day by day, which is probable becoming the cause to raise the global temperatures of atmosphere, the change in temperature is causing disturbance in the distribution of annual rain fall and precipitation which caused intensified drought conditions in semiarid and arid areas of the world, it is leading to a reduced growth and development of grass lands productivity which is responsible for drought and heat stress in cereal crop plants (XU and ZHOU, 2006; ASSENG *et al.*, 2011; KRASENSKY and JONAK, 2012). There are several finding and studies which showed the combine effects of drought and heat on growth and development of wheat, maize, rice, barley and sorghum along with various grasses from grass family (WANG and HUANG, 2004; XU and ZHOU, 2006; JHA *et al.*, 2011). It has been identified from various studies that a combine stress of heat and drought showed sever and harmful effects on the plant growth, productivity and development of these cereal crops as compared with all each of the different biotic and abiotic stresses which applied in individually to cereal crop plants (JAIN *et al.*, 2007; BAI *et al.*, 2009).

In a study conducted on the *Leymus chinensis* a perennial grass, it was recommended that high heat and drought, joined with serious soil dry spell, may decrease the capacity of PSII, debilitate nitrogen (N) anabolism in cells, fortify proteins catabolism and incite the lipid peroxidation in cells (XU and ZHOU, 2006; PRASAD *et al.*, 2008a). The diverse stresses may require conflicting or antagonistic reactions or responses for each other. Along with heat and drought stress together, for instance, the plants usually open up their leaf stomata to keep cool their leaves through transpiration process. In any case, if heat and drought stresses joined together spell the crop plants can't open up their leaf stomata, so the temperature of leaves stays higher and caused damage for leaves (XU *et al.*, 2009; VILE *et al.*, 2012). Moreover, a blend of dry spell and higher temperature or heat stress has been found to modify the plant digestion in a novel way as compared with the single environmental stress. The transcriptome investigation of *Arabidopsis thaliana* plants exposed to a mix of heat and drought stresses uncovered another

example of barrier reaction, including the halfway mix of two multi-quality resistance pathways and additionally 454 transcriptomes which were explicitly communicated in crop plants along with a mix of heat and drought stress (RAMPINO *et al.*, 2006; CHINNUSAMY *et al.*, 2008; CHAVES *et al.*, 2009). The metabolic profiling uncovered that the plants exposed to a blend of heat and drought stress aggregated sucrose and different sugars, for example, glucose and maltose. On the contrary, proline (an amino acid), which collected in the plants exposed to dry spell, did not accumulate in plants along with a combine effect of heat and drought stresses. The heat stress was found to alleviate the poisonous quality of proline to cells, recommending that accompanied by combined effects of heat and drought stress, sucrose supplanted proline acts as the major osmoprotectant (VERSLUES and BRAY, 2005; WAHID *et al.*, 2007). In view of physiological and atomic portrayal, there were numerous similarities between the reactions of *Arabidopsis* and *Nicotiana* to this pressure mix or combine effects of drought and heat stresses, recommending that this method of protection reaction is rationed among various plant species. Resilience to a mix of various pressure conditions, especially those that impersonate the field condition, ought to be the focal point of future research programs went for creating transgenic crops with improved resistance to normally happening ecological conditions. At present, in any case, data on the joined impact of heat and drought weight on the regenerative advancement of grains is somewhat constrained, so it may be talked about further at formative stages where adequate information are as of now accessible (WIGLEY and RAPER, 2001; MEINSHAUSEN *et al.*, 2009).

Combine effects of drought and heat on flowering

The vegetative tissues protect the generative organs during their initiation and early development. The procreative cell structures react indirectly towards unfavorable environments, as arbitrated by somatic plant organs, unless stress is lethal. Therefore, the pressure affectability of conceptive procedures and the biochemical and atomic foundation of stress reactions must be translated in relationship with the reactions happening in the vegetative organs (SHAH and PAULSEN, 2003; WAHID *et al.*, 2007). Contingent upon the cereal species and on the land area of plant development, drought and heat stresses may happen amid the period of vegetative/generative change in the shoot apical meristems. The suitable coordinating of the example of inflorescence improvement and the season of blooming to the fleeting variety in water accessibility is perceived as a standout amongst the most imperative characteristics giving adjustment to dry season. In spite of the fact that grain crops demonstrate affectability to dry spell amid botanical inception and the pre-meiotic separation of flower parts, the impacts of dry season on flower meristems are among the slightest comprehended parts of yield conceptive advancement submerged controlled conditions (LIU *et al.*, 2005; KRASENSKY and JONAK, 2012; SUZUKI *et al.*, 2014).

Heat stress can be attributed to losses in cereals yields brought on metabolic variations, to a lower inside the length of developing stages of vegetation and resulting discount in light notion over the abbreviated existence cycles, and towards perturbation of procedures associated with carbon acclimatization may additionally result in less and/or abnormal and/or reduced organs. Most effective a restricted variety of reports had been posted at the impact of abiotic strains, mainly higher temperature, on provisional segment of improvement in cereals plants (KOTAK *et al.*, 2007; REJEB *et al.*, 2014; VISHWAKARMA *et al.*, 2017). Wheat vegetation have four

to 8 leaves on primary shoot at growing apex modifications from somatic to the re-productive level. Above 30°C temperature, at some stage in floret formation cause complete sterility pronounced a fantastic relationship in between the span of the somatic part and the wide variety of spikelet's in keeping with spike. Therefore, shortens the period of the vegetative level of apex that induces fewer spikelet's in step with spike. The primary impact of warmth stress after/all through floral instigation is discovered on kernel array. Wide variety of kernel consistent with component location reduces at 4% price for every grade growth in approach temperature throughout 30 d forgoing anthesis. As a first-rate aspect within the grain wide variety, significant experimental effort has been devoted to analyze carbohydrate availability for developing wheat florets (CHAUHAN *et al.*, 2011; THITISAKSAKUL *et al.*, 2012). The time of floret death related with the period while the stem and ear had been accumulate dry material at their maximum quick charge and that insufficient assimilate accessibility might be crucial in the loss of florets (KIRBY, 1988; REYNOLDS *et al.*, 2009). Availability of nitrogen also looks important on this level of growth. Charge of spikelet production and length are managed through temperature of maize and genotypic results occur for such types of trait. Heat stress (i.e. pistil hyperplasia and stamen hypoplasia), brought floral abnormalities leads to sterility of spikelet, constitute enormous issues in the production of rice (FOULKES *et al.*, 2010; FAROOQ *et al.*, 2011).

Effects on reproductive growth

Incidence of concurrent drought and heat strain in the course of the initial reproductive tiers of cereal ontogeny used to be occasional, so it is of little interest. But, inside mild of the progressively more common incidence of initial season temperature excesses in most of the regions, many studies might be defensible. Blended effects of those stress is greater typical of advanced phases of re-productive improvement in cereal (e.g. Grain filling and early seed formation), as conferred in addition (TRETOWAN *et al.*, 2002; COSSANI and REYNOLDS, 2012; ALI *et al.*, 2016; YAQOOB, 2020). Ovary and embryo sac improvement impact of water insufficiency on female gametophyte development and ovary although grain vegetation show sensitivity to drought for the duration of floral initiation and the pre-meiotic differentiation of floral components, the maximum dramatic outcomes on yield were recorded while stress concurs with the length connected by early grain initiation and means of the onset of meiosis (PRASAD *et al.*, 2008b; DOLFERUS *et al.*, 2011).

In wheat, pre-anthesis stem reserve accumulation is taken into consideration to be a full-size factor affecting flower and grain development under pressure conditions. Whilst carbon assimilation all through stem elongation is reduced by drought stress, the storage capacity inside the stems additionally decreases. The authors of a latest overview factor out that the grain variety in wheat is surprisingly depending on the conditions of environment previous to and at some point of flower formation (SAINI and WESTGATE, 1999; MACCAFERRI *et al.*, 2008). They claim that grain wide variety can't be taken into consideration as a main determinant of last yield, but due to nutrient aid accumulation. This view offers greater significance to vegetative boom inside the dedication of very last yield, emphasizing the significance of nitrogen availability for floret improvement. Restrained nitrate uptake from the dehydrated soil and the decreased nitrate concentration inside the xylem could cause the alkalization of the xylem sap, as a consequence affecting ABA accumulation both in the leaves and the reproductive structures, resulting in

reduced yield (VERSLUES and BRAY, 2005; IZANLOO *et al.*, 2008; ALI *et al.*, 2020b; SAEED *et al.*, 2020).

Drought stress can cause a huge put off in female organ development in maize, whilst male in-florescence is least affected additionally ABA may have a function on this method. A growth in contents of ABA material in propagative organs is one of the factors recommended to play a position in yield discount in response to drought strain. The ABA attention of ovary became located to upsurge considerably because the end result of extreme, long-lasting strain previous to flowering in comparison with moistened maize plant life, but this distinction disappeared via flowering. No matter this, authors did not eliminate the opportunity that ABA can also play a role in the abortion of lady plants. Even though increase in the ABA awareness without decreasing the water supply did no longer result in low grain numbers in wheat, inside the case of low water elements the ABA concentration augmented within the developing floral organs of every wheat and maize (VERSLUES and BRAY, 2005; CUTLER *et al.*, 2010; FUJITA *et al.*, 2011). Excessive ABA tiers in early reproductive structures resulting from environmental stresses might also inhibit mobile division and impair floret after which seed improvement. Reproduction of plant substantially depends upon sufficient supply of photo-synthetic products. Water scarcity is the outcome in the reticence of the photosynthesis system, and thus in the reduction within the nutrient deliver to the generative organs. An inadequate deliver can inhibit the growth of generative structures, causing abortion. Disturbances inside the carbohydrate metabolism of the ovary due to inhibited photosynthetic inflow in the course of early improvement can be presumed to be answerable for those developmental stages (CHAVES *et al.*, 2009; BOWNE *et al.*, 2012).

Effect reproduction cycles

Under low water or drought stress conditions kernel abortion became able to prevent by sucrose infusion. Similarly, many studies have shown that sucrose alone is also capable of rescuing the ovaries and that delivery of sucrose from leaves to the ovaries might also purpose a start to induce the developmental and molecular responses (CHAVES *et al.*, 2003; CATTIVELLI *et al.*, 2008). Reproductive tissues of maize contain starch reserves inside the maternal tissues of the cob, pedicle and pericarp and those reserves are concept to be re-mobilized to help reproductive upsurge when photosynthesis is blocked for the duration of water deficit, photosynthesis can be blocked for days, and the reserves grow to be in particular essential due to the fact respiratory maintains to demand substrates. In the absence of stream of substrates from photosynthesis, most of the cell activities can't hold. Though, growing proof shows that the reserve repute of the cells may function a signal that affects gene expression (HUANG *et al.*, 2012; DANSANA *et al.*, 2014). The expressional regions have revised and recognized numerous genes that seemed to be involved in expression while the sugar repute of the cells modified (KOCH, 1996; KOCH *et al.*, 1996). SCHUSSLER and WESTGATE (1994) found that a bigger pool of reserves in maize growth changed into incapable to uphold ovary boom all through water deficit and that abortion persisted inside the female florets. Sucrose may additionally have a dual role as substrate and signal. Feeding sucrose to the stems at some stage in water insufficiency might motive the stream of substrates to resume, but might also signal to the growing reproductive shape that metabolism could continue (SCHUSSLER and WESTGATE, 1994). Genes that responds to

sugar sign would be those stopping floret abortion and controlling the phenotype (MCLAUGHLIN and BOYER, 2004b). Around anthesis, maize ovaries acquire ~1 mg dry mass an afternoon, broadly speaking within the form of carbohydrate. Dry mass is introduced by using the phloem as far as the pedicel, in which the phloem terminates. In an effort to input most of ovary tissue, sucrose or its break down products must find their way without help of phloem transportation (SMITH and STITT, 2007; RUAN *et al.*, 2010). In the course of water deficit, the phloem cell caused stopping of sap to the maize stem and located much less motion to the ovary than in controls furnished with water. This showed that much low sugar becomes brought by means of the phloem towards the pedicel during water scarcity. With much lesser sucrose, starch turned into depleted and the glucose gradient vanished (MÄKELÄ *et al.*, 2005; RUAN, 2014).

Ovaries additionally showed much less cell wall-bound invertase interest when the plants have been exposed to a water deficiency. All of the downstream metabolites have been depleted by way of biosynthesis of starch in the ovaries, which shows that the lack of invertase fashioned a metabolic inhibition further to the deficiency of sucrose delivery because of decreased photosynthesis (CHAVES *et al.*, 2009; COSSANI and REYNOLDS, 2012). Other studies for signaling comes from the reaction of invertase within the discern plant in comparison with the ovaries. Numerous authors suggested that invertase interest elevated inside the roots and leaves of young maize flowers during a water scarcity, while it has been found less effects on ovaries on the time of anthesis. This evaluation means that the sign to abort growth is probably missing in roots and leaves, however gift within ovaries (ZINSELMEIER *et al.*, 1999; CAKIR, 2004). Past those physiological and biochemical strategies, there is now interest in viable adjustments in gene expression. Recent molecular researches found out that many genes recognized to be worried in sucrose processing in young maize ovaries have been down-regulated soon after water insufficiency started to have an effect on the flora. These are the sucrose synthases (SS1, SS2) and invertases (Incw1-four, Ivr1-2), and their down-law turned into dignified by evaluating mRNA large quantity in ovaries before and after water scarcity took place. Because of the down-law started earlier than glucose wiped out from ovaries, the sign for genes can also was little in sucrose. For an inhibitor peptide the gene coding for invertase (Zminh1) turned into unaltered in expression and Ivr1 become not expressed (WESCHKE *et al.*, 2000; KIM *et al.*, 2015). Kim and his colleagues pronounced that Incw3 turned into also now not expressed (KIM *et al.*, 2015), CHENG and his colleagues discovered that Incw4 had less expression under drought stress in maize (CHENG *et al.*, 1996). Andersen and his coworkers located a strong connection among the reduced effects of such varieties of ovary invertase enzymes and the expression in their genes (ANDERSEN *et al.*, 2002). There are 4 genes involved in the breakdown of sugar molecules under drought stress. The ribosome inactivating protein 2 gene has become strongly up-regulated two days after the down regulation of sucrose processing genes in maize, starting up senescence inside the ovary tissues (MCLAUGHLIN and BOYER, 2004a; LOPES *et al.*, 2011). Two days later, phospholipase D (PLD1) changed into up-regulated gene, suggesting that membrane breaking down might had been initiated which might also initiate the ovary abortion (MCLAUGHLIN and BOYER, 2004a). Genome aggressively responds to the reduced availability of sugar. Genes for 2 different enzymes, cysteine protease (CCP1) and a bi-purposeful nuclease (Bfn1), had been down regulated at about the time while sucrose processing genes have been down regulated. Those genes are supposed to characteristic in nucleotide and protein turnover throughout

everyday increase in drought stress, which did not occur in aborting ovaries (ZINSELMEIER *et al.*, 1999; JI *et al.*, 2010).

Multi genic nature of the ovary reaction and issue in recognizing controlling gene (ZINSELMEIER *et al.*, 1999; MCLAUGHLIN and BOYER, 2004b) has been found through the development of cDNA micro arrays to degree differential gene expression in pedicel tissues and maize ovaries while water scarcity happened across the time of anthesis. More than 1500 genes representing 27 regulatory and metabolic pathways had been explored out of these 15–45 confirmed difference in expression under slight water scarcity changed into imposed, with some genes down-regulated and others up-regulated (MCDOWELL, 2011). More quantity of genes had been differentially expressed as the lack exaggerated. In case of floral abortion, it has currently showed feasible to opposite the phenotype with the aid of biochemical/physiological approach without changing the genetics of cereals. At some stage in this useful reversion, just a few genes answered, as a result identifying the ones likely to be worried in regulatory abortion phenotype (YANG and ZHANG, 2006; MCDOWELL *et al.*, 2013). These data imply that the down-turn in contents of sucrose of the cells of ovary, attributable to curtailed sucrose transport due to the reduction in photosynthesis all through the water scarcity, may be the prime number one sign to the growing reproductive systems. The second would be reduction of glucose as starch changed into fed on within the ovary tissues. On the basis of those results, these genes have appear as targets for stopping abortion (CENTRITTO *et al.*, 2009; ZHU *et al.*, 2010).

Heat stress effects on embryo sac and ovary development

There may be a lack of facts on the impact of excessive temperature female reproductive structures development. A rise in the range of antipodal cells is as a result of high temperature in the maize embryo sac. It has been found that a phase of heat stress that causes male sterility in wheat had no unfavorable impact at the features of female sexual generation, proposing that the girl gametophyte had extra tolerance of heat strain (CHEBOTARU, 1965; BATYGINA, 2009). Whilst the Australian wheat range ‘Gabo’ turned into exposed to excessive temperature 30°C at some stage in meiosis, a 3rd of ovaries were located to showcase strange improvement (SAINI and WESTGATE, 1999; NEVO and CHEN, 2010). In a number of the ovaries, no embryo sac become discriminated, and the hollow space changed into filled because of the proliferation of the cell layer of the external integument or the encroachment of inner integument. The incidence of minor embryo sacs with ordinary cell formation changed into additionally frequently found. in lots of cases pollen tube growth was inhibited within style and ovule, probably due to the destruction to sign switch mechanisms (BLUM, 1998; CENTRITTO *et al.*, 2009). Seed putting reduced through an usual of 21%.these authors sketched devotion to the realism that, although drought itself likely has a less drastic effect at the structure and functioning of the female sexual technology than at male gametophyte, it is able to still motive excessive yield losses when associated with higher temperature and drought (ASSENG *et al.*, 2011).

Effects on megasporogenesis and reproductive structures

Drought and excessive temperature both, 3 to 4 weeks before flowering, induced asynchrony inside the tasselling and silking of maize, even as increase and receptiveness of the

style had been additionally blocked. Range of kernels each year did not raise when clean pollen of un-stressed plant life became carried out to overdue-appearing silks. On the idea of the formerly discussion, it is clear that structural and purposeful abnormalities occurs as a result of stresses within the procedures main to improvement of the gametes have a critical impact on fulfillment of fertilization due to the production of dysfunctional female or male gametophyte, even supposing fertilization takes area under greatest environmental situations (BATYGINA, 2009; BITA and GERATS, 2013).

It is predominantly shown by experiments that two phases of ontogeny during the reproductive development i.e. meiosis in gametes and second flowering which are very sensitive to the environmental stresses like drought, heat, and cold (SAINI and WESTGATE, 1999; BOYER and WESTGATE, 2004; REJEB *et al.*, 2014). It has been found that among various crop plant cultivars like wheat as self-pollinated crop plants (SAINI and ASPINALL, 1981; THAKUR *et al.*, 2010) and rice (SHEORAN and SAINI, 1996; LANCERAS *et al.*, 2004) the percentage of water deficit or drought during meiotic stage of cell division may cause to reduce 35-75% grain setting in cereals. Due to restricted transpiration within two or more enclosing leaf sheaths, plants like wheat, rice and maize can resist changes in water status of inflorescence/anthesis previous to its emergence even maturity (SHEORAN and SAINI, 1996; WAHID *et al.*, 2007; IQRA *et al.*, 2020). Consequently, in response to meiotic stage water stress or drought caused reduction in cereals grain set while the water stress or drought showed no any correlation with the water or moisture status of the male and female reproductive parts and their structures. Pollen sterility due to drought stress increases in the case of wheat where self-fertilization takes place (SAINI and WESTGATE, 1999). The abnormalities due to drought caused in the microsporogenesis which resulted in the development of sterile, dysfunctional pollen grains in cereals. The metabolic events relating to the failure of pollen development confirms the abnormalities in the anatomy of drought stressed anthers of wheat and rice (FAROOQ *et al.*, 2009; FAROOQ *et al.*, 2011). The water deficiency during male meiosis forced the acidic invertases to play a decisive role was confirmed by recent research (KOONJUL *et al.*, 2004; FISCHER, 2011). The cDNA library has been prepared from the wheat anthers which showed that three invertase genes were isolated and out of two (Ivr1, Ivr3) genes cod for cell wall invertase and one (Ivr5) codes for vacuolar invertases of wheat plant cells. RNA samples deriving from the generative organs of irrigated wheat plants generating data from a western blot indicating that invertase isoforms were preferentially but not exclusively expressed in anthers. Water deficiency at meiosis demonstrated by quantitative RT-PCR analysis selectively inhibits the transcription of Ivr5 and Ivr1 genes however it don't show any effect on Ivr3 gene. After irrigation, the expression of relevant genes was not detectable. In situ hybridization demonstrated the cell specific expression of stress sensitive genes in cereals (KOONJUL *et al.*, 2004; JI *et al.*, 2010). The gene OSINV4 was anther specific and down regulated by cold stress which was shown by expression analysis of cell wall from two different cultivars (OSINV4) and acid invertases from cell vacuolar (OSINV2). The drought stress caused up regulation of OsCIN2 which acts as multiple invertase gene for cell wall in rice and caused in each of the sink rice tissues. The corn Incw2 gene, showed similar expression as that of OsCIN2 invertase gene (JI *et al.*, 2005; WASSMANN *et al.*, 2009). The same situation was with Ivr2 which was soluble invertase gene and also the maize gene ortholog of rice cell vacuolar invertase

OsVIN2 gene, which always expressed in rice and maize throughout pollination and fertilization in rice and maize.

Effects on anthesis

The drought and heat stresses caused a huge loss of cereal crop plants in producing pollens as the higher heat and drought caused late anthesis even if there is formation of pollens, there will no viable pollens. The most drought and heat sensitive organ of cereals are pollens as compared with other cell organs and plant organs of cereals crop plants (SAKATA *et al.*, 2000). The pollen grain mitosis 1 and 2 showed higher sensitivity of wheat and barley with increase in temperature and drought stress (SAKATA and HIGASHITANI, 2008; NAVEED *et al.*, 2014). The higher temperature and drought stresses can cause two types of abnormalities in grain and pollen development of wheat. When the microspores showed not ability to complete the first mitotic division, caused the degradation of pollen cells and nucleus. They may remain immature due to the loss of cytoplasm but may contain exine. It may also be in the form that the first meiotic cell division completed successfully but only a few of the cells grown into mature pollen grains (SAKATA *et al.*, 2000; LEE and LEE, 2003). During panicle development and meiosis, the barley crop plants become hypersensitive to drought and higher temperature conditions. Abnormal developments and complete sterility was caused by high temperature treatment for several days in barley. The increased temperatures (35°C day/25°C night) always resulted in the transcriptional inhibitions of regulating genes that were inactive in anthers while under optimal or normal temperature and water conditions and this was shown by histological examinations and serial analysis for the expression of genes (ABIKO *et al.*, 2005; SAKATA *et al.*, 2010). It has been found that the higher temperature and drought caused the damaging of pollen mother cells which caused irreversible changes in the pollen mother cells of cereals. The pollen formation in anthers of maize show response to heat and drought stress conditions, there are several groups of lower and higher molecular weight heat shock proteins such as HSP101, HSP60, HSP70 and HSP90. These HSP proteins are produced in the anthers at low moisture and higher heat levels which prevent pollens from dehydration (SUN *et al.*, 2001; SUZUKI *et al.*, 2014).

Effect on fertilization and flowering

It is most important for successful seed growth and development, some important factors which influence the embryo formation process are pollen availability for stigma and pollen tubes growth must be maximum so that they can reach ovules, double fertilization should be efficacious, and after all these successful factors lead towards the fulfillment of embryo and endosperm normal growth. All these processes may not be accomplished properly due to some environmental factors as heat, drought stress, as many times seen in cereals field. The pollen viability and seed germination is one of the sensitive processes in cereals (SAINI and ASPINALL, 1981; SHAO *et al.*, 2008). Water stress cause pollen sterility in maize (SAKATA *et al.*, 2000; SATO *et al.*, 2006; SAKATA and HIGASHITANI, 2008) high temperature stress could be observed in genotype dependent pollen (SCHOPER *et al.*, 1987; MITCHELL and PETOLINO, 1988; MITTLER and BLUMWALD, 2010). Maize pollen could survive even after loss 80% of water and no abnormality seen in any normal function. 60% of harvest index reduces when water stress occurs during flowering, which results in reduction of grains (MITCHELL and PETOLINO, 1988; LYAKH *et al.*,

1991). Panicle exertion and anther dehiscence are two events which are drought sensitive. The 25-30% of spikelet sterility is due to failure of panicle insertion this is because anthesis cannot be completed without complete insertion of panicle (FONSECA and WESTGATE, 2005; ERCOLI *et al.*, 2008). When few pollen grains reached stigma surface and incomplete anther dehiscence occurred in this situation pollen grains seems to be co-operating than compete (SAINI, 1997; LIU *et al.*, 2005). Dry winds may cause water deficiency before flowering or immediately after flowering causes less seed production. Due to water deficiency panicle unable to free itself from leaf flag and spikelets not open at anthesis. Less pollen are available for fertilization when anthers shrivel up. Fertilization can completely be prevented due to these reproductive abnormalities (SAINI, 1997). Reduction in number of rice is also due to grain abortion. In Maize water stress timings cause abortion if water availability low before pollination it will result in abortion (XIE *et al.*, 2010). After stress treatment embryo and endosperm before fertilization not present these findings suggests that after water stress ovaries affected badly. Anthesis, double fertilization and embryo development did not show any affect if water stress up to 30% more than that percentage or lethal shortage of water affect all these processes. Genomic methods can be used for detailed discussion of stress effect on development and fertilization (SCHOPER *et al.*, 1987; LUO, 2011). Zinselmeier and his colleagues discussed the effect of low light and drought on maize flowering using DNA chip which contains 384 genes through metabolic pathway. 47 % to 74 % yield loss in early stage of flowering when plant placed in shade for 5 days and caused changes in expression of detected genes. ABA signaling includes several genes activity ABI insensitive, ABA and stress responsive ASR1, glycerine-rich RNA binding-ABA inducible protein all the increase while enzymes that code for starch as G-6P/Pi translocator, ADP-G pyrophosphorylase (AGPase), Sh type 2, granule bound starch synthase (GBSS) decreased (ZINSELMEIER *et al.*, 2002).

A-amylase, starches, b-amylase and the starch phosphorylase these starch degradation genes not affected by drought and heat stress. All these data suggest that starch pool decrease in young maize ovaries induced due to shading, starch synthesis started at the level of transcription and co-ordinates other multiple genes which present in those pathways (ZINSELMEIER *et al.*, 1999; YANG and ZHANG, 2006). In wheat, when temperature reaches up to 30°C with drought at the stage of meiosis pollen damage and it effect pollen grains viability and all this result in failure of fertilization and this ultimately in low seed production (SAINI and ASPINALL, 1981; SAINI and WESTGATE, 1999). If temperature increases at anthesis the grain of wheat per year reduces (WHEELER *et al.*, 2000), this indicates heat stress effect on grain production. All HSPs cannot be synthesize in heat stress this explains pollen sensitivity of heat (SAKATA *et al.*, 2000; SUN *et al.*, 2001). In rice at flowering stage heat stress causes spikelet fertility. Sterility is due to low pollen dehiscence and poor number of pollen production, which results in less germinating pollen grains on the stigma (MAESTRI *et al.*, 2002; NAVEED *et al.*, 2014). In maize plant, low number of seed production is because of high temperature more than 38C, this heat stress causes less germination of pollen and reduces the growth of pollen tube. Kernel number per year reduces due to lateral ear heating (CÁRCOVA and OTEGUI, 2001). Kernel formation started in the non-heated side in ovaries when embryo present but their development stopped soon. Metabolic activity differentiates between heated and normal ovary during post fertilization time, it promotes uneven distribution of assimilates along same position of ovaries along maize ear.

When the sink activity enhanced in heated side the assimilate partition within ear occur and ultimately kernel abortion increased in normal sides (SANGOI *et al.*, 2002). In cereals post anthesis period is characterized by repeatedly occurrence of high ambient temperature in field. Pollination is non-synchronous in cereals even within the same ear, high temperature effect on fertilization from initial development of embryo (CAI *et al.*, 2011). On the other hand, in anthers at anthesis and in mature pollen, where the developmental gene expression of HSP101 and HSPs are not sufficient to meet the heat as well as drought stress demand, the level of HSP101 protein expression enough in silks prior to and ongoing fertilization in maize relates with high degree of heat-tolerance in tissues (CÁRCOVA and OTEGUI, 2001; SUN *et al.*, 2001; SANGOI *et al.*, 2002). There was no any remarkable high level of the HSP101 protein in thermos-stressed maize embryo or endosperm in any developmental stage that was watched for 12-48 hours in post pollination period (ARAUS *et al.*, 2012). These results showed that kernels/grains are not remarkably heat and drought responsive with regard to the HSP101 gene expression. In this filed no systematically analysis have been carried out, so more research work is required to justify the function of HSP genes that are expressed when sexual phase going on in cereals (EDREIRA *et al.*, 2011; REZAEI *et al.*, 2015). Asynchrony in tasseling and silking of maize at flowering/anthesis stage caused due to Drought and high temperature. Kernel number did not increase when pollination with pollen of untreated plants occurs, this happens in the case of late appearing of silks in maize (SANGOI *et al.*, 2002; CAI *et al.*, 2011). In spite of all these, fertilization completed and zygote develop under these circumstances, abortion of zygote within 2-3 days caused when there is lack of seed setting and cessation of pre-embryo and endo-sperm and differentiation of seed coat fails (WAHID *et al.*, 2007).

Effects on grain formation and development

Grain filling stage is the final stage of growth in cereals, in which caryopses develop from fertilized ovaries. The time and rate determines the weight of grain, it is a key to total yield. In many production areas the major stress factors during the maturation and grain ripening of pulses are increased temperature and drought. In cereals limited water supply and high temperature while the grain is at maturation or developmental stage cause a huge loss in yield. This loss is mainly due to less accumulation of starch, 65 % of dry weight of cereals is starch. The grain weight is also decreases due to heat and drought stress, in early stage of grain filling there are lower number of endosperm cells and this in return cause (NICOLAS *et al.*, 1985), in later stages of grain filling stress cause impairment of starch production and due to limited supply of accumulation for grains (BLUM, 1998; ATKINSON and URWIN, 2012), this directly effects on synthesis of grain (TURNER, 1996; YANG *et al.*, 2000). There are number of paper published on wheat grain development (YANG *et al.*, 2000) all these facts are mainly discussed to use as guidelines for mentioning the effects of heat and drought on grain filling time in cereals or pulses.

The number of endosperm cells is very important as proteins and starches that accumulate in the grain both are depend on these cells, these endosperms actually decided the grain filling and, final cell size, which depends upon the rate and time of grain fill (EGLI, 1998; GOODING *et al.*, 2003). Heat and drought directly effects on the division of cell of endosperm has been well known and studied (SLAFER *et al.*, 2005) In wheat plants, when water stress given in

endosperm division period, this drought which resulted in 30-40 % less endosperm cells, and 45 % small starch cells also reduced (THAKUR *et al.*, 2010; SUZUKI *et al.*, 2014). High temperature stress of 30 C-40 C OR 6d in maize plant during mitotic phase of the endosperm cell cycle 6, 4 and 8 d which was resulted in more damaging as they inhibit the entry of mitotic cell entry into endo-reduplication phase (YANG and ZHANG, 2006; WAHID *et al.*, 2007). During grain filling period heat stress up to 35°C was given in barley and it was found that endosperm showed some structural changes, which included damage of storage product (ZINSELMEIER *et al.*, 1999; ZARGAR *et al.*, 2011). Stem storage and whole plant senescence is closely related to grain filling 10-40% of the grain weight is assimilation of wheat and rice sheath and stem reserve (XU *et al.*, 2009; GHAFOR *et al.*, 2020). Photosynthesis reduces when water stress occurs during grain filling time it shortens the grain filling time and initiate early senescence, but all this loss enhances the remobilization of storage from straw to grains (WESCHKE *et al.*, 2000; FAROOQ *et al.*, 2011). Under controlled conditions like soil drying, in this condition plant could rehydrate itself at night the better results found as remobilization of stem reserve could be seen and faster and enhanced whole senescence of plant observed (ZHANG *et al.*, 2006). During kernel filling and height temperature stress of more than 30°C at whole day time has same effect as drought and remarkable reduction in grain filling only margins rate increase (WHEELER *et al.* 2000). At anthesis and till maturity high temperature more than 37°C cause significant reduction of starch storage in under developing wheat grains in comparison with plant which grown under controlled condition (HURKMAN *et al.*, 2003; CAI *et al.*, 2011; NASEEM *et al.*, 2020). The starch storage completed 21 day earlier when extra high temperature applied at night and day it was earlier than controlled one. Shorter starch accumulation could be seen at high temperatures in wheat and barley plants when there is high ratio of A type granules and low ratio of B type granules (CÁRCOVA and OTEGUI, 2001; CHAVES *et al.*, 2003). Grain filling process can be enhanced by increasing temperature and this depends upon farmer who is cultivating wheat (FISCHER, 2011). Increased enzyme activity and high rate of metabolic activity increases the rate of grain filling. This results in overall increased rate of grain development and depressed at higher temperatures. Grain dry matter storage might collaborate for less time duration (EDREIRA *et al.*, 2011). In maize plant grain filling time prolongs when the temperature stress reaches up to 33.5/25°C day or night in green house after post pollination or after 15th day of pollination (MACCAFERRI *et al.*, 2008). In wheat and maize plants grains the effect of heat stress is different due to Starch metabolism enzymes sensitivity difference.

Modern technologies for improvement in tolerance

Cereals yield greatly affected by environment i.e. water, temperature, and wind etc. these environmental factors have complex mechanism which includes a long complicated process, heat and stress directly effect on yield and change the process of stem reserves and gametogenesis, embryo development, and zygote formation and seed and grain development. These processes are complex and current knowledge of today era is not enough to explain these complexes interactions and systems. Modern research and methods has just begun to increase the yield of cereals and higher plants, it's beginning to understand the molecular level complexes and responses. Modern genetic and genetic approaches for cereals crop improvement and potential and in minimizing the effects of abiotic factors and tolerance of stress in plants have

currently started to study deeply (SLAFER *et al.*, 2005; SREENIVASULU *et al.*, 2007; IQBAL *et al.*, 2017; MUQADAS *et al.*, 2020).

Molecular markers

Important and major cereals species genetic maps and marker technology are available now, these genetic maps based on molecular marker (SNAPE *et al.*, 2005; BUNTA and BUCUREAN, 2011; ALI *et al.*, 2020a). Quality and quantity of yield is controlled by large number of genes, these genes have low effect as single and great effect when work together. To assist breeding efforts Quantitative trait loci analysis is very important, in crops species there is large complicated genomic system to understand this system and to identify genetic markers QTL is required. In wheat this access is complex because of polyploidy and polymorphism and it is very simple and straight in case of wheat, barley and rice crops (ELANGOVAN, 2007). There is strong co-relation between genetic roads of cereals they help to further transfer knowledge that gained for rice or wheat. Critical study base results include abiotic stress factors analysis of QTLs which linked to evaluation for field of stress tolerated factors (LANGRIDGE *et al.*, 2006; FLEURY *et al.*, 2010). After many trails and efforts, it is seen that QTLs identification related to grain yield is not easy, as there is higher consistency in different conditions (REYNOLDS *et al.*, 2007; JAMIL *et al.*, 2011). Root ABA1 However is a major QTL which continuously affects the intra structure of root, quantity of leaf ABA, yield grain and other production traits of maize under drought stress and watered system it was found recently, it defines the benefits of practical/experimental approach (SUPRUNOVA *et al.*, 2007; ZOU *et al.*, 2012). In rice, genomic regions have been identified which are associated with grain production when there is drought or water stress (YUE *et al.*, 2006; BERNIER *et al.*, 2007), one more study performed on rice yield genetic bases of traits presenting source through QTL relationship between sink and transporter tissue and their link to yield (KUMAR, 2011; KUMAR *et al.*, 2018). New varieties development which could be drought resistance using genetic marker breeding is possible now, this could happen by interacting the genetic information with physical and morphological traits and these also related to high yield production. This experiment will also helpful for drought and heat tolerance genotypes which includes land crops and cereals relatives. QTLs in various cereals help to compare the stress tolerance this may help to locate genes and loci, for example, to drought tolerance (TRACHSEL *et al.*, 2009; HAO *et al.*, 2010).

Functional genomics

The molecular events like stress and grain development as well their internal interaction can be identifying by expression profiling. The public data base is increasing day by day by EST expressed sequence tag. Libraries of c DNA produces these ESTs they showed many tissues and growth conditions, but dominated libraries are yield and stress tolerance. In wheat genomics ESTs are especially important, wheat have a complicated genome and large size it is hard to be completed in near future. Wheat abiotic stress resistance showed the digital analysis of EST with the combination of gene annotation. Cereal research micro and macro array platform also increasing every day (BADAWI *et al.*, 2007). A DNA chip of around 2100 genes hybridized by (ZHU, 2003; SLIWERSKA *et al.*, 2007), it represents about half of the rice genome associated with c DNA properties grain filling. After hybridization of genes they test the known genes patterns

which functionally involved in processing for example genes that linked to fatty acid and carbohydrates degradation. 98 and 491 genes showed correlated expression of grain filling. On further study of genes, it was found that 171 genes also have similar regulation which suggested that it might also help in grain development or grain filling. One more experimental study suggests that there are 28 more same genes (JAIN *et al.*, 2007), all these previous results of different studies suggests that total 297 genes are linked or related to grain filling process in rice. The study about rice genome sequence has opened a pathway for further study of promoter regions which is the central control of genes and to discovered further elements of these regions. This all resulted in discover of nine different transcriptional factors which actually regulate the expressions of genes (ZHU, 2003; LAN *et al.*, 2012). The rice grain filling at high temperature and drought stress which ultimately effect when rice at milky stage. Several starch synthesis genes GBSS and SBE showed down regulation while starch using alpha amylase showed up regulation it was not only observed but these results also verified. When rice caryopses observed at high temperature there was decrease in transcription of genes that codes for AGPs and there was no effect on SSS isoforms (YAMAKAWA *et al.*, 2008). The changes that observed at this stress showed changes in transcription level and also changes observed in biochemical formation of starch grains at normal temperature and high temperature, there was reduction in amylase content and increased length of side chain of amylopectin and shortening in size of grain. Water stress observed in maize by water hold for 5-9-day post pollination drought stress, endosperm and pedicle tissue, c DNA micro array observed under this stress (SLIWERSKA *et al.*, 2007; MIR *et al.*, 2012). A remarkable difference seen in both tissue types 89 % of 79 % transcription affected (MAESTRI *et al.*, 2002; MEIR *et al.*, 2010). These were up regulated in pedicel, and 82 % out of 56 % transcription altered genes down regulated in endosperm. Genes that were affected were also different sets: HSP and stress related genes where increased in first case on the other hand cell division related genes and some degrading genes were down regulated. It was observed that endosperm division decreased under water stress after pollination, and this directly related to grain or kernel size and in maize (OBER *et al.*, 1991; LANGRIDGE *et al.*, 2006; YOUSEF *et al.*, 2020) and wheat (YANG *et al.*, 2006). 1502 expressions of maize have been analyzed and these expressions were found in response of water deficiency after pollination, changes were observed in gene expression of silk and grain. The one more interesting thing was that drought causes no change in starch synthesis genes, as compare to under shade (ZINSELMEIER *et al.*, 2002). In cereals micro array profiling of water stress cause response in whole plant it is conducted in many species (YOUNIS *et al.*, 2014; SAJEEVAN *et al.*, 2017; LI *et al.*, 2018; SHAFIQUE *et al.*, 2020a; SHAFIQUE *et al.*, 2020b). This study importantly helps in yield production increment and plants safety under drought conditions. Differences in wheat gene expression progeny were studied by XUE *et al.* (2006). They observed the low and high transpiration efficiency. Transpiration efficiency high water use water use efficiency is concerned with more yield at low or limited water condition (XUE *et al.*, 2006). Transpiration efficiency levels contrast with 93 genes from profiling 16000 genes they showed different expression in progeny lines. 1/5th of these genes were responsible to water stress. Adding more to this many other genes were also identified which were related to growth related genes they expressed with high level of transpiration efficiency. More analysis of genes will provide more information about genes which helpful in more yield in drought conditions in growth period it will provide markers which

will be useful for future breeders. Female sexual generation occur in deep female tissue it could make useful in biological experiments, like in vitro cell techniques could be possible and zygote access will be easy for scientist (FLEURY *et al.*, 2010). The mRNA from cell is now made easy to isolate by molecular biological techniques for the study of gene expression and sequence/pattern in zygote and egg cells of cereals with help of PCR (ALBA *et al.*, 2004; CONN *et al.*, 2011; YAN *et al.*, 2011; BASHIR *et al.*, 2020; TAHIR *et al.*, 2020) and by genomic method (HAZEN *et al.*, 2003; RODRÍGUEZ *et al.*, 2005) another one proteomic (NGARA and NDIMBA, 2014; PARVATHI and NATARAJA, 2016; PARVATHI and NATARAJA, 2017) technique.

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GENETSKI ODGOVOR FAZA RASTA ZA TOLERANCIJU NA ABIOTIČKI STRES SPOLJAŠNJE SREDINE KOD ŽITA

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Izvod

Potencijal prinosa i kvalitet glavnih žitarica, uključujući kukuruz, pšenicu, pirinač i ječam, poboljšali su se oplemenjivanjem i uvođenjem transgenih biljaka u poslednje tri decenije. Intenzivno se istražuje poboljšanje otpornosti na biotičke i abiotičke uslove spoljašnje sredine kako bi se zaštitio potencijal žitarica. Među abiotskim stresovima suša i toplota su dva najvažnija faktora koja su prouzrokovala velike gubitke u prinosu i kvalitetu useva. Toplotni stres dovodi do suše usled gubitka vode iz zemljišta i sa površine biljaka, pa su suša i toplota prouzrokovali kombinovane štetne efekte na morfološke, fiziološke i osobine prinosa što dovodi do smanjenja potencijala useva. Oduvek je postojala interakcija između uslova okoline i useva biljaka radi proizvodnje žita i zadrže produktivnosti. Suša i toplotni stres izazvali su promene na ćelijskom nivou, molekularne promene i promene ekspresije gena u žitaricama u različitim vegetativnim i reproduktivnim fazama / fazama rasta i razvoja useva. Kod žitarica je identifikovan veliki broj gena koji imaju povećanu ili smanjenu ekspresiju tokom uslova suše i toplotnog stresa. Međutim, postoji potreba za poboljšanjem otpornosti žitarica na nivou gena kako bi se održao potencijal prinosa i kvaliteta pod abiotskim stresnim uslovima poput suše, visokih temperature, slanosti i hladnoće.

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