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RESEARCH PROGRESS OF AP2/ERF TRANSCRIPTION FACTOR FAMILY IN IMPORTANT CROPS

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ABSTRACT

Plants have the ability to show responses against various environmental stresses. It is one of the necessities to understand stress response mechanisms to improve crops productivity and quality, under the stressed condition. The AP2/ERF transcription factors are one of the putative candidates that are involved in the regulation of biotic and abiotic stress. Most of the research has been conducted on functional analysis of AP2/ERF genes in many plants; however, a comprehensive review is required to show a broad picture of functionally characterized AP2/ERF in different plants. In this study, a comprehensive review is carried on genome-wide studies of AP2/ERF gene family and their evolutionary divergence in plant species including mustard (*Arabidopsis*, *brassica*), cereal (rice, wheat, maize, sorghum), and fiber (upland cotton and island cotton). Review exhibited that AP2/ERF superfamily is classified into four sub-families *e.g.* AP2, DREB, ERF, RAV and solicit, in which the ERF was the largest sub-family of AP2/ERF superfamily. Each subfamily was further divided into multiple groups and sub-groups. Furthermore, each plant species showed different number of paralogs showing correspondence to the plant genome size *e.g.* higher genome possess higher gene copy number. The change in copy number may be due to either tandem gene duplication or whole genome duplication during evolutionary adaptation that developed special feature in plant species under environmental stresses. Moreover, current study also surveyed on the expression of AP/ERF genes with the conclusion that expression of AP2/ERF produced tolerance against biotic and abiotic stresses. However further studies are required to improve crops resistance by studying the same variables and gene families in different plants.

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INTRODUCTION

Environmental stress like drought, high salinity, extreme temperature, lack of oxygen have an adverse impact on plant growth and this, in turn, leads to the loss of crop yield and the crop quality (Awasthi *et al.*, 2014; Qaisrani *et al.*, 2022). According to Peters *et al.* (2012), due to the increase in the level of carbon dioxide all over the world, the climatic conditions are changing rapidly with the considerable increase in the temperature leading to the poor the quality of agricultural land. These type of stresses alter the morphology and physiology of the plant's cell, resulting changes in function, such as cell division and cell growth as well as metabolism alteration (Agarwal *et al.*, 2006; Yamasaki *et al.*, 2013). It has been hypothesized that for the survival of the plant, it gets a signal from surrounding and produce a response to regulate and fix its mechanism. Most of plant hormones, transcriptional factors or regulators, signalling molecules and other secondary messenger molecules in stress condition gets activated and allows the plants to respond and act so to allow them to withstand such harsh conditions (Cvikrová *et al.*, 2013; Gilroy *et al.*, 2014). Activation of such a signal cascade acts to induce activation of certain stress responsive plant genes which produces enzyme and other different kind of proteins that help the plant to regulate its metabolic activities that are involved in helping the plant in response to withstand stress stimuli (Casaretto *et al.*, 2016). Commonly, hormones like abscisic acid act as important growth stimulator supporting the plant against high salt and drought stress (Danquah *et al.*, 2014). The main focus of this review is about the action of certain stress-responsive transcription factors that help in activating the genes that aid in plant survival. Therefore, in such responsive stress conditions, it is important to examine the responsive genes and its expression to improve crop yield under stress condition (Trewavas, 2005). In Signaling transcription factor plays important role in activation and inactivation of defence gene expression as well as regulation and interaction of these genes with other gene families.

Transcription Factors

In molecular biology transcription factors (TFs) are a protein that controls gene expression at DNA to mRNA level. This protein bind to DNA sequences at upstream

and downstream of the gene to regulate any gene transcription. This also acts as co-activator or co-suppressor that controls the expression of a gene at right time, in right cell and the right amount. Group of Transcription factors coordinate to direct a cell for cell division, cell growth and cell death (Mizoi *et al.*, 2012; Sun *et al.*, 2016). The number of transcription factor depends on genome size, for example, there are 2600 TFs in human genome and plants have multiple times of human TFs (Asensi-Fabado *et al.*, 2017). The selective activation and inactivation of genes enable us to understand the cellular behaviour towards internal and external environment (Schmid *et al.*, 2005). Different transcription factor families regulate different processes like light and stress signalling, seed maturation, flower development, development of the embryo, root cells maturation and pathogen defence etc (Mizoi *et al.*, 2012; Sun *et al.*, 2016; Hussain *et al.*, 2016b; Zandalinas *et al.*, 2017).

Transcription factors (TFs) are directly involved in gene expression by interaction with DNA-binding element and cis-element in the promoter region (Mizoi *et al.*, 2012; Sun *et al.*, 2016). Particular environmental signals activate specific responsive mechanisms in plants. These processes are involved in the regulation of gene through transcription factors (Mizoi *et al.*, 2012; Ohme-Takagi and Shinshi, 1995).

Transcription Factors Families

According to transcription factor classification, 129-288 TFs classes were identified in 83 species. These classes were categorized into 58 families such as AP2, ERF, WORKY, MYB, RAV, MICK etc. Plants species has more transcription factor them mammals. For example, 2296 TFs found in *Arabidopsis thaliana* and 1891 TFs in *Oryza sativa*, are classified into 58 and 56 transcription families respectively (Jin *et al.*, 2014). Several other families of transcription factors like bZIP, HSF, C2H2 and NAC have been identified that have an important role in growth and stress response (Jin *et al.*, 2014; Li *et al.*, 2008). As the expression profiles of Arabidopsis under stress identified 7000 genes upregulate and downregulate under specific stress like cold, drought and salinity condition (Sun *et al.*, 2016; Seki *et al.*, 2002) (Figure 1). So, transcription factor has a crucial role under biotic and abiotic stress to maintain plant growth and development and each transcription family response

to a specific stress.

AP2/ERF Transcription Factors and its Classification

In the past decade, the AP2/ERF family has become more attention gene family. A hypothesis states AP2/ERF family originated in result of horizontal transfer from bacteria/viruses to plants (Magnani *et al.*, 2004; Shigyo *et al.*, 2006). Many AP2/ERF genes were identified and characterized in angiosperms (both monocotyledons and dicotyledons), gymnosperms and microorganisms (bacteria, ciliates, and viruses) (Shigyo *et al.*, 2006; Xu *et al.*, 2008; Hussain *et al.*, 2016b). An important role of AP2/ERF gene family has been reported in the regulation of transcriptional signaling linked with stress response. A single AP2/ERF gene can control various stress factors and in the regulation of different processes, there developed proteins contribute as positive and negative regulators (Chen *et al.*, 2012). The regulatory involvement of AP2/ERF family has been studied in the biotic and abiotic stresses like UV radiation, salicylic acid, H₂O₂

and in plant defense (Rahaie *et al.*, 2013). Moreover, a number of studies had identified the involvement of these factors in other morpho-physiological activities like embryogenesis, development of seed coat and trichomes, regulation of biosynthetic pathways and hormonal signaling. However, the exact mechanism in response to stress is not yet fully understood. But in these days researchers have worked for the functional analysis of the AP2/ERF transcription factor in the response against stresses (Ülker and Somssich, 2004; Rushton *et al.*, 2010). The AP2/ERF transcription factor is involved in diverse regulatory function of plant development, growth and biotic and abiotic stress responses such as reproductive and vegetative development cell division, cell propagation, plant hormone responses, high salinity, low temperature, embryogenesis (Jofuku *et al.*, 1994; Guillaumot *et al.*, 2008; Jin *et al.*, 2014; Licausi *et al.*, 2010). In view of these important function of AP2/ERF transcription family, the identification and characterization of AP2/ERF family became the main subject of transgenic plant researchers.

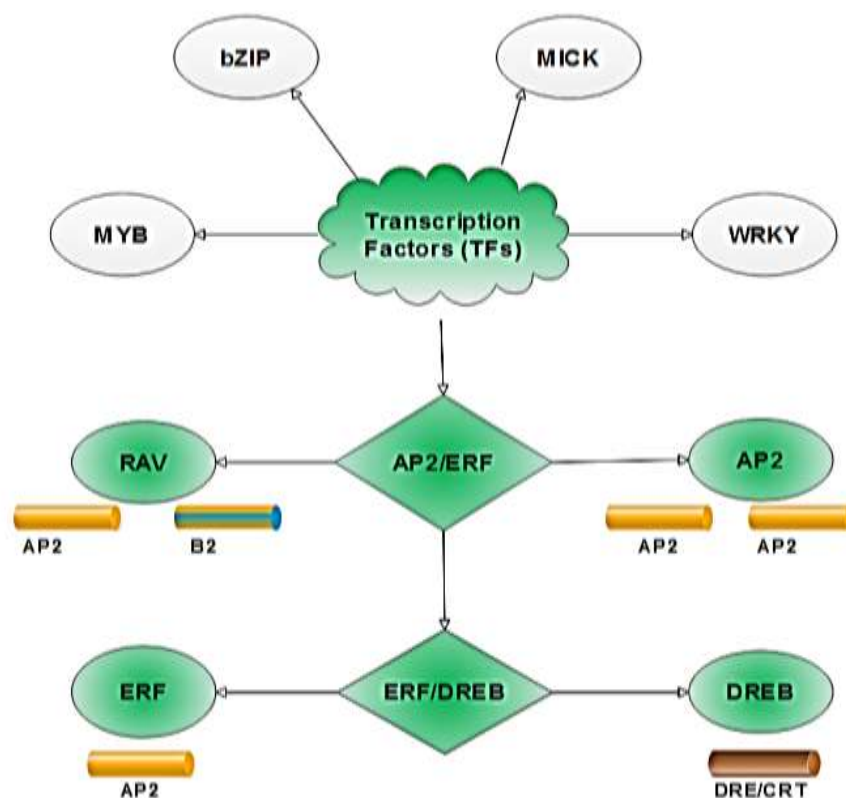


Figure 1. Classification of Transcription factors drawn through Edraw Max 8.4. Coloured classification is the current subject of this paper. Cylindrical shapes its number and colour are showing protein domain present in respective families.

The first step of AP2/ERF TFs understanding was its classification i.e. AP2 (APETALA2) with 2 AP2/ERF domain in protein sequence, ERF (Ethylene responsive Factor) with one AP2/ERF domain, RAV (related to ABI3/VP1) with two different domains; AP2/ERF domain and B3 binding domain, DREB (Dehydration Responsive Element Binding protein), and other related binding domain, (Table 1; Figure 1), (Nakano *et al.*, 2006; Sakuma *et al.*, 2002). The AP2/ERF TFs have

DNA-binding domain, consist of about 60 to 70 amino acid, that directly interacts with the dehydration-responsive element (DREB), c-repeat element (CRT) and *cis*-acting element (CE) at the downstream of the target gene of a promoter. Thus, stress-responsive genes, having DREB, stress-responsive elements and CRT elements in their promoters shows strong expression under biotic and abiotic stress that lead plants protection in adverse condition.

Table 1. Genome-wide survey of AP2/ERF in different plant species.

Plants	Total AP2/ERF	Classification					Reference
		AP2	ERF	DREB	RAV	Soloist	
Foxtail Millet	171	28	90	48	5	-	(Lata <i>et al.</i> , 2014)
Chines cabbage	291	49	139	109	14	1	(Song <i>et al.</i> , 2013)
Peach	131	21	104	-	5	1	(Zhang <i>et al.</i> , 2012)
Sorghum	126	16	105	-	4	1	(Yan <i>et al.</i> , 2013)
Maize	184	22	107	51	3	1	(Du <i>et al.</i> , 2014; Hussain <i>et al.</i> , 2016b)
Moso Bamboo	116	28	80		7	1	(Wu <i>et al.</i> , 2015)
Carrot	267	38	143	71	12	3	(Yao <i>et al.</i> , 2015)
Arabidopsis	147	18	65	57	6	1	(Sakuma <i>et al.</i> , 2002)
Grapevine	149	20	86	36	6	1	(Licausi <i>et al.</i> , 2010)
Rice	164	26	79	52	7	0	(Wu <i>et al.</i> , 2015)
Banana	265	67	119	81	16	3	(Lakhwani <i>et al.</i> , 2016)
Banana wild	318	71	144	99	22	4	(Lakhwani <i>et al.</i> , 2016)

Regulatory Mechanism of AP2/ERF Transcription Factor

ERFs and DREBs are two major subfamilies of the AP2/ERF family and play important roles in the regulation of abiotic and biotic stress responses (Mizoi *et al.*, 2012; Sun *et al.*, 2016). Generally, DREB transcription factors activate diverse dehydration and cold-regulated (RD/COR) genes by interacting with DRE and CRT elements (A/GCCGAC) present in the promoters of RD/COR genes that are responsive to both low-temperature and water deficiency, such as COR15A, RD29A/COR78, and COR6.6 (Mizoi *et al.*, 2012; Liu *et al.*, 1998; Lucas *et al.*, 2011; Sharoni *et al.*, 2011; Stockinger *et al.*, 1997). Recently it is studied that DREB bind to DRE and GCC-cis element and their binding activity is higher to DRE then GCC-box (Mizoi *et al.*, 2012; Sun *et al.*, 2016). For binding activities, Lys9 plays a key role in GCC box-binding activity and Val14th and Glu19 are essential in the AP2 domain of DREB (Cao *et al.*, 2001). V1114 when replaced with the other like Alanine then

show no binding activities while Leucine at Leu19 shows strong binding activities (Cao *et al.*, 2001; Sakuma *et al.*, 2002; Yao *et al.*, 2015).

ERF transcription factors directly regulate pathogenesis-related (PR) gene expression by interaction with DNA-binding factor at GCC-box (GCCGCC) (Büttner and Singh, 1997; Sakuma *et al.*, 2002; Zarei *et al.*, 2011a). Although there is large divergent among sequences the two important residues, 14th Val/Ala and 19th Glu conserved in AP2/ERF domain are important to recognize cis-Element. It was reported that the changes of Phe62 to Serine and Gly156 to Arginine enhance the GCC-box binding activity of *Brassica napus* ERF-B3-hy15 protein (De Boer *et al.*, 2011).

The Tobacco ERF factor-ORC1, required for both GCC-motif (TGCGCCC) and G-box (GCACGTTG) elements for maximum transactivation in the promoters of tobacco nicotine genes (De Boer *et al.*, 2011). So it is possible that the different AP2/ERFs are involved in the regulation of downstream target genes. It is reported that AP2

subfamily binds to the element GCAC(A/G)N(A/T)-TCCC(A/G)ANG(C/T) (Gong *et al.*, 2008; Nole-Wilson and Krizek, 2000). This DNA sequence is quite different from

the consensus sequence CCGA/CC bound by ERF and DREB subfamilies and not consist of two similar-half sites (Figure 2) (Krizek, 2003).

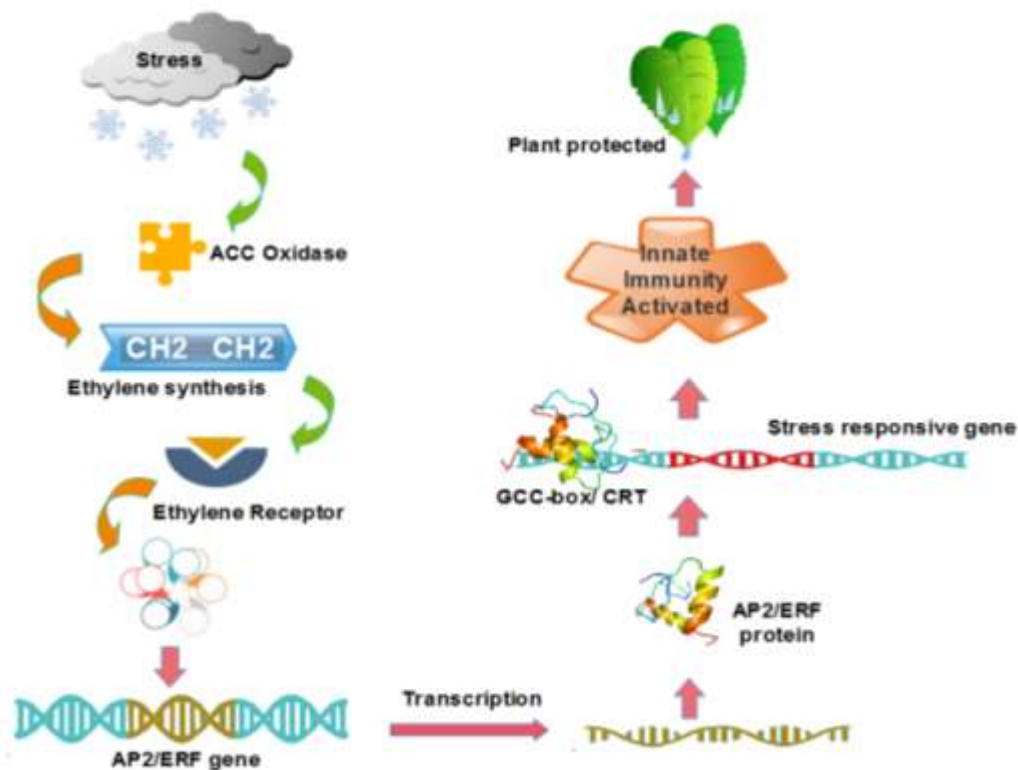


Figure 2. Biotic and Abiotic stress regulatory pathway through AP2/ERF genes, drawn through Edraw Max 8.4.

Genome-wide studies of AP2/ERF TF in important crops

The genome-wide analysis is to study the gene epidemiology, the genetic association among the different groups of genes. These studies compare the DNA of different participants. In contrast to the analysis methods of one or few genes, the genome-wide analysis study analyzes whole genome (Pearson and Manolio, 2008). Genome-wide analysis studies are a very important advancement in investigating the variations among the genes and genome of different species. Different approaches have been used in Genome-wide studies to investigate the genome of species. In different plant species, genome-wide analysis has been used to identify different groups of genes, variations among different genes and among different species. Classification on the basis of genetic differences and homology among genes has also been done by using genome-wide analysis. Genome distribution and protein

domains analysis is also be practised. The evolutionary study of genes through phylogeny analysis to identify the different group's evolution and parental gene relationship had also been studied (Table 1). The comparative genome-wide studies showed that transcription regulatory genes are abundantly present in plant and animal genomes. This study also revealed that the diversity and evolution of eukaryotes seem to be related to the expansion of lineage specific transcription regulator families (Table 1) (Agarwal *et al.*, 2011).

Arabidopsis (*Arabidopsis thaliana*)

The first genome-wide study of AP2/ERF family was carried in *Arabidopsis thaliana* (Sakuma *et al.*, 2002) and classified into ERF, AP2, RAV and soloist. Later, Nakano *et al.* (2006) carried again genome-wide study and identified 147 AP2/ERF characterizing into AP2, ERF, DREB, RAV and soloist. *Arabidopsis thaliana* has a

relatively small genome of approximately 135 megabase pairs (Mbp) (Initiative, 2000). It was long thought to have the smallest genome of all flowering plants, showing a genome size of approximately 61 Mb (Fleischmann *et al.*, 2014). So, the number of genes in *Arabidopsis* lesser as compared to other large genomes plant species (Shigyo *et al.*, 2006; Xu *et al.*, 2008; Hussain *et al.*, 2016b). Based on the identification and characterization of AP2/ERF superfamily in *Arabidopsis*, many research have been done to identify their role in plants. For instance, Rashotte, 2006, determined that the Ap2 transcription factor in generating cytokinin response, Zhu *et al.* (2010) identified the involvement of AP2/ERF in BA, salt and osmotic stress responses, Zarei *et al.* (2011b) showed the AtAP2/ERF GCC boxes in jamonate/ethylene mediated activation. Abogadallah *et al.* (2011) over express AP2/ERF gene in *Arabidopsis* showed improvement in drought and salt tolerance, Huang *et al.* (2015) review also discussed detail ERF factor responses in the immunity of *Arabidopsis*. Dubois *et al.* (2015) identified the role of ERF6 and ERF11 in the antagonistic relation with the mannitol-induced growth inhibition in *Arabidopsis*. Park *et al.* (2016) suggested the positive regulation of cuticular wax biosynthesis in *Arabidopsis* by AP2/ERF transcription factor. The overexpression of *Camellia sinensis* DREB in increased salt and drought tolerance in transgenic *Arabidopsis* (Wang *et al.*, 2017), similarly, over expression of NnDREB1, NnDREB2, VrDREB2A, ScDREB8, AhERF in transgenic *Arabidopsis* improved drought and salt tolerance (Cheng *et al.*, 2015; Massange-Sánchez *et al.*, 2016; Chen *et al.*, 2016; Cheng *et al.*, 2017; Liang *et al.*, 2017). Sun *et al.* (2018) identified positive regulation of AP2/ERF in osmotic modulation and disease resistance in *Arabidopsis*, Li et al expressed sweet potato AP2/ERF in *Arabidopsis*, the transgenic *Arabidopsis* showed tolerance against salt and drought, the Giuntoli and Perata (2018) review summarized crucial role of ERF transcription factor in the regulation of physiological role in *Arabidopsis*. Huang *et al.* (2018b) determined the negative regulation of ERF19 when associated with NINJA in *Arabidopsis*. The heterologous over expression of *Lithospermum erythrorhizon* (LeERF-1) increased drought and pathogen resistance in *Arabidopsis* (Fang *et al.*, 2019). There are may be many others studies that may not included in this study. But still we need to carry more functional analysis of AP2/ERF genes, as there are 147 AP2/ERF genes in *Arabidopsis* and much of them

are still undiscovered regarding there functional analysis.

Rice (*Oryza sativa*)

Rice is another important crop, just after availability of whole genome sequence of, the trend of genome-wide study also started in the rice plant. Just like *Arabidopsis* genome-wide study AP2/ERF, this superfamily was also studied in rice in 2006 that identified only 139 ERF genes (Nakano *et al.*, 2006), later rice a complete genome-wide study of AP2/ERF superfamily was conducted by Rashid et al 2012 (Rashid *et al.*, 2012), which identified 170 AP2/ERF genes and classified into AP2, ERD, DREB, RAV and soloist. The rice genome was sequenced in 2002 with 420Mb genome size that much higher than *Arabidopsis* (61Mb). So, the number of AP2/ERF genes in rice was higher than *Arabidopsis*, showing duplication and originated multiple paralogs during divergence from dicot and monocot. However, the number of AP2/ERF gene in rice was not so much higher as compared to the size of genomes. Because monocot has lower number of AP2/ERF gene then dicots (Table 1). In the case of AP2/ERF role in rice multiple research have been conducted that showed the crucial role of these transcription factor in the development and growth of rice plant. For instance, OsDREB gene activate the drought, high salt and cold stress tolerance mechanism in rice (Dubouzet *et al.*, 2003). Similarly, the overexpression of sub1A ERF gene produced tolerance to submergence (Xu *et al.*, 2006), the TSRF1-ERF transcription factor improved drought tolerance in rice (Quan *et al.*, 2010), the OsAP2LP gene cloning and expression depicted its role in stresses in response (ZHOU *et al.*, 2010), OsDREB1F overexpression increased drought, salt and low temperature tolerance in *Arabidopsis* and rice (Wang *et al.*, 2008), expression of OsDEB2A also enhanced dehydration, and salt stress tolerance in rice (Mallikarjuna *et al.*, 2011), OsEATB regulate gibberellin biosynthetic mechanism in rice (Qi *et al.*, 2011), OsEREBP1 overexpression improved biotic and abiotic stress in rice (Jisha *et al.*, 2015), the OsRMC is also controlled by AP2/ERF in rice (Serra *et al.*, 2013), over expression of TERF2 transcription factor conferred cold tolerance in rice (Tian *et al.*, 2011), the AP2/ERF genes also regulated RLK6 gene in rice (Wang *et al.*, 2011b), Sun *et al.* (2017a) reviewed the function and structure of AP2/ERF in rice summarized the important

contribution of AP2/ERF gene in multiple biological and physiological function in rice plant. Recent studies also demonstrated AP2/ERF superfamily contribution in the water deficit response (Mawlong *et al.*, 2018), the transcriptional regulatory network also demonstrated AP2/ERF gene responses under drought stress in transgenic rice (Ahn *et al.*, 2017), Sun *et al.* (2017b) also demonstrated involvement of AP2/ERF transcription factor in the trichom formation in rice, Tezuka *et al.* (2019) depicted the OsERF83 positively regulated *Magnaporthe oryzae* disease resistance (Tezuka *et al.*, 2019), AtDREB1A expression in transgenic rice showed tolerance to salt stress, overexpression of OSDREB1G conferred resistance cold stress in rice (Moon *et al.*, 2019), expression of OsDRAP1 also conferred tolerance in rice (Huang *et al.*, 2018a), the SbAP37 over expression in transgenic rice modulate stresses and protein profiling in leaf (Parveda *et al.*, 2017). The literature survey listed many AP2/ERF genes in rice, but still there are many other members that are still unknown. The expression of AP2/ERF genes showed different biological and physiological effect on rice. We need further improvement in the rice plant against biotic and abiotic stresses, because rice is one of the most important edible crops in the world.

Maize (*Zea mays*)

Maize, also known as corn, an annual crop that belongs to the family of grass and is considered as the 3rd most significant cereal crops in the world. In addition to human food, maize has a major contribution in animal feeds and many other purposes like bioethanol production and phytochemical metabolites. In viewing these important features, now maize has become the main subject of researchers. Maize plant was sequenced in 2009 with 2.3 Gb genome size. The availability of *Zea mays* genome provides facility to carry genomic and functional studies of maize genes.

The AP2/ERF transcription factor was also extensively studied in maize plants and their important role in plant growth and physiology was also exhibited. In 2002, Kizis and Pagès (2002) identified the role of DBF1 and DBF2 in the regulation of ABA-dependent pathway to induced drought tolerant in maize. Similarly, the DREB1/CBF AP2/ERF transcription factor over expression in maize improved cold stress tolerance (Qin *et al.*, 2004), in 2007, Qin *et al.* (2007) identified the functional analysis of

ZmDREB2A under drought and heat stresses in maize (Qin *et al.*, 2007), the over expression of *ZmDBP3* gene in transgenic *Arabidopsis* enhanced the drought and cold tolerance (Wang and Dong, 2009). In 2010 the Zhuang *et al.* (2010) carried identification, evolution and expression of AP2-like gene in maize (Zhuang *et al.*, 2010), Wang *et al.* (2011a) isolated ZmDBP2 and overexpressed in transgenic *Arabidopsis* that improved the drought stress tolerance in plant. The first genome-wide analysis of AP2/ERF in *Zea mays* in 2012 (Zhou *et al.*, 2012) just after availability of whole genome assembly of maize. This genome-wide study identified 292 AP2/ERF genes and classified them into AP2, DREB, ERF and RAV. The number of AP2/ERF genes in maize was greater than both *Arabidopsis* (139 AP2/ERF) and rice (172 AP2/ERF), because of its large genome size then the two mentioned plants. After Genome-wide data availability multiple genome wide association and expression profiling was carried in maize. For instance, in 2013, Liu *et al.* (2013) carried *ZmDREB* genetic association with drought at seedling stage of maize. In 2014, Du *et al.* (2014) carried genome-wide analysis of AP2/ERF in maize under waterlogging stress and showed their role in drought tolerant, in 2016, Hussain *et al.* (2016a) performed a detailed genome-wide characterization, structural and functional prediction of ERF family in maize. After genome-wide identification and characterization of AP2/ERF in maize, the functional analysis of individual genes become the research target of researchers. In 2016, Zhou *et al.* (2016) identify ZmDB3 as novel AP2/ERF transcription factor involved in multiple abiotic stress tolerance. Similarly, the ZmDREB4.1 identified as negative regulation of plant growth and development (Li *et al.*, 2018), the ZmEREB94 involve in the starch granules formation in maize (Li *et al.*, 2017), ZmERF1 is involve in hormone and stress response, ZmEREB156 gene involved in sucrose and ABA regulation in starch biosynthesis in maize (Huang *et al.*, 2016), over expression of DREB genes increased maize yield (Simmons and Sivasankar, 2018), ZmEREB180 shows water logging tolerance in maize (Yu *et al.*, 2019). The genome-wide study of AP2/ERF genes shows 184 AP2/ERF genes classifying into five subfamilies i.e. ERF (107 genes), DREB (51 genes), AP2 (22 genes), RAV (3 genes) and one soloist gene (Du *et al.*, 2014; Hussain *et al.*, 2016a). Phylogenetic tree shows further subgroups of DREB and ERF that were also similar to other crop. The literature

survey of AP2/ERF genes in maize summarized that AP2/ERF genes have great contribution in the regulation of plant growth and development; however, lots of AP2/ERF genes are still uncharacterized regarding their function. So, to improve the crop quality of maize, it is require uncovering important AP2/ERF genes for future use.

Wheat (*Triticum aestivum*)

Wheat is a grass, also known as *Triticum aestivum* (common wheat), belongs to poaceae family. It produces cereal grains which is use as a staple food. Wheat is the one of a leading crop that is cultivated and exported much more than any other crop. It is an important source of carbohydrates for human as well as animals. Wheat genome is more complicated than other poaceae family, as it is hexaploid with AABBDD (A genome from *T. monococcum* wheat, B genome from *T. turgidum*, D genome from *T. tauschii*) genome composition. The first genome sequence assembly was done in 2014, but later in 2018 a new wheat genome assembly was also published by international wheat genome sequence consortium (IWGSC).

Wheat production is promising due to multiple biotic and abiotic factors. One of an abiotic factor is drought which is a major problem in wheat production. Plant breeding and genetics are trying to developed drought tolerant wheat through conventional breeding methods. A drought tolerant screening strategy is not only increase its tolerance against drought but also enhance its yield.

In order to find the genetic makeup of tolerant plants multiple studies have been done on different drought related genes including, transcription factor and other aquaporins gene families. The Plant transcription factor database

(<http://plantfdb.cbi.pku.edu.cn/index.php?sp=Tae>)

identified 3606 Transcription factors with 51 families using denovo approach. Of these 51 families, AP2/ERF gene family is one of a largest family that contributed in drought tolerant. A genome-wide study has been done by Jin et al 2010;

(<https://link.springer.com/article/10.1007%2Fs11033-010-0162-7>), and predicted 117 AP2/ERF gene (57 DREB, 47ERF, 9AP2, 3RAV and one Soloist). However, this number is very low as compared to other monocots, so new genome-wide study is required using latest

wheat genome assembly with advance approaches. Multiple AP2/ERF genes have been isolated and functionally characterized. For instance, in 2010 Dong et al overexpressed TaPIEP1, a pathogen-induced ERF, confer resistant to fungal pathogen(<https://link.springer.com/article/10.1007/s10142-009-0157-4>), Similarly, in 2012 Dong et al (<https://doi.org/10.1016/j.gene.2012.09.039>), cloned TaERF4 and expressed in wheat (<https://www.sciencedirect.com/science/article/pii/S037811912011201>), that enhance sensitivity of plants to salinity, suggesting that TaERF4 may act a transcription repressor.

Chinese cabbage (*Brassica rapa*)

Brassica crops are used for human nutrition and are important in daily life. Chinese cabbage (*Brassica rapa*) is one of best worldwide grown crops of Brassica crops, economically important due to its high yielding capacity and good quality, which attracted researchers to study its genetic and genomic characteristics. Genome sequencing of Brassica was completed in 2011 under *Brassica rapa* Genome Sequencing Project Consortium (Wang *et al.*, 2011c). The *Brassica rapa* genome contains 41,174 coding genes. In viewing the importance of AP2/ERF gene family, a genome-wide study was made by Song *et al.* (2013). They identified 291 AP2/ERF genes, consisting of 109 DREB, 139 ERF, 49 AP2, 14RAV and 1 Soloist gene. The number of genes in chines cabbage is higher than the above-mentioned species because the genome of chines cabbage is larger as compared to foxtail millet and Arabidopsis. Furthermore, expression of AP2/ERF gene in *Brassica rapa* also identified that maximum expression takes place in the root, which is 31.95%, and minimum in buds, which is 5.85% (Table 1; Figure 3) (Song *et al.*, 2013). A similar expression was also seen in Arabidopsis and foxtail millet. So, it means most of the AP2/ERF genes are express in root tissue that is the main tissue which deals the drought and salinity condition.

Sorghum (*Sorghum bicolor*)

Sorghum belongs to grass species and is used as food for animals and humans, as well as sorghum is also used for biofuel production. It is among tropical and subtropical grown crops (Dillon *et al.*, 2007). Sorghum

is considered as the world's fifth most commonly grown cereal crops. It is an annual as well perennial crop (Prasad and Staggenborg, 2009). Sorghum has the high tolerance to drought, salinity and toxic environment (Almodares *et al.*, 2011; Bibi *et al.*, 2012). Research is being conducted to develop a

genetic cross that will make the plant more tolerant to cooler temperatures and to unravel the drought tolerance mechanisms since it is native to tropical climate (Ogbaga *et al.*, 2014). The genome of *Sorghum bicolor* was sequenced between 2005 and 2007 (Paterson *et al.*, 2009).

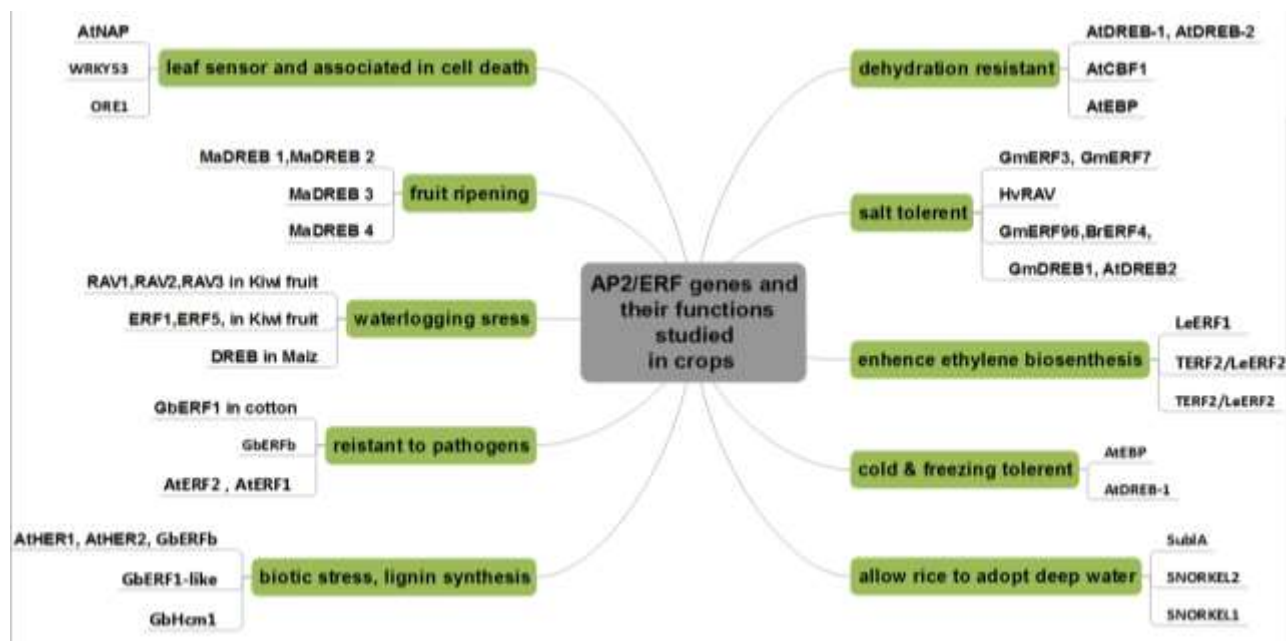


Figure 3. AP2/ERF transgenic expressions in different crops against biotic and abiotic stress, drawn through Edraw Max 8.4.

In sorghum, the total of 126 AP2/ERF gene families was predicted and distributed into 16 AP2, 105 ERF, 4 RAV and 1 soloist subfamilies (Yan *et al.*, 2013). On the basis of phylogenetic analysis, the ERF family was divided into 12 subgroups, from A1-A6 (group A) and B1-B2 (group B). Group A encodes CBF/DREB proteins and Group B encodes ERF proteins (Sakuma *et al.*, 2002). The total of 105 SbERFs genes was spread into 33 sister groups. Among 105 SbERF genes, 13 genes were predicted to have tissue-specific expression; SbERF 5 in the embryo; SbERF 7 in the root; SbERF 1, 19, 20, 26, 57, 72, and 74 in seedlings; SbERF 45 in the rhizome; SbERF 14 and 71 in leaves and SbERF 105 in the ear. Also, the genes are irregularly distributed on 10 chromosomes, and the maximum number is on chromosome 2, which contains 18 genes, and the minimum number is on chromosome 8 which contains 2 genes, and the interesting thing is that all genes are located on either the top or bottom of the chromosome (Table 2; Figure 3).

Sea Island cotton (*Gossypium barbadense*)

Cotton is one of the major crops grown in Pakistan and is also a worldwide renowned crop grown for its economic importance. A lot of stress factors (biotic and abiotic stress factors) are known to cause a reduction of quality and yield in the cotton crop worldwide (Liu *et al.*, 2017). Among all those stress factors in cotton, fungal-induced *Verticillium wilt* (*V. wilt*) is one of the major problems that has been studied extensively (Cai *et al.*, 2009). *Gossypium barbadense* (Sea Island cotton) is more tolerant of the pathogenic fungus wilt (*V. wilt*).

Liu *et al.* (2017) by using the technique of RACE in *Gossypium barbadense* identified and reported another AP2/ERF TFs gene which is of novel kind and they named it as *Gossypium barbadense* ethylene responsive factors (*GbERFb*), they induced the *GbERFb* gene expression by applying treatments with ethylene, methyl jasmonate, salicylic acid, by inducing wounds, H₂O₂ and by infecting with soil-borne pathogenic fungus *Verticillium dahliae*

which showed that in response to such stresses GbERFb recognizes and binds to the GCC box involving cis-acting elements and it can also interact with *Gossypium barbadense* mitogen-activated protein kinase (GbMAPKb). Evidence indicate that *GbERF1-like* TFs are produced in response to the biotic stresses and provide resistance to wilt caused by *Verticillium dahliae* and are involved in lignin synthesis (Guo *et al.*, 2016; Meng *et al.*,

2010). Over-expression of the EREB1 in cotton can increase tolerance of cotton cultivars to *Verticillium dahliae* (Meng *et al.*, 2010). Similarly, over-expression of ethylene responsive factors like *GbERF1-like* in Sea Island cotton, can enhance the tolerance of cotton and *A. thaliana* against the *Verticillium dahliae*, while its down-regulation increases the cotton susceptibility to *Verticillium wilt* (Table 1; Figure 3) (Liu *et al.*, 2017).

Table 2. Transgenic plants expressing different AP2/ERF transcription factors and their roles.

Gene Name	Plant	Functions	Reference
RAV1			
RAV2			
ERF1	Kiwi fruit	Water logging treatment	(Zhang <i>et al.</i>)
ERF5			
DRED			
MaDRED1			
MaDRED2	Banana	Regulatory roles in fruit ripening	(Xiao <i>et al.</i> , 2013)
MaDRED3			
MaDRED4			
AtNAP			
ORE1	<i>Arabisopsis</i>	Significantly involved in leaf senescence	(Guo and Gan, 2006)
WRKY53			(Kim <i>et al.</i> , 2009)
GbERFb	Sea island cotton	Disease resistance to <i>Verticillium dahliae</i> (<i>V. dahliae</i>) infection, Crop resistance to pathogens	(Miao <i>et al.</i> , 2004)
GbERF1-like			(Liu <i>et al.</i> , 2017)
GbHcm1			(Guo <i>et al.</i> , 2016)
GbWRKY1		Response to biotic stress	(Zhang <i>et al.</i> , 2016)
rd29A			(Li <i>et al.</i> , 2014)
DRER2	<i>Arabidopsis</i>	Dehydration	(Jaglo-Ottosen <i>et al.</i> , 1998;
CBF1			Kasuga <i>et al.</i> , 1999;
DREB-1			Sakuma <i>et al.</i> , 2002)
AtEBP			(Hsieh <i>et al.</i> , 2002)
JERF3			(Liu <i>et al.</i> , 1999)
GmERF3			(Büttner and Singh, 1997)
GmERF7			(Wang <i>et al.</i> , 2004)
SodERF3	Tobacco	Salt tolerance	(Zhang <i>et al.</i> , 2009)
GERF1			(Zhai <i>et al.</i> , 2013)
ERF96			(Trujillo <i>et al.</i> , 2008)
HARDY			(Wang <i>et al.</i>)
HvRAF			(Karaba <i>et al.</i> , 2007)
DREB2			<i>Arabidopsis</i>

BrERP4			
GmDREB1	Soybean		(Jin <i>et al.</i> , 2010)
PDF1.1			(Meng <i>et al.</i> , 2013)
PDF1.2	<i>Arabidopsis</i>	Enhance resistance to Botrytis	(Meng <i>et al.</i> , 2013)
AtERF73	<i>Arabidopsis</i>		(Li <i>et al.</i> , 2007)
LeERF1	Tomato	Enhance Ethylene Biosynthesis	(Xiao <i>et al.</i> , 2013)
TERF2/LeERF2			(Zhang and Huang, 2010)
SubIA			
SNORKEL1	Rice	Allow rice to adept deep water	(Hattori <i>et al.</i> , 2009)
SNORKEL2			

CONCLUSION

With the advancement in genome sequencing technologies, now, several complete with highly refined genome assemblies are available. Due to availability of these assemblies and bioinformatics tools, it became possible to carry genome-wide studies of gene families. The genome-wide study is a powerful approach to identify gene families in new assembled genomes. It also provides clear classifications, based on genes and proteins features, which is helpful for functional validation. One example of genome-wide study is the classification and expression profiling of AP2/ERF superfamily in many important crops. In this review we have provided a detail report of all genome-wide studies in agronomically important crops. As AP2/ERF superfamily is a large family of transcriptino factor that regulate stress responsive genes. The literature servary also demonstrated its involvedmen in multiple biotic and abiotic stress reponses in many crops. Howeve, still, there is limited infomration regarding its fucntional validation. The current assembeled genome-wide studies might be helpful for the crops improvement, especially plant tolerance under drought, salinity, cold and freezing and diseases, by applying advance molecular biology tools like genetic engineering and genome editting on AP2/ERF genes.

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Consent for publication

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Availability of data and materials

All data generated or analyzed during this study are included in this published article and its supplementary information files.

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CONFLICT OF INTEREST

The authors have not declared any conflict of interests.

AUTHORS CONTRIBUTIONS

All the authors contributed equally to this work.

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