

REVIEW

Open Access



# Multiple regulatory roles of AP2/ERF transcription factor in angiosperm

Chao Gu\*, Zhi-Hua Guo, Ping-Ping Hao, Guo-Ming Wang, Zi-Ming Jin and Shao-Ling Zhang\*

## Abstract

APETALA2/ethylene response factor (AP2/ERF) transcription factor (TF) is a superfamily in plant kingdom, which has been reported to be involved in regulation of plant growth and development, fruit ripening, defense response, and metabolism. As the final response gene in ethylene signaling pathway, AP2/ERF TF could feedback modulate phytohormone biosynthesis, including ethylene, cytokinin, gibberellin, and abscisic acid. Moreover, AP2/ERF TF also participates in response to the signals of auxin, cytokinin, abscisic acid, and jasmonate. Thus, this superfamily is key regulator for connecting the phytohormonal signals. In this review, based on the evidence of structural and functional studies, we discussed the multiple regulator roles of AP2/ERF TF in angiosperm, and then constructed the network model of AP2/ERF TF in response to various phytohormonal signals and regulatory mechanism of the cross-talk.

**Keywords:** AP2/ERF TF, Stress, Plant growth and development, Fruit ripening, Phytohormones

## Background

The superfamily APETALA 2/ethylene response factor (AP2/ERF) has been studied in many plants, which have a range of 119–200 members (Du et al. 2014; Nakano et al. 2006; Rao et al. 2015; Zhuang et al. 2008), and have been reported in responses to ethylene, stress, metabolic, fruit ripening and senescence (Han et al. 2016; Koyama et al. 2013; Lee et al. 2012; Li et al. 2007; Fits and Memelink 2000; Trujillo et al. 2008; Zhu et al. 2014). All the time, regulatory mechanism of AP2/ERF TF in these fields were wide-spread studies by many scientists and their research teams, and increasing experimental evidence was exploited to elucidate the detailed roles in each field (Guo and Ecker 2004; Liu et al. 2014; Pré et al. 2008; Taketa et al. 2008; Tang et al. 2016; Xiao et al. 2013; Yin et al. 2016). Herein, research advance of AP2/ERF TF was reviewed in plant, and the doubtful viewpoints were also discussed.

## Classification and DNA-binding elements

According to previous reports, the superfamily AP2/ERF members contain a common DNA binding domain, AP2 domain. Based on the difference of this domain in copy numbers, AP2/ERF TF could usually be divided into four families, AP2, ERF, RAV, and Soloist (Nakano et al. 2006; Licausi et al. 2010a). AP2 members constitute by one or additionally taking a tandem repeated AP2 domain (Kagaya et al. 1999; Licausi et al. 2013). ERF members characterize by a single AP2 domain (Nakano et al. 2006; Licausi et al. 2013). RAV members comprise by a consensus sequence elements for both AP2 domain and B3 domains (Kagaya et al. 1999; Swaminathan et al. 2008). Soloist family have little members (one or two) that also contain a single AP2 domain in all sequenced plant genome, but they strongly diverged in gene sequence from other AP2/ERF members (Du et al. 2013; Licausi et al. 2010a; Rao et al. 2015; Zhuang et al. 2008). Because of ERF family members could bind to two mainly DNA-binding elements (Hao et al. 2002; Sakuma et al. 2002), resulting in a novel DREB family is separated from ERF family (Du et al. 2013; Rao et al. 2015; Sakuma et al. 2002; Zhuang et al. 2008). Of the DREB and ERF families, all the members are further classified into six groups, A1 to A6 and B1 to B6, respectively (Sakuma et al. 2002). However, these twelve groups are re-designated with group I

\*Correspondence: guchao@njau.edu.cn; zhangsl@njau.edu.cn  
State Key Laboratory of Crop Genetics and Germplasm Enhancement,  
Center of Pear Engineering Technology Research, Nanjing Agricultural  
University, Nanjing 210095, China

to X, VI-L, and Xb-L or group A to J (Nakano et al. 2006). The re-designated classification is employed in horticultural plants, such as *Vitis vinifera*, *Prunus mume*, and *Solanum lycopersicon* (Licausi et al. 2010a; Du et al. 2013; Pirrello et al. 2012), whereas the traditionally classification is used in other plant species, including *Salix arbutifolia*, *Nicotiana tabacum*, and *Populus trichocarpa* (Rao et al. 2015; Sasaki et al. 2007; Zhuang et al. 2008).

AP2/ERF proteins have strongly capacity to bind a wide range of cis-regulatory elements in promoter of target genes (Sasaki et al. 2007). Of these cis-regulatory elements, GCC-box (AGCCGCC element) and DRE/CRT (dehydrationresponsive element/C-repeat, RCCGCC element) are the mainly two DNA-binding elements (De Boer et al. 2011; Fujimoto et al. 2000; Hao et al. 1998, 2002; Oñate-Sánchez et al. 2007; Wang et al. 2012). Noteworthy, most AP2/ERF proteins can bind GCC-box containing promoter, but the activation degree is different among members in various groups. For instance, the members are weak activators in group A, B and E, neutral in class G and H, and strong in group C, whereas that are as repressor in group F (Pirrello et al. 2012). Besides GCC-box and DRE/CRT, the elements diverged from these two also belong to cis-regulatory elements, which may be in response to different stimuli underlying various stresses (Mizoi et al. 2012; Shaikhali et al. 2008; Welsch et al. 2007). Moreover, ERF protein can also bind to VWRE (vascular wounding responsive element, GAAAAGAAAATTTTC) and CE1 (coupling element, CACCG) in tobacco (Sasaki et al. 2007; Wu et al. 2008). In addition, few reports reveal that ERF proteins could interact directly with a non-GCC element containing promoters (Chakravarthy et al. 2003).

### Ethylene response

Ethylene is an important phytohormone for plant growth, development, senescence, and stress tolerance. Ethylene is synthesized by ACS (1-aminocyclopropane-1-carboxyla synthase) catalyzing substrate of SAM (S-adenosyl methionine) to form ACC (1-aminocyclopropane-1-carboxyla acid), and then impel by ACO (1-aminocyclopropane-1-carboxyla oxidase). Sequentially, how much ethylene produced in plant tissues are positive correlated to ACS and ACO activities. The produced ethylene in plant tissues is combined with ETR (Ethylene receptor) to activate constitutive triple response (CTR), and then induce expression of a set of ethylene insensitive (EIN) and Ethylene insensitive-like (EIL). The EIN/EIL proteins bind to upstream regions of ERF TFs to promote it expressed in tissues (Alexander and Grierson 2002; Guo and Ecker 2003; Solano et al. 1998). However, due to GCC-box usually presented in the promoter of ACS and ACO in many plants, the expressed *ERF* genes will

enhance the activities of the two genes, thereby accelerate ethylene biosynthesis and signal transduction, such as *LeERF1*, *AtERF73/HRE1*, *TERF2/LeERF2*, and *MaERF9* (Li et al. 2007; Xiao et al. 2013; Yang et al. 2011; Zhang et al. 2009). Besides the positive feedback genes, few ERF TFs also represent as repressor of ACS and ACO activities to prevent ethylene biosynthesis, including *AtERF4*, *AtERF11*, *SlERF6*, and *MaERF11* (Lee et al. 2012; Li et al. 2011; Xiao et al. 2013; Yang et al. 2005). In addition, ERF. B3 has the ability to modulate the transcription levels of a subset of other ERF TFs (Liu et al. 2013). Noteworthy, this subset contains the aforementioned activators and repressors of ethylene biosynthesis and signal pathway genes. Thus, AP2/ERF TF is not only in response to ethylene signal transduction, but also can feedback regulate ethylene synthesis in plant tissues.

### Stress tolerance

Stresses are the negative environment factors around plant growth and development. Both abiotic and biotic stresses are mediated by multiple transcriptional factors, such as NAC, WRKY, MYB, bHLH, bZIP, and ERF (Abe et al. 2003; Li et al. 2013; Puranik et al. 2012; Rushton et al. 2010; Singh et al. 2002; Zhang et al. 2012a). Most studies have found the importance of AP2/ERF TF in defense of various stresses. In general, the AP2/ERF TFs in response to abiotic stresses are the members of DREB family (Licausi et al. 2013; Sakuma et al. 2002). Such as *AtERF98*, *MsERF8*, *JcERF011*, and *CaERFLP1* that enhance tolerance to salt (Chen et al. 2012; Lee et al. 2004; Tang et al. 2016; Zhang et al. 2004, 2012b). *TERF2/LeERF2*, *CBF1*, and *CBF3* exalt cold and freezing tolerances (Novillo et al. 2007; Tian et al. 2011; Zhang et al. 2010b). *Sub1A*, *SNORKEL1* and *SNORKEL2* allow rice to adapt to deep water (Fukao et al. 2006, 2011; Hattori et al. 2009; Xu et al. 2006). *HRE1* and *HRE2* improve the tolerance of the plant to the hypoxia stress (Licausi et al. 2010b). *OsWRI*, *JERF1*, *TERF1*, and *SHINE* are positive regulators of resistance to drought (Aharoni et al. 2004; Wang et al. 2012; Zhang et al. 2005, 2010a). Moreover, few of AP2/ERF TFs are involved to modulate at least two different abiotic stresses in defense response. For example, over-expression of *SlERF5* in transgenic tomato plants result in high tolerance to drought and salt stress (Pan et al. 2012). Over-expression of *JERF3* and *SodERF3* improve resistance to drought, osmotic, salt, and freezing stresses in transgenic rice and tobacco (Trujillo et al. 2008; Wu et al. 2008; Zhang et al. 2010c). Ectopic expression of *DREB2A* in *Arabidopsis* increase endurance to drought, stress, and heat stresses (Sakuma et al. 2006a, b).

Unless enhanced tolerance to abiotic stresses, AP2/ERF TF also are reported to be concerned in raising

resistance to biotic stresses. Over-expression of *NtERF5* contributes to high tolerance to *Tobacco mosaic virus* in *Nicotiana tabacum* (Fischer and Droge-Laser 2004). Silence-expression of *ORA59* or *RAP2.2* results in low tolerance to *Botrytis cinerea* in *Arabidopsis thaliana* (Pré et al. 2008; Zhao et al. 2012). Loss-of-function mutants of *AtERF2* or *AtERF14* are more susceptible against *Fusarium oxysporum* in *Arabidopsis thaliana* (McGrath et al. 2005; Oñate-Sánchez et al. 2007). Exceptionally, *AtERF4* is the negatively genes in regulating *Fusarium oxysporum* resistance (McGrath et al. 2005). Similar to that in abiotic stress defense, few of AP2/ERF TFs have the ability to coordinate two or more biotic stresses in defense response. For instance, Over-expression of *MtERF1-1* improves tolerance to *Rhizoctonia solani* and *Phytophthora medicaginis* in *Medicago* roots (Anderson et al. 2010). Over-expression of *ERF1* in *Arabidopsis* conferred resistance to necrotrophic fungi including *B. cinerea* and *Plectosphaerella cucumerina* (Berrocal-Lobo et al. 2002). The tomato Transcription Factor *Pti4* Regulates Defense-Related Gene Expression for *Pseudomonas syringae* and *Erysiphe orontii* by combined to GCC Box and Non-GCC Box cis Elements (Chakravarthy et al. 2003).

In addition, few AP2/ERF TFs had been reported responsible for biotic and abiotic stress, simultaneously. A typical example is the positively regulator *TaPIE1* that raise the defense responses to *R. cerealis* and freezing stresses by activating defense- and stress-related genes (Zhu et al. 2014). Taken together, AP2/ERF TF plays very important roles in regulating defense response to all kinds of biotic and abiotic stresses.

### Plant growth, development, and senescence

The life of plant is cycled through seed germination, seedling growth, organ development, and senescence. In this cycle, AP2/ERF TF also displays their regulatory roles for shaping many architectural traits. In the process of seed germination, *SlERF2* positively improve transcription level of marker gene, mannanase 2, resulting in a stimulation of premature germination, and enhance hook formation of darkgrown (Pirrello et al. 2006). In the progression of plant growth and development, *AINTEGUMENTA* and *AINTEGUMENTA-LIKE6* are related to flower organ growth and ovule development in *Arabidopsis* (Elliott et al. 1996; Jofuku et al. 1994; Klucher et al. 1996; Krizek 2009; Mizukami and Fischer 2000). Rice ethylene-response AP2/ERF factor *OsEATB* restricts internode elongation by down-regulating ent-kaurene synthase A, leading to a reduction of rice plant height and panicle length at maturity (Qi et al. 2011). In contrast, *AtERF1*, *AtDREB1*, and *TINYT* present their ability in dwarfing plant height (Liu et al. 1998; Solano et al. 1998; Wilson et al. 1996). Moreover, *NtERF3*, *AtERF4* and

*AtERF8* had been found to be associated with plant aging (Koyama et al. 2013). Of these three genes, *AtERF4* and *AtERF8* belonged to class II ERFs in *Arabidopsis*, which can accelerate precocious leaf senescence by targeting the *EPITHIOSPECIFIER PROTEIN/EPITHIOSPECIFYING SENESCENCE REGULATOR* gene and regulating the expression of many genes related to senescence (Koyama et al. 2013). In addition, AP2/ERF TF is involved in regulating metabolite productions, such as chlorophyll, wax and cutin. The present evidences show that *CitERF13* is negative regulator for chlorophyll degradation during *Citrus* fruit degreening by directly binding to the *Cit-PPH* promoter and enhancing the activity of a metabolite of pheophorbide hydrolase (Yin et al. 2016). *AtWIN1*, *AtSHN*, and *HvNUD* could increase an accumulation of wax and cutin on the epidermis by regulating a lipid biosynthesis pathway (Aharoni et al. 2004; Broun et al. 2004; Taketa et al. 2008). Obviously, the functions of these AP2/ERF TFs are distinctly elucidated in these reported traits, but the regulatory roles of other members should be further explored in unknown properties in future.

### Fruit ripening

Fruit is one of important tissues in fruited plants, which harbors seed formation, development, and maturity. According to respiratory intensity during ripening, fruit is divided into climacteric and non-climacteric phenotypes. The climacteric fruit must release massive ethylene at ripening, also called ethylene-dependent fruit. On the contrary, the non-climacteric fruit is ethylene-independent. To date, ethylene-dependent fleshy-fruits are the primary materials for studying fruit ripening, such as tomato, apple, and banana. In ethylene-dependent fruits, *ERF*, as the final response gene in ethylene signaling pathway, directly regulate fruit ripening by binding to the promoters of their downstream genes, including *ACO*, *ACS*, *PG*, *EXP*, and *PSY* (Han et al. 2016; Lee et al. 2012; Liu et al. 2014). At present, *LeERF1*, *MaERF9*, *MdERF1*, and *MdERF3* has been reported as the positive activator (Li et al. 2007, 2016; Wang et al. 2007; Xiao et al. 2013), whereas *SlERF6*, *MaERF11*, and *MdERF2* are the negative repressors for fruit ripening (Han et al. 2016; Lee et al. 2012). Of these *ERFs*, *MaERF9* and *MaERF11* could not only regulate the transcription levels of *ACO1* and *ACS1* by binding to their promoter, but also physically interacted with *ACO1* (Xiao et al. 2013). Interestingly, *MaERF11* also interact with *MaHDA1*, the complex repress expression levels of downstream genes targeted by *MaERF11* via histone deacetylation (Han et al. 2016). Moreover, the regulatory route of *ERF* genes is intricate during fruit ripening. In apple, *MdERF2* presents at least three roads in regulating *MdACS* expression. *MdERF2* repressor and *MdERF3* activator could

regulate the transcription level of *MdACS* by binding to their promoter, respectively. Meanwhile, *MdERF2* inhibit *MdERF3* activity by combining to the DRE element in the promoter, indirectly suppressed the expression level of *MdACS*. Thirdly, a directly interaction between *MdERF2* and *MdERF3* restrain the binding of *MdERF3* to the *MdACS* promoter, and then suppress the *MdACS* expressed in fruit flesh (Li et al. 2016). In tomato, *SlERF.B3* has the ability to activate the regulatory network for fruit ripening. A dominant repressor version of *SlERF.B3* (*SlERF.B3-SRDX*) down-regulates ethylene receptor levels, but enhances triple response and up-regulated the expression levels of *EIN3-like* gene, contributing to an acceleration of fruit ripening (Liu et al. 2013). Further study found that *SlERF.B3-SRDX* could alter the expression pattern of other ERF family members. Most notably, *SlERF.B3-SRDX* also stimulate the transcription levels of ripening regulators, including *RIPENING INHIBITOR* (*RIN*), *NON-RIPENING* (*NOR*), *COLORLESS NON-RIPENING* (*CNR*), and *Homeodomain-leucine zipper HOMEBOX* (*HB-1*) (Liu et al. 2014). Therefore, the regulatory role of AP2/ERF TF is multiple, and their regulated mechanism is very complex during fruit ripening.

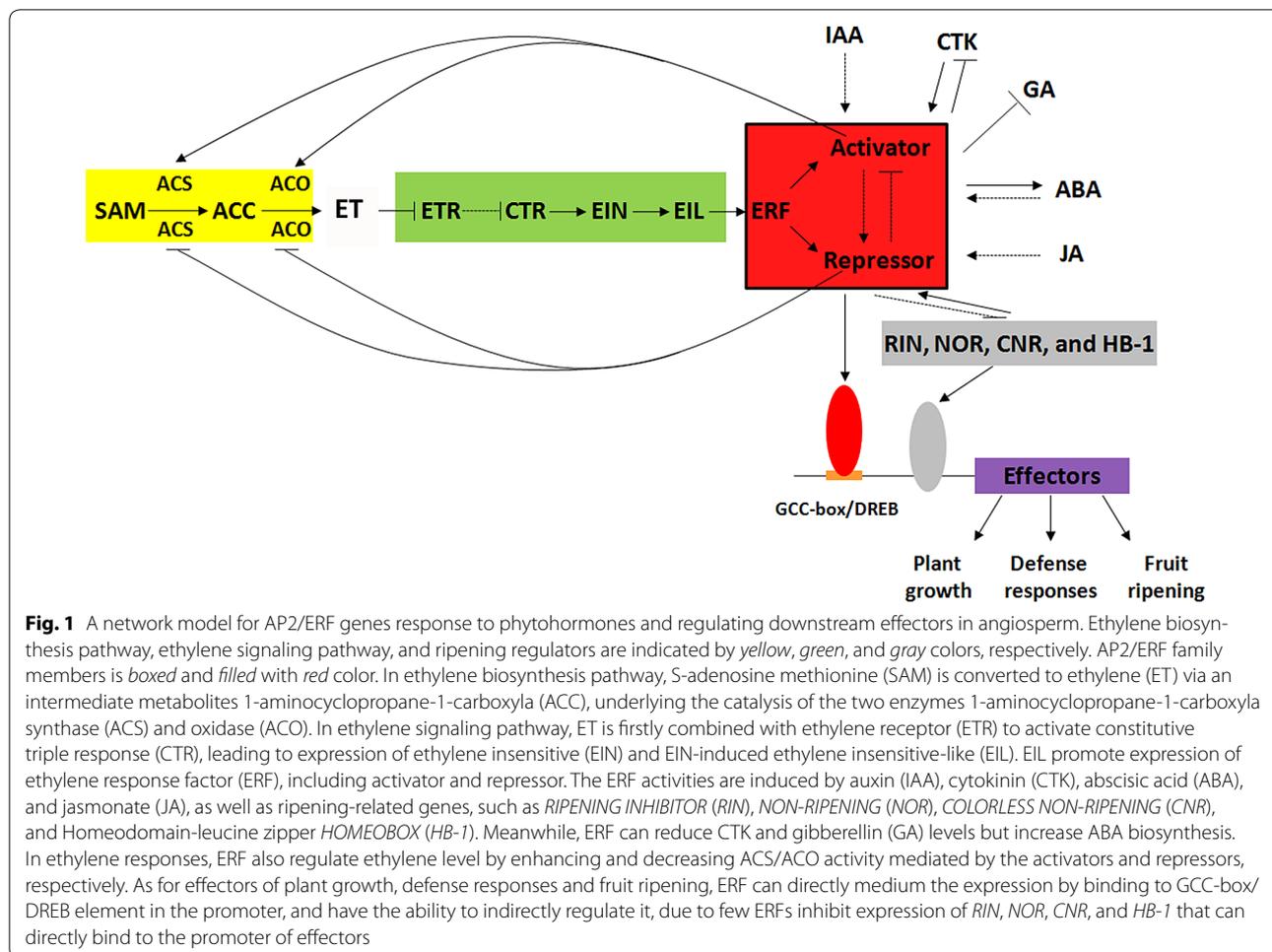
### Integration of phytohormonal signals

Phytohormones are a group of naturally occurring, organic substances which affected plant growth, development, and senescence at low concentrations. Of these phytohormones, auxin, cytokinin, and gibberellin are reported to be involved in regulation of seed germination and plant growth (Pacifci et al. 2015; Urbanova and Leubner-Metzger 2016; Werner et al. 2001). Ethylene plays extremely important roles in climacteric fleshy fruit ripening and senescence (Hayama et al. 2006; Xiao et al. 2013; Yin et al. 2008), and together with jasmonate and abscisic acid, participate in defense response to biotic and abiotic stresses (Li et al. 2011; Lorenzo et al. 2003; Pré et al. 2008). Obviously, cross-talk among these phytohormones must be carried out in plant tissues. This cross-talk is always surveyed by many scientists, and increasing evidences are emerged to elucidate the talk mechanism. Ethylene signal transduction is a general pathway during the life cycle of plant. As the final response gene in ethylene signaling pathway, AP2/ERF are also documented to be involved in response to other hormones. In rice, an

AP2/ERF TF *OsCRL5* is induced by treating with exogenous auxin, and inhibits cytokinin signal transduction by enhancing the activities of two repressors (Kitomi et al. 2011). Interestingly, several AP2/ERF TFs in subgroup B-5 are responsible for exogenous cytokinin, thereby designated as cytokinin response factor (Rashotte et al. 2006). Also in rice, *OsEATB*, which is restrained by ethylene and abscisic acid in expression level, negative regulate gibberellin biosynthesis by down-regulating a pathway gene (Qi et al. 2011). In *Arabidopsis*, tobacco and tomato, however, few AP2/ERF TFs are shown to modulate abscisic acid responses, such as *AtERF11* and *TSRF1* (Li et al. 2011; Zhang et al. 2008). The ethylene-, jasmonate-, and abscisic acid-responsive *JERF1* regulates abscisic acid biosynthesis-related gene in expression level (Zhang et al. 2004; Wu et al. 2007). Moreover, *NIC2* participate in mediating jasmonate-elicited nicotine biosynthesis (De Boer et al. 2011). *ORA59*, which was induced by jasmonate and ethylene in expression level, is the key regulator of jasmonate- and ethylene-responsive PLANT DEFENSIN 1.2 expression by binding to GCC-box element in the promoter (Pré et al. 2008; Zarei et al. 2011). *AtERF2* is a positive regulator of jasmonate-responsive defense genes, while *AtERF4* negative adjust jasmonate-responsive defense gene expression (McGrath et al. 2005). Overall, AP2/ERF TF is the key regulator to integrate all kinds of phytohormonal signals.

### Conclusions

The AP2/ERF superfamily has hundreds of members in various plants, which contains at least one AP2 domain in all designated families. Generally, AP2/ERF TF mediates downstream responsible genes by binding to the GCC-box and/or DREB element in the promoter. Unless responses to ethylene signal, a large number of AP2/ERF members are stimulated by auxin, cytokinin, abscisic acid, and jasmonate signals. Meanwhile, several members also modulate gibberellin, cytokinin, and abscisic acid contents by directly regulating biosynthesis pathway genes of these phytohormones. Moreover, the stimulated genes would further regulate downstream effectors, resulting in changes of agronomic traits, including plant growth, defense responses, and fruit ripening (Fig. 1). In summary, AP2/ERF TF presents multiple regulatory roles in angiosperm.



**Authors' contributions**

CG and SLZ conceived and wrote the manuscript. ZHG provided the advance of classification and DNA-binding elements of AP2/ERF TF, ethylene signal transduction pathway, and ethylene-induced fruit ripening. PPH contributed the integration of phytohormone signals related to AP2/ERF. GMW and ZMJ conducted the advance of AP2/ERF TFs involved in regulating stress, plant growth and development. All authors read and approved the final manuscript.

**Acknowledgements**

This work was supported by the National Natural Science Foundations of China (31471856 and 31672118).

**Competing interests**

The authors declare that they have no competing interests.

Received: 15 November 2016 Accepted: 26 December 2016

Published online: 03 January 2017

**References**

Abe H, Urao T, Ito T, Seki M, Shinozaki K, Yamaguchi-Shinozaki K (2003) Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. *Plant Cell* 15:63–78  
 Aharoni A, Dixit S, Jetter R, Thoenes E, van Arkel G, Pereira A (2004) The SHINE clade of AP2 domain transcription factors activates wax biosynthesis,

alters cuticle properties, and confers drought tolerance when overexpressed in Arabidopsis. *Plant Cell* 16:2463–2480  
 Alexander L, Grierson D (2002) Ethylene biosynthesis and action in tomato: a model for climacteric fruit ripening. *J Exp Bot* 53:2039–2055  
 Anderson JP, Lichtenzveig J, Gleason C, Oliver RP, Singh KB (2010) The B-3 ethylene response factor MTERF1-1 mediates resistance to a subset of root pathogens in *Medicago truncatula* without adversely affecting symbiosis with rhizobia. *Plant Physiol* 154:861–873  
 Berrocal-Lobo M, Molina A, Solano R (2002) Constitutive expression of ETHYLENE-RESPONSE-FACTOR1 in *Arabidopsis* confers resistance to several necrotrophic fungi. *Plant J* 29:23–32  
 Broun P, Poindexter P, Osborne E, Jiang CZ, Riechmann JL (2004) WIN1, a transcriptional activator of epidermal wax accumulation in Arabidopsis. *Proc Natl Acad Sci USA* 101:4706–4711  
 Chakravarthy S, Tuori RP, D'Ascenzo MD, Fobert PR, Despres C, Martin GB (2003) The tomato transcription factor Pti4 regulates defense-related gene expression via GCC box and non-GCC box cis elements. *Plant Cell* 15:3033–3050  
 Chen TT, Yang QC, Gruber M, Kang JM, Sun Y, Ding W, Zhang TJ, Zhang XQ (2012) Expression of an alfalfa (*Medicago sativa* L.) ethylene response factor gene MsERF8 in tobacco plants enhances resistance to salinity. *Mol Biol Rep* 39:6067–6075  
 De Boer K, Tilleman S, Pauwels L, Vanden Bossche R, De Sutter V, Vanderhaeghen R, Hilson P, Hamill JD, Goossens A (2011) APETALA2/ETHYLENE RESPONSE FACTOR and basic helix-loop-helix tobacco transcription factors cooperatively mediate jasmonate-elicited nicotine biosynthesis. *Plant J* 66:1053–1065

- Du DL, Hao RJ, Cheng TR, Pan HT, Yang WR, Wang J, Zhang QX (2013) Genome-wide analysis of the AP2/ERF gene family in *Prunus mume*. *Plant Mol Biol Rep* 31:741–750
- Du HW, Huang M, Zhang ZX, Cheng SY (2014) Genome-wide analysis of the AP2/ERF gene family in maize waterlogging stress response. *Euphytica* 198:115–126
- Elliott RC, Betzner AS, Huttner E, Oakes MP, Tucker WQJ, Gerentes D, Perez P, Smyth DR (1996) AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth. *Plant Cell* 8:155–168
- Fischer U, Droge-Laser W (2004) Overexpression of NtERF5, a new member of the tobacco ethylene response transcription factor family enhances resistance to Tobacco mosaic virus. *Mol Plant Microbe Interact* 17:1162–1171
- Fujimoto SY, Ohta M, Usui A, Shinshi H, Ohme-Takagi M (2000) Arabidopsis ethylene-responsive element binding factors act as transcriptional activators or repressors of GCC box-mediated gene expression. *Plant Cell* 12:393–404
- Fukao T, Xu K, Ronald PC, Bailey-Serres J (2006) A variable cluster of ethylene response factor-like genes regulates metabolic and developmental acclimation responses to submergence in rice. *Plant Cell* 18:2021–2034
- Fukao T, Yeung E, Bailey-Serres J (2011) The submergence tolerance regulator SUB1A mediates crosstalk between submergence and drought tolerance in rice. *Plant Cell* 23:412–427
- Guo H, Ecker JR (2003) Plant responses to ethylene gas are mediated by SCF(EBF1/EBF2)-dependent proteolysis of EIN3 transcription factor. *Cell* 115:667–677
- Guo HW, Ecker JR (2004) The ethylene signaling pathway: new insights. *Curr Opin Plant Biol* 7:40–49
- Han YC, Kuang JF, Chen JY, Liu XC, Xiao YY, Fu CC, Wang JN, Wu KQ, Lu WJ (2016) Banana transcription factor MaERF11 recruits histone deacetylase MaHDA1 and represses the expression of MaACO1 and expansins during fruit ripening. *Plant Physiol* 171:1070–1084
- Hao DY, Ohme-Takagi M, Sarai A (1998) Unique mode of GCC box recognition by the DNA-binding domain of ethylene-responsive element-binding factor (ERF domain) in plant. *J Biol Chem* 273:26857–26861
- Hao DY, Yamasaki K, Sarai A, Ohme-Takagi M (2002) Determinants in the sequence specific binding of two plant transcription factors, CBF1 and NtERF2, to the DRE and GCC motifs. *Biochem* 41:4202–4208
- Hattori Y, Nagai K, Furukawa S, Song XJ, Kawano R, Sakakibara H, Wu JZ, Matsuoto T, Yoshimura A, Kitano H, Matsuoka M, Mori H, Ashikari M (2009) The ethylene response factors SNORKEL1 and SNORKEL2 allow rice to adapt to deep water. *Nature* 460:1026–1030
- Hayama H, Shimada T, Fujii H, Ito A, Kashimura Y (2006) Ethylene-regulation of fruit softening and softening-related genes in peach. *J Exp Bot* 57:4071–4077
- Jofuku KD, Denboer BGW, Vanmontagu M, Okamoto JK (1994) Control of Arabidopsis flower and seed development by the homeotic gene *ap2*. *Plant Cell* 6:1211–1225
- Kagaya Y, Ohmiya K, Hattori T (1999) RAV1, a novel DNA-binding protein, binds to bipartite recognition sequence through two distinct DNA-binding domains uniquely found in higher plants. *Nucleic Acids Res* 27:470–478
- Kitomi Y, Ito H, Hobo T, Aya K, Kitano H, Inukai Y (2011) The auxin responsive AP2/ERF transcription factor CROWN ROOTLESS5 is involved in crown root initiation in rice through the induction of OsRR1, a type-A response regulator of cytokinin signaling. *Plant J* 67:472–484
- Klucher KM, Chow H, Reiser L, Fischer RL (1996) The AINTEGUMENTA gene of Arabidopsis required for ovule and female gametophyte development is related to the floral homeotic gene APETALA2. *Plant Cell* 8:137–153
- Koyama T, Nii H, Mitsuda N, Ohta M, Kitajima S, Ohme-Takagi M, Sato F (2013) A regulatory cascade involving class II ETHYLENE RESPONSE FACTOR transcriptional repressors operates in the progression of leaf senescence. *Plant Physiol* 162:991–1005
- Krizek B (2009) AINTEGUMENTA and AINTEGUMENTA-LIKE6 act redundantly to regulate Arabidopsis floral growth and patterning. *Plant Physiol* 150:1916–1929
- Lee JH, Hong JP, Oh SK, Lee S, Choi D, Kim WT (2004) The ethylene-responsive factor like protein 1 (CaERFLP1) of hot pepper (*Capsicum annuum* L.) interacts in vitro with both GCC and DRE/CRT sequences with different binding affinities: possible biological roles of CaERFLP1 in response to pathogen infection and high salinity conditions in transgenic tobacco plants. *Plant Mol Biol* 55:61–81
- Lee JM, Joung JG, McQuinn R, Chung MY, Fei ZJ, Tieman D, Klee H, Giovannoni J (2012) Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor SlERF6 plays an important role in ripening and carotenoid accumulation. *Plant J* 70:191–204
- Li YC, Zhu BZ, Xu WT, Zhu HL, Chen AJ, Xie YH, Shao Y, Luo YB (2007) LeERF1 positively modulated ethylene triple response on etiolated seedling, plant development and fruit ripening and softening in tomato. *Plant Cell Rep* 26:1999–2008
- Li ZF, Zhang LX, Yu YW, Quan RD, Zhang ZJ, Zhang HW, Huang RF (2011) The ethylene response factor AtERF11 that is transcriptionally modulated by the bZIP transcription factor HY5 is a crucial repressor for ethylene biosynthesis in Arabidopsis. *Plant J* 68:88–99
- Li XP, Zhu XY, Mao J, Zou Y, Fu DW, Chen WX, Lu WJ (2013) Isolation and characterization of ethylene response factor family genes during development, ethylene regulation and stress treatments in papaya fruit. *Plant Physiol Bioch* 70:81–92
- Li T, Jiang Z, Zhang L, Tan D, Wei Y, Yuan H, Li T, Wang A (2016) Apple (*Malus domestica*) MdERF2 negatively affects ethylene biosynthesis during fruit ripening by suppressing MdACS1 transcription. *Plant J* 88:735–748
- Licausi F, Giorgi FM, Zenoni S, Osti F, Pezzotti M, Perata P (2010a) Genomic and transcriptomic analysis of the AP2/ERF superfamily in *Vitis vinifera*. *BMC Genom* 11:719
- Licausi F, van Dongen JT, Giuntoli B, Novi G, Santaniello A, Geigenberger P, Perata P (2010b) HRE1 and HRE2, two hypoxia-inducible ethylene response factors, affect anaerobic responses in *Arabidopsis thaliana*. *Plant J* 62:302–315
- Licausi F, Ohme-Takagi M, Perata P (2013) APETALA2/Ethylene Responsive Factor (AP2/ERF) transcription factors: mediators of stress responses and developmental programs. *New Phytol* 199:639–649
- Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamaguchi-Shinozaki K, Shinozaki K (1998) Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding domain separate two cellular signal transduction pathways in drought- and low-temperature-responsive gene expression, respectively, in Arabidopsis. *Plant Cell* 10:1391–1406
- Liu M, Pirrello J, Kesari R, Mila I, Roustan JP, Li Z, Latche A, Pech JC, Bouzayen M, Regad F (2013) A dominant repressor version of the tomato Sl-ERF.B3 gene confers ethylene hypersensitivity via feedback regulation of ethylene signaling and response components. *Plant J* 76:406–419
- Liu MC, Diretto G, Pirrello J, Roustan JP, Li ZG, Giuliano G, Regad F, Bouzayen M (2014) The chimeric repressor version of an ethylene response factor (ERF) family member, Sl-ERF.B3, shows contrasting effects on tomato fruit ripening. *New Phytol* 203:206–218
- Lorenzo O, Piqueras R, Sanchez-Serrano JJ, Solano R (2003) ETHYLENE RESPONSE FACTOR1 integrates signals from ethylene and jasmonate pathways in plant defense. *Plant Cell* 15:165–178
- McGrath KC, Dombrecht B, Manners JM, Schenk PM, Edgar CI, Maclean DJ, Scheible WR, Udvardi MK, Kazan K (2005) Repressor- and activator-type ethylene response factors functioning in jasmonate signaling and disease resistance identified via a genome-wide screen of *Arabidopsis* transcription factor gene expression. *Plant Physiol* 139:949–959
- Mizoi J, Shinozaki K, Yamaguchi-Shinozaki K (2012) AP2/ERF family transcription factors in plant abiotic stress responses. *Bba-Gene Regul Mech* 1819:86–96
- Mizukami Y, Fischer RL (2000) Plant organ size control: AINTEGUMENTA regulates growth and cell numbers during organogenesis. *Proc Natl Acad Sci USA* 97:942–947
- Nakano T, Suzuki K, Fujimura T, Shinshi H (2006) Genome-wide analysis of the ERF gene family in Arabidopsis and rice. *Plant Physiol* 140:411–432
- Novillo F, Medina J, Salinas J (2007) Arabidopsis CBF1 and CBF3 have a different function than CBF2 in cold acclimation and define different gene classes in the CBF regulon. *Proc Natl Acad Sci USA* 104:21002–21007
- Oñate-Sánchez L, Anderson JP, Young J, Singh KB (2007) AtERF14, a member of the ERF family of transcription factors, plays a nonredundant role in plant defense. *Plant Physiol* 143:400–409
- Pacifici E, Polverari L, Sabatini S (2015) Plant hormone cross-talk: the pivot of root growth. *J Exp Bot* 66:1113–1121
- Pan Y, Seymour GB, Lu C, Hu Z, Chen X, Chen G (2012) An ethylene response factor (ERF5) promoting adaptation to drought and salt tolerance in tomato. *Plant Cell Rep* 31:349–360
- Pirrello J, Jaimes-Miranda F, Sanchez-Ballesta MT, Tournier B, Khalil-Ahmad Q, Regad F, Latche A, Pech JC, Bouzayen M (2006) Sl-ERF2, a tomato

- ethylene response factor involved in ethylene response and seed germination. *Plant Cell Physiol* 47:1195–1205
- Pirrello J, Prasad BC, Zhang W, Chen K, Mila I, Zouine M, Latche A, Pech JC, Ohme-Takagi M, Regad F, Bouzayen M (2012) Functional analysis and binding affinity of tomato ethylene response factors provide insight on the molecular bases of plant differential responses to ethylene. *BMC Plant Biol* 12:190
- Pré M, Atallah M, Champion A, De Vos M, Pieterse CM, Memelink J (2008) The AP2/ERF domain transcription factor ORA59 integrates jasmonic acid and ethylene signals in plant defense. *Plant Physiol* 147:1347–1357
- Puranik S, Sahu PP, Srivastava PS, Prasad M (2012) NAC proteins: regulation and role in stress tolerance. *Trends Plant Sci* 17:369–381
- Qi WW, Sun F, Wang QJ, Chen ML, Huang YQ, Feng YQ, Luo XJ, Yang JS (2011) Rice ethylene-response AP2/ERF factor OsEATB restricts internode elongation by down-regulating a Gibberellin biosynthetic gene. *Plant Physiol* 157:216–228
- Rao GD, Sui JK, Zeng YF, He CY, Zhang JG (2015) Genome-wide analysis of the AP2/ERF gene family in *Salix arbutifolia*. *Febs Open Bio* 5:132–137
- Rashotte AM, Mason MG, Hutchison CE, Ferreira FJ, Schaller GE, Kieber JJ (2006) A subset of Arabidopsis AP2 transcription factors mediates cytokinin responses in concert with a two-component pathway. *Proc Natl Acad Sci USA* 103:11081–11085
- Rushton PJ, Somssich IE, Ringler P, Shen QJ (2010) WRKY transcription factors. *Trends Plant Sci* 15:247–258
- Sakuma Y, Liu Q, Dubouzet JG, Abe H, Shinozaki K, Yamaguchi-Shinozaki K (2002) DNA-binding specificity of the ERF/AP2 domain of Arabidopsis DREBs, transcription factors involved in dehydration- and cold-inducible gene expression. *Biochem Biophys Res Commun* 290:998–1009
- Sakuma Y, Maruyama K, Osakabe Y, Qin F, Seki M, Shinozaki K, Yamaguchi-Shinozaki K (2006a) Functional analysis of an Arabidopsis transcription factor, DREB2A, involved in drought-responsive gene expression. *Plant Cell* 18:1292–1309
- Sakuma Y, Maruyama K, Qin F, Osakabe Y, Shinozaki K, Yamaguchi-Shinozaki K (2006b) Dual function of an Arabidopsis transcription factor DREB2A in water-stress-responsive and heat-stress-responsive gene expression. *Proc Natl Acad Sci USA* 103:18822–18827
- Sasaki K, Mitsuhashi I, Seo S, Ito H, Matsui H, Ohashi Y (2007) Two novel AP2/ERF domain proteins interact with cis-element VWRE for wound-induced expression of the Tobacco *tpoxN1* gene. *Plant J* 50:1079–1092
- Shaikhali J, Heiber I, Seidel T, Stroher E, Hiltscher H, Birkmann S, Dietz K-J, Baier M (2008) The redox-sensitive transcription factor Rap2.4a controls nuclear expression of 2-Cys peroxidoxin A and other chloroplast antioxidant enzymes. *BMC Plant Biol* 8:48
- Singh KB, Foley RC, Oñate-Sánchez L (2002) Transcription factors in plant defense and stress responses. *Curr Opin Plant Biol* 5:430–436
- Solano R, Stepanova A, Chao QM, Ecker JR (1998) Nuclear events in ethylene signaling: a transcriptional cascade mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1. *Gene Dev* 12:3703–3714
- Swaminathan K, Peterson K, Jack T (2008) The plant B3 superfamily. *Trends Plant Sci* 13:647–655
- Taketa S, Amano S, Tsujino Y, Sato T, Saisho D, Kakeda K, Nomura M, Suzuki T, Matsumoto T, Sato K, Kanamori H, Kawasaki S, Takeda K (2008) Barley grain with adhering hulls is controlled by an ERF family transcription factor gene regulating a lipid biosynthesis pathway. *Proc Natl Acad Sci USA* 105:4062–4067
- Tang YH, Qin SS, Guo YL, Chen YB, Wu PZ, Chen YP, Li MR, Jiang HW, Wu GJ (2016) Genome-wide analysis of the AP2/ERF gene family in physic nut and overexpression of the JcERF011 gene in rice increased its sensitivity to salinity stress. *PLoS ONE* 11:e0150879
- Tian Y, Zhang HW, Pan XW, Chen XL, Zhang ZJ, Lu XY, Huang RF (2011) Overexpression of ethylene response factor TERF2 confers cold tolerance in rice seedlings. *Transgenic Res* 20:857–866
- Trujillo LE, Sotolongo M, Menendez C, Ochogavía ME, Coll Y, Hernandez I, Borrás-Hidalgo O, Thomma BPHJ, Vera P, Hernandez L (2008) SoderF3, a novel sugarcane ethylene responsive factor (ERF), enhances salt and drought tolerance when overexpressed in tobacco plants. *Plant Cell Physiol* 49:512–525
- Urbanova T, Leubner-Metzger G (2016) Gibberellins and seed germination. *Annu Plant Rev* 49:253–284
- van der Fits L, Memelink J (2000) ORCA3, a jasmonate-responsive transcriptional regulator of plant primary and secondary metabolism. *Science* 289:295–297
- Wang A, Tan D, Takahashi A, Li TZ, Harada T (2007) MdERFs, two ethylene-response factors involved in apple fruit ripening. *J Exp Bot* 58:3743–3748
- Wang YH, Wan LY, Zhang LX, Zhang ZJ, Zhang HW, Quan RD, Zhou SR, Huang RF (2012) An ethylene response factor OsWR1 responsive to drought stress transcriptionally activates wax synthesis related genes and increases wax production in rice. *Plant Mol Biol* 78:275–288
- Welsch R, Maass D, Voegel T, DellaPenna D, Beyer P (2007) Transcription factor RAP2.2 and its interacting partner SINAT2: stable elements in the carotenogenesis of Arabidopsis leaves. *Plant Physiol* 145:1073–1085
- Werner T, Motyka V, Strnad M, Schmulling T (2001) Regulation of plant growth by cytokinin. *Proc Natl Acad Sci USA* 98:10487–10492
- Wilson K, Long D, Swinburne J, Coupland G (1996) A dissociation insertion causes a semidominant mutation that increases expression of TINY, an Arabidopsis gene related to APETALA2. *Plant Cell* 8:659–671
- Wu LJ, Chen XL, Ren HY, Zhang ZJ, Zhang HW, Wang JY, Wang XC, Huang RF (2007) ERF protein JERF1 that transcriptionally modulates the expression of abscisic acid biosynthesis-related gene enhances the tolerance under salinity and cold in tobacco. *Planta* 226:815–825
- Wu LJ, Zhang ZJ, Zhang HW, Wang XC, Huang RF (2008) Transcriptional modulation of ethylene response factor protein JERF3 in the oxidative stress response enhances tolerance of tobacco seedlings to salt, drought, and freezing. *Plant Physiol* 148:1953–1963
- Xiao YY, Chen JY, Kuang JF, Shan W, Xie H, Jiang YM, Lu WJ (2013) Banana ethylene response factors are involved in fruit ripening through their interactions with ethylene biosynthesis genes. *J Exp Bot* 64:2499–2510
- Xu K, Xu X, Fukao T, Canlas P, Maghirang-Rodriguez R, Heuer S, Ismail AM, Bailey-Serres J, Ronald PC, Mackill DJ (2006) Sub1A is an ethylene-response-factor-like gene that confers submergence tolerance to rice. *Nature* 442:705–708
- Yang Z, Tian L, Latoszek-Green M, Brown D, Wu K (2005) Arabidopsis ERF4 is a transcriptional repressor capable of modulating ethylene and abscisic acid responses. *Plant Mol Biol* 58: 585–596
- Yang CY, Hsu FC, Li JP, Wang NN, Shih MC (2011) The AP2/ERF transcription factor AtERF73/HRE1 modulates ethylene responses during hypoxia in Arabidopsis. *Plant Physiol* 156:202–212
- Yin XR, Chen KS, Allan AC, Wu RM, Zhang B, Lallu N, Ferguson IB (2008) Ethylene-induced modulation of genes associated with the ethylene signalling pathway in ripening kiwifruit. *J Exp Bot* 59:2097–2108
- Yin XR, Xie XL, Xia XJ, Yu JQ, Ferguson IB, Giovannoni JJ, Chen KS (2016) Involvement of an ethylene response factor in chlorophyll degradation during citrus fruit degreening. *Plant J* 86:403–412
- Zarei A, Korbes AP, Younessi P, Montiel G, Champion A, Memelink J (2011) Two GCC boxes and AP2/ERF-domain transcription factor ORA59 in jasmonate/ethylene-mediated activation of the PDF1.2 promoter in Arabidopsis. *Plant Mol Biol* 75:321–331
- Zhang Z, Huang R (2010) Enhanced tolerance to freezing in tobacco and tomato overexpressing transcription factor TERF2/LeERF2 is modulated by ethylene biosynthesis. *Plant Mol Biol* 73:241–249
- Zhang HW, Huang ZJ, Xie BY, Chen Q, Tian X, Zhang XL, Zhang HB, Lu XY, Huang DF, Huang RF (2004) The ethylene-, jasmonate-, abscisic acid- and NaCl-responsive tomato transcription factor JERF1 modulates expression of GCC box-containing genes and salt tolerance in tobacco. *Planta* 220:262–270
- Zhang X, Zhang Z, Chen J, Chen Q, Wang XC, Huang R (2005) Expressing TERF1 in tobacco enhances drought tolerance and abscisic acid sensitivity during seedling development. *Planta* 222:494–501
- Zhang HB, Yang YH, Zhang ZJ, Chen J, Wang XC, Huang RF (2008) Expression of the ethylene response factor gene TSRF1 enhances abscisic acid responses during seedling development in tobacco. *Planta* 228:777–787
- Zhang ZJ, Zhang HW, Quan RD, Wang XC, Huang RF (2009) Transcriptional regulation of the ethylene response factor LeERF2 in the expression of ethylene biosynthesis genes controls ethylene production in tomato and tobacco. *Plant Physiol* 150:365–377
- Zhang Z, Li F, Li D, Zhang H, Huang R (2010a) Expression of ethylene response factor JERF1 in rice improves tolerance to drought. *Planta* 232:765–774
- Zhang H, Liu W, Wan L, Li F, Dai L, Li D, Zhang Z, Huang R (2010b) Functional analyses of ethylene response factor JERF3 with the aim of improving tolerance to drought and osmotic stress in transgenic rice. *Transgenic Res* 19:809–818
- Zhang Z, Liu X, Wang X, Zhou M, Zhou X, Ye X, Wei X (2012a) An R2R3 MYB transcription factor in wheat, TaPIMP1, mediates host resistance to

- Bipolaris sorokiniana and drought stresses through regulation of defense- and stress-related genes. *New Phytol* 196:1155–1170
- Zhang ZJ, Wang J, Zhang RX, Huang RF (2012b) The ethylene response factor AtERF98 enhances tolerance to salt through the transcriptional activation of ascorbic acid synthesis in *Arabidopsis*. *Plant J* 71:273–287
- Zhao Y, Wei T, Yin KQ, Chen Z, Gu H, Qu LJ, Qin G (2012) *Arabidopsis* RAP2.2 plays an important role in plant resistance to *Botrytis cinerea* and ethylene responses. *New Phytol* 195:450–460
- Zhu XL, Qi L, Liu X, Cai SB, Xu HJ, Huang RF, Li JR, Wei XN, Zhang ZY (2014) The wheat ethylene response factor transcription factor PATHOGEN-INDUCED ERF1 mediates host responses to both the necrotrophic pathogen *Rhizoctonia cerealis* and freezing stresses. *Plant Physiol* 164:1499–1514
- Zhuang J, Cai B, Peng RH, Zhu B, Jin XF, Xue Y, Gao F, Fu XY, Tian YS, Zhao W, Qiao YS, Zhang Z, Xiong AS, Yao QH (2008) Genome-wide analysis of the AP2/ERF gene family in *Populus trichocarpa*. *Biochem Bioph Res Co* 371:468–474

Submit your manuscript to a SpringerOpen<sup>®</sup> journal and benefit from:

- Convenient online submission
- Rigorous peer review
- Immediate publication on acceptance
- Open access: articles freely available online
- High visibility within the field
- Retaining the copyright to your article

---

Submit your next manuscript at ► [springeropen.com](http://springeropen.com)

---