

植物AP2/ERF类转录因子研究进展

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摘要 植物AP2/ERF是一个庞大的转录因子基因家族，含有由60~70个氨基酸组成的AP2/ERF结构域而得名，存在于所有的植物中。AP2/ERF转录因子参与多种生物学过程，包括植物生长、花发育、果实发育、种子发育、损伤、病菌防御、高盐、干旱等环境胁迫响应等。AP2/ERF类转录因子参与水杨酸、茉莉酸、乙烯、脱落酸等多种信号转导途径，而且是逆境信号交叉途径中的连接因子。文章对国内外近年来有关植物AP2/ERF类转录因子的分类、生物学功能、基因调控等方面的研究进行了综述。

关键词： AP2/ERF转录因子 生物学功能 研究进展

Abstract: Plant AP2/ERF transcription factor with AP2/ERF domain containing 60-70 amino acids is a huge gene family present in all plant. AP2/ERF transcriptional factors are involved in various biological functions such as plant development, flower development, fruit and seed maturation, wounding, pathogen defense, high salty, drought, and so on. AP2/ERF transcription factor are involved in salicylic acid, jasmonic acid, ethylene, abscisic acid signal transduction pathways and among them. The transcription factors are cross-talk factor in stress signal pathway. This paper summarizes the most advanced researches on types, biological functions, and gene regulations of plant AP2/ERF transcription factors.

Keywords: AP2/ERF transcription factor, biological functions, progress

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- [1] Jofuku KD, den Boer BG, van Montagu M, Okamuro JK. Control of *Arabidopsis* flower and seed development by the homeotic gene *APETALA2*. *Plant Cell*, 1994, 6(9): 1211-1225.
- [2] Ohme-Takagi M, Shinshi H. Ethylene-inducible DNA binding proteins that interact with anethylene-responsive element. *Plant Cell*, 1995, 7 (2): 173-182.
- [3] Kagaya Y, Ohmiya K, Hattori T. 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*, 1999, 27(2): 470-478. 
- [4] Velasco R, Zharkikh A, Affourtit J, Dhingra A, Cestaro A, Kalyanaraman A, Fontana1 P, Bhatnagar SK, Troggio M, Pruss D, Salvi S, Pindo M, Baldi P, Castelletti S, Cavaiuolo M, Coppola G, Viola R. The genome of the domesticated apple (*Malus × domestica* Borkh.). *Nature Genet*, 2010, 42: 833-839.
- [5] Nakano T, Suzuki K, Fujimura T, Shinshi H. Genome wide analysis of the ERF gene family in *Arabidopsis* and rice. *Plant Physiol*, 2006, 140(2): 411-432. 
- [6] Elliott RC, Betzner AS, Huttner E, Oakes MP, Tucker WQ, Gerentes D, Perez P, Smyth DR. *AINTEGUMENTA*, an APETALA2-like gene of *Arabidopsis* with pleiotropic roles in ovule development and floral organ growth. *Plant Cell*, 1996, 8(2): 155-168.
- [7] Chuck G, Meeley RB, Hake S. The control of maize spikelet meristem fate by the APETALA2-like gene indeterminate spikelet. *Genes Dev*, 1998, 12(8): 1145-1154. 

- [8] Boutilier K, Offringa R, Sharma VK, Kieft H, Ouellet T, Zhang L, Hattori J, Liu CM, van Lammeren AA, Miki BL, Custers JB, van Lookeren Campagne MM. Ectopic expression of BABY BOOM triggers a conversion from vegetative to embryonic growth. *Plant Cell*, 2002, 14(8): 1737-1749. 
- [9] Alonso JM, Stepanova AN, Leisse TJ, Kim CJ, Chen H, Shinn P, Stevenson DK, Zimmerman J, Barajas P, Cheuk R, Gadrinab C, Heller C, Jeske A, Koesema E, Meyers CC, Parker H, Prednis L, Ansari Y, Choy N, Deen H, Geralt M, Hazari N, Hom E, Karnes M, Mulholland C, Ndubaku R, Schmidt I, Guzman P, Aguilar-Henonin L, Schmid M, Weigel D, Carter DE, Marchand T, Risseeuw E, Brogden D, Zeko A, Crosby WL, Berry CC, Ecker JR. Genome-wide insertional mutagenesis of *Arabidopsis thaliana*. *Science*, 2003, 301(5633): 653-657.
- [10] Hu YX, Wang YX, Liu XF, Li JY. *Arabidopsis RAV1* is down-regulated by brassinosteroid and may act as a negative regulator during plant development. *Cell Res*, 2004, 14(1): 8-15. 
- [11] Sohn KH, Sung Chul Lee SC, Jung HW, Hong JK, Kook Hwang BK. Expression and functional roles of the pepper pathogen-induced transcription factor RAV1 in bacterial disease resistance, and drought and salt stress tolerance. *Plant Mol Biol*, 2006, 61(6): 897-915. 
- [12] Sakuma Y, Liu Q, Dubouzet JG, Abe H, Shinozaki K, Yamaguchi-Shinozaki K. 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*, 2002, 290(3): 998-1009. 
- [13] Yamaguchi-Shinozaki K, Shinozaki K. A novel *cis*-acting element in an *Arabidopsis* gene is involved in responsiveness to drought, low-temperature, or high-salt stress. *Plant Cell*, 1994, 6(2): 251-264.
- [14] Thomashow MF. PLANT COLD ACCLIMATION: freezing tolerance genes and regulatory mechanisms. *Annu Rev Plant Physiol Plant Mol Biol*, 1999, 50: 571-599. 
- [15] Hao DY, Ohme-Takagi M, Sarai A. Unique mode of GCC box recognition by the DNA-binding domain of ethylene responsive element-binding factor (ERF domain) in plants. *J Biol Chem*, 1998, 273(41): 26857-26861.
- [16] Raikhel NV. Nuclear targeting in plants. *Plant Physiol*, 1992, 100(4): 1627-1632. 
- [17] Fujimoto SY, Ohta M, Usui A, Shinshi H, Ohme-Takagi M. *Arabidopsis* ethylene-responsive element binding factors act as transcriptional activators or repressors of GCC box-mediated gene expression. *Plant Cell*, 2000, 12(3): 393-404.
- [18] Pearson RB, Kemp BE. Protein kinase phosphorylation site sequences and consensus specificity motifs: tabulations. *Methods Enzymol*, 1991, 200: 62-81. 
- [19] Sanchez-Ballesta MT, Lluch Y, Gosálbez MJ. A survey of genes differentially expressed during long-term heat-induced chilling tolerance in citrus fruit. *Planta*, 2003, 218(1): 65-70.
- [20] Zhang G, Chen M, Chen X, Xu Z, Guan S, Li LC, Li A, Guo J, Mao L, Ma Y. Phylogeny, gene structures, and expression patterns of the ERF gene family in soybean (*Glycine max* L.). *J Exp Bot*, 2008, 59(15): 4095-4107.
- [21] Zhuang J, Anyia A, Vidmar J, Xiong A S, Zhang J. Discovery and expression assessment of the AP2-like genes in *Hordeum vulgare*. *Acta Physiol Plant*, 2011, 33(5): 1639-1649. 
- [22] Zhuang J, Yao QH, Xiong AS, Zhang J. Isolation, phylogeny and expression patterns of AP2-like genes in Apple (*Malus × domestica* Borkh). *Plant Mol Biol Rep*, 2011, 29(1): 209-216. 
- [23] Zhuang J, Chen JM, Yao QH, Xiong F, Sun CC, Zhou XR, Zhang J, Xiong AS. Discovery and expression profile analysis of AP2/ERF family genes from *Triticum aestivum*. *Mol Biol Rep*, 2011, 38(2): 745-753. 
- [24] Zhuang J, Deng DX, Yao QH, Zhang J, Xiong F, Chen JM, Xiong AS. Discovery, phylogeny and expression patterns of AP2-like genes in maize. *Plant Growth Regul*, 2010, 62(1): 51-58. 
- [25] Kunkel BN, Brooks DM. Cross talk between signaling pathways in pathogen defense. *Curr Opin Plant Biol*, 2002, 5(4): 325-331. 
- [26] Chinnusamy V, Schumaker K, Zhu JK. Molecular genetic perspectives on cross-talk and specificity in abiotic stress signalling in plants. *J Exp Bot*, 2004, 55(395): 225-236.
- [27] Fujita M, Fujita Y, Noutoshi Y, Takahashi F, Narusaka Y, Yamaguchi-Shinozaki K, Shinozaki K. Crosstalk between abiotic and biotic stress responses: a current view from the points of convergence in the stress signaling networks. *Curr Opin Plant Biol*, 2006, 9(4): 436-442. 
- [28] Ton J, Jakab G, Toquin V, Flors V, Iavicoli A, Maeder MN, Métraux JP, Mauch-Mani B. Dissecting the β -aminobutyric acid-induced priming phenomenon in *Arabidopsis*. *Plant Cell*, 2005, 17(3): 987-999. 
- [29] Ton J, Mauch-Mani B. β -amino-butryic acid-induced resistance against necrotrophic pathogens is based on ABA-dependent riming for callose. *Plant J*, 2004, 38(1): 119-130. 
- [30] Zhang G, Chen M, Li LC, Xu Z, Chen X, Guo J, Ma Y. Overexpression of the soybean *GmERF3* gene, an AP2/ ERF type transcription factor for increased tolerances to salt, drought, and diseases in transgenic tobacco. *J Exp Bot*, 2009, 60(13): 3781-3796. 
- [31] Menke FL, Champion A, Kijne JW, Memelink J. A novel jasmonate-and elicitor-responsive element in the periwin-kle secondary metabolite biosynthetic gene *Str* interacts with a jasmonate-and elicitor-inducible AP2-domain transcription factor, ORCA2. *EMBO J*, 1999, 18(16): 4455-4463. 
- [32] van der Fits L, Memelink J. ORCA3, a jasmonate responsive transcriptional regulator of plant primary and secondary metabolism. *Science*, 2000, 289(5477): 295-297.
- [33] van der Fits L, Memelink J. The jasmonate-inducible AP2/ ERF-domain transcription factor ORCA3 activates gene expression via interaction with a jasmonate-responsive promoter element. *Plant J*, 2001, 25(1): 43-53. 

- [34] Pré M, Atallah M, Champion A, de Vos M, Pieterse CMJ, Memelink J. The AP2/ERF domain transcription factor ORA59 integrates jasmonic acid and ethylene signals in plant defense. *Plant Physiol*, 2008, 147(3): 1347-1357.
- [35] Memelink J. Regulation of gene expression by jasmonate hormones. *Phytochemistry*, 2009, 70(13-14): 1560-1570.
- [36] Bowman JL, Sakai H, Jack T, Weigel D, Mayer U, Mey-erowitz EM. Superman, a regulator of floral homeotic genes in *Arabidopsis*. *Development*, 1992, 114(3): 599-615.
- [37] Irish VF, Sussex IM. Function of the Apetala-1 gene during *Arabidopsis* floral development. *Plant Cell*, 1990, 2(8): 741-753.
- [38] Huala E, Sussex IM. Leafy interacts with floral homeotic genes to regulate *Arabidopsis* floral development. *Plant Cell*, 1992, 4(8): 901-913.
- [39] Haughn GW, Somerville CR. Genetic control of morpho-genesis in *Arabidopsis*. *Dev Genet*, 1988, 9(2): 73-89.
- [40] Bowman JL, Smyth DR, Meyerowitz EM. Genes directing flower development in *Arabidopsis*. *Plant Cell*, 1989, 1(1): 37-52.
- [41] Bowman JL, Drews GN, Meyerowitz EM. Expression of the *Arabidopsis* floral homeotic gene agamous is restricted to specific cell types late in flower development. *Plant Cell*, 1991, 3(8): 749-758.
- [42] Kunst L, Klenz JE, Martinez-Zapater J, Haughn GW. AP2 gene determines the identity of perianth organs in flowers of *Arabidopsis thaliana*. *Plant Cell*, 1989, 1(12): 1195- 1208.
- [43] Maes T, van de Steene N, Zethof J, Karimi M, D' Hauw M, Mares G, van Montagu M, Gerats T. Petunia AP2-like genes and their role in flower and seed development. *Plant Cell*, 2001, 13(2): 229-244.
- [44] Keck E, McSteen P, Carpenter R, Coen E. Separation of genetic functions controlling organ identity in flowers. *EMBO J*, 2003, 22(5): 1058-1066.
- [45] Nilsson L, Carlsbecker A, Sundas-Larsson A, Vahala T. APETALA2 like genes from *Picea abies* show functional similarities to their *Arabidopsis* homologues. *Planta*, 2007, 225(3): 589-602.
- [46] Bartley GE, Ishida BK. Digital fruit ripening: data mining in the TIGR tomato gene index. *Plant Mol Biol Rep*, 2002, 20(2): 115-130.
- [47] Alba R, Payton P, Fei ZJ, McQuinn R, Debbie P, Martin GB, Tanksley SD, Giovannoni JJ. Transcriptome and se-lec-ted metabolite analyses reveal multiple points of eth-ylene control during tomato fruit development. *Plant Cell*, 2005, 17(11): 2954-2965.
- [48] Chung MY, Vrebalov J, Alba R, Lee J, McQuinn R, Chung JD, Klein P, Giovannoni J. A tomato (*Solanum lycopersicum*) APETALA2/ERF gene, SiAP2a, is a negative regulator of fruit ripening. *Plant J*, 2010, 64(6): 936-947.
- [49] Niu X, Helentjaris T, Bate NJ. Maize ABI4 binds coupling element1 in abscisic acid and sugar response genes. *Plant Cell*, 2002, 14(10): 2565-2575.
- [50] Jofuku KD, Omidyar PK, Gee Z, Okamuro JK. Control of seed mass and seed yield by the floral homeotic gene APETALA2. *Proc Natl Acad Sci USA*, 2005, 102(8): 3117-3122.
- [51] Ohto MA, Fischer RL, Goldberg RB, Nakamura K, Harada JJ. Control of seed mass by APETALA2. *Proc Natl Acad Sci USA*, 2005, 102(8): 3123-3128.
- [52] Kunst L, Klenz JE, Martinez-Zapater J, Haughn GW. AP2 gene determines the identity of perianth organs in flowers of *Arabidopsis thaliana*. *Plant Cell*, 1989, 1(12): 1195-1208.
- [53] Bowman JL, Alvarez J, Weigel D, Meyerowitz EM, Smyth DR. Control of flower development in *Arabidopsis thaliana* by APETALA1 and interacting genes. *Development*, 1993, 119(1): 721-743.
- [54] Schultz EA, Haughn GW. Genetic analysis of the floral initiation process (FLIP) in *Arabidopsis*. *Development*, 1993, 119(1): 745-765.
- [55] Okamuro JK, den Boer BGW, Jofuku KD. Regulation of *Arabidopsis* flower development. *Plant Cell*, 1993, 5(10): 1183-1193.
- [56] Koornneef M, Bentsink L, Hilhorst H. Seed dormancy and germination. *Curr Opin Plant Biol*, 2002, 5(1): 33-36.
- [57] Kucera B, Cohn MA, Leubner-Metzger G. Plant hormone interactions during seed dormancy release and germination. *Seed Sci Res*, 2005, 15(4): 281-307.
- [58] Jacobsen JV, Pearce DW, Poole AT, Pharis RP, Mander LN. Abscisic acid, phaseic acid and gibberellin contents associated with dormancy and germination in barley. *Physiol Plant*, 2002, 115(3): 428-441.
- [59] Finkelstein RR. Mutations at two new *Arabidopsis* ABA response loci are similar to the *abi3* mutations. *Plant J*, 1994, 5(6): 765-771.
- [60] Nambara E, Naito S, McCourt P. A mutant of *Arabidopsis* which is defective in seed development and storage protein accumulation is a new *abi3* allele. *Plant J*, 1992, 2(4): 435-441.
- [61] Giraudat J, Hauge BM, Valon C, Smalle J, Parcy F, Goodman M. Isolation of the *Arabidopsis* ABI3 gene by positional cloning. *Plant Cell*, 1992, 4(10): 1251-1261.
- [62] Finkelstein RR, Wang ML, Lynch TJ, Rao S, Goodman HM. The *Arabidopsis* abscisic acid response locus ABI4 encodes an APETALA2 domain protein. *Plant Cell*, 1998, 10(6): 1043-1054.
- [63] Arenas-Huertero F, Arroyo A, Zhou L, Sheen J, León P. Analysis of *Arabidopsis* glucose insensitive mutants, *gin5* and *gin6*, reveals a central role of the plant hormone ABA in the regulation of plant vegetative development by sugar. *Genes Dev*, 2000, 14(16): 2085-2096.
- [64] Huijser C, Kortstee A, Pego J, Weisbeek P, Wisman E, Smekens S. The *Arabidopsis* SUCROSE UNCOUPLED-6 gene is identical to ABSCISIC ACID INSENSITIVE-4: Involvement of abscisic acid in sugar responses. *Plant J*, 2000, 23(5): 577-585.
- [65] Laby RJ, Kincaid MS, Kim D, Gibson SI. The *Arabidopsis* sugar-insensitive mutants sis4 and sis5 are defective in abscisic acid synthesis and response. *Plant J*, 2000, 23(5): 587-596.

- [66] Rook F, Corke F, Card R, Munz G, Smith C, Bevan MW. Impaired sucrose-induction mutants reveal the modulation of sugar-induced starch biosynthetic gene expression by abscisic acid signalling. *Plant J*, 2001, 26(4): 421-433.
- [67] Wang C, Wang H, Zhang J, Chen S. A seed-specific AP2-domain transcription factor from soybean plays a certain role in regulation of seed germination. *Sci China Ser C-Life Sci*, 2008, 51(4): 336-345. 
- [68] Dekkers BJ, Schuurmans JA, Smekens SC. Glucose de-lays seed germination in *Arabidopsis thaliana*. *Planta*, 2004, 218(4): 579-588.
- [69] Price J, Li TC, Kang SG, Na JK, Jang J. Mechanisms of glucose signaling during germination of *Arabidopsis*. *Plant Physiol*, 2003, 132(3): 1424-1438. 
- [70] Zhao L, Luo Q, Yang C, Han Y, Li W. A RAV-like tran-scription factor controls photosynthesis and senescence in soybean. *Planta*, 2008, 227(6): 1389-1399.
- [71] Song CP, Agarwal M, Ohta M, Guo Y, Halfter U, Wang P, Zhu JK. Role of an *Arabidopsis* AP2/EREBP-type transcriptional repressor in abscisic acid and drought stress responses. *Plant Cell*, 2005, 17(8): 2384-2396. 
- [72] Tsutsui T, Kato W, Asada Y, Sako K, Sato T, Sonoda Y, Kidokoro S, Yamaguchi-Shinozaki K, Tamaoki M, Ara-kawa K, Ichikawa T, Nakazawa M, Seki M, Shinozaki K, Matsui M, Ikeda A, Yamaguchi J. DEAR1, a transcriptional repressor of DREB protein that mediates plant de-fense and freezing stress responses in *Arabidopsis*. *J Plant Res*, 2009, 122(6): 633-643. 
- [73] Mittler R, Kim Y, Song L, Coutu J, Coutu A, Ciftci-Yil-maz S, Lee H, Stevenson B, Zhu JK. Gain-and loss-of-function mutations in *Zat10* enhance the tolerance of plants to abiotic stress. *FEBS Lett*, 2006, 580(28-29): 6537-6542. 
- [74] Ciftci-Yilmaz S, Morsy MR, Song L, Coutu A, Krizek BA, Lewis MW, Warren D, Cushman J, Connolly EL, Mittler R. The EAR-motif of the Cys2/His2-type zinc finger pro-tein Zat7 plays a key role in the defense response of *Arabidopsis* to salinity stress. *J Biol Chem*, 2007, 282(12): 9260-9268. 
- [75] Kasuga M, Liu Q, Miura S, Yamaguchi-Shinozaki K, Shinozaki K. Improving plant drought, salt, and freezing tolerance by gene transfer of a single stress-inducible transcription factor. *Nat Biotech*, 1999, 17(3): 287-291. 
- [76] Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamagu-chi-Shinozaki K, Shinozaki K. Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding domain, separate two cellular signal transduction path-ways in drought and low temperature-responsive gene expression, respectively, in *Arabidopsis*. *Plant Cell*, 1998, 10(8), 1391-1406.
- [77] Gilmour SJ, Sebolt AM, Salazar MP, Everard JD, Thomashow MF. Overexpression of the *Arabidopsis* CBF3 transcriptional activator mim-ics multiple biochemical changes associated with cold acclimation. *Plant Physiol*, 2000, 124(4): 1854-1865. 
- [78] Sakuma Y, Maruyama K, Osakabe Y, Qin F, Seki M, Shinozaki K, Yamaguchi-Shinozaki K. Functional analysis of an *Arabidopsis* transcription factor, DREB2A, involved in drought-responsive gene expression. *Plant Cell*, 2006, 18(5): 1292-1309. 
- [79] Kizis D, Pages M. Maize DRE-binding proteins DBF1 and DBF2 are involved in rab17 regulation through the drought responsive element in an ABA-dependent pathway. *Plant J*, 2002, 30(6): 679-689. 
- [80] Wei G, Pan Y, Lei J, Zhu YX. Molecular cloning, phylogenetic analysis, expressional profiling and in vitro studies of TINY2 from *Arabidopsis thaliana*. *J Bio-chem Mol Biol*, 2005, 38(4): 440-446.
- [81] Huang B, Liu JY. A cotton dehydration responsive element binding protein functions as a transcriptional rep-ressor of DRE mediated gene expression. *Biochem Biophys Res Commun*, 2006, 343(4): 1023-1031. 
- [82] Chen M, Wang QY, Cheng XG, Xu ZS, Li LC, Ye XG, Xia LQ, Ma YZ. GmDREB2, a soybean DRE-binding transcription factor, conferred drought and high-salt tol-erance in transgenic plants. *Biochem Biophys Res Commun*, 2007, 353(2): 299-305. 
- [83] Peng X, Ma X, Fan W, Su M, Cheng L, Iftekhar A, Lee B, Qi D, Shen S, Liu G. Improved drought and salt tolerance of *Arabidopsis thaliana* by transgenic expression of a novel DREB gene from *Leymus chinensis*. *Plant Cell Rep*, 2011, 30(8): 1493-1502. 
- [84] Hong B, Ma C, Yang Y, Wang T, Yamaguchi-Shinozaki K, Gao J. Over-expression of *AtDREB1A* in chrysan-themum enhances tolerance to heat stress. *Plant Mol Biol*, 70(3): 231-240.
- [85] Dong J, Wang X, Wang K, Wang Z, Gao H. Isolation and characterization of a gene encoding an ethylene responsive factor protein from *Ceratoides arborescens*. *Mol Biol Rep*, 2012, 39(2): 1349-1357. 
- [86] Abogadallah GM, Nada RM, Malinowski R, Quick P. Overexpression of *HARDY*, an AP2/ERF gene from *Arabidopsis*, improves drought and salt tol-erance by reducing transpiration and sodium uptake in transgenic *Trifolium alexandrinum* L. *Planta*, 2011, 233(6): 1265-1276.
- [87] Karaba A, Dixit S, Greco R, Aharoni A, Trijatmiko K R, Marsch-Martinez N, Krishnan A, Nataraja KN, Udayaku-mar M, Pereira A. Improvement of water use efficiency in rice by expression of *HARDY*, an *Arabidopsis* drought and salt tolerance gene. *Proc Natl Acad Sci USA*, 2007, 104(39): 5270-15275.
- [88] Gao S, Zhang H, Tian Y, Li F, Zhang Z, Lu X, Chen X, Huang R. Expression of *TERF1* in rice regulates expression of stress-responsive genes and enhances tolerance to drought and high-salinity. *Plant Cell Rep*, 2008, 27(11): 1787-1795. 
- [89] Zhang H, Liu W, Wan L, Li F, Dai L, Li D, Zhang Z, Huang R. Functional analyses of ethylene response factor *JERF3* with the aim of improving tolerance to drought and osmotic stress in transgenic rice. *Transgenic Res*, 2010, 19(5): 809-818. 
- [90] Zhang Z, Li F, Li D, Zhang H, Huang R. Expression of ethylene response factor *JERF1* in rice improves tolerance to drought. *Planta*, 2010, 232(3): 765-774.
- [91] Zhang Z, Huang R. Enhanced tolerance to freezing in to-bacco and tomato overexpressing transcription factor *TERF2/LeERF2* is modulated by ethylene biosyn-thesis. *Plant Mol Biol*, 2010, 73(3): 241-249. 

- [92] Chen JR, Lu JJ, Liu R, Xiong ZY, Wang TX, Chen SY, Guo LB, Wang HF. *DREB1C* from *Medicago truncatula* enhances freezing tolerance in transgenic *M. truncatula* and China Rose (*Rosa chinensis* Jacq.). *Plant Growth Regul*, 2010, 60(3): 199-211.
- [93] Jin T, Chang Q, Li W, Yin D, Li Z, Wang D, Liu B, Liu L. Stress-inducible expression of *GmDREB1* con-ferred salt tolerance in transgenic alfalfa. *Plant Cell Tissue Organ Cult*, 2010, 100(2): 219-227.
- [94] Yang Z, Tian L, Latoszek-Green M, Brown D, Wu K. *Arabidopsis* ERF4 is a transcriptional repressor capable of modulating ethylene and abscisic acid re-sponses. *Plant Mol Biol*, 2005, 58(4): 585-596.
- [95] Park JM, Park CJ, Lee SB, Ham BK, Shin R, Paek KH. Overexpression of the tobacco *Tsi1* gene encoding an EREBP/AP2-type transcription factor enhances resis-tance against pathogen attack and osmotic stress in to-bacco. *Plant Cell*, 2001, 13(5): 1035-1046.
- [96] Shin R, Park JM, An JM, Paek KH. Ectopic expression of *Tsi1* in transgenic hot pepper plants enhances host resistance to viral, bacterial, and oomycete pathogens. *Mol Plant Microbe Interact*, 2002, 15(10): 983-989.
- [97] Gutierrez N, Reuber TL. Regulation of disease resistance pathways by AP2/ERF transcription factors. *Curr Opin Plant Biol*, 2007, 7(4): 465-471.
- [98] Yi SY, Kim JH, Joung YH, Lee S, Kim WT, Yu SH, Choi D. The pepper transcription factor CaPF1 confers patho-gen and freezing tolerance in *Arabidopsis*. *Plant Physiol*, 2004, 136(1): 2862-2874.
- [99] Zuo KJ, Qin J, Zhao JY, Ling H, Zhang LD, Cao YF, Tang KX. Over-expression GbERF2 transcription factor in tobacco enhances brown spots disease resistance by activating expression of downstream genes. *Gene*, 2007, 391 (1-2): 80-90.
- [100] Fischer U, Dröge-Laser W. Overexpression of *NtERF5*, a new member of the tobacco ethylene response transcription factor family enhances resistance to tobacco mosaic virus. *Mol Plant Microbe Interact*, 2004, 17(10): 1162-1171.
- [101] Tang W, Charles TM, Newton RJ. Overexpression of the pepper transcription factor CaPF1 in transgenic Virginia pine (*Pinus virginiana* Mill.) confers multiple stress tolerance and enhances organ growth. *Plant Mol Biol*, 2005, 59(4): 603-617.
- [102] Ohta M, Matsui K, Hiratsu K, Shinshi H, Ohme-Takagi M. Repression domains of class II ERF transcriptional rep-ressors share an essential motif for active repression. *Plant Cell*, 2001, 13(8): 1959-1968.
- [103] Ohta M, Ohme-Takagi M, Shinshi H. Three ethylene responsive transcription factors in tobacco with distinct transactivation functions. *Plant J*, 2000, 22(1): 29-38.
- [104] Pan I, Li CW, Su RC, Cheng CP, Lin CS, Chan MT. Ec-topic expression of an EAR motif deletion mutant of *SiERF3* enhances tolerance to salt stress and *Ralstonia solanacearum* in tomato. *Planta*, 2010, 232(5): 1075-1086.
- [105] Brown RL, Kazan K, McGrath KC, Maclean DJ, Manners JM. A role for the GCC-box in jasmonate-mediated activation of the *PDF1.2* gene of *Arabidopsis*. *Plant Physiol*, 2003, 132(2): 1020-1032.
- [106] McGrath KC, Dombrecht B, Manners JM, Schenk PM, Edgar CI, Maclean DJ, Scheible WR, Udvardi MK, Kazan K. 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*, 2005, 139(2): 949-959.
- [107] Zhou J, Tang X, Martin GB. The Pto kinase conferring resistance to tomato bacterial speck disease interacts with proteins that bind a *cis*-element of pathogene-sis-related genes. *EMBO J*, 1997, 16(11): 3207-3218.
- [108] Tournier B, Sanchez-Ballesta MT, Jones B, Pesquet E, Regad F, Latché A, Pech JC, Bouzayen M. New members of the tomato ERF family show specific expression pattern and diverse DNA-binding capacity to the GCC box ele-ment. *FEBS Lett*, 2003, 550(1-3): 149-154.
- [109] Lee JH, Hong JP, Oh SK, Lee S, Choi D, Kim WT. 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*, 2004, 55(1): 61-81.
- [110] Xu ZS, Xia LQ, Chen M, Cheng XG, Zhang RY, Li LC, Zhao YX, Lu Y, Ni ZY, Liu L, Qiu ZG, Ma YZ. Isolation and molecular characterization of the *Triticum aesti-vum* L. ethylene-responsive factor 1 (TaERF1) that increases multiple stress tolerance. *Plant Mol Biol*, 2007, 65(6): 719-732.
- [111] Hao D, Yamasaki K, Sarai A, Ohme-Takagi M. Determi-nants in the sequence specific binding of two plant tran-scription factors, CBF1 and NtERF2, to the DRE and GCC motifs. *Biochemistry*, 2002, 41(13): 4202-4208.
- [112] Gu YQ, Wildermuth MC, Chakravarthy S, Loh YT, Yang C, He X, Han Y, Martin GB. Tomato transcription factors pti4, pti5, and pti6 activate defense responses when expressed in *Arabidopsis*. *Plant Cell*, 2002, 14(4): 817-831.
- [113] Sasaki K, Mitsuhashi I, Seo S, Ito H, Matsui H, Ohashi Y. Two novel AP2/ERF domain proteins interact with *cis*-element VWRE for wound-induced expression of the Tobacco *tpxN1* gene. *Plant J*, 2007, 50(6): 1079-1092.
- [114] Sasaki K, Hiraga S, Ito H, Seo S, Matsui H, Ohashi Y. A wound-inducible tobacco peroxidase gene expresses preferentially in the vascular system. *Plant Cell Physiol*, 2002, 43(1): 108-117.
- [115] Sasaki K, Ito H, Mitsuhashi I, Hiraga S, Seo S, Matsui H, Ohashi Y. A novel wound-responsive *cis*-element, VWRE, of the vascular system-specific expression of a tobacco peroxidase gene, *tpxN1*. *Plant Mol Biol*, 2006, 62(4-5): 753-768.

[1] 宋健, 郭勇, 于丽杰, 邱丽娟. 大豆种皮色相关基因研究进展[J]. 遗传, 2012, 34(6): 687-694

[2] 陈凡国, 侯丙凯. 巴氏小体案例在遗传学教学中的应用[J]. 遗传, 2012, 34(4): 503-508

[3] 罗军玲, 赵娜, 卢长明. 植物Trihelix转录因子家族研究进展[J]. 遗传, 2012, 34(12): 1551-1560

[4] 高运臻, 潘玉春. 转录因子CCAAT增强子结合蛋白 β (C/EBP β)的研究进展[J]. 遗传, 2011, 33(3): 198-206

- [5] 景花, 宋沁馨, 周国华. MicroRNA定量检测方法的研究进展[J]. 遗传, 2010, 32(1): 31-40
- [6] 封华 ;陈晨 ;王义琴 ;邱金龙 ;储成才 ;杜希华 .植物可溶性N-乙基马来酰亚胺敏感因子连接物复合体(SNAREs)及其生物学功能研究进展[J]. 遗传, 2009, 31(5): 471-478
鄂志国 ;王磊
- [7] .水稻抗病性基因的克隆和功能研究进展[J]. 遗传, 2009, 31(10): 999-1005
- [8] 余文博; 江松敏; 余龙.先天性聋哑会遗传吗? [J]. 遗传, 2008, 30(9): 1107-1107
- [9] 王彦 许恒勇 朱庆.哺乳动物DGAT基因及其生物学功能研究进展[J]. 遗传, 2007, 29(10): 1167-1167—1172
- [10] 朱克军; 汪振诚; 王学敏ZHU Ke-Jun; WANG Zhen-Cheng; WANG Xue-Min.线粒体DNA修复系统相关酶的研究进展 Progress of Enzyme in Mitochondrial DNA Repair System[J]. 遗传, 2004, 26(2): 274-282
- [11] 张振霞;; 符义坤; 储成才.豆科牧草基因工程研究进展 [J]. 遗传, 2002, 24(5): 607-612
- [12] 鲁绍雄;; 吴常信 LU Shao-xiong; ;WU Chang-xin.动物遗传标记辅助选择研究及其应用 Research and Application of Animal Genetic Marker-assisted Selection[J]. 遗传, 2002, 24(3): 359-362
- [13] 黄银花; 李宁; 孙汉; 黄路生 HUANG Yin-hua; LI Ning; SUN Han; HUANG Lu-sheng.家禽数量性状基因座定位的研究进展 The Advanced Research Progress of QTL Mapping in Poultry[J]. 遗传, 2001, 23(6): 588-376