1. 請翻譯下面二段文字
專有名詞請直接抄錄
每一段翻譯之後請列出三個關鍵字 (英文)
25%

Resurrection plants constitute a unique cadre within the angiosperms: they alone have the remarkable capability to survive the complete dehydration of their leaves and roots. How the dry and visually "dead" plants come alive when water becomes available has long fascinated plant biologists and the lay public alike. The majority of plants, including all our crops, can rarely survive tissue water potentials of less than −4 Mpa. Resurrection plants can, in contrast, survive tissue water potentials of −100 MPa (equilibration to air of 50% relative humidity) and below. The ability to desiccate and resurrect vegetative tissues is considered a primal strategy for surviving extensive periods of drought. Desiccation tolerance (DT) has played a major role in plant evolution (1): Postulated as critical for the colonization of terrestrial habitats. DT, as it relates to seed survival and storage, is also arguably the primary plant trait that governs global agriculture and food security. Vegetative DT was lost early in the evolution of tracheophytes and is rare in the angiosperms, but has since reappeared within several lineages, at least 13 of which belong to the angiosperms. (Xiao et al. PNAS 2015. 112: 5833–5837).

25%

Glutathione (c-glutamylcysteinylglycine) is an essential metabolite with multiple functions in plants. It is an important thiol antioxidant as well as a scavenger of reactive electrophilic compounds that functions with glutathione-Stransferases (GSTs; EC 2.5.1.18) to detoxify a range of herbicides by tagging electrophilic compounds for removal during oxidative stress. In both animals and plants, glutathione is synthesized from L-Glu, L-Cys and Gly in an ATP-dependent two-step pathway catalyzed by the enzymes c-glutamylcysteine synthetase (c-ECS; EC 6.3.2.2) and glutathione synthetase (EC 6.3.2.3). In *Arabidopsis thaliana*, three genes involved in glutathione synthesis have been identified: one coding for plastidial c-ECS (GSH1) and two glutathione synthetases (GSH2), a cytosolic protein and a chloroplast targeted protein. Knocking out the expression of *GSH1* causes lethality at the embryo stage, whereas the knock-out of both *GSH2* genes results in a seedling-lethal phenotype. (Cheng et al. 2015 The Plant Journal 83, 926–939)

見背面

2. 25%

Heat stress response (HSR) is a conserved mechanism developed to increase the expression of heat shock proteins (HSPs) via a heat shock factor (HSF)-dependent mechanism. Signaling by the stress phytohormone abscisic acid (ABA) is involved in acquired thermotolerance as well. Analysis of Arabidopsis thaliana microarray databases revealed that the expression of *HSFA6b*, a class-A *HSF*, extensively increased with salinity, osmotic, and cold stresses, but not heat. Here, we show that *HSFA6b* plays a pivotal role in the response to ABA and in thermotolerance. Salt-inducible *HSFA6b* expression was downregulated in ABA insensitive and deficient mutants; however exogenous ABA application restored expression in ABA-deficient, but not insensitive plants. Thus, ABA signaling is required for proper *HSFA6b* expression. A transcriptional activation assay of protoplasts revealed that ABA treatment and coexpression of an ABA-signaling master effector, ABA-RESPONSIVE ELEMENT-BINDING PROTEIN1, could activate the *HSFA6b* promoter. In addition, HSFA6b directly bound to the promoter of *DEHYDRATION-RESPONSIVE ELEMENT-BINDING PROTEIN2A* and enhanced its expression. Analysis of ABA responses in seed germination, cotyledon greening, and root growth as well as salt and drought tolerance in *HSFA6b*-null, overexpression, and dominant-negative mutants revealed that *HSFA6b* is a positive regulator participating in ABA mediated salt and drought resistance. Thermoprotection tests showed that *HSFA6b* was required for thermotolerance acquisition. Our study reveals a network in which HSFA6b operates as a downstream regulator of the ABA-mediated stress response and is required for HS resistance. This new ABA-signaling pathway is integrated into the complex HSR network in *planta*. (Huang et al. Plant Physiology Aug 4. pii: pp.00860.2016.)

1)給此研究下一個英文標題? (英文)
2)以下除了專有名詞外，需用中文敘述
　a)這篇摘要敘述此研究在研究什麼樣的問題?
　b)此研究用了哪些研究方法，這些研究得到什麼樣的結論?
　c)此研究最主要的結論是什麼?

接次頁

3. 25%

Ethylene response factors (ERFs) are a large plant-specific transcription factor family and play diverse important roles in various plant functions. However, most tomato ERFs have not been characterized. In this study, we showed that the expression of an uncharacterized member of the tomato ERF-IX subgroup, ERF68, was significantly induced by treatments with different bacterial pathogens, ethylene (ET) and salicylic acid (SA), but only slightly induced by bacterial mutants defective in the type III secretion system (T3SS) or non-host pathogens. The ERF68-green fluorescent protein (ERF68-GFP) fusion protein was localized in the nucleus. Transactivation and electrophoretic mobility shift assays (EMSAs) further showed that ERF68 was a functional transcriptional activator and was bound to the GCC-box. Moreover, transient overexpression of *ERF68* led to spontaneous lesions in tomato and tobacco leaves and enhanced the expression of genes involved in ET, SA, jasmonic acid (JA) and hypersensitive response (HR) pathways, whereas silencing of *ERF68* increased tomato susceptibility to two incompatible *Xanthomonas* spp. These results reveal the involvement of ERF68 in the effector-triggered immunity (ETI) pathway. To identify ERF68 target genes, chromatin immunoprecipitation combined with high-throughput sequencing (ChIP-seq) was performed. Amongst the confirmed target genes, a few genes involved in cell death or disease defence were differentially regulated by ERF68. Our study demonstrates the function of ERF68 in the positive regulation of hypersensitive cell death and disease defence by modulation of multiple signalling pathways, and provides important new information on the complex regulatory function of ERFs. (Liu et al. Mol Plant Pathol. 2016. doi: 10.1111/mpp.12460)

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試題隨卷繳回