※ 注意：請於試卷內之「非選擇題作答區」作答，並應註明作答之題號。

1. 25%

Oligogalacturonides (OGs) are fragments of pectin released from the plant cell wall during insect or pathogen attack. They can be perceived by the plant as damage signals, triggering local and systemic defence responses. Here, we analyse the dynamics of local and systemic responses to OG perception in tomato roots or shoots, exploring their impact across the plant and their relevance in pathogen resistance. Targeted and untargeted metabolomics and gene expression analysis in plants treated with purified OGs revealed that local responses were transient, while distal responses were stronger and more sustained. Remarkably, changes were more conspicuous in roots, even upon foliar application of the OGs. The treatments differentially activated the synthesis of defence-related hormones and secondary metabolites including flavonoids, alkaloids and lignans, some of them exclusively synthetized in roots. Finally, the biological relevance of the systemic defence responses activated upon OG perception was confirmed, as the treatment induced systemic resistance to *Botrytis cinerea*. Overall, this study shows the differential regulation of tomato defences upon OGs perception in roots and shoots and reveals the key role of roots in the coordination of the plant responses to damage sensing. (Plant, Cell and Environment, 2021, 44: 275-289)

1) 給此研究下一個英文標題(英文)
2) 以下除了專有名詞外，需用英文敘述
   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?

2. 25%

Plants coordinate the expression of photosynthesis-related genes in response to growth and environmental changes. In species that conduct two-cell C4 photosynthesis, expression of photosynthesis genes is partitioned such that leaf mesophyll and bundle sheath cells accumulate different components of the photosynthetic pathway. The identities of the regulatory networks that facilitate this partitioning are unknown. Here, we show that differences in light perception between mesophyll and bundle sheath cells facilitate differential regulation and accumulation of photosynthesis gene transcripts in the C4 crop maize (*Zea mays*). Key components of the photosynthesis gene regulatory network differentially accumulated between mesophyll and bundle sheath cells, indicative of differential network activity across cell types. We further show that blue (but not red) light is necessary and sufficient to activate photosystem II assembly in mesophyll cells in etiolated maize. Finally, we demonstrate that 61% of all light-induced mesophyll and bundle sheath genes were induced only by blue light or only by red light, but not both. These findings provide evidence that subdivision of light signaling networks is a component of cellular partitioning of C4 photosynthesis in maize. (Plant Physiology, 2020, 182: 1297–1309)

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見背面

3. 25%

Drought stress often limits plant growth and global crop yields. Catalase (CAT)-mediated hydrogen peroxide (H_2O_2) scavenging plays an important role in the adaptation of plant stress responses, but the transcriptional regulation of the *CAT* gene in response to drought stress is not well understood. Here, we isolated an APETALA2/ETHYLENE-RESPONSIVE FACTOR (AP2/ERF) domain-containing transcription factor (TF), *NtERF172*, which was strongly induced by drought, abscisic acid (ABA) and H_2O_2, from tobacco (*Nicotiana tabacum*) by yeast one-hybrid screening. *NtERF172* localized to the nucleus and acted as a transcriptional activator. Chromatin immunoprecipitation, yeast one-hybrid assays, electrophoretic mobility shift assays and transient expression analysis assays showed that NtERF172 directly bound to the promoter region of the *NtCAT* gene and positively regulated its expression. Transgenic plants overexpressing *NtERF172* displayed enhanced tolerance to drought stress, whereas suppression of *NtERF172* decreased drought tolerance. Under drought stress conditions, the *NtERF172*-overexpressed lines showed higher catalase activity and lower accumulation of H_2O_2 compared with wild-type (WT) plants, while the *NtERF172*-silenced plants showed the inverse correlation. Exogenous application of amino-1,2,4-triazole (3-AT), an irreversible CAT inhibitor, to the *NtERF172*-overexpression lines showed decreased catalase activity and drought tolerance, and increased levels of cellular H_2O_2. Knockdown *of NtCAT* in the *NtERF172*-overexpression lines displayed a more drought stress-sensitive phenotype than *NtERF172*-overexpression lines. We propose that *NtERF172* acts as a positive factor in drought stress tolerance, at least in part through the regulation of CAT-mediated H_2O_2 homeostasis. (Plant Biotechnology Journal, 2020, 18: 2444-2455)

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4. 25%

Fruit ripening is a complex and genetically programmed process modulated by transcription factors, hormones, and other regulators. However, the mechanism underlying the regulatory loop involving the membrane-protein targets of RIPENING-INHIBITOR (RIN) remains poorly understood. To unravel the function of tomato (*Solanum lycopersicum*) *FERONIA Like* (*SlFERL*), a putative MADS-box transcription factor target gene, we investigated and addressed the significance of *SlFERL* in fruit ripening by combining reverse genetics, biochemical, and cytological analyses. Here, we report that RIN and Tomato AGAMOUS-LIKE1 (TAGL1) directly bind to the promoter region of *SlFERL* and further activate its expression transcriptionally, suggesting a potential role of *SlFERL* in fruit ripening. Overexpression of *SlFERL* significantly accelerated the ripening process of tomato fruit, whereas RNA interference knockdown of *SlFERL* resulted in delayed fruit ripening. Moreover, a surface plasmon resonance assay coupled with tandem mass spectrometry and a protein interaction assay revealed that SlFERL interacts with the key enzyme *S*-adenosyl-Met synthetase 1 (SlSAMS1) in the ethylene biosynthesis pathway, leading to increased *S*-adenosyl-Met accumulation and elevated ethylene production. Thus, SlFERL serves as a positive regulator of ethylene production and fruit ripening. This study provides clues to the molecular regulatory networks underlying fruit ripening. (Plant Physiology, Published December 2020. DOI: https://doi.org/10.1104/pp.20.01203)

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試題隨卷繳回