



2018年第41期总155期

## 蔬菜育种专题

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## ▶ 前沿资讯

### 1. Variation in abundance of predicted resistance genes in the *Brassica oleracea* pangenome (甘蓝泛基因组抗性基因丰度的变异)

**简介:** 甘蓝是一种重要的农作物, 包括了卷心菜、花椰菜、西兰花及羽衣甘蓝在内的多种蔬菜作物, 然而甘蓝容易受到包括根瘤病、黑胫病、叶斑病和霜霉病在内的多种真菌病害所侵染。对于这些疾病的抗性由特异性疾病抗性基因类似物RGA所介导, 这类基因在不同的甘蓝品系中存在差异。由于基因存在/缺失变异PAV的原因。栽培种甘蓝的参考基因组并不包含所有的RGA, 因此在甘蓝泛基因组中鉴定候选RGA就显得尤为重要。来自澳大利亚的研究人员对甘蓝泛基因组中的候选RGA进行了比较分析, 结果显示不同甘蓝品系中候选RNA具有差异, SNP和PAV通过不同的机制驱动不同品种甘蓝的RGA多样化。该研究团队鉴定了32个与菌核病、根瘤病及枯萎病抗性QTL相关的候选RGA。该研究发现对于将来的甘蓝育种具有重要的参考意义, 同时对于其它作物的育种也具有借鉴价值。

**来源:** Plant Biotechnology Journal

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**全文链接:**

<http://agri.ckcest.cn/ass/41b05050-d5e7-4059-ba4a-88e7317f00aa.pdf>

## ▶ 学术文献

### 1. *Leptosphaeria maculans* Effector Protein AvrLm1 Modulates Plant Immunity by Enhancing MAP Kinase 9 Phosphorylation (油菜黑胫病菌效应物调控植物免疫)

**简介:** *Leptosphaeria maculans*, the causal agent of blackleg disease in canola (*Brassica napus*), secretes an array of effectors into the host to overcome host defense. Here we present evidence that the *L. maculans* effector protein AvrLm1 functions as a virulence factor by interacting with the *B. napus* mitogen-activated protein (MAP) kinase 9 (BnMPK9), resulting in increased accumulation and enhanced phosphorylation of the host protein. Transient expression of BnMPK9 in *Nicotiana benthamiana* induces cell death, and this phenotype is enhanced in the presence of AvrLm1, suggesting that induction of cell death due to enhanced accumulation and phosphorylation of BnMPK9 by AvrLm1 supports the initiation of necrotrophic phase of *L. maculans* infection. Stable expression of BnMPK9 in *B. napus* perturbs hormone signaling, notably salicylic acid response genes, to facilitate *L. maculans* infection. Our findings provide evidence that a MAP kinase is directly targeted by a fungal effector to modulate plant immunity.

**来源:** iScience

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<http://agri.ckcest.cn/ass/e72f879d-28d7-4c15-8195-dbbcf7276b24.pdf>

### 2. Identification and expression pattern analysis of the glucosinolate

## **biosynthetic gene BoCYP83B1 from broccoli(西兰花硫苷生物合成基因BCYP83B1的鉴定及表达模式分析)**

**简介:** Glucosinolates are a branch of amino acid-derived metabolites, which are specifically found in Brassicales. In Arabidopsis, tryptophan derived indolic glucosinolates are required for plant defense against a wide range of pathogens and herbivores due to their strong antimicrobial activity and potential signaling function. An important enzyme in indolic glucosinolate biosynthesis pathway is CYP83B1, which oxidizes indole-3-acetaldoxime, a precursor of indole-3-acetic acid (IAA). In this study, we reported isolation and expression characterization of a CYP83B1 gene from Brassica oleracea L. var. italica Plenck, which we termed BoCYP83B1. Overexpression of BoCYP83B1 in Arabidopsis resulted in an altered glucosinolate profile and early flowering phenotype. By expressing the reporter gene  $\beta$ -glucuronidase under the control of the BoCYP83B1 promoter in Arabidopsis, we analyzed the spatial expression pattern of BoCYP83B1 under normal growth conditions as well as in response to several hormones and stresses. The BoCYP83B1 was primarily expressed in vascular tissue through the almost whole plant. It was strongly induced by methyl jasmonate, 1-amino-1-cyclopropanecarboxylic acid, salicylic acid (SA), gibberellin, and IAA, suggesting its involvement in complex signaling pathways. Mannitol, NaCl, UV, and Flagelin 22 significantly up-regulated BoCYP83B1 expression, indicating its possible role in stress response. Interestingly, the response of BoCYP83B1 to SA and NaCl showed tissue specificity. Thus, BoCYP83B1 might have different functions in different tissues.

**来源:** Biologia Plantarum

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**全文链接:**

<http://agri.ckcest.cn/ass/154fb9fe-f054-4a99-aca2-d55d686f80fc.pdf>

## **3. Expression of rice OsMyb4 transcription factor improves tolerance to copper or zinc in canola plants (水稻OsMYB4转录因子的表达提高油菜对铜或锌的耐受性)**

**简介:** The effects of copper and zinc salts on transgenic canola plants expressing rice transcription factor (TF) OsMYB4 were investigated. Transgenic plants (TPs), which showed a high OsMyb4 expression in response to either Cu or to Zn excess, were used for the current study. In leaves of TPs, the content of Cu was equal and the content of Zn was significantly higher than in non-transformed plants (NTPs). The TPs grown on an extremely high concentration of heavy metals (HMs; 150  $\mu$ M CuSO<sub>4</sub> or 5 000  $\mu$ M ZnSO<sub>4</sub>) were able to survive for more than 15 d, while NTPs died after 7 - 9 d of incubation. This indicates that expression of OsMyb4 in canola plants improved their HM tolerance. The TPs tolerance to HMs was confirmed by a higher shoot biomass than that in NTPs. Excess of HMs caused oxidative stress (indicated by increase in malondialdehyde content) especially in leaves of NTPs. This data suggests a protective role of the OsMyb4 TF in oxidative stress. The HMs caused a lower decrease in activities of superoxide dismutase and guaiacol peroxidase in TPs than in NTPs. Higher tolerance of TPs to HMs was also suggested by a considerable increase in the content of low-molecular phenolic compounds, including flavonoids and anthocyanins,

as well as proline (a potential antioxidant and chaperone). These data suggest that OsMYB4 may play a role as a positive regulator of phenylpropanoid pathway and proline synthesis. The created canola OsMyb4 TPs may be useful for future applications in phytoremediation of HM-polluted soils.

来源: *Biologia Plantarum*

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全文链接:

<http://agri.ckcest.cn/ass/5b9fc92d-01cc-4ca8-b313-c9a8b4d09566.pdf>

#### **4. Effectiveness of Rlm7 resistance against *Leptosphaeria maculans* (phoma stem canker) in UK winter oilseed rape cultivars (英国冬油菜品种RLM7对油菜茎基溃疡病菌抗性的研究)**

简介: The Rlm7 gene in *Brassica napus* is an important source of resistance for control of phoma stem canker on oilseed rape caused by the fungus *Leptosphaeria maculans*. This study shows the first report of *L. maculans* isolates virulent against Rlm7 in the UK. *Leptosphaeria maculans* isolates virulent against Rlm7 represented 3% of the pathogen population when cultivars with the Rlm7 gene represented 5% of the UK oilseed rape area in 2012/13. However, the Rlm7 gene has been widely used since then, representing >15% of the UK oilseed rape area in 2015/16. Winter oilseed rape field experiments included cultivars with the Rlm7 gene, with the Rlm4 gene or without Rlm genes and took place at five sites in the UK over four cropping seasons. An increase in phoma leaf spotting severity on Rlm7 cultivars in successive seasons was observed. Major resistance genes played a role in preventing severe phoma leaf spotting at the beginning of the cropping season and, in addition, quantitative resistance (QR) in the cultivars examined made an important contribution to control of phoma stem canker development at the end of the cropping season. Deployment of the Rlm7 resistance gene against *L. maculans* in cultivars with QR in combination with sustainable disease management practices will prolong the use of this gene for effective control of phoma stem canker epidemics.

来源: *Plant Pathology*

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全文链接:

<http://agri.ckcest.cn/ass/4c7fd2bf-fb27-4280-9cc8-f302c29dd3c8.pdf>