



2018年第31期总145期

蔬菜育种专题

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中国农业科学院农业信息研究所

联系人：王爱玲

联系电话：010-51503648

邮箱：agri@ckcest.cn

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➤ 前沿资讯

1. Spatio-temporal expression dynamics differ between flowering time gene homologues in the allopolyploid *Brassica napus* (异源多倍体甘蓝型油菜的复制基因功能分化)

简介: 多倍化是真核生物演化过程中反复出现的特性,与基因组复杂性、适应性辐射及物种形成的增加相关。被子植物中的许多植物支系都发生过多多次多倍化事件。日前来自英国约翰英尼斯研究中心的科研人员研究了欧洲油菜中与成花转变相关复制基因的保留和时空表达动态,结果显示开花基因相比于其他基因更容易在油菜基因组中保留下来。成果在线发表于《植物杂志》(the plant journal)。

研究发现,叶和茎尖在不同发育阶段的转录组时间序列数据显示67%的保留下来的开花时间相关基因表达。此外,64%的叶片和74%的茎尖组织保留的同源基因在不同发育阶段显示出不同的表达模式,说明这些基因存在新功能或者亚功能化。茎分生组织决定基因TFL1同源基因的研究显示在顺式元件上存在差异,也许可以解释同源基因之间的分化。复制基因表达模式的差异突出了将二倍体模式系统中的基因调控网络应用到更加复杂的多倍体作物物种的挑战。

来源: the plant journal

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全文链接:

<http://agri.ckcest.cn/ass/fd7f154e-14c1-4a0c-9436-8aa01476b4f8.pdf>

➤ 学术文献

1. First evidence of the occurrence of Turnip mosaic virus in Ukraine and molecular characterization of its isolate (乌克兰首次出现芜菁花叶病毒,并对病毒分离物分子特征进行分析)

简介: A total of 54 samples of Brassicaceae crops showing symptoms of mosaic, mottling, vein banding and/or leaf deformation were collected in Kyiv region (northern central part of Ukraine) in 2014-2015. A half of collected samples was found to be infected with Turnip mosaic virus (TuMV), and TuMV was detected in samples from *Brassica oleracea* var. capitata (cabbage), *Raphanus sativus*, *Brassica juncea*, *Raphanus* sp., *Sinapis alba*, *Camelina sativa* and *Bunias orientalis* (weed). The full-length sequence of the genomic RNA of a Ukrainian isolate (UKR9), which was isolated from cabbage, was determined. Recombination analysis of UKR9 isolate showed that this isolate was an interlineage recombinant of world-*Brassica* and Asian-*Brassica/Raphanus* phylogenetic groups. This study shows for the first time the occurrence of TuMV in Ukraine.

来源: Journal of Phytopathology

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<http://agri.ckcest.cn/ass/f0a70f6e-fea4-438e-ab61-6a6e3efc585a.pdf>

2. Genome-wide identification and expression analysis of chitinase gene family in *Brassica rapa* reveals its role in clubroot resistance (通过对芜菁几丁质酶基因家族进行全基因组鉴定和表达分析, 发现几丁质酶能够促进根肿病抗性)

简介: Chitinases, a category of pathogenesis-related proteins, are responsible for catalyzing the hydrolysis of chitin into the N-acetyl-D-glucosamine. Therefore, chitinases are believed to function as a guardian against chitin-containing pathogens. Here, we examined the role of the *Brassica rapa* chitinase family genes in clubroot disease. A total of 33 chitinase genes were identified and grouped into five classes based on their conserved domain. They were distributed unevenly across eight chromosomes in *B. rapa*, and 31 of them contained few introns (≤ 2). In addition, the expression of these genes was organ-specific, and 14 genes were expressed differentially in response to *Plasmodiophora brassicae* challenge of clubroot-susceptible (CS NIL) and resistant (CR NIL) lines. Furthermore, reduced pathogen DNA content and clubroot symptoms were observed in the CS NILs after their treatment with chitin oligosaccharides 24 h prior to inoculation with *P. brassicae*. The findings indicate that chitinases play a crucial role in pathogen resistance of the host plants. The results offer an insight into the role of chitinase in *B. rapa*-*P. brassicae* interaction.

来源: Plant Science

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<http://agri.ckcest.cn/ass/3f7dd9ce-c86b-42af-b865-8921a4038192.pdf>

3. Infection cycle of *Alternaria brassicicola* on *Brassica oleracea* leaves under growth room conditions (温室条件下羽衣甘蓝叶片上的甘蓝链格孢菌侵染循环)

简介: Development of the necrotrophic fungus *Alternaria brassicicola* was evaluated during infection of three cabbage varieties: *Brassica oleracea* var. *capitata* f. *alba* 'Stone Head' (white cabbage), *B. oleracea* var. *capitata* f. *rubra* 'Langedijker Dauer' (red cabbage) and *B. oleracea* var. *capitata* f. *sabauda* 'Langedijker Dauerwirsing' (Savoy cabbage). Following inoculation of cabbage leaves, conidial germination, germ tube growth, and appressorium formation were analysed during the first 24 h of infection. Differences in the dynamics of fungal development on leaves were observed, e.g. approximately 40% of conidia germinated on Savoy cabbage leaves at 4 h post-inoculation (hpi) while only 20% germinated on red and white cabbage leaves. Leaf penetration on the three cabbage varieties mainly occurred through appressoria, rarely through stomata. Formation of infection cushions was found exclusively on red cabbage. Appressoria were first observed on red cabbage leaves at 6 hpi, and on white and Savoy cabbage leaves at 8 hpi. Conidiogenesis occurred directly from mature conidia at an early stage of fungal development (10 hpi), but later (48 hpi) it occurred through conidiophores. Disease progress and changes in the morphology of leaf surfaces were also observed. At the final 120 hpi measurement point, necroses on all investigated varieties were approximately the same size. Based on detailed light and electron microscopic analyses, an outline of the *A. brassicicola* infection cycle on *B. oleracea* leaves under growth

room conditions has been proposed. According to the authors' knowledge, this report represents the most detailed up-to-date description of infection of *B. oleracea* varieties by *A. brassicicola*.

来源: Plant Pathology

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全文链接:

<http://agri.ckcest.cn/ass/49b82d24-5dd8-42c3-be18-f1a4533418e7.pdf>

4. Comprehensive analyses of the BES1 gene family in *Brassica napus* and examination of their evolutionary pattern in representative species (甘蓝型油菜BES1基因家族综合分析及代表种进化方式分析)

简介: Background: The BES1 gene family, an important class of plant-specific transcription factors, play key roles in the BR signal pathway in plants, regulating various development processes. Until now, there has been no comprehensive analysis of the BES1 gene family in *Brassica napus*, and a cross-genome exploration of their origin, copy number changes, and functional innovation in plants was also not available.

Results: We identified 28 BES1 genes in *B. napus* from its two subgenomes (AA and CC). We found that 71.43% of them were duplicated in the tetraploidization, and their gene expression showed a prominent subgenome bias in the roots. Additionally, we identified 104 BES1 genes in another 18 representative angiosperms and performed a comparative analysis with *B. napus*, including evolutionary trajectory, gene duplication, positive selection, and expression pattern. Exploiting the available genome datasets, we performed a large-scale analysis across plants and algae suggested that the BES1 gene family could have originated from group F, expanding to form other groups (A to E) by duplicating or alternatively deleting some domains. We detected an additional domain containing M4 to M8 in exclusively groups F1 and F2. We found evidence that whole-genome duplication (WGD) contributed the most to the expansion of this gene family among examined dicots, while dispersed duplication contributed the most to expansion in certain monocots. Moreover, we inferred that positive selection might have occurred on major phylogenetic nodes during the evolution of plants.

Conclusions: Grossly, a cross-genome comparative analysis of the BES1 genes in *B. napus* and other species sheds light on understanding its copy number expansion, natural selection, and functional innovation.

来源: BMC Genomics

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全文链接:

<http://agri.ckcest.cn/ass/42a5a419-e158-49bd-8e9c-515420fc24c1.pdf>