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前沿资讯

1. Biologists have studied enzymes that help wheat to fight fungi（小麦抵抗真菌的机理研究获得突破）

简介：俄罗斯Medical University的科学家们研究了小麦对致病真菌引起的破坏做出的响应。他们检测了因感染导致的细胞死亡过程中涉及的酶的活性，发现植物对病原体的抗性大小主要取决于一组编码在DNA中的蛋白酶，这些酶会参与到感染细胞的死亡过程并防止感染进一步扩散。研究结果发表于《International Journal of Molecular Sciences》上。

尽管小麦在农业中占据十分重要的位置，然而小麦对病原体做出的响应只有泛泛的描述，并没有关注特定的蛋白质。由于小麦和大多数其他植物一样，是同源多倍体，即每一个细胞都拥有多组染色体。加之小麦基因组十分复杂，包含了107000个基因，几乎超过人类基因组的五倍，进而导致了研究的复杂性。

小麦暴露在细菌、病毒、真菌、线虫动物门、昆虫等各种各样的病原体中。其中有些有害微生物寄生在活的植物细胞上，减缓细胞的生长速度（生物营养性病原菌），其他则以细胞为食，导致细胞死亡（坏死性病原菌）。

科学家们使用了引起小麦叶锈病的生物营养性病原菌和损害叶片、麦穗、籽粒的坏死性病原菌两种病原菌，研究了其对Khakasskaya和Daria两种小麦品种感染真菌后的响应。他们采用了液相色谱和质谱相结合的特殊方法。液相色谱法是一种用来鉴别液体流中混合物的技术。由于物质被不同程度地吸收，混合物被分成不同的组分。质谱是一种根据中性原子和分子的质量电荷比将其电离成带电离子的技术，甚至可以精确测定复杂的有机化合物。

通过以上方法，科学家们发现了1554种酶，属于丝氨酸、半胱氨酸、天冬氨酸、苏氨酸、金属蛋白酶等五种催化型蛋白酶，并确认了不同植物栽培品种中常见的蛋白酶比例比预期的要低。但是，不同类型的蛋白酶之间的差异几乎是均等的，表明这些酶可能相互替代。

蛋白酶的研究有助于预测在结构中的精确位置。这些区域的水解过程可能会在蛋白水解级联的过程中被激活。这一连锁反应能让有机物迅速激活大量酶来帮助自己抵御感染。

最重要的是，在受感染植物中发现的蛋白酶的激活不涉及具有半胱天冬酶样或半胱天冬酶样活性的酶。尽管早先有人认为这种蛋白酶会启动蛋白水解酶级联激活，从而导致植物有机体的细胞死亡。但结论是，其他一些独特的蛋白酶可能参与小麦对生物营养性病原体和坏死性病原体感染的早期反应。当然，这一结果应该通过实验用其他方法加以证实。

对酶进行详尽的研究能够帮助科学家澄清它们的分类，科学家描述了多组酶的同源（最相似的蛋白质），并说明了这些酶在系统发生树（展示蛋白质之间的演化距离）上的位置。例如，科学家们已经确认了不同类型的天冬氨酸蛋白酶的差异很大，可能没有亲缘关系，却各自独立获得了类似的功能。

这项研究也有助于阐明植物细胞凋亡的具体机制。众所周知，动物体内主要的凋亡调节因子之一是半胱天冬酶，这种蛋白水解酶能将细胞破坏成不同的元素。科研人员越来越清晰地意识到存在细胞凋亡现象，但是植物却没有凋亡蛋白酶。研究发现植物还有其他酶会进行凋亡蛋白酶的活动。这些酶很有可能就像在动物体内一样，在植物细胞内

执行着同样的细胞死亡过程。不过研究已经证明，在小麦的植物细胞凋亡激活剂中，有些酶不会进行凋亡蛋白酶的活动。这再一次验证了各种真核生物中存在不同的细胞凋亡机制。

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学术文献

1. Genome-Wide Identification and Expression Profiling of Sugar Transporter Protein (STP) Family Genes in Cabbage (Brassica oleracea var. capitata L.) Reveals their Involvement in Clubroot Disease Responses(甘蓝（Brassica oleracea var.capitata L.）中糖转运蛋白（STP）家族基因的全基因组鉴定和表达谱分析揭示其在根肿病反应中的作用)

简介： Sugar transporter protein (STP) genes are involved in multiple biological processes, such as plant responses to various stresses. However, systematic analysis and functional information of STP family genes in Brassica oleracea are very limited. A comprehensive analysis was carried out to identify BoSTP genes and dissect their phylogenetic relationships and to investigate the expression profiles in different organs and in response to the clubroot disease. A total of 22 BoSTP genes were identified in the B. oleracea genome and they were further classified into four clades based on the phylogenetic analysis. All the BoSTP proteins harbored the conserved sugar transporter (Sugar_tr, PF00083) domain, and the majority of them contained 12 transmembrane helices (TMHs). Rates of synonymous substitution in B. oleracea relative to Arabidopsis thaliana indicated that STP genes of B. oleracea diverged from those of A. thaliana approximately 16.3 million years ago. Expression profiles of the BoSTP genes in different organs derived from RNA-Seq data indicated that a large number of the BoSTP genes were expressed in specific organs. Additionally, the expression of BoSTP4b and BoSTP12 genes were induced in roots of the clubroot-susceptible cabbage (CS-JF1) at 28 days after inoculation with Plasmodiophora brassicae, compared with mock-inoculated plants. We speculated that the two BoSTPs might be involved in monosaccharide unloading and carbon partitioning associated with P. brassicae colonization in CS-JF1. Subcellular localization analysis indicated that the two BoSTP proteins were localized in the cell membrane. This study provides insights into the evolution and potential functions of BoSTPs.

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http://agri.ckcest.cn/file1/M00/06/6A/CsgkOFy27ECAZwn5ADVvSMtf5DO488.pdf

2. The Gene Structure and Expression Level Changes of the GH3 Gene Family in Brassica napus Relative to Its Diploid Ancestors(甘蓝型油菜GH3基因家族相对于二倍体祖先的基因结构和表达水平变化)

简介：The GH3 gene family plays a vital role in the phytohormone-related growth and developmental processes. The effects of allopolyploidization on GH3 gene structures and expression levels have not been reported. In this study, a total of 38, 25, and 66 GH3 genes were identified in Brassica rapa (ArAr), Brassica oleracea (CoCo), and Brassica napus (AnACnCn), respectively. BnaGH3 genes were unevenly distributed on chromosomes with 39 on An and 27 on Cn, in which six BnaGH3 genes may appear as new genes. The whole genome triplication allowed the GH3 gene family to expand in diploid ancestors, and allopolyploidization made the GH3 gene family re-expand in B. napus. For most BnaGH3 genes, the exon-intron compositions were similar to diploid ancestors, while the cis-element distributions were obviously different from its ancestors. After allopolyploidization, the expression patterns of GH3 genes from ancestor species changed greatly in B. napus, and the orthologous gene pairs between An/Ar and Cn/Co had diverged expression patterns across four tissues. Our study provides a comprehensive analysis of the GH3 gene family in B. napus, and these results could contribute to identifying genes with vital roles in phytohormone-related growth and developmental processes.

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3. Development of a Molecular Marker Using GWAS to Select the Resistance Resource for the Yeoncheon Strain Causing Kimchi Cabbage Clubroot Disease(利用GWAS分子标记技术筛选泡菜白菜根肿病Yeoncheon菌株的抗性资源)

简介：Resistant cultivars have been developed as a response to clubroot disease, which poses a challenge to Kimchi cabbage cultivation in Korea. However, the recent problem of disease vulnerability in resistant varieties has led to collective efforts to promote genetically diverse resistant sources. The National Institute of Horticultural & Herbal Science (NIHHS, Vegetable Research Division) promotes and conserves resistant resources, and despite using the molecular markers reported thus far in analyzing the resources, a need for novel molecular markers has become apparent owing to the large number of resources that could not be amplified. To address this problem, 96 resources for resistance and vulnerability were selected among the ones conserved at the NIHHS, from which 20,540 SNPs were detected using genotype-by-sequencing (GBS) analysis. Subsequently, a molecular marker associated with resistance to the Yeoncheon strain that causes clubroot disease was developed using a genome-wide association study (GWAS). The corresponding gene had an SNP (G↔T) at the 23098380 position of A07, which was used to develop the CAPS marker that can differentiate resistance and susceptibility to the Yeoncheon strain causing clubroot disease.

The gene at the position of the CAPS marker was found to be an associated gene within 21 kb, encoding a glucose-methanol-choline (GMC) oxidoreductase family protein with four V-type H^+-transporting ATPase subunit Gs. In this study, a molecular marker specific for the Yeoncheon strain was developed. Its use, alongside other previously developed markers in selecting resistance resources, is expected to prove useful in the selection of a wide array of disease-resistant breeding sources. Furthermore, the resulting GBS data could be used for future analysis of the resistance genes associated with various strains causing clubroot disease.

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http://agri.ckcest.cn/file1/M00/06/6A/CsgkOFy26RKAZviUACaktGHvMtw630.pdf

4．Hotspots of Independent and Multiple Rounds of LTR-retrotransposon Bursts in Brassica Species(芸苔属植物LTR-反转录转座子独立和多轮突发热点研究)

简介：Long terminal repeat retrotransposons (LTR-RTs) are a predominant group of plant transposable elements (TEs) that are an important component of plant genomes. A large number of LTR-RTs have been annotated in the genomes of the agronomically important oil and vegetable crops of the genus Brassica. Herein, full-length LTR-RTs in the genomes of Brassica and other closely related species were systematically analyzed. The full-length LTR-RT content varied greatly (from 0.43% to 23.4%) between different species, with Gypsy-like LTR-RTs constituting a primary group across these genomes. More importantly, many annotated LTR-RTs (from 10.03% to 33.25% of all detected LTR-RTs) were found to be enriched in localized hotspot regions. Furthermore, all of the analyzed species showed evidence of having experienced at least one round of a LTR-RT burst, with Raphanus sativus experiencing three or more. Moreover, these relatively ancient LTR-RT amplifications exhibited a clear expansion at specific time points. To gain a further understanding of this timing, Brassica rapa, B. oleracea, and R. sativus were examined for the presence of syntenic regions, but none were present. These findings indicate that these LTR-RT burst events were not inherited from a common ancestor, but instead were species-specific bursts that occurred after the divergence of Brassica species. This study further exemplifies the complexities of TE amplifications during the evolution of plant genomes and suggests that these LTR-RT bursts play an important role in genome expansion and divergence in Brassica species.

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