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▶ 前沿资讯

1. Horticulture Research 精选2021 | 沈阳农大李天来团队揭示S1SWEET7a和S1SWEET14调控番茄果实中糖的运输和储存

简介: 2021年8月, Horticulture Research在线发表了教育部设施园艺重点实验室、沈阳农业大学李天来院士研究团队题为Plasma membrane-localized S1SWEET7a and S1SWEET14 regulate sugar transport and storage in tomato fruits的研究论文。

本研究首先对番茄中29个SWEETs家族成员在Micro-Tom果实中进行了定量分析,发现S1SWEET7a和S1SWEET14在这些成员中具有相对较高的果实特异性表达。随后,研究者对S1SWEET7a和S1SWEET14进行了详细的时空表达模式的分析,发现它们在果实中尤其在维管束中具有较高的表达。进一步的亚细胞定位分析发现,S1SWEET7a和S1SWEET14均为质膜定位的糖转运体。因此推测,S1SWEET7a和S1SWEET14可能参与番茄果实中糖的卸载。

此外,底物特异性分析结果表明,S1SWEET7a和S1SWEET14不仅转运己糖,也可以转运蔗糖,进一步表明了S1SWEET7a和S1SWEET14可能在番茄果实中糖的运输中扮演着重要的角色。

为了进一步探索S1SWEET7a和S1SWEET14在番茄果实中糖的运输和储存上的功能,研究者分别获得了RNAi介导的S1SWEET7a和S1SWEET14的沉默株系,通过对沉默株系中可溶性糖含量的分析,发现相比于WT,沉默株系果实中果糖和葡萄糖的含量显著增加,转化酶活性和蔗糖代谢相关基因表达增加,揭示了S1SWEET7a和S1SWEET14在调控番茄果实己糖积累中的重要作用。此外研究还发现糖分和激素能够调控S1SWEET7a和S1SWEET14的表达,进而对番茄植株株高有显著影响。

本研究结果丰富了SWEETs成员在番茄尤其是果实中的功能,同时为提高番茄果实中糖含量进而提高番茄果实品质提供了一个潜在的思路。

来源: 园艺研究

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全文链接:

http://agri.ckcest.cn/file1/M00/03/40/Csgk0YeX1NGAExp0AChprRWY_4o460.pdf

▶ 学术文献

1. Differential Physiological Response and Potential Toxicological Risk of White Cabbage Grown in Zinc-Spiked Soil (施锌土壤中白菜的生理差异及潜在毒理风险)

简介: Physiological, agricultural and toxicological impact of an excess of Zn in the soil is an important issue, as Zn is a heavy metal and impairs many processes of plants and animals. The novelty of this work is that it is a comprehensive approach to facilitate visualization not only of the condition of cabbage plants under Zn stress, but also prediction of the toxicity associated with consumption of such cabbages. We treated plants of two cabbage cultivars, differing in their earliness, with 50 and 200 mg Zn kg⁻¹ soil (Zn50 and Zn200, respectively) above the natural Zn levels of 118.13 mg kg⁻¹ soil (Zn0). Leaf cell membrane integrity,

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condition of the photosynthetic apparatus (reflected by relative chlorophyll content (SPAD) and F_v/F_m parameter of chlorophyll a fluorescence), head biomass, and Zn bioaccumulation in the heads were analyzed. Toxicological risk was also assessed by Daily Intake of Metal (DIM) and Health Risk Index (HRI) indicators. The data revealed that plants of the late cultivar were more sensitive to soil Zn than those of the early one. Detrimental effects of Zn (especially at the higher dose, Zn200) were manifested in the seedlings just after three weeks of treatment, and then reflected in the yield. We assume that, due to their fast and prolonged response to Zn, the seedlings of the late cultivar can be used as biomarkers of Zn toxicity. Although Zn plants did not indicate toxicological risk, based on DIM and HRI, Zn concentration in the soil should be taken into account prior to cabbage planting, because plants which do not reveal symptoms of injury can accumulate Zn above the permissible level.

来源: Agronomy

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<http://agri.ckcest.cn/file1/M00/03/3F/Csgk0YeX0n2AdbzdAAidU-FBMNQ865.pdf>

2. Dissecting the genetic basis of bioactive metabolites and fruit quality traits in blueberries (*Vaccinium corymbosum* L.) (蓝莓生物活性代谢产物和果实品质性状的遗传基础解析)

简介: Blueberry is well-recognized as a healthy fruit with functionality derived largely from anthocyanin and chlorogenic acid. Despite their importance, no study to date has evaluated the genetic basis of these bioactives in blueberries and their relationship with fruit quality traits. Hence, to fill this gap, a mapping population including 196 F_1 individuals was phenotyped for anthocyanin and chlorogenic acid concentration and fruit quality traits (titratable acidity, pH, and total soluble solids) over 3 years and data were used for QTL mapping and correlation analysis. Total soluble solids and chlorogenic acid were positively correlated with glycosylated anthocyanin and total anthocyanin, respectively, indicating that parallel selection for these traits is possible. Across all the traits, a total of 188 QTLs were identified on chromosomes 1, 2, 4, 8, 9, 11 and 12. Notably, four major regions with overlapping major-effect QTLs were identified on chromosomes 1, 2, 4 and 8, and were responsible for acylation and glycosylation of anthocyanins in a substrate and sugar donor specific manner. Through comparative transcriptome analysis, multiple candidate genes were identified for these QTLs, including glucosyltransferases and acyltransferases. Overall, the study provides the first insights into the genetic basis controlling anthocyanins accumulation and composition, chlorogenic acid and fruit quality traits, and establishes a framework to advance genetic studies and molecular breeding for anthocyanins in blueberry.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/10/11/Csgk0GNBI5qAfWq9AMs1MJRXHR8177.pdf>

3. Integrated Analysis of Transcriptome and Metabolome Reveals New Insights into the Formation of Purple Leaf Veins and Leaf Edge Cracks in Brassica juncea (通过转录组和代谢组学分析, 探索紫色叶脉和叶缘开裂形成的调控途径)

简介: Purple leaf veins and leaf edge cracks comprise the typical leaf phenotype of Brassica juncea; however, the molecular mechanisms and metabolic pathways of the formation of purple leaf veins and leaf edge cracks remain unclear. In this study, transcriptome and metabolome analyses were conducted to explore the regulation pathway of purple leaf vein and leaf edge crack formation based on four mustard samples that showed different leaf colors and degrees of cracking. The results showed genes with higher expression in purple leaf veins were mainly enriched in the flavonoid biosynthesis pathway. Integrating related genes and metabolites showed that the highly expressed genes of ANS (BjuA004031, BjuB014115, BjuB044852, and BjuO009605) and the excessive accumulation of dihydrokaempferol and dihydroquercetin contributed to the purple leaf veins by activating the synthetic pathways of pelargonidin-based anthocyanins and delphinidin-based anthocyanins. Meanwhile, “alpha-farnesene synthase activity” and “glucan endo-1, 3-beta-D-glucosidase activity” related to the adversity were mainly enriched in the serrated and lobed leaves, indicating that the environmental pressure was the dominant factor controlling the change in leaf shape. Overall, these results provided new insights into the regulation pathways for formation of purple leaf veins and leaf edge cracks, which could better accelerate the theoretical research on purple leaf vein color and leaf edge cracks in mustard.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/11/Csgk0GM2jDSADPWmAGmvDI94wmI115.pdf>

4. Genetic dissection of Brassica napus photosynthetic pigment content diversity and identification of loci associated with photoperiod and alkaline soil responses (甘蓝型油菜光合色素含量多样性的遗传分析及与光周期和碱性土壤反应相关基因座的鉴定)

简介: The photosynthetic pigment content of plants is a key physiological trait as it is closely related to photosynthetic efficiency and crop yield potential, and which is extremely susceptible to environmental factors. However, the genetic factors controlling the photosynthetic pigment content in Brassica napus have not yet been completely elucidated. Here, we performed a genome-wide association study (GWAS) of photosynthetic pigment content using a diversity panel comprising 518 B. napus inbred lines grown in four different soil and light environments. We identified 281 single-nucleotide polymorphisms (SNPs) significantly associated with photosynthetic pigment content-related traits. A total of 46 candidate genes involved in chlorophyll and carotenoid metabolism were identified. The identified SNPs and potential candidate genes may facilitate the study of natural variation in photosynthetic pigment accumulation and provide valuable resources for future high photosynthetic efficiency breeding that will adapt to different soil and light conditions.

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