



2019年第2期总169期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. 研究揭示土壤干旱致全球河流日渐干涸

#### ▶ 学术文献

1. 大白菜莲座叶与叶球变异相关性的遗传分析
2. 芸薹属植物抗黑腐病分子育种最新进展
3. 大白菜BpPMSR3过表达增强拟南芥对镉的耐受性
4. 十字花科蔬菜黑腐病致病菌第三生理小种的特异性分子标记研究

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## ▶ 前沿资讯

### 1. The long dry: why the world's water supply is shrinking (研究揭示土壤干旱致全球河流日渐干涸)

**简介:** 澳大利亚新南威尔士大学的研究团队采用160个国家43000个降水站点和5300个河流监测点的真实数据对全球降雨和河流做了一次极为透彻的分析,结果揭示了一个自相矛盾的现状:气候变化导致越来越频繁的降雨,但全球水资源却在不断减少,这其中的罪魁祸首就是干旱的土壤。

由于暖空气会带来更多湿气,气候模型预测的是降雨量会增加。但出人意料的是,尽管全世界各地的降雨量都有所增加,大型河流却日渐干涸。研究认为其中的原因就在于流域内的土壤因全球变暖而日益干旱。以前,在暴雨来临之前土壤是湿润的,多余的降雨就能流入河流;如今土壤却越来越干,吸收的雨水多了,流入河流的水也就越来越少。土壤越干旱,农民种植同样的作物就需要灌溉更多的水。之前美国的研究也表明,发生极端降雨事件时,如果土壤是湿润的,那么62%的雨水量会形成洪水;而如果土壤是干旱的,则仅有13%的雨水会形成洪水。

自然降水中仅有36%为“蓝水”(流入湖泊、河流、蓄水层的降雨),这部分水资源可被抽提以满足人类需求。剩下三分之二的降雨大部分会成为土壤含水量(即“绿水”),即景观用水和生态用水。由于温度升高,越来越多的水分从土壤中蒸发出去,干旱的土壤就会在降雨时吸收更多的雨水,于是人类所需的“蓝水”也就越来越少。

这一结果和过去政府间气候变化专门委员会(IPCC)有关洪水增加的报道相悖。研究还指出干旱将成为全球新常态,对于那些已然干旱的地区来说尤其如此。为了适应这一新常态,需要制定新的政策,并完善水利基础设施。水资源不断缩减的地区要减少耗水型农业活动,或者转移到别处,同时加大水库蓄水容量。

**来源:** AAAS

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**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0Fwsa96AVjEnAAMmrOmoCCK551.pdf>

## ▶ 学术文献

### 1. Genetic Analysis of Chinese Cabbage Reveals Correlation Between Rosette Leaf and Leafy Head Variation (大白菜莲座叶与叶球变异相关性的遗传分析)

**简介:** To understand the genetic regulation of the domestication trait leafy-head formation of Chinese cabbages, we exploit the diversity within *Brassica rapa*. To improve our understanding of the relationship between variation in rosette-leaves and leafy heads, we phenotyped a diversity set of 152 Chinese cabbages. This showed correlation between rosette-leaf traits and both head traits and heading capacity. Interestingly, the leaf number of the mature head is not correlated to heading degree nor head shape. We then chose a non-heading pak choi genotype to cross to a Chinese cabbage to generate populations segregating for the leafy head traits. Both a large F<sub>2</sub> (485 plants) and a smaller Doubled

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Haploid (88 lines) mapping population were generated. A high density DH-88 genetic map using the Brassica SNP array and an F2 map with a subset of these SNPs and InDel markers was used for quantitative trait locus (QTL) analysis. Thirty-one quantitative trait loci (QTLs) were identified for phenotypes of rosette-leaves in time and both heading degree and several heading traits. On chromosome A06 in both DH-88 and F2-485 QTLs for rosette leaf length and petiole length at different developmental days and an F2 QTL for head height co-located. Variation in head height, width and weight all correlate with variation in heading degree with co-locating QTLs, respectively, on chromosome A03, A05, and A08 in F2-485. The correlation between rosette-leaf and heading traits provides not only insight in the leaf requirements to form a head, but also can be used for selection by Chinese cabbage breeders.

来源: Frontiers in Plant Science

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwsZI6AWgPvADAXgbFShzQ798.pdf>

## **2. Molecular breeding for resistance to black rot [*Xanthomonas campestris* pv. *campestris* (Pammel) Dowson] in Brassicas: recent advances (芸薹属植物抗黑腐病分子育种最新进展)**

简介: The Brassicas are affected by several diseases, of which black rot, *Xanthomonas campestris* pv. *campestris* (Pam.) Dowson (Xcc), is one of the most widespread and devastating worldwide. The black rot bacteria causes systemic infection in the susceptible plants and penetrate the plants through the hydathodes or wounds. Typical disease symptoms are 'V' shaped necrotic lesions appearing from the leaf margins with blackened veins. Periodic outbreaks of the black rot pathogen have occurred worldwide, especially in the continental regions, where high temperatures and humidity favor the incidence of disease occurrence causing huge yield loss. The challenge to control the losses in vegetable brassicas production is made more difficult by the adverse climatic changes and evolution of new pathogenic races. The development of black rot resistant hybrids/varieties is the most reliable long term practical solution for effective disease control. Identification of new resistant genetic resources, tightly linked markers with resistance loci and QTL mapping would facilitate the breeding programme for black rot resistance. Information regarding genetics of resistance and mapping of resistance genes/QTLs will accelerate the marker assisted resistance breeding in brassica crops against Xcc. In future we need to identify the race specific candidate genes for and their validation through transgenics and gene expression. Moreover, it is imperative to identify functional markers for resistance genes through identification of R gene families and their relationship with resistance expression. This comprehensive review will help the researchers working in this area to understand the dynamics of black resistance breeding and to formulate future breeding strategies.

来源: Euphytica

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[http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwsYDKAG\\_RxAA6fJGUPz20471.pdf](http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwsYDKAG_RxAA6fJGUPz20471.pdf)

### 3. Overexpression of Chinese flowering cabbage BpPMSR3 enhances the tolerance of *Arabidopsis thaliana* to cadmium (大白菜BpPMSR3过表达增强拟南芥对镉的耐受性)

简介: Soil pollution by the heavy metal cadmium (Cd) is a global environmental problem that adversely affects plants and humans. For example, Cd easily contaminates Chinese flowering cabbage (*Brassica rapa parachinensis*). To investigate the molecular mechanism of Cd tolerance in Chinese flowering cabbage, we cloned a Cd tolerance-related gene named BpPMSR3 in this study. The full-length cDNA of BpPMSR3 is 555 bp with an open reading frame encoding 184 amino acids. Phylogenetic analysis indicated that BpPMSR3 was closely related to *Brassica rapa* PMSR in different species. Functional analysis showed that the root lengths and fresh weights of transgenic *Arabidopsis thaliana* plants overexpressing BpPMSR3 decreased a lower ratio than Col-0 under 50  $\mu$  M Cd condition, compared to plants grown under -Cd condition. However, Cd absorption did not differ between Col-0 and transgenic lines. The methionine (Met), glutathione (GSH), and phytochelatin concentrations in transgenic lines were higher than those in Col-0, whereas the methionine sulfoxide (MetSO) concentration in transgenic lines was lower than that in the wild type Col-0. These results reveal that the tolerance of transgenic *Arabidopsis* plants to Cd was higher than that of Col-0. The transcription levels of AtHMA3, AtMAN3, and AtNramp1, which were related to Cd tolerance, were significantly higher in transgenic lines than in Col-0 in the presence of Cd. Therefore, Chinese flowering cabbage BpPMSR3 improved the tolerance of transgenic *Arabidopsis* plants to Cd.

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### 4. Development of race-specific molecular marker for *Xanthomonas campestris* pv. *campestris* race 3, the causal agent of black rot of crucifers (十字花科蔬菜黑腐病致病菌第三生理小种的特异性分子标记研究)

简介: Race-specific molecular markers were established to distinguish *Xanthomonas campestris* pv. *campestris* (Xcc) race 3, the causal agent of black rot disease of crucifers. The available genome sequences of Xcc races were aligned and identified three DNA fragments specific to Xcc race 3. The identified race-specific DNA fragments namely XccR3-49, XccR3-52, and XccR3-55 were used for designing the race-specific primers to detect and identify Xcc race 3. The specificity of race-specific primers was tested against the genomic DNA extracted from Xcc (races 1-7), Xcc strains, Xc pathovars, and other bacterial species. XccR3-49, a specific sequence characterized amplified region (SCAR) primer set, gave a single band with 867 bp length for Xcc race 3 only. The remaining two markers XccR3-52 and XccR3-55 showed polymorphic amplification with amplicon sizes of 1889 and 2109 bp

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for Xcc race 3, respectively. Additionally, the SCAR primer set detected Xcc race 3 rapidly and efficiently in artificially infected cabbage leaves with bio-PCR. This result showed that the newly developed race-specific markers can successfully and efficiently detect and identify Xcc race 3 from *Xanthomonas campestris* pv. *campestris* races, *Xanthomonas* species/ pathovars, as well as other plant pathogenic bacteria (*Pseudomonas syringae* pv. *maculicola* and *Erwinia carotovora* subsp. *carotovora*). Up to now, this is the first report describing the race-specific marker for the detection of Xcc race 3.

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