



2019年第15期总55期

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## ▶ 前沿资讯

### 1. Scouting for Naturally Low-Toxicity Wheat Genotypes by a Multidisciplinary Approach (通过多学科方法寻找天然低毒小麦基因型)

**简介:** 在过去的几年里,人们一直致力于研发有效的麸质解毒策略,从而对工艺性能进行优化。在不影响小麦流变特性的情况下,获取低筋产品仍然是一个新的挑战。在这项研究中,我们对硬粒小麦的基因型进行了全面的鉴定,目的是识别低面筋蛋白的基因型,这种基因型结合了潜在的低毒性/免疫原性、保守的产量和流变学特性,具有良好的面包或意大利面制作的前景。通过定量的免疫分析和液相色谱结合紫外检测技术,初步分析了麸质蛋白,重点研究了麦胶蛋白组分在腹腔疾病患者免疫反应中的主要作用。此外,还收集了小麦籽粒蛋白质含量、穗粒产量、干谷蛋白和谷蛋白指数等数据,为小麦营养价值及其技术特性的产量相关性状和品质定量特征提供补充信息。对整个数据池进行统计评估,以首选的低毒性基因型,进行体外模拟胃十二指肠消化和非靶向HR-MS/MS肽鉴定。最后,根据欧洲食品安全局提供的最新指导,对腹腔疾病患者的潜在毒性进行风险评估。

**来源:** Nature

**发布日期:** 2019-02-07

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fyq-fOALm8ACJ7KvxZTos238.pdf>

## ▶ 学术文献

### 1. Compositional equivalence of event IND-00412-7 to non-transgenic wheat (非转基因小麦的成分等价事件IND-00412-7)

**简介:** 小麦是种植最广泛的谷类作物,占耕地总面积的很大一部分。干旱是影响作物生产的主要环境压力源,在缺水条件下保持产量是作物改良的一个非常理想的表型。向日葵的HaHB4 (*Helianthus annuus* homeobox 4) 基因编码是一种与环境胁迫耐受有关的转录因子。HaHB4小麦的引入导致了IND-00412-7 (HB4小麦) 事件的发展,在生产潜力低的环境中表现出较高的产量。对IND-00412-7小麦进行成分分析,包括41种营养素、2种谷物抗营养素和10种饲料营养素。这些研究结果表明, IND-00412-7构图相当于非转基因小麦。

**来源:** Springer

**发布日期:** 2019-01-17

**全文链接:**

[http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fyq\\_vCASVuZAAak0q0q-t4556.pdf](http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fyq_vCASVuZAAak0q0q-t4556.pdf)

### 2. Mapping of dwarfing gene Rht14 in durum wheat and its effect on seedling vigor, internode length and plant height (硬粒小麦矮化基因Rht14的定位及其对幼苗活力、节间长度和株高的影响)

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**简介:** Short coleoptiles associated with GA-insensitive Rht-1 alleles in wheat reduces yield due to poor seedling establishment under dry, or stubble-retained conditions. Hence there is a need for alternative dwarfing genes for wheat improvement programs. GA-sensitive dwarfing gene Rht14 confers semidwarf stature in wheat while retaining longer coleoptiles and early seedling vigor. Two RIL populations were used to identify the map position of Rht14 and to estimate its effect on plant height, coleoptile length, seedling shoot length, spike length and internode length. Rht14 on chromosome 6A was mapped in the genomic region 383422 Mbp flanked by GA2oxA9 and wmc753 in a Bijaga Yellow/Castelporziano RIL population. Recombination events between Rht14 and GA2oxA9 in the RIL population indicated that Rht14 might not be allelic to GA2oxA9. The conserved DNA sequence of GA2oxA9 and its flanking region in Castelporziano also suggested that the point of mutation responsible for the Rht14 allele must be a few Mbp away from GA2oxA9. The dwarfing effects of Rht14 on plant height, internode length and seedling vigor were compared with those of Rht-B1b in an HI 8498/Castelporziano RIL population. Both genes significantly reduced plant height and internode length. Rht-B1b conferred a significant reduction in coleoptile length and seedling shoot length, whereas Rht14 reduced plant height, but not coleoptile and seedling shoot length. Therefore, Rht14 can be used as an alternative to Rht-B1b for development of cultivars suitable for deeper sowing in dry environments and in conditions of conservation agriculture where crop residues are retained.

**来源:** The Crop Journal

**发布日期:** 2018-11-26

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0FyrAeuAUjIHAA2KMRzU8rA822.pdf>

### **3. Dataset on phenolic profile of seven wheat genotypes along maturation (七种成熟期小麦基因型的酚类谱数据集)**

**简介:** This article contains data on phenolic-profiling of seven wheat genotypes along maturation (softy, milky, physiological maturity and mature). This supplementary data is related to research “Metabolomic approach for characterization of phenolic compounds in different wheat genotypes during grain development” (Santos et al., 2018). Briefly, free and bound phenolic compounds were extracted with 80% ethanol (v/v) and hydrolysis processes, respectively. The aliquots resultants were separated by ultra-performance liquid chromatography (UPLC) and analyzed by quadrupole time-of-flight mass spectrometry (QTOF). Data were acquired using a multiplexed MS/MS acquisition with alternating low and high energy acquisition (MS<sup>E</sup>). The phenolic compounds with their respective abundances are showed here through characterization table and multivariate analysis (hierarchical cluster analysis—HCA—and principal component analysis—PCA).

**来源:** Data in Brief

**发布日期:** 2018-10-04

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0FyrBOKANNLtAAZiWcVCiDg558.pdf>

## ➤ 相关专利

### 1. 小麦-中间偃麦草广谱抗条锈T4DL . 4DS-3Ai易位系及SCAR标记的开发

**简介:** 本发明公开了一种广谱抗锈的小麦-中间偃麦草E<sup>6</sup>染色体组T4DL . 4DS-3Ai小片段易位系CH4131及追踪该易位片段的SCAR标记。通过对小麦与中间偃麦草杂交后代进行条锈病和GISH鉴定, 获得高抗条锈病的小麦-中间偃麦草小片段易位系CH4131, 并开发特异性追踪SCAR标记1个。该易位系对条锈病具有广谱抗性, 农艺性状优良、具有优异亚基14+15, 品质性状好, 在小麦育种上具有广泛的利用价值。

**来源:** 国家知识产权局专利检索及分析

**发布日期:** 2018-11-21

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0FyrBc2AXcLUABK2t6IAN-E068.PDF>