

BẢN TIN THỨ BA 19-9-2023

BẢN TIN SỐ 1

Chinese Scientists Develop New Gene Editing Tool



A team of scientists in Beijing have developed a new [gene editing](#) tool called CyDENT. The tool is more efficient than [CRISPR](#) technology and can be used to edit DNA in mitochondria and chloroplasts.

CyDENT is a protein-based tool that does not rely on a guide RNA. Instead, it uses a protein signal to transport the editor inside the cell, bypassing the need for a guide RNA. This makes CyDENT more efficient than [CRISPR-Cas9](#), especially for editing DNA in mitochondria and chloroplasts.

CyDENT works by first binding to the target DNA sequence with the transcription-activator-like effector (TALEs). The FokI nickase then cuts the DNA at that location, creating a single-stranded DNA substrate. The single-strand-specific cytidine deaminase then converts the cytidines in the single-stranded DNA to uracils. The uracils are then recognized by the cell's DNA repair machinery, which replaces them with cytosines. This process is called base editing.

This new tool could lead to new therapies for diseases caused by mitochondrial DNA mutations and it could also be used to engineer crops with higher yields.

Read more from [Nature](#) and [South China Morning Post](#).
<https://www.isaaa.org/kc/cropbiotechupdate/ged/article/default.asp?ID=20419>

BẢN TIN SỐ 2

EU Ag Ministers Discuss NGTs in Cordoba Meeting

ISAAA September 13, 2023



The informal meeting of the European Union (EU) agriculture ministers in Cordoba on September 3-5, 2023 focused on the use of new technologies to advance food security, combat [climate change](#), and achieve agricultural sector profitability in the region. The meeting was held in the Palacio de Congresos of the Andalusian city and chaired by Spain's acting Minister for Agriculture and Fisheries, Luis Planas, and was attended by the European Commissioner, Janusz Wojciechowski.

Industry leaders from the EU presented their ideas and proposals on which techniques and solutions they consider most effective in the fight against climate change and for better food production. One of the main topics of the meeting was food security, a priority of the Spanish presidency for its six-month term. Another issue discussed during the meeting was the fight against climate change and its effects on the agri-food sector in the EU and globally. However, the key topic during the informal meeting was [new genomics techniques](#) (NGTs), which make it possible to breed more resilient and resistant plant varieties quickly and with greater precision.

During the meeting, the Spanish minister highlighted the potential of new genomic techniques in breeding new plant varieties to meet the challenge of food production sustainability, tackle climate change, and reduce the use of plant protection products and fertilizers.

European decision-makers were able to express their concerns, doubts, and worries as part of a transparent debate to guarantee the production of both seeds and plants for food production in sufficient quantities. This is all without harming the environment and guaranteeing the future of the sector. The Ministers also emphasized their interest in ensuring transparency and information for consumers to achieve more sustainable technological solutions.

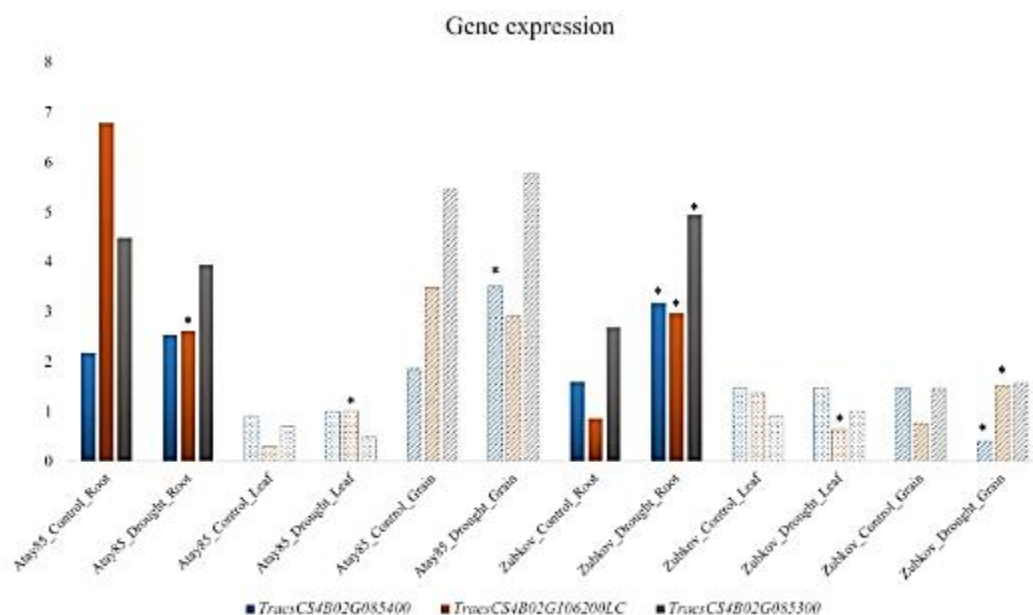
For more details, read the news release on the website of the [Council of the European Union](#).

BẢN TIN KHOA HỌC

Identification of KASP markers and candidate genes for drought tolerance in wheat using 90K SNP array genotyping of near-isogenic lines targeting a 4BS quantitative trait locus

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Abstract

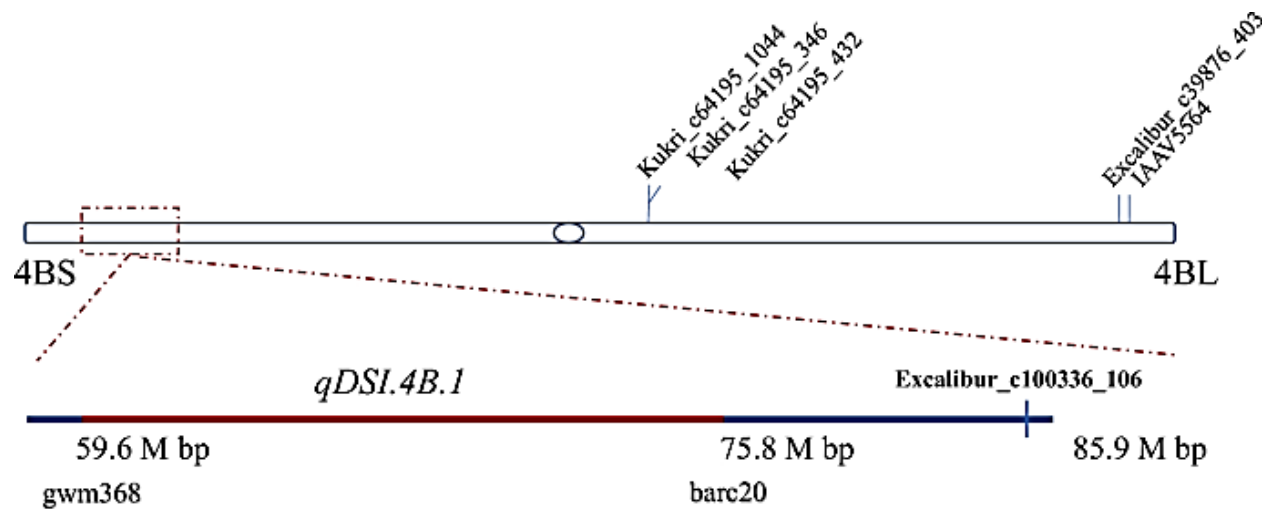
Key message

This study identified a novel SNP and developed a highly efficient KASP marker for drought tolerance in wheat by genotyping NILs targeting a major QTL for drought tolerance using an SNP array and validation with commercial varieties.

Abstract

Common wheat (*Triticum aestivum* L.) is an important winter crop worldwide and a typical allopolyploid with a large and complex genome. With global warming, the environmental volatility and incidence of drought in wheat-producing areas will increase. Molecular markers for drought tolerance are urgently needed to enhance drought tolerance breeding. Here, we genotyped four near-isogenic line (NIL) pairs targeting a major QTL qDSI.4B.1 on wheat chromosome arm 4BS for drought tolerance using the 90K SNP Illumina iSelect array and discovered a single nucleotide polymorphism (SNP) (Excalibur_c100336_106) with consistent genotype–phenotype associations among all four NIL pairs and their parents. Then, we converted the SNP into a Kompetitive Allele-Specific PCR (KASP) marker, with an accuracy of 100% for the four NIL pairs and their parents and as high as 81.8% for the 44 tested wheat lines with known phenotypes collected from Australia and China. Two genes near this SNP were suggested as candidate genes for drought tolerance in wheat after checking the Chinese Spring reference genome annotation version 1.1. One gene, TraesCS4B02G085300, encodes an F-box protein reportedly related to the ABA network, a main pathway for drought tolerance, and another gene, TraesCS4B02G085400, encodes a calcineurin-like metallophosphoesterase transmembrane protein, which participates in Ca²⁺-dependent phosphorylation regulatory system. Based on this work and previous research on pre-harvest sprouting, we established a quick and efficient general SQV-based approach for KASP marker development, integrating genotyping by SNP arrays (S) using NILs targeting major QTL for a specific trait (Q) and validating them with commercial varieties (V). The identified SNP and developed KASP marker could be applied to marker-assisted selection in drought breeding, and further study of the candidate genes may improve our understanding of drought tolerance in wheat.

See <https://link.springer.com/article/10.1007/s00122-023-04438-3>



Physical distance for the SNP

SNP	Physical Distance
Excalibur_c100336_106	85,895,716-85,895,856
Excalibur_c39876_403	650,488,177-650,488,277
IAAV5564	650,893,009-650,893,229
Kukri_c64195_1044	372,844,125-372,844,227
Kukri_c64195_346	372,843,437-372,843,532
Kukri_c64195_432	372,843,518-372,843,618

Fig. 1: Locations of the six selected SNPs with their physical positions on chromosome 4B. SNP marked as bold shows genotype–phenotype associations in all four NIL pairs; red line is the peak region of the target QTL (*qDSI.4B.1*); QTL markers are bolded; the details of each SNP’s physical distance (based on Chinese Spring genome version 1.1) were listed in the embedded table