BẢN TIN THỨ TƯ 7-6-2023

BẢN TIN SỐ 1

Engineered Yeast to Help Boost Drug Supply

Synthetic biology can be used to make more drugs or raw materials for the transformation of the pharmaceutical supply chains. This is according to Dr. Christian Smolke, CEO and co-founder of Antheia—science and technology company developing next-generation plant-inspired medicines.

Dr. Smolke explained that this transformation could be achieved through the use of engineered yeast that can yield active pharmaceutical ingredients (APIs). This breakthrough could lead to the reduction of drug shortages through less dependence on ingredients derived from nature. She said that sourcing active ingredients from nature is very inefficient and time-consuming. To address this problem, Antheia developed engineered yeast to produce APIs. The yeast is grown in a fermenter, thus, can make a batch of purified product in less time.

To date, Antheia has approximately 70 active ingredients in the pipeline, and the first batch will be produced in full-scale this 2023.

Know more in Genetic Engineering and Biotechnology News.
https://www.isaaa.org/kc/cropbiotechupdate/article/default.asp?ID=20191

BẢN TIN SỐ 2

Groundbreaking Images of Root Chemicals Reveal New Insights on Plant Growth

Researchers from the University of California San Diego and Stanford University have provided insights into a new understanding of essential root chemicals that are responsible for plant growth. Using a mass spectrometer, the researchers produced a “roadmap” that shows the distribution of small molecules along stem cells of maize plant roots and how their placement factors into the plant's maturation.

As a visiting scientist at Stanford University, Assistant Professor Alexandra Dickinson collaborated with Sarah Noll and Professor Richard Zare who developed a mass spectrometry imaging system that helps surgeons distinguish between cancerous and benign tissue during tumor-removal operations. Dickinson, Zare, and Noll adapted the technology called “desorption electrospray ionization mass spectrometry imaging” (DESI-MSI) to probe plant roots for the chemicals involved in growth and energy production. The team initially focused on maize plants at the root tips, where stem cells play an active role in the plant's development. Zare said that to understand plant roots from the biology side, they needed to find out which chemicals are present.

The team then produced images, believed to be some of the first to reveal the transition between stem cells and mature root tissue. The images show the foundational role of metabolites—molecules involved in the plant's energy production. Tricarboxylic acid (TCA) cycle metabolites became the focus of the research since they were found to be a key player in controlling root development. Also seen in the new images were previously unidentified compounds that could be critical for plant growth.

For more details, read the article in UC San Diego Today.
https://www.isaaa.org/kc/cropbiotechupdate/article/default.asp?ID=20205

BẢN TIN KHOA HỌC

Mining genes regulating root system architecture in maize based on data integration analysis

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Key message

A new strategy that integrated multiple public data resources was established to construct root gene co-expression network and mine genes regulating root system architecture in maize. A root gene co-expression network, containing 13,874 genes, was constructed. A total of 53 root hub genes and 16 priority root candidate genes were identified. One priority root candidate was further functionally verified using overexpression transgenic maize lines.

Abstract

Root system architecture (RSA) is crucial for crops productivity and stress tolerance. In maize, few RSA genes are functionally cloned, and effective discovery of RSA genes remains a great of challenge. In this work, we established a strategy to mine maize RSA genes by integrating functionally characterized root genes, root transcriptome, weighted gene co-expression network analysis (WGCNA) and genome-wide association analysis (GWAS) of RSA traits based on public data resources. A total of 589 maize root genes were collected by searching well-characterized root genes in maize or homologous genes of other species. We performed WGCNA to construct a maize root gene co-expression network containing 13874 genes based on public available root transcriptome data, and further discovered the 53 hub genes related to root traits. In addition, by the prediction function of obtained root gene co-expression network, a total of 1082 new root candidate genes were explored. By further overlapping the obtained new root candidate gene with the root-related GWAS of RSA candidate genes, 16 priority root candidate genes were identified. Finally, a priority root candidate gene, *Zm00001d023379* (encodes pyruvate kinase 2), was validated to modulate root open angle and shoot-borne roots number using its overexpression transgenic lines. Our results develop an integration analysis method for effectively exploring

regulatory genes of RSA in maize and open a new avenue to mine the candidate genes underlying complex traits.
See https://link.springer.com/article/10.1007/s00122-023-04376-0