

**BẢN TIN NGÀY THỨ HAI 21-8-2023**

**BẢN TIN SỐ 1**

**Pinoy Biotek Seminar: Mudfish Spawning Technology**  
ISAAA August 16, 2023



 Hybrid Event

**Pinoy Biotek Seminar:  
Mudfish Spawning  
Technology**

01 SEP 2023 | 9am to 12nn  
Philippine Carabao Center, Nueva Ecija

**Join via Zoom for free:  
bit.ly/MudfishPH2023**

ISAAA Inc., in partnership with the Department of Agriculture-Fisheries Biotechnology Center (DA-FBC) will hold the hybrid event titled *Pinoy Biotek Seminar: Mudfish Spawning Technology* on September 1, 2023, at 9:00 AM (GMT+8). The [registration](#) is now open.

The seminar will discuss:

- Status of Fishing Industry and Mudfish Production in the Philippines
- Mudfish Spawning Technology
- Access to Mudfish Spawning and Outreach Initiatives by the DA-FBC
- Economic Viability of Mudfish Spawning

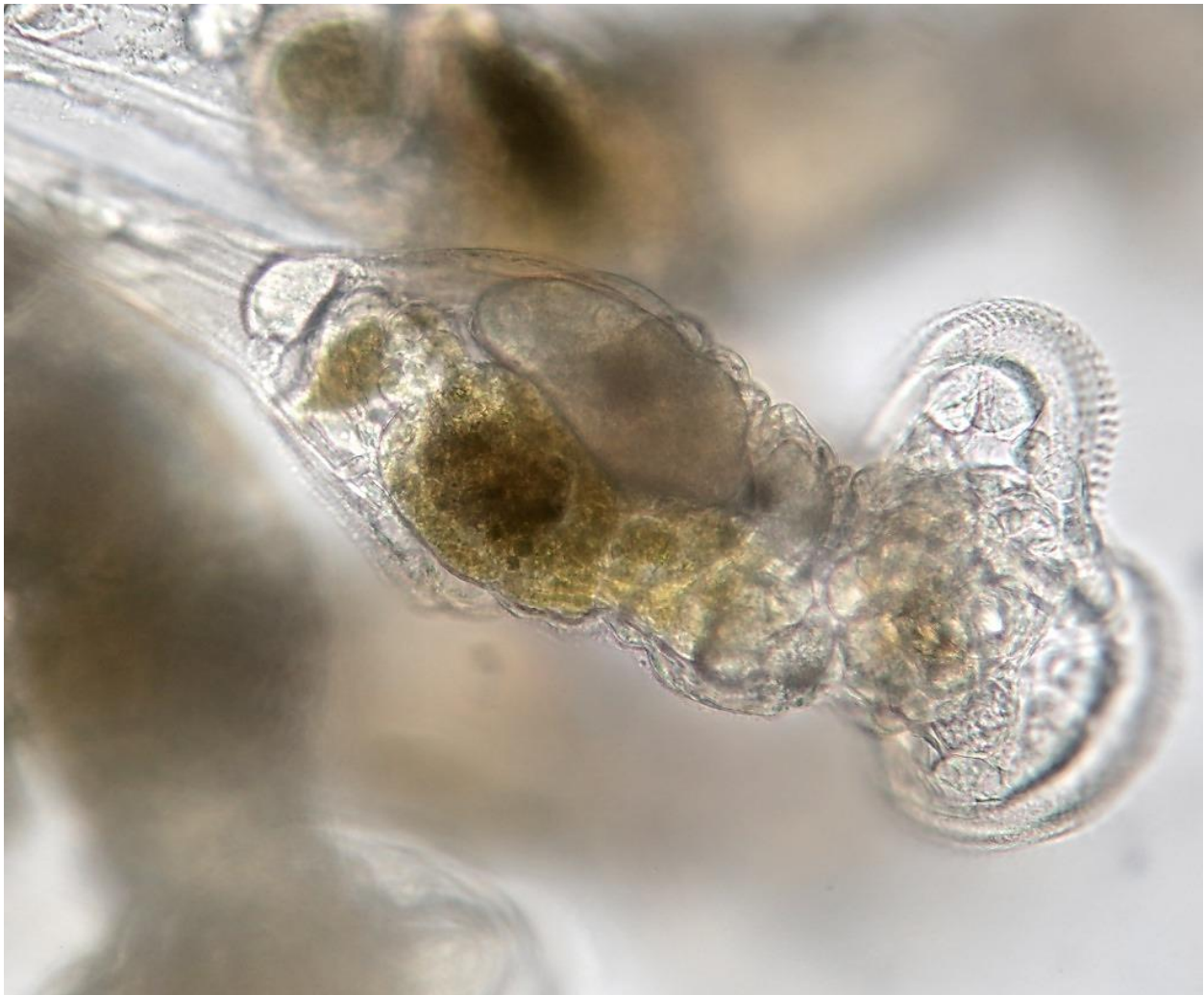
- Farmer's Experience With Mudfish Spawning

The event is part of a series of seminars that aims to increase awareness and appreciation of Pinoy biotechnologies and products by the general public, especially in the Philippines. It will also provide science-based information to target stakeholders for acceptance and adoption of the Pinoy-developed biotechnologies that can contribute to the improvement of the country's agriculture sector.

Register now to join online via [Zoom](#). For inquiries, email [lpunzalan@isaaa.org](mailto:lpunzalan@isaaa.org).

## **BẢN TIN SỐ 2**

### **CRISPR Gene Editing in a Rotifer**



Researchers have developed a protocol for quick and efficient [CRISPR-Cas9](#) gene editing of the rotifer *Brachionus manjavacas*. The results of the study will open new possibilities for rotifer research and biological discoveries.

Rotifers have been used as a model system to study [genome](#) evolution, DNA repair, aging, and other aspects of biology. However, scientists have not been able to manipulate the genetics of rotifers for further studies. That is why researchers from the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution devised a method to alter the genomes of rotifers using CRISPR-Cas9.

The team immersed the rotifers in a highly viscous solution and gave them a low-level anesthetic, which slowed them down. The researchers were then able to grab the rotifers one at a time using light suction through a hollow needle. The [gene editing](#) system was then injected into the part of the rotifer that provides nutrients to their eggs.

The researchers inactivated the developmental [gene](#) *vasa*, which led to the rotifers ceasing reproduction after several generations. They also turned off the DNA mismatch repair gene *mlh3*, which prohibited the rotifers from creating a male offspring. Finally, they inserted a stop codon cassette into *mlh3*, which had the same effect. Some of these mutations were passed down to the next generations.

For more information, read the journal article in [PLOS Biology](#).

<https://www.isaaa.org/kc/cropbiotechupdate/article/default.asp?ID=20364>

## BẢN TIN KHOA HỌC

### Metabolomic and transcriptomic analyses provide insights into metabolic networks during cashew fruit development and ripening



Li Zhao, Bei Zhang, Haijie Huang, Weijian Huang, Zhongrun Zhang, Qiannan Wang, Hongli Luo, Bang An.

Food Chem.; 2023 Mar 15; 404(Pt B):134765. doi: 10.1016/j.foodchem.2022.134765.

#### Abstract

Cashew nut is a popular food around the world. The high-resolution profiles and dynamics of metabolomes in cashew fruits are poorly understood till now. In this study, we analyzed the temporal metabolome of cashew nut via a non-targeted method based on UHPLC-Q-

Exactive-MS, and analyzed that of cashew apple via a widely targeted method based on UHPLC-QTRAP-MS/MS (MRM). Furthermore, we performed integrative analyses of temporal metabolome and transcriptome data, characterized the accumulation of specific metabolites, and identified the transcriptional changes during cashew fruit development. Specifically, we found that phosphatidylinositol species were the predominant fractions in the unsaturated glycerophospholipids, and we identified a transcription factor that was the potential regulator of

phosphatidylinositol biosynthesis. Analysis of cashew apple revealed metabolic genes and transcription factors involved in sugar biosynthesis. Taken together, our results provide insights into metabolic networks during cashew fruit development and generate a valuable resource for further cashew breeding studies.

See <https://pubmed.ncbi.nlm.nih.gov/36444096/>

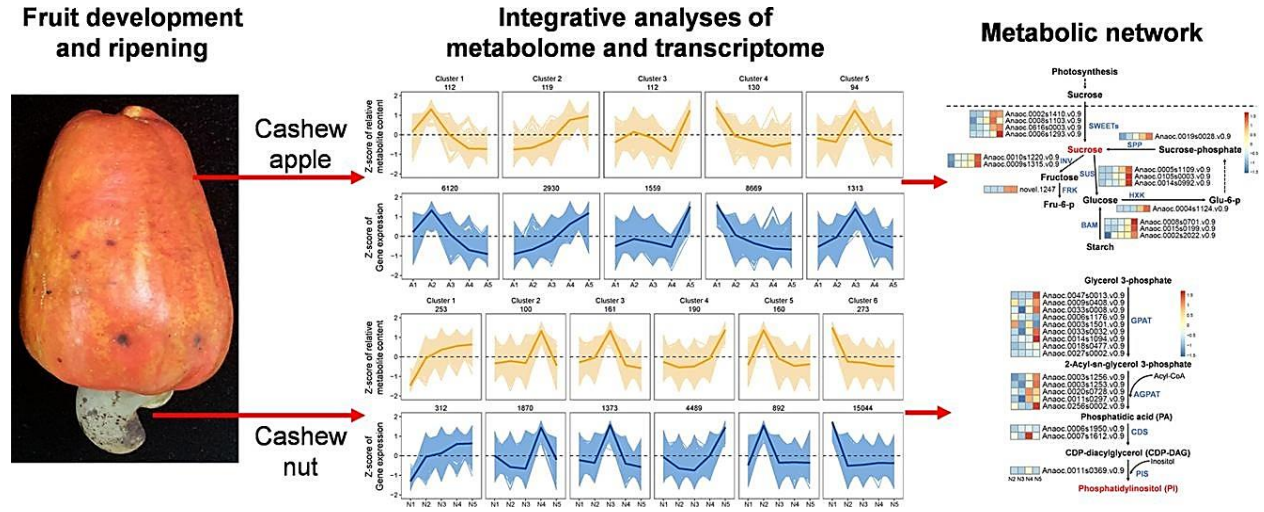


Figure: Fruit development and ripening - Zhao et al. 2023