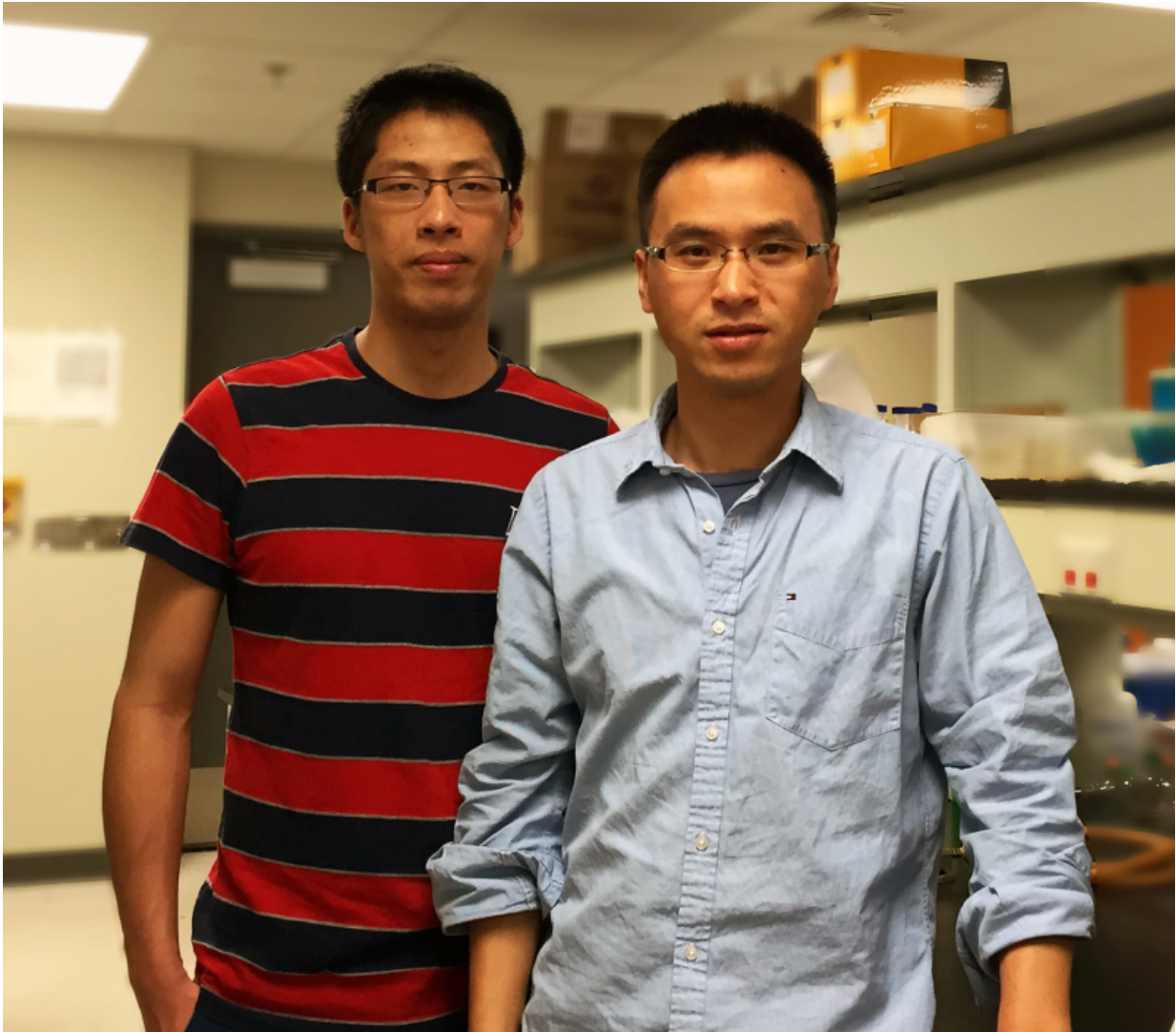


# Unlocking fermentation secrets open the door to new biofuels

June 24 2015, by Rick Kubetz

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(l-r) BioE graduate student Chen Liao, first author of the PNAS article, in the lab with Assistant Professor Ting Lu.

Researchers from the University of Illinois at Urbana-Champaign have, for the first time, uncovered the complex interdependence and orchestration of metabolic reactions, gene regulation, and environmental cues of clostridial metabolism, providing new insights for advanced biofuel development.

"This work advances our fundamental understanding of the complex, system-level process of clostridial acetone-butanol-ethanol (ABE) [fermentation](#)," explained Ting Lu, an assistant professor of bioengineering at Illinois. "Simultaneously, it provides a powerful tool for guiding strain design and protocol optimization, therefore facilitating the development of next-generation biofuels."

Microbial metabolism is a means by which a microbe uses nutrients and generates energy to live and reproduce. It typically involves complex biochemical processes implemented through the orchestration of metabolic reactions and gene regulation, as well as their interactions with environmental cues. One canonical example is the ABE fermentation by *Clostridium acetobutylicum*, during which cells convert carbon sources to organic acids that are later re-assimilated to produce solvents as a strategy for cellular survival.

"*Clostridium* is very much like a factory during fermentation which converts carbon sources into renewable, advanced biofuels that can be directly used to fuel your cars," added Lu, who is also affiliated with the Department of Physics and Carl R. Woese Institute for Genomic Biology at Illinois. "The complexity and systems nature of the process have been largely underappreciated, rendering challenges in understanding and optimizing solvent (ABE) production."

"In this study, we developed an integrated computational framework for

the analysis and exploitation of the solvent metabolism by *C. acetobutylicum*," said Chen Liao, a bioengineering graduate student and first author of the paper, "Integrated, Systems Metabolic Picture of Acetone-Butanol-Ethanol Fermentation by *Clostridium acetobutylicum*," appearing in this week's Early Edition of *Proceedings of the National Academy of Sciences*.

"To our knowledge, this framework elucidates, for the first time, the complex system-level orchestration of [metabolic reactions](#), [gene regulation](#), and [environmental cues](#) during clostridial ABE fermentation," Lu said. "It also provides a quantitative tool for generating new hypotheses and for guiding strain design and protocol optimization—invaluable for the development of efficient metabolic engineering strategies, expediting the development of advanced biofuels. More broadly, by using the ABE fermentation as an example, the work further sheds light on systems biology toward an integrated and quantitative understanding of complex microbial physiology."

**More information:** *Proceedings of the National Academy of Sciences*, [www.pnas.org/content/early/2015/06/24/1423143112.abstract](http://www.pnas.org/content/early/2015/06/24/1423143112.abstract)

Provided by University of Illinois at Urbana-Champaign

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