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Researchers identify caffeine-consuming bacterium

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As it turns out, humans aren't the only organisms that turn to caffeine for a pick-me-up. University of Iowa scientists have identified four different bacteria that actually can live on caffeine.

One of them, known as Pseudomonas *putida* CBB5, was found in a flowerbed outside a UI research laboratory. The research team says the discovery -- and the new understanding of how the process works -- could in the future allow scientists to convert waste from leftover coffee, tea and even chocolate into useful substances, like pharmaceuticals, animal feed or biofuels.

Previous studies have also discovered caffeine-degrading bacteria, but the UI team took the research one step further. They identified the gene sequence that enables the bacterium to break down the caffeine compound in nature.

Caffeine is found naturally in more than 60 different plants and is composed of carbon, hydrogen, nitrogen and oxygen. Its molecular structure features three clusters of carbon and hydrogen atoms known as methyl groups, enabling caffeine to resist degradation by most bacteria.

Led by UI chemical and biochemical engineering doctoral student Ryan Summers, the study found that Pseudomonas putida CBB5 uses four newly discovered digestive proteins to break caffeine down into xanthine and then to carbon dioxide and ammonia. It removes the methyl groups from the molecule (a process called N-demethylation), allowing the bacteria to feed on the nitrogen atoms in the interior of the molecule (xanthine).

The caffeine digestive proteins from CBB5 can be used to convert caffeine into building blocks for drugs used to treat asthma, improve blood flow and stabilize heart arrhythmias.

"With one or two methyl groups removed, the remainder of the molecule can be used as the base for a number of pharmaceuticals," Summers said. "You basically use the new genes and enzymes that could take something we have a lot of -- like caffeine -- and make drugs that are typically very expensive. And that process could lower the costs for people who need them."

Summers said the bacterium's digestive proteins could also be used to remove caffeine and related compounds from large amounts of waste generated from coffee and tea processing, which pollute the environment. The decaffeinated waste from these industries could be used for animal feed, or for production of transportation fuel, especially in areas where corn (for ethanol) is scarce.

The team originally thought only one enzyme was responsible for extracting methyl groups. Ultimately, they identified four (NdmA, NdmB, NdmC, and reductase) involved in the N-demethylation process. This helped them to pinpoint the genes responsible for enzyme production in the bacterium.

Summers, with UI research scientists Michael Louie and Chi Li Yu, studied the bacterium in professor Mani Subramanian's lab in the Chemical and Biochemical Engineering Department, and the Center for Biocatalysis and Bioprocessing. They initially set out to craft a dipstick measurement for nursing mothers to test caffeine levels in breast milk, but the gene discovery took the research down a different path.

"These findings are a significant leap, as other researchers have shown bacteria can grow on caffeine, but, until now, the exact mechanism was a mystery," Subramanian said. "Now that we are starting to work on this, we are finding completely new genes, and reactions that we never expected."

Summers presented the findings at the American Society for Microbiology in New Orleans in late May. He anticipates seeking a scientific publication of the study this summer.

Provided by University of Iowa

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