

Bugs provide new insights into relationships between animals and bacteria

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The mealybug needs its nested bacterial helpers to turn plant sap into usable nutrients. Credit: Husnik et al. (2013), *Cell* 153(7). Photo by Alex Wild (alexanderwild.com), courtesy of John McCutcheon.

Scientists have come closer to untangling a unique and intricate relationship between animals and bacteria, providing potential insights



into the complex association between humans and the microbes we rely on for our health.

Mealybugs, scaly insects that feed on plant juices, have a rare tag-team relationship with bacteria that help the bugs turn plant sap into usable nutrients. Similar to Russian nesting dolls, the bugs house two kinds of bacteria, with one <u>bacterium</u> called *Moranella endobia* living inside another called *Tremblaya princeps*. This three-tiered system has never been observed in other animals, and scientists, including CIFAR Associate John McCutcheon (University of Montana), are interested in untangling its inner workings.

"Previous work by me and my collaborators revealed that *Tremblaya* has a very tiny <u>genome</u>—the smallest cellular genome yet observed—and that it is missing many essential <u>genes</u>," explains McCutcheon. "With such a small and degenerate genome, how is this bacterium surviving? This question was the focus of our new study. We wanted to untangle the role of *Moranella* and the mealybug in the functioning of *Tremblaya*."

The team's findings were published in *Cell* on June 20, 2013, with a special appearance on the cover of the issue.

Using the latest technologies to sequence genomes and measure <u>gene</u> <u>expression</u>, the researchers unravelled the mechanisms used by *Tremblaya* to survive. "We approached our experiments similar to the way an archaeologist might," says McCutcheon. "It's hard to manipulate this <u>natural bacteria</u>-animal system, but we can do experiments in the lab to figure out how the relationship works and then make predictions about what we should see in different kinds of situations."

The team found that *Moranella* is playing a big role in providing genes to *Tremblaya* to help it function. Once it acquired *Moranella*, *Tremblaya* must have dropped many of its own genes, since many of them were



similar to those in Moranella and therefore no longer needed.

McCutcheon and his team were particularly interested in exploring what genes *Tremblaya* had transferred to the mealybug genome over time, essentially making the mealybug a keeper of some its essential genes. But surprisingly, they saw no evidence of this kind of gene transfer.

"What we discovered instead was a surprising parallel universe of other genes in the mealybug that were transferred from historical bacterial infections," says McCutcheon.

His team found that the mealybug didn't have any genes from *Tremblaya*, but rather had at least 22 genes that were transferred to its genome from other bacteria and that were keeping the *Moranella-Tremblaya*-mealybug relationship alive. These 22 genes seem to complement the genes missing in *Tremblaya* and *Moranella* by providing, for example, help in nutrient synthesis and bacterial cell wall maintenance. McCutcheon and his team are now doing experiments to further investigate the role of these genes.

The findings from this study suggest that gene transfer from *Tremblaya* to the mealybug is not an explanation for *Tremblaya*'s small genome. It also means that the development of the relationship is different from what happens in organelle evolution.

Organelles like mitochondria (the energy powerhouse of complex cells) and chloroplasts (responsible for photosynthesis in plants) were originally bacteria that started living in other cells millions of years ago. Today, mitochondria and chloroplasts still have their own genome, but many of their genes have been transferred to their host genome.

"From this study, it looks like *Tremblaya* is not progressing along an evolutionary path analogous to mitochondria and chloroplasts," explains



McCutcheon.

This research drives home the idea that these extremely intimate relationships between animals and bacteria with very small genomes are often developing with the help of genomes from other organisms. This study has shown scientists just how complicated the association between animals and bacteria can be.

"Some of the bacteria we work on are quite unusual, so much so that it becomes difficult to still think of them as bacteria," says McCutcheon. "The members of CIFAR's program in Integrated Microbial Biodiversity understand and appreciate microbial diversity like no other group of scientists that I am aware of—from the complexity of organelle evolution to the population genetics of microbial eukaryotes—and my interactions with them have been critical in helping me consider the broad context of my work."

All animals have important relationships with bacteria that are complex and hard to see. A deeper understanding of systems like the mealybug leads scientists to a better understanding of the bacteria humans depend on today and how interactions with <u>bacteria</u> have shaped the evolution of animals in general.

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