

# Gut microbes affect MicroRNA response to bacterial infection

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When it comes to fighting off pathogens like *Listeria*, your best allies may be the billions of microorganisms that line your gut, according to new research published in *mBio*, the online open-access journal of the American Society for Microbiology. The study reveals that germ-free mice are more susceptible to infection with the foodborne pathogen *Listeria monocytogenes* than mice with conventional intestinal microbiota.

The authors were also able to show that expression of five intestinal microRNA (miRNA) molecules decreases in conventional mice upon *Listeria* infection while it did not in germ-free mice, indicating that the gut microbiota may determine, at least in part, how the mouse genome expression is reprogrammed in the gut and how the animal responds to an infection.

"We were surprised by the robustness of the intestinal miRNA signature in germ-free mice and conventional mice," says corresponding author Pascale Cossart of the Institut Pasteur in Paris, France. "Our results show that even very small variations in miRNA expression can have important outcomes," for the health of the animals, says Cossart.

In recent years, researchers have come to recognize that the gut microbiota is an indispensable partner in the development of an animal's immune response and in maintaining its internal stability, but few studies have addressed the impact the microbiota has on miRNA expression during bacterial infections. Cossart and her colleagues approached the

matter using the system they know best: *Listeria* infection. *L. monocytogenes* is a frequent contaminant of raw milk products, and a highly publicized outbreak traced to *Listeria*-contaminated cantaloupe left 30 people dead in the fall of 2011.

Previous studies in Cossart's lab have shown that during infection with *Listeria*, the bacterium AND the host both reprogram their protein manufacturing using small non-coding RNA molecules like miRNA - pieces of genetic material that are used to selectively regulate the creation of proteins. Here, the researchers used conventional mice and germ-free mice to address the question of whether - and how - the [gut microbiota](#) has an effect on the course of infection and on the production of these regulatory miRNA molecules.

When it comes to susceptibility to infection, the results were unequivocal: 24 hours after infection, germ-free mice harbored 10,000 times more *L. monocytogenes* bacteria in their small intestines and about 1,000 times more *Listeria* in their mesenteric lymph nodes than did the conventional mice.

At the level of miRNA, however, the differences were not immediately evident: the most highly expressed miRNAs were produced at the same levels in both types of mice and they didn't change much after infection. Nevertheless, the production of five miRNAs decreased after infection only in the conventional mice, indicating that the presence of the microbiota influences the level of miRNA expression.

"We found that even though the intestinal miRNA signature is globally stable, *Listeria* infection can affect the host miRNA response in a microbiota-dependent manner," says Cossart. When paralleled with the lower susceptibility of the conventional mice to infection, these down-regulated regulatory molecules present an intriguing result, write the authors.

Cossart says that this study and others indicate that miRNA may be involved in protecting the host from infection, but their precise role isn't yet clear. She notes that although this study was conducted in mice, miRNA and the protein coding gene targets they regulate may be very similar in mice and in humans. Cossart and her colleagues are planning to follow up on the work to try and figure out what impacts the changes in miRNA expression mean for the networks of protein-coding genes they regulate.

Provided by American Society for Microbiology

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