Experiment IDs influence of antibiotics, isolation on host bacteria

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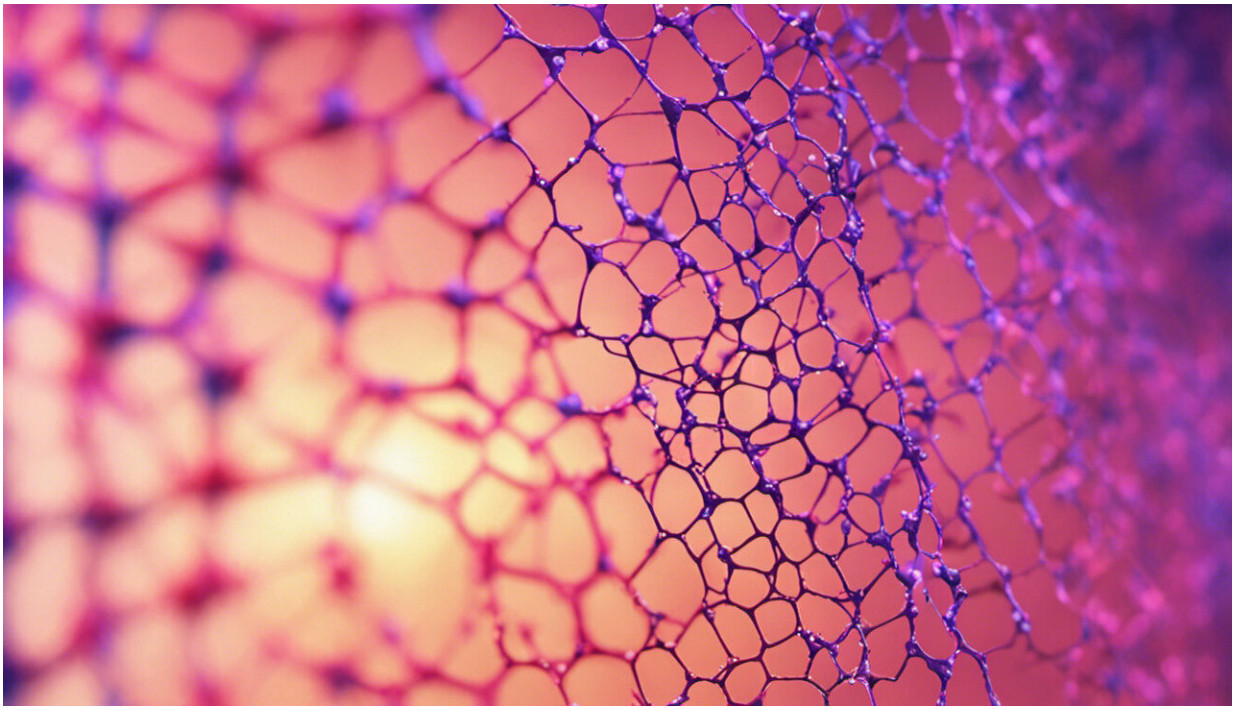

Credit: AI-generated image (disclaimer)

Bacteria regularly develop and deploy new antibiotics in a never-ending arms race to kill other bacterial species that compete for mutual resources. Humans have capitalized on that evolutionarily honed capability by administering antibiotics to strike at harmful bacteria that invade and infect their bodies.

But antibiotics can also attack innocent bystanders—among them, the oft-beneficial bacterial species that inhabit the guts of humans and many other animals. With the use and environmental spread of antibiotics increasing, especially via application in livestock, their effect on host bacteria is joining the rise of antibiotic resistance as a potential cause for concern.

Prior research indicates that exposure to antibiotics can reduce the presence and modify the makeup of a host's bacterial community, or microbiome, potentially driving changes in metabolism and greater susceptibility to pathogens, obesity and antibiotic-resistant bacteria. Studies have even shown that antibiotics can influence microbiomes in the next generation of offspring, which receive those bacteria from parents or the environment. Less is known, though, about how those effects play out across multiple generations.

In search of answers, Nebraska's Reilly Cooper and colleagues turned to Daphnia magna, a species of crustacean that grows to mere millimeters in length but is emerging as a go-to organism for studying microbiome dynamics. The team raised five generations of D. magna; half of the first generation was raised antibiotic-free, the other half in an antibiotic-rich cocktail. Subsequent generations of the antibiotic-free crustaceans continued to be raised that way. Each generation born to antibiotic-exposed parents, meanwhile, was evenly split between an antibiotic-rich or antibiotic-free existence.

As expected, antibiotics appeared to drastically alter the population of bacteria in first-generation D. magna, increasing the number of one prominent bacterial group while curbing the abundance of another. And the diversity of bacterial species continued to decline across generations of the antibiotic-exposed crustaceans.

Nevertheless, D. magna whose parents were exposed to antibiotics, but

which themselves were raised antibiotic-free, boasted bacterial communities that were mostly indistinguishable from crustaceans' whose ancestors were never exposed. That finding, which ran counter to the team's expectations, suggests that just one generation may be enough for a microbiome to effectively recover—regardless of how many generations of antibiotic exposure preceded it.

The team was in for another surprise: The simple act of isolating the individual crustaceans, whether antibiotic-exposed or -free, also corresponded with less bacterial diversity across generations of D. magna. Though survival rates dropped across the generations of isolated crustaceans, both body size and total reproduction increased. So, too, did the disappearance of relatively rare bacterial groups—hinting that those groups might be playing detrimental roles.

Having demonstrated the effects of various conditions on microbiomes, D. magna should continue to serve as a model organism for investigating the resilience, diversity and trajectory of bacterial communities across generations, the team said.

Cooper especially hopes that researchers follow up on the influences of isolation, which indicate that maintaining a diverse microbiome could depend on whether an animal grows up alongside members of its own species. If so, that could have implications for a whole host of host species, he said.

The study is published in *FEMS Microbiology Ecology*.

More information: Reilly O Cooper et al, Multiple generations of antibiotic exposure and isolation influence host fitness and the microbiome in a model zooplankton species, *FEMS Microbiology Ecology* (2022). DOI: 10.1093/femsec/fiac082

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