

Brown bear saliva found to contain chemical that kills *Staphylococcus aureus*

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A team of researchers affiliated with multiple institutions in Russia and the U.S. has found that Siberian brown bears have a chemical in their saliva that has been found able to kill *Staphylococcus aureus* bacteria. In

their paper published in *Proceedings of the National Academy of Sciences*, the group describes their study of the microbiome of a subspecies of brown bear and what they found.

The Siberian brown bear lives in Mongolia, northern parts of China, and in Siberia. While mostly vegetarian, they will on occasion kill and eat caribou, elk and fish—giving them a varied diet that has a profound impact on their microbiome. The researchers were interested in studying the biome of the brown bear as part of a larger effort to study the biome of a large number of wild animals. The goal of the larger effort is to find naturally occurring chemicals that are able to kill bacteria that infect humans—bacteria that are evolving to become resistant to traditional treatments.

To learn more about the microbiome of Siberian brown bears, the team captured several specimens in the taiga (a forested part of Siberia) and took [saliva](#) swabs which they carried back to their lab. There they used what they describe as state-of-the-art screening techniques to identify chemicals and organisms in the saliva samples.

The team reports that they found evidence of *Bacillus pumilus* in the saliva, which produces an antibiotic chemical called amicoumacin A. The researchers suggest the bears get the microbes when they consume certain types of vegetation. After they found *B. pumilus* in the saliva, the researchers focused their study on it specifically and in so doing discovered the means by which it does battle with bacteria, specifically *S. aureus*—a type of bacteria associated with human skin infections. *S. aureus* is also one of the types of bacteria that are becoming resistant to traditional treatments, thus a naturally occurring [chemical](#) that can help humans fight it would be quite valuable.

The team plans to continue studying the biome of the [brown bear](#), along with other [wild animals](#), in hopes of discovering the means by which

they ward off [bacteria](#) that are giving us humans so many problems.

More information: Stanislav S. Terekhov et al., "Ultrahigh-throughput functional profiling of microbiota communities," *PNAS* (2018).

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Abstract

Microbiome spectra serve as critical clues to elucidate the evolutionary biology pathways, potential pathologies, and even behavioral patterns of the host organisms. Furthermore, exotic sources of microbiota represent an unexplored niche to discover microbial secondary metabolites.

However, establishing the bacterial functionality is complicated by an intricate web of interactions inside the microbiome. Here we apply an ultrahigh-throughput (uHT) microfluidic droplet platform for activity profiling of the entire oral microbial community of the Siberian bear to isolate *Bacillus* strains demonstrating antimicrobial activity against *Staphylococcus aureus*. Genome mining allowed us to identify antibiotic amicoumacin A (Ami) as responsible for inhibiting the growth of *S. aureus*. Proteomics and metabolomics revealed a unique mechanism of *Bacillus* self-resistance to Ami, based on a subtle equilibrium of its deactivation and activation by kinase AmiN and phosphatase AmiO, respectively. We developed uHT quantitative single-cell analysis to estimate antibiotic efficacy toward different microbiomes and used it to determine the activity spectra of Ami toward human and Siberian bear microbiota. Thus, uHT microfluidic droplet platform activity profiling is a powerful tool for discovering antibiotics and quantifying external influences on a microbiome.

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