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## *Bdellovibrio* genome sequenced

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Understanding the life strategy of highly motile *Bdellovibrio bacteriovorus*, which preys on other gram-negative bacteria, including plant, animal, and human pathogens, could lead to the identification of novel antimicrobials, but this has been hampered by a lack of fundamental knowledge of the organism. In the January 30 *Science*, Snjezana Rendulic and colleagues from the Max-Planck-Institute for Developmental Biology report the complete sequence of the *B. bacteriovorus* genome, facilitating further study of this bacterium (*Science* 2004 **303**:689-692).

"We wanted to use a genomic approach in order to understand [*Bdellovibrio*]," said Stephan C. Schuster, senior author of the study, who together with colleagues from the University of Nottingham and Bielefeld University sequenced *B. bacteriovorus* strain HD100.

Analysis of the *B. bacteriovorus* genome revealed a number of insights into its lifecycle, the first being that this extremely small bacterium - it averages 0.2-0.5 by 0.5-2.5  $\mu\text{m}$  - has a relatively large genome of over 3.7 Mb, encoding 3584 predicted genes.

The researchers also found no indication of horizontal gene transfer from its prey, even though *B. bacteriovorus* has easy access to its prey's genomic information. Additionally, the genome lacks the genes to synthesize 11 and to degrade 10 amino acids, suggesting it relies on its prey for some essential amino acids. "The most important finding is that *Bdellovibrio* depends on prey because it can not make and degrade some of the essential amino acids needed for growth," Schuster told us.

The bacterium also harbors a huge contingent of lytic enzymes, numbering over 200 genes. "We were intrigued to find so many genes that code for lytic enzymes, which decomposed proteins, polysaccharides, DNA, RNA, and lipids," Schuster said. "These peptide-based substances are potential new antimicrobial substances."

"That is really cool news. This may greatly help invigorate the field of predatory interactions within the prokaryotic realm," Edouard Jurkevitch, from the Hebrew University of Jerusalem, told us. "One of the most striking features in the genome presented is the very large number of hydrolytic enzymes which are used in a very controlled manner to enable the entry, settling, growth, protection, and finally release of the predator and its progeny cell."

Jurkevitch, who was not involved in the study, believes this assortment of lytic enzymes offers great potential as an antimicrobial compound, since it works on a variety of targets. "I think that the concoction of strong antibacterial mixtures may be an option to explore. This type of approach, if feasible and successful, may help reduce the rate of development of resistance in target organisms," Jurkevitch said.

*Bdellovibrio* has been considered for use as a living biocontrol agent, and Mark O. Martin from Occidental College in Los Angeles, California, believes knowing its genome sequence will allow this to be investigated further. "I could see *Bdellovibrio* used to reduce or modify populations of pathogenic microbes," Martin told us. "After all, there have been some old papers about *Bdellovibrio* used to attack plant pathogenic *Erwinia*. But are people ready for this?"

"It's delightful and surprising work," Martin said. However, he noted that most of the field uses stain 109 J, and not HD100. "But from its 16S [ribosomal DNA], it looks the same," he said. Nonetheless, "its an excellent piece of structure genomics. The good news is, with this data, many new experiments can be done," he said.

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