

Antimicrobial resistance gene found in marine pathogen

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A team of Chinese investigators has discovered a gene for resistance to β lactamase antibiotics, in the pathogenic marine bacterium, *Vibrio parahaemolyticus*. The β -lactamase gene, bla_{VEB-2}, has never before been found in *V. parahaemolyticus*, and in fact, has been found almost exclusively in non-marine pathogens. The research is published Monday, September 19, 2016 in *Antimicrobial Agents and Chemotherapy*, a journal of the American Society for Microbiology.

The <u>resistance genes</u> were contained within a novel, highly unusual plasmid. Plasmids are pieces of independent DNA that can jump from one species of bacteria to another, and which frequently carry multiple resistance genes—as this plasmid did. The authors suspect that these plasmids may be enabling Vibrios, and likely other marine bacterial pathogens, to spread resistance—which they note has been gradually climbing among marine pathogens.

"Interestingly, we found that this plasmid can be transferred back to E. coli through a process called conjugation," said corresponding author Sheng Chen, PhD, Associate Professor in Microbiology, Department of Applied Biology and Chemical Technology, The Hong Kong Polytechnic University. "Such plasmid may serve as machinery to collect resistance genes from the environment, and transfer them to other marine organisms, or even other bacteria."

"The results suggest that the Vibrios can readily acquire various types of resistance genes presumably through horizontal gene transfer from other



organisms in the marine environment," said Chen. "This may be the reason why there has been a gradual increase in resistance rate among the marine pathogens such as V. parahaemolyticus, which is a common causative agent of food-borne infections but has until recently remained susceptible to most <u>antimicrobial agents</u>."

The motivation for the research was Chen's interest in studying the transmission kinetics and host specificity of various mobile resistance elements, notably plasmids, that are responsible for causing an increase in <u>antibiotic resistance</u> in major bacterial pathogens. Researchers had thought that there was little selection pressure for resistance in the oceans, because antibiotics are thought to be absent from the oceans, "despite the fact that antibiotics may be released into the sea via the sewage system," Chen said. Furthermore, gastroenteritis caused by V. parahaemolyticus is generally self-limiting, so that most cases do not require antibiotic treatment, further reducing selection pressure.

 β -lactamases are enzymes that disable β -lactam antibiotics. The penicillin and cephalosporin β -lactams are among the most commonly used antibiotics, and thus, β -lactamases are significant threats to the antibiotic armory.

More information: Ruichao Li et al. Genetic Characterization of acarrying plasmid in, *Antimicrobial Agents and Chemotherapy* (2016). DOI: 10.1128/AAC.01749-16

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