

Novel antibiotic resistance gene in milk

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Researchers of the University of Bern have identified a new antibiotic resistance gene in bacteria from dairy cows. This gene confers resistance to all beta-lactam antibiotics including the last generation of cephalosporins used against methicillin-resistant Staphylococcus aureus. A transfer to S. aureus which is likely according to the researchers would jeopardize the use of reserve antibiotics to treat human infections caused by multidrug-resistant bacteria in hospitals.

Macrococcus caseolyticus is a harmless bacterium naturally found on the skin of dairy cows which can spread to milk during the milking process. It can also be present in dairy products made from raw milk like e.g. cheese. Researchers of the Institute of Veterinary Bacteriology of the University of Bern have identified a new methicillin <u>resistance</u> gene in



strains of M. caseolyticus isolated from milk. Transfer of the gene to Staphylococcus aureus, a bacteria found on the skin and mucosa of animals and humans, would have dramatic consequences for public health. This methicillin resistance gene would turn this bacteria into a hazardous methicillin-resistant S. aureus (MRSA), which is known to cause difficult-to-treat infections in hospitals. Acquired methicillin resistance in bacteria is associated with genes mecA, mecB, or mecC. However, none of these genes were present in the M. caseolyticus strains – they carried the novel resistance gene mecD. This discovery has now been published in *Scientific Reports*.

The discovery

Over the last years, researchers of Vincent Perreten's group at the Institute of Veterinary Bacteriology in Bern investigated M. caseolyticus present in milk of <u>dairy cows</u> suffering from mastitis. Mastitis is an infection of the udder which is frequently treated with penicillins and cephalosporins, which are <u>antibiotics</u> of the beta-lactam class like methicillin. These bacteria isolated from milk showed an unusual resistance pattern to beta-lactam antibiotics with a resistance profile resembling that of MRSA, but the known <u>genes</u> responsible for resistance were missing. "We were intrigued by this novel resistance in M. caseolyticus and wanted to know what was behind this resistance," says Vincent Perreten. Bacteria have the extraordinary ability to acquire novel genetic information such as <u>antibiotic resistance genes</u>. Using Next Generation Sequencing (NGS), the researchers rapidly found that the M. caseolyticus isolates acquired a novel antibiotic resistance island which contains a new methicillin resistance gene designated mecD.

The new mecD gene confers resistance to anti-MRSA cephalosporins



The group of Vincent Perreten demonstrated that the novel methicillin resistance gene mecD confers resistance to all classes of β -lactams including anti-MRSA cephalosporins. It was located on a "resistance island" which has been acquired by M. caseolyticus. Further experimental investigations of the "resistance island" showed that it also has the potential for integration into the chromosome of S. aureus. "It is not excluded that this event may happen in nature, since S. aureus and M. caseolyticus share the same habitats," says Perreten.

M. caseolyticus containing the novel mecD gene has been so far mainly found in cattle but in one case it has been isolated from skin infection in a dog indicating that this bacteria has the potential to colonize different animal species.

"So far, we do not have any indication of the presence of mecD in humans, but its transfer from M. caseolyticus to S. aureus would further limit therapeutic options of this nosocomial pathogen." Selection of this gene should be avoided limiting the inadequate use of antibiotics in animals and humans. "It is imperative to keep an eye on the evolution and spread of this novel resistance gene in both human and animal <u>bacteria</u>," says Perreten.

More information: Sybille Schwendener et al. Novel methicillin resistance gene mecD in clinical Macrococcus caseolyticus strains from bovine and canine sources, *Scientific Reports* (2017). <u>DOI:</u> <u>10.1038/srep43797</u>

Provided by University of Bern

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