Discovery increases understanding how bacteria spread

June 20 2012

A University of Alberta researcher is moving closer to understanding how infection is caused by the spread of bacteria.

In a study published in the high-impact Cell Press journal called *Structure*, Joel Weiner and his collaborators, Gerd Prehna and Natalie Stynadka at the University of British Columbia, share new knowledge about how bacteria release proteins.

Proteins are complex molecules that perform all sorts of functions in the cells of living things. The group studied a specific protein called YebF in *E. coli* bacteria. It is widely found in other bacteria as well.

Solving the structure and understanding the mechanism by which this protein spreads bacterial pathogens was a big step forward. As humans develop more resistance to antibiotics, researchers are in search of new ways to stop bacteria from spreading.

"Most pathogenic bacteria induce special structures in order to release proteins that allow them to infect a host," said Weiner of the Department of Biochemistry, whose lab is funded by the Natural Sciences & Engineering Research Council and the Canadian Institutes of Health Research. "What we show here is that normal, run-of-the-mill bacteria can actually release a protein through the pores [of the bacterial membrane] which are normally there to take in small molecules."

YebF proved to be an interesting protein molecule because in addition to

its release through the bacterial pore, which is the most recent discovery, it has the unique property of secreting "passenger proteins" that are attached to it. This unique property was a prior discovery patented by the U of A because it has potential use for the production of protein-based drugs by the pharmaceutical and biotechnology industry.

"What we found in the structure is that there are regions that are very flexible in YebF that seem to be very important in getting it out of the bacteria," said Weiner. "If you make mutants in those regions you can prevent the protein from going out.

"We're not investing enough in identifying new targets for antibiotics," he said. "What this system does suggests a new target. We're looking at drugs that could block the ability of YebF to go out.

"That's really easy to test for," he added. Because the screen is easy, it's good for pharmaceutical companies."

This step in the research took several years, because solving the structure of this protein wasn't easy. The lab typically uses crystallization but stubborn YebF wouldn't work, so instead they had to use nuclear magnetic resonance.

Typically researchers know what action takes place and they try to find the protein that triggers it. In this case the researchers have been working the opposite direction. They have the protein, YebF, but they need to find out its purpose in the cell.

Provided by University of Alberta Faculty of Medicine & Dentistry