New software improves ability to catalog bacterial pathogens

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Washington State University researchers have developed a new software tool that will improve scientists' ability to identify and understand bacterial strains and accelerate vaccine development.

RepeatAnalyzer is able to track, manage, analyze and catalogue the short, repeating sequences of bacterial DNA.

The researchers used the software to characterize Anaplasma marginale, a tick-borne bacteria that affects cattle, and published their work in the journal *BMC Genomics*. The research team includes computer science student Helen Catanese; Kelly Brayton, Department of Veterinary Microbiology and Pathology; and Assefaw Gebremedhin, School of Electrical Engineering and Computer Science.

Like many types of bacterial pathogens, A. marginale has a huge variety of strains and is widely distributed geographically, which makes vaccine development challenging. Scientists use short repeating sequences of DNA, called repeats, to understand the bacteria, its heredity and geographic distribution and to determine how harmful it is.

But for A. marginale, for instance, researchers have found more than 235 short, repeating DNA sequences. Without any kind of database, researchers had to mine published literature to keep track of the sequences. The task is also error prone when done manually, said Brayton.

"We developed RepeatAnalyzer precisely to bridge that gap," said Gebremedhin.

They developed the software for A. marginale, but it can be extended to any other species with similar repeating DNA sequences. It also provides a visualization tool so researchers can track strains on a world map, said Catanese.

"This reliable software tool can fuel research and collaboration and accelerate the path to the discovery of a vaccine," said Gebremedhin.

RepeatAnalyzer has garnered significant interest, and Brayton's collaborators in South Africa and China are already using it, she said.

"Here is something that was overlooked and didn't exist," said Gebremedhin. "More than anything, it will help people. When you have a tool, and the right metrics and analysis, you may find things you might not have known before."

The researchers are working to extend the software to collect and handle similar datasets on other bacteria, as well as expanding on the visualization and analysis functionalities.

More information: Helen N. Catanese et al, RepeatAnalyzer: a tool for analysing and managing short-sequence repeat data, *BMC Genomics* (2016). DOI: 10.1186/s12864-016-2686-2

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