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Improved identification of war wound infections promises more successful treatment

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War wounds that heal successfully frequently contain different microbial species from those that heal poorly, according to a paper published ahead of print in the *Journal of Clinical Microbiology*. These and other findings have important implications for improving wound healing, says first author Nicholas Be of Lawrence Livermore National Laboratory, Livermore, California.

The problem the researchers were addressing is that culture-based identification, which has been used to assay war wound infections, misses the many species that are difficult or impossible to culture. But Be and his collaborators posited that using microarrays and whole genome sequencing to detect microbial species in wound samples would reveal infections caused by microbes that cannot be cultured, as these molecular methods can detect all species for which reference DNA is available.

"We also hypothesized that different microorganisms could be associated with successful or unsuccessful healing, and we felt that this information could be used for guiding medical treatment," says Be.

In the study, the investigators found that genetic sequences from certain bacteria, including *Pseudomonas* species and *Acinetobacter baumannii*, were frequently observed in wounds that failed to heal, while bacteria typically associated with the gastrointestinal system, such as *E. coli* and

Bacteroides species, were found in wounds that did heal successfully.

"This surprising finding further emphasizes the need for specific molecular detection," says Be. "We also observed via whole genome sequencing that the complex microbial populations present in wounds vary between patients and change over time in a single patient, further emphasizing the need for personalized treatment of individual wounds."

The investigators examined 124 wound samples from 61 wounds in 44 patients injured in combat in Iraq and Afghanistan. They used a microbial detection microarray developed at Lawrence Livermore National Laboratory, which contains DNA probes capable of detecting any microorganisms that have previously been sequenced.

"This represents a cost-effective, high-throughput platform for analysis of wound infections," says Be. A subset of samples was also subjected to whole genome sequencing.

"Information on the presence of specific bacteria that more significantly affect the success of the healing response could guide therapy and allow for more accurate prediction of outcome," says Be. "More effective, specific, and timely diagnosis of infection would improve treatment, accelerate rehabilitation, and decrease the length of hospital stays."

The manuscript can be found online. The final version of the article is scheduled for the July 2014 issue of the *Journal of Clinical Microbiology*.

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