Algorithm maps protein degradation patterns to improve infection diagnosis and treatment

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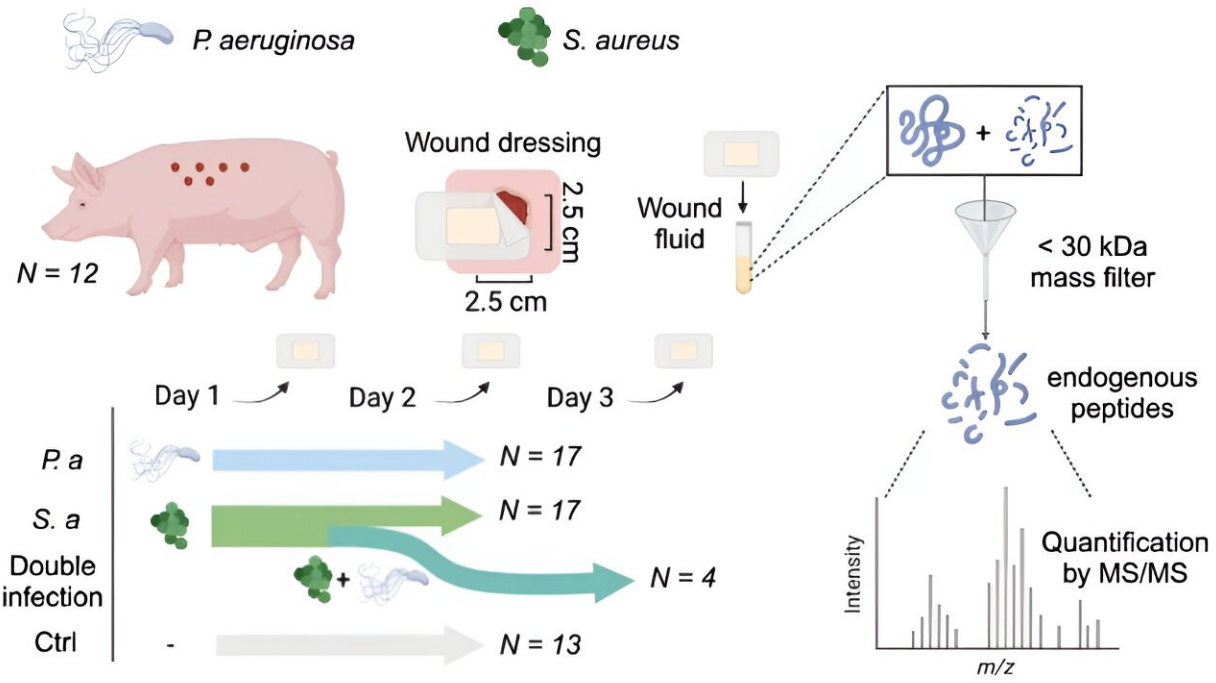

Wounds were created on pigs and overlaid with a dressing. The wound drainage, containing proteins and peptides, is absorbed into the dressing. The dressings were changed and sampled every day over a two- to three-day period. The fluid was extracted from the dressings, whereafter proteins were filtered out by a mass filter of 30 kDa. Credit: *Nature Communications* (2024). DOI: 10.1038/s41467-024-51589-y

Peptides are small fragments of proteins, mainly found in the skin and

mucous membranes. Some peptides act as a barrier, protecting the body against infections by fighting off microorganisms like bacteria, viruses, and other pathogens, while others participate in the regulation of inflammation.

When we have a wound or undergo surgery, this balance can sometimes be disrupted, allowing microorganisms to penetrate and cause acute infection and, in the worst cases, sepsis.

"To be able to diagnose infections today, the doctor first makes a clinical assessment and then sends a culture sample for further analysis. It usually takes a couple of days to get results on which bacteria are present in the wound, and this does not always provide a clear picture of the severity of the infection," says Artur Schmidtchen, professor of dermatology and venereology at Lund University, and consultant at Skåne University Hospital, Sweden.

In an infected wound, there is a battle between the immune system and bacteria. Bacteria break down proteins into peptides as a strategy to acquire nutrients and spread, while the body uses similar strategies to fight bacteria and regulate inflammation. This interaction is incredibly complex, influenced by the types of bacteria present as well as the severity of the infection.

The research team aimed to understand the degradation patterns of proteins to more quickly identify the bacteria involved and assess the risk of sepsis. The rise of antibiotic resistance has also increased the demand for alternative ways to diagnose and combat infections. The work is published in the journal *Nature Communications*.

"In order to investigate the number and types of peptides in a wound, we 'squeezed' peptides out of wound dressings and then analyzed them using mass spectrometry. This allowed us to identify up to 45,000 different

peptides from a single infected wound," says Johan Malmström, Professor of mass spectrometry at Lund University.

This enormous amount of information is difficult to grasp and utilize for understanding the degradation patterns of proteins. It was not until Erik Hartman, an engineer and Ph.D. student at Lund University, developed an algorithm that reduces the compilation of peptides by 95%, down to just a few hundred peptide clusters, that the data could be analyzed and used.

By clustering the peptides, he was able to train machine-learning models to determine the quantities and types of bacteria present in the wound. After identifying unique peptide patterns and changes in these patterns based on different types of bacteria, the researchers can now assess the severity of the infection.

"We have mapped how protein degradation patterns vary in different types of wound infections, gaining better insight into how they differ by systematically analyzing the peptide clusters. This allows us to easily identify subgroups that can guide treatments," says Erik Hartman.

These unique biomarkers can lead to earlier and more accurate diagnoses, enabling the faster detection and treatment of potential infections. With mass spectrometry and machine learning, the entire process takes only a few minutes.

"The cool thing is that the algorithm is not limited to wound infections; it is general and can be applied to many different diseases where protein degradation plays a significant role. Peptides thus become a new source of information that can, in the next step, help tailor treatments and contribute to finding new drug candidates," says Erik Hartman.

The next step for the researchers is to conduct larger studies to further

validate the results, refine the methodology and analyze other types of diseases, such as sepsis. They also want to explore how the method can be applied clinically in real diagnostic situations to assess its practical usefulness.

More information: Erik Hartman et al, Peptide clustering enhances large-scale analyses and reveals proteolytic signatures in mass spectrometry data, *Nature Communications* (2024). DOI: 10.1038/s41467-024-51589-y

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