

AI-POWERED DIAGNOSTICS

A Proteomics-approach For Biological Threat Agents Detection And Identification

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Biological threats agents (BTAs) remain a concern for military forces and for civil security. When confronted with a potential biological incident, accurate and timely identification is essential to launch protective, medical and strategic countermeasures. Reach back facilities have the capability to quickly identify a well-known subset of potentially hazardous micro-organisms. However, besides the common BTAs there are many other pathogens that can potentially pose a threat to our forces by intentional or natural distribution. Additionally, the increasing prevalence of antimicrobial resistance (AMR) strains and the developed awareness of future pandemics empathizes the need of an untargeted broad spectrum analytic capability.

To enable accurate, trustworthy identification in a timely manner of a broad spectrum of potential pathogens, we developed a liquid chromatography-tandem mass spectrometry (LC-MS/MS) based identification method including two digital applications; Proteome to Pathogen (P2P) and Proteome for Pandemic Preparedness (P4PP). The P2P system enables identification of bacteria and direct determines if the identified bacterium is a high-risk AMR strain. P4PP can be used to identify 1895 difference virus species, including genetic variants. In both methods trypsin digests are subjected to LC-MS/MS where the masses of the peptides and their fragments are measured. The obtained data is processed in PEAKS X, utilizing one of the two developed database (P2Pdb or P4PPdb). Retrieved peptides lists are then subsequently analyzed in the in P2P or P4PP application, respectively. P2P determines the identity of the bacteria and whether it is expressing a high-risk AMR phenotype and P4PP determines the identity of a virus. P2P and P4PP identify micro-organisms based on multiple peptides. Therefore, in contrast to traditional targeted detection methods also deliberate or natural genetically modified pathogens will be identified.

With P2P we have demonstrated that BTAs (*Bacillus anthracis*, *Brucella abortus*, *Brucella melitensis*, *Brucella suis*, *Burkholderia pseudomallei*, *Burkholderia mallei*, *Francisella tularensis*, *Yersinia pestis*) and other pathogens can be identified directly from positive blood culture flasks. With P4PP we have demonstrated that viruses can be identified including *Togaviridae*, *Poxviridae* but also *Coronaviridae* after in cell cultivation. Currently, we are in the process of starting a study to assess if we can identify viruses direct from clinical samples.

The implementation of our developed proteomics approach will serve our biological defenses, as no biothreat or AMR-threat can escape identification by P2P or P4PP.

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