

Evaluation of Mass Spectrometry Proteomics Method as a Rapid Screening Tool for Bacterial Contamination of Food

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Background

Possibilities of a bioterror attack on civilian or military installations require rapid detection and accurate identification of pathogens in a near real-time approach. We have developed a high throughput mass spectrometry-based proteomics method (MSPM) that addresses such requirements and is showing promising progress.

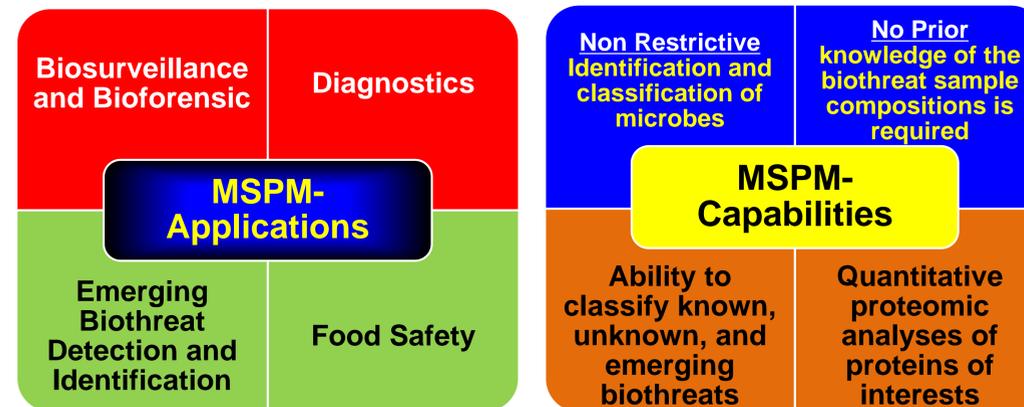
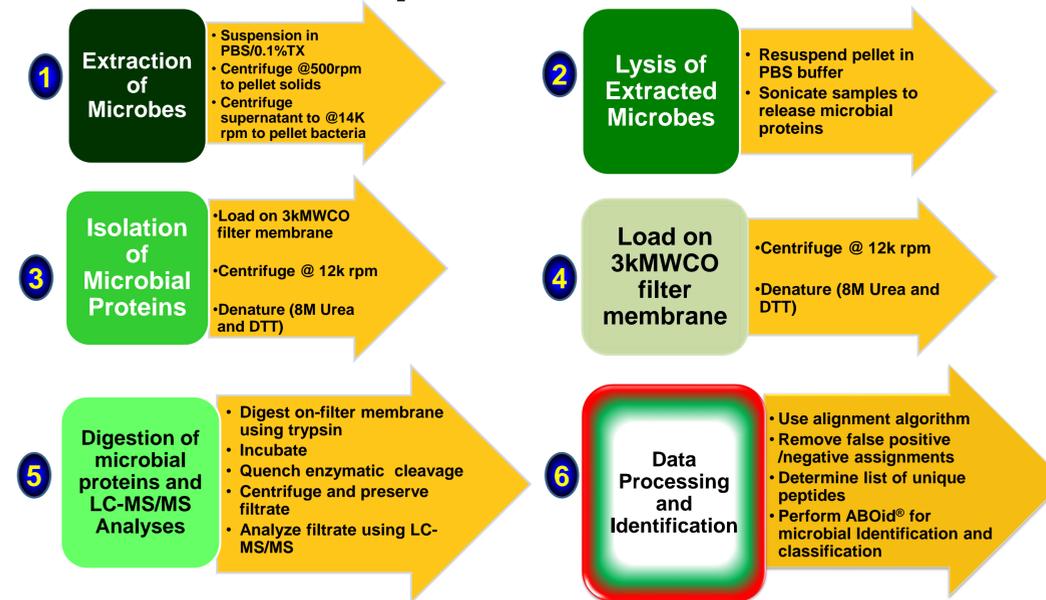
This approach utilizes the knowledge of amino acid sequences of peptides derived from proteolysis as a basis for the reliable microbial identification. Amino acid sequences have wide diversity in their sequence contents and can provide sufficient discrimination power that enables our in-house method to provide strain level identification and classification. This poster addresses the capability of the MS-proteomic based approach toward microbial and toxin identification present in blind samples and in a complex matrix.

Methods

- 150 blinded samples of mashed potatoes were prepared by the U.S. Army Public Health Command Food and Diagnostics Laboratory (FADL) in San Antonio, Texas.
- All samples were received with a coded number and processed according to in-house developed protocol (Jabbour et al, J. Proteome Res., 10, 907, 2011).
- Processed samples were digested and the tryptic peptides were analyzed on an LC-MS/MS system operated in data dependent acquisition (DDA) mode.
- Acquired mass spectral data for all unknown blind samples were processed using an in-house developed identification software (ABOid®).
- Constructed proteome database consisted of all publically available *E. coli* strains, *Shigella* species, *Bacillus* sp., *Salmonella* sp. all laboratory common contaminants and all DoD toxins.
- Bacterial identification and classification uses assignments of organisms to taxonomic group (phylogenetic classification) based on an organized scheme that begins at the phylum level and follows through classes, orders, families, genus and species down to strain level.

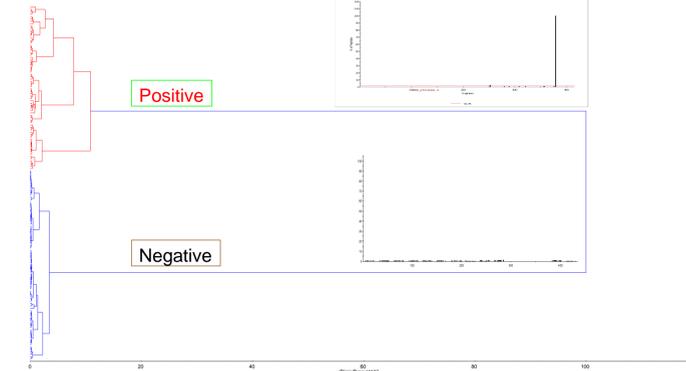
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Experimental



Results

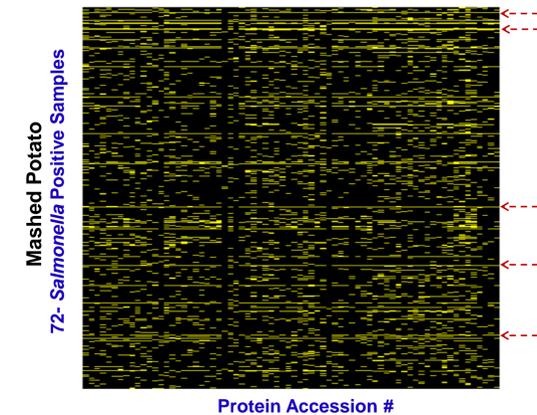
100 % Correct ID of all microbes in 150 samples



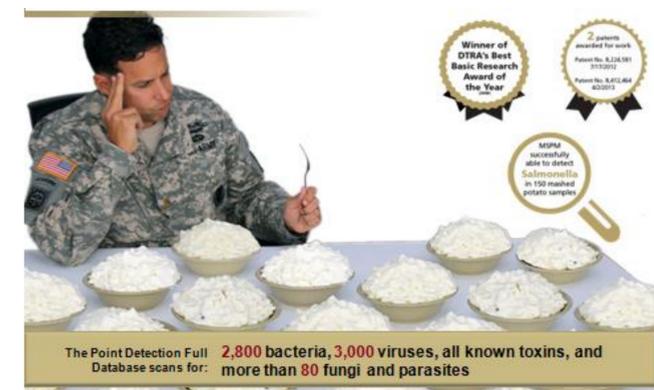
Bioforensic Profile of Blind Samples

Sample Type	Mashed Potato				
Samples analyzed	C-01	C-02	C-03	C-04	C-05
ID- Microbes	Salmonella	Negative	Salmonella	Salmonella	Negative
ID- Background Microbes	<i>Frankia alni ACN14a</i> <i>Dehalococcoides ethenogenes 195</i> <i>Carboxydotherrmus hydrogenoformans Z-2901</i>	<i>T.thermophilus HB27</i> <i>hydrogenoformans Z-2901</i> <i>Frankia alni ACN14a</i>	<i>Acidobacterium bacterium Ellin345</i> <i>Frankia alni ACN14a</i> <i>Thermophilus HB27</i>	<i>Frankia alni ACN14a</i> <i>Thermophilus HB27</i>	<i>Acidobacterium bacterium Ellin345</i> <i>Thermophilus HB27</i>

Potential Biomarkers for *Salmonella newport*



Accurate Identification of Bioterror in Unknown Samples



Conclusions

- MSPM correctly identified all 150 blind samples and showed no compromise in performance when microbes are present in complex matrix.
- MSPM was capable of differentiating true positive/true negative from false positive/negative
- MSPM successfully identified all microorganisms present in various biological matrices, i.e. blood, serum, culture, aerosol
- MSPM has been selected to participate in the Joint U.S. Forces Korea Portal and Integrated Threat Recognition (JUPITR) Advanced Technology Demonstration (ATD) program. The JUPITR ATD is the largest ATD in the history of the Department of Defense Chemical and Biological Defense Program with the goal to establish a biosurveillance capability to protect U.S. forces.
- MSPM will be participating in an operational demonstration that will occur at Osan Air Base beginning on 6 June 2015 for the detection and identification of Toxins.



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