

Invited presentation to be presented at the workshop "Mass Spectrometry in Homeland Security: Past, Present and Future", September 16-18, 2003, Knoxville, Tennessee

Impact Of Genomics On Protein Mass Spectrometry For Biodefense

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High throughput DNA sequencing has provided access to hundreds of complete proteomes from microorganisms. We now have the opportunity to construct comprehensive proteomic profiles in great detail for select organisms. These profiles can form the basis for development of diagnostics as well as counter-measures for threat microorganisms, as well as pathogens in general, through the use of characteristic protein signatures. Direct and indirect methodologies have been developed for interpreting peptide mass fingerprints. Nonstandard translation, post-translational modification, and mis-annotation remain substantial barriers to comprehensive and accurate protein identification by mass spectrometry. In addition, genome sampling of variant strains and near neighbor species indicates that both highly conserved sequences as well as rapidly diverging sequences can further restrict the usefulness of specific protein signatures. At the same time, comparative genomics affords the opportunity to resolve those shortcomings. Recent developments in multiple genome comparison tools will expedite data-mining these rapidly expanding comparative sequence sets.

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