used to protect the bean crop, but the proteins governing resistance are not well-resolved, especially compared to model plant-pathogen systems. To characterize the nature of resistance, we have used high-throughput tandem mass spectrometry to detect and analyze more than 3000 proteins from infected bean leaves. By statistically comparing the amounts of proteins detected in a single plant variety that is either susceptible to infection or resistant, depending on the fungal strains introduced, we have distinguished resistance from susceptibility at a proteomic level. Several other plant proteomic responses, some of which may favor the pathogen, also change during the course of infection. These results provide a basic foundation for understanding the proteomics of disease responses for a major crop plant.

S17

Sugarbeet Protein Changes and Interactions Associated with Resistance and Susceptibility to *Beet necrotic yellow vein virus*

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Rhizomania, caused by *Beet necrotic yellow vein virus* (BNYVV), is a devastating viral pathogen of sugar beet. There are limited sources of resistance against the virus, and resistance-breaking isolates are becoming increasingly problematic worldwide. Developing more effective disease-control strategies starts with gaining a better understanding of the basis for resistance and the mechanism of disease. Multidimensional liquid chromatography was employed to examine proteins differentially expressed in nearly isogenic lines of sugar beet either resistant or susceptible to BNYVV infection. Protein expression was temporally regulated, and in total, 7.4 and 11% of the detected proteome was affected by BNYVV-challenge in the resistant and susceptible genotype, respectively. Sixty-five of the proteins induced or repressed by the virus were identified by tandem MALDI-TOF mass spectrometry, and expression of key defense- and disease-related proteins was further verified using qualitative reverse transcriptase polymerase chain reaction. The proteomic data suggest involvement of classic systemic resistance components in *Rz*1-mediated resistance and phytohormones in hairy root symptom development. Movement between cells may be linked to disease severity. Recent efforts have focused on developing effective protein-protein interaction techniques (pull-down assays, Far Westerns, yeast 2-hybrid) for determining host factors involved in interactions with viral movement proteins.

S18

Composite Sequence Proteomic Analysis of Bacterial Protein Biomarkers: Proteomic Evidence of Lateral Gene Transfer Across *Campylobacter* Species?

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A method is presented demonstrating the sequencing of amino acid residues of proteins from non-genomically sequenced bacteria using only MS and MS/MS techniques. The method involves *combining* multiple, non-overlapping proteomic identifications from homologous sequence regions of proteins from genomically sequenced bacterial strains. This "composite" sequence proteomic analysis (CSPA) involves "bottom-up" proteomic identification of protein biomarkers from non-genomically sequenced *Campylobacter* species/strains by combining multiple, non-overlapping, sequence regions from genomically sequenced *Campylobacter* species/strains. The genomically sequenced strains are phylogenetically proximate or distant to the non-genomically sequenced strain. Composite sequences were confirmed by both MS and MS/MS analysis. In addition, gene sequencing was also used to confirm the correctness of the composite sequence. The composite sequence obtained can be utilized for: (1) protein molecular weight–based algorithms for pathogen identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS); (2) strain-specific biomarker for analysis by "top-down" proteomics techniques; (3) peptide-centric databases used for bacterial microorganism identification. CSPA can be used to identify the full amino acid sequence of protein biomarkers of emerging bacterial strains (i.e., non-genomically sequenced strains) without the necessity of either genetically sequencing biomarker genes or attempting full *de novo* MS/MS sequencing. Finally, CSPA is discussed with respect to whether lateral (horizontal) gene transfer across *Campylobacter* species is responsible for the non-overlapping homologous sequence regions observed.

DISRUPTIVE TECHNOLOGIES

S19

DNA and DNA Gel: A New Material in Life Sciences and Beyond

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Our research centers on molecular engineering DNA as a nanoscale material for real-world applications. In particular, our group focuses on three directions: DNA nanobarcodes, DNA gels, and DNA nanoparticles. By taking advantage of the amazing chemical, physical, and biological properties of DNA and by utilizing a myriad of DNA manipulating enzymes, we have created, on a bulk scale with a high yield, DNA dendrimers, DNA-based addressable molecules and materials, DNA-based nanobarcode systems, DNA hydrogels, DNA liposomes, and DNA organized Au nanoparticles. New properties and applications are expected from DNA-based materials. For this