LARSON, REBECCA[1*], ALBERTO NUNEZ[2] and WILLIAM M. WINTERMANTEL[3], [1]USDA-ARS, 1701 Centre Avenue, Fort Collins, CO 80526, [2]USDA-ARS, 600 E. Mermaid Lane, Wyndmoor, PA 19038 and [3]USDA-ARS, 1636 E. Alisal Street, Salinas, CA 93905. **Rhizomania as seen from inside the beet cell: Identifying proteome differences between sugarbeet infected with *Beet necrotic yellow vein virus* and healthy sugarbeet.**

ABSTRACT

Rhizomania, caused by *Beet necrotic yellow vein virus* (BNYVV) is one of the most economically important disease affecting sugarbeet. The disease is characterized by excessive growth of lateral roots and constriction of the taproot, the main sucrose storage site in sugarbeet, resulting in decreased sugar yield. The importance of this disease has been reemphasized by the emergence of new resistance-breaking isolates in many areas where resistant sugarbeet is universally planted. This project focuses on identification of proteins induced or repressed during BNYVV infection, with a goal of determining key protein interactions between BNYVV and sugarbeet that contribute to disease. Near isogenic sugarbeet lines varying for the presence/absence of the *Rz1* resistance allele were grown under identical environmental conditions in a growth chamber in noninfested soil or soil infested with BNYVV. At 3 and 6 weeks after planting, plant material was tested to confirm the presence/absence of BNYVV, and total plant protein was extracted from roots, quantified and fractionated using multidimensional liquid chromatography. Subtractive proteomics determined that only approximately 20% of the sugarbeet proteome was influenced by BNYVV infection compared with healthy sugarbeet. Protein identification using tandem MALDI-TOF-MS and sequence analysis has identified several major proteins influenced by infection that are known to be involved in cellular defense, including, polyphenol oxidase, germin-like proteins, polyubiquitin, among others. Downstream analysis will involve arrays for the identification of interactions between BNYVV and sugarbeet proteins in an effort to identify key interactions driving infection and symptom development.