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[1]USDA-ARS, 1636 East Alisal St., Salinas, CA 93905 and [2]USDA-ARS, 1701 Centre Ave., Ft. Collins, CO 80526. **Advantages of using 'omics' technologies and bioinformatics for analyzing the impact of pathogens on sugarbeet.**

Throughout the history of American sugarbeet production, research has proceeded hand-in-hand with the emergence of new diseases, and sugarbeet scientists have used the technologies available to improve disease management and crop yield in the face of the emerging disease pressures. Many traditional methods will always remain important for disease management, including host range studies, and pathogen isolation and inoculation of sugarbeet to confirm causative nature of the pathogen. In the late 20th Century the advent of molecular biology revolutionized plant pathology, leading to DNA and RNA based detection methods. The development of methods for analysis of the complete sequence of the genome (total DNA), transcriptome (RNA produced from DNA), proteome (all expressed proteins), and metabolome (total biochemical compounds produced) now allow scientists the ability to essentially begin putting together a systemic analysis of how sugarbeet responds to pathogen infection. While the technology is complex, the end result can be used to decipher how sugarbeet responds to pathogen attack. Studies by our laboratories have addressed changes in sugarbeet using proteome and metabolome analysis to understand the effects of Rhizomania and Rhizoctonia crown and root rot on sugarbeet, while others have used transcriptome and genomic analysis. The advantage of such methods is that they can be used to obtain both knowledge of gene expression by healthy sugarbeet as well as when sugarbeet is impacted by a pathogen at the molecular level. This information can facilitate targeted strategies, leading to improved control. By integrating omics technologies into traditional sugarbeet pathology, we can advance our ability to protect sugarbeet from disease and environmental stresses.