Plant Pathology Seminar Series

USING TRANSCRIPTOMICS TO INVESTIGATE PLANT-PATHOGEN INTERACTIONS: REVEALING DYNAMIC MECHANISMS OF RESISTANCE AND SUSCEPTIBILITY

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Abstract

Plant disease exists in the conducive environments where susceptible hosts and virulent pathogens meet. When diseased individuals are compared, a spectrum of disease resistance is revealed instead of a binary scale (Mehta, 2014). Historically, wheat breeders have successfully selected on this visible spectrum of disease for multiple pathogens without needing to understand the actual mechanisms involved. As breeding goals shift towards using more complex forms of resistance, accurately identifying the genes and mechanisms responsible for enduring resistance has become a more urgent goal (Khanfri et al., 2018). In the case of virulent pathogens such as stripe rust, transcriptomics can be a valuable tool for understanding the dynamic mechanisms involved in plant-pathogen interactions and identifying biomarkers for breeding resistant lines (Garnica et al., 2013).

Transcriptomics is a method for identifying and quantifying the total transcripts (RNA) of an individual. Advances in Next Generation Sequencing (NGS) over the last decade has made direct sequencing of transcripts more accessible, increasing the number of transcriptomics studies. Transcriptomics can be applied to identify differentially expressed genes and gene regulatory networks. Studies that utilize NGS can also be used for exploratory transcript discovery and the identifying alternative transcript splicing. Plant pathologists are already utilizing transcriptomics to explore differential gene expression between resistant and susceptible hosts, as well as investigating if different genes are used by different spore types of the same pathogen to colonize their hosts (Wang et al., 2021;) (Zhao et al, 2020).

Transcriptomics is a cutting-edge technology that allows researchers to measure dynamic processes within organisms in response to a variety of conditions. In the future, transcriptomics is likely to evolve to include spatially resolved measurements and simultaneous proteomics studies (Song et al., 2019). While there are many applications of transcriptomics yet to be explored by plant pathologists, there are already examples of how the technology is being applied for crop improvement. Ultimately, transcriptomics is a single tool in the plant pathologists' toolbox that can help us understand how genetic potential is translated into observable phenotypes.

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