CRISPR TECHNOLOGIES FOR IMPROVED POINT-OF-CARE DIAGNOSTICS

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Clustered regularly interspaced short palindromic repeats (CRISPR) were first detected in 1987 by scientist Yoshizumi Ishino in *Escherichia coli*. While at the time, the lack of sufficient DNA sequence data made it impossible to predict their function, advances on sequencing technologies and further studies on sequence similarities allowed scientists to understand how CRISPR work alongside CRISPR-associated enzymes (Cas) as a system (CRISPR-Cas) to protect prokaryotic cells against invading viruses and plasmids. Further studies on CRISPR-Cas systems led to the discovery of CRISPR-Cas9 genetic editing and the 2020 Nobel Prize in Chemistry awarded to Jennifer Doudna and Emanuelle Charpentier.

CRISPR-Cas systems have been the focus of extensive research and development for their application in genome editing. With the recent discovery of trans-cleavage activity by specific Cas nucleases, they have also gained attention as an emerging technology in the field of infectious disease diagnostics for their potential portability and sensitivity. CRISPR-Cas-based detection systems using various enzymes and approaches such as SHERLOCK and DETECTR have since emerged. CRISPR-Cas-based assays have been developed for detecting potato virus X (PVX), potato virus Y (PVY), and tobacco mosaic virus (TMV), tomato brown rugose fruit virus (ToBRFV), and citrus huanglongbing pathogen ('*Candidatus* Liberibacter asiaticus') among others. Despite the novelty CRISPR-Cas-based tools developed by the research community, optimization and validation of these technologies for 'real world' diagnostic use remains a challenge. In this presentation, we will discuss our experience with this technology as a potential diagnostic tool for point-of-care detection of plant pathogens.

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