Next-generation sequencing technology has made it easier than ever for quick diagnosis of plant diseases. "It's really exciting to see how sequencing technologies have evolved and how this new technology facilitates sequencing of entire genomes in such a short amount of time," said Yazmín Rivera, a plant pathologist with the United States Department of Agriculture's Plant Protection and Quarantine program, who recently published a research paper on the efficacy of Oxford Nanopore Technologies protocols.

"We wanted to provide an unbiased assessment of the technology and protocols available for long read sequencing," Rivera explained. Along with other plant pathologists, Rivera used the company's protocols to prepare RNA and DNA libraries from virus-infected plant material and from a plant pathogenic bacterium, respectively. After one hour of data sequencing, scientists had enough data to assemble small genomes.

"Diagnosticians will welcome an objective review of this technology," Rivera said. Rivera and her colleagues published their findings in *Plant Health Progress*, presenting a side-by-side comparison of the protocols that will allow the reader to identify which library preparation kit is best suited for their needs.

The ability to quickly obtain the entire genome of an organism has great implications for the plant pathology field. "Having more information readily available facilitates identification of emerging pathogens and of pathogens that are difficult to identify," explains Rivera. For more information, read "Comparison of Nanopore Sequencing Protocols and Real-Time Analysis for Phytopathogen Diagnostics"? published in the March issue of Plant Health Progress.

More information: Tommy Phannareth et al, Comparison of Nanopore Sequencing Protocols and Real-Time Analysis for Phytopathogen Diagnostics