

# Plant Pathology Seminar Series

## “BIOLOGICAL AND MOLECULAR STUDIES ON THREE ORTHOTOSPOVIRUS SPECIES”

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This research was focused on three orthospoviruses (genus *Orthospovirus*, family *Tospoviridae*, order *Bunyvirales*) causing economically important diseases in horticultural and agronomic crops worldwide. *Tomato chlorotic spot virus* (TCSV) was reported for the first-time infecting peanut (*Arachis hypogea*) in Haiti. This finding has practical implications for the peanut industry in the major peanut producing states in the U.S. Using a combination of Sanger and nextgeneration sequencing, the complete sequences of the large (L)-, medium(M), and small (S)-RNA genome segments were determined, to be 8873 nucleotides (nt), 4847 nt, and 3311 nt respectively. The complete genome sequences of TCSV will lead to a better understanding of the ecological and epidemiological aspects of this emerging orthospovirus to deploy robust control strategies. The complete nucleotide sequence of M- and S-RNA segments of thirteen isolates of *Impatiens necrotic spot virus* (INSV) collected from eight plant species from California, New York and Washington was determined. A global phylogenetic analysis of full-length M- and S-RNA segment sequences showed for the first time the presence of naturally occurring reassortant variants due to the exchange of genomic RNA segments. The generation of reassortant isolates has biological implications in understanding genetic diversity and rapid evolution of new variants of INSV and examining epidemiological characteristics and impacts on crop management strategies. The biological and genome sequence characteristics of two isolates of *Tomato spotted wilt virus* (TSWV) were examined to delineate factors contributing to phenotypic differences. Although the two variants are thrips vector transmissible, have similar virion morphologies, are serologically indistinguishable and nearly identical at the genome level, the mild isolate showed limited host range compared to the severe isolate. In *Agrobacterium*-mediated transient expression assays, the role of specific amino acid changes in NSs, a non-structural protein encoded by the S-RNA, on its silencing suppressor ability was examined. Due to the lack of a reverse genetics system for orthospoviruses, the genetic analyses of TSWV isolates with distinct phenotypes will better aid understanding of host-virus interactions for deployment of improved virus resistance in breeding programs.

9 am | Friday, August 31 | Johnson Hall 343

*PhD Exit Seminar*



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