

# Plant Pathology Seminar Series

“The influence of transposable elements on plant pathogen evolution”

By: Alex Batson



Transposable elements (TEs) are mobile genetic elements that can change position in a genome through duplication or translocation. Originally described by Dr. Barbara McClintock in maize (McClintock 1950), TEs were demonstrated first to influence kernel color, revealing a potential mechanism for generating diversity without sexual recombination or replication-induced mutations. Since McClintock's work, the functional role of TEs and their impact on evolution has been debated: some have described TEs as parasitic genetic elements whose proliferation in genomes is costly to the host metabolically (Doolittle and Sapienza 1980), while others have described TEs as agents promoting rapid adaptation to environmental change through genomic rearrangements (Crombach and Hogeweg 2007).

For plant pathogens, TEs have been implicated in large-scale genomic expansion and compartmentalization (Grandaubert et al. 2014; Haas et al. 2009), as well as the emergence of novel pathogenic races through the gain and loss of avirulence genes and effector genes (Kim et al. 1998; Rivas et al. 2005). For example, the genomes of *Phytophthora infestans* and *Leptosphaeria maculans*, the causal agents of potato late blight and black leg of brassicas, respectively, underwent extensive genome expansion compared to the genomes of their respective ancestral taxa (Grandaubert et al. 2014; Haas et al. 2009). Approximately 74% of the *P. infestans* genome is composed of repetitive elements, and regions of the genome that play an important role in pathogenicity are enriched with TEs and lack *Phytophthora*-orthologs (Haas et al. 2009). Similarly, the *L. maculans* genome is enriched with TEs (~32%) compared to those of closely related *Leptosphaeria* taxa (~4%). A majority of TEs in the genome were associated with chromosomal rearrangements, which were hypothesized to have played a role in the speciation of this organism (Grandaubert et al. 2014). *In addition to large-scale genomic changes*, there is strong associative evidence that the mobility of TEs has given rise to novel pathogenic races of the causal agent of halo blight of bean, *Pseudomonas syringae* pv. *phaseolicola* (Rivas et al. 2005), and other pathovars of *P. syringae* (Kim et al. 1998) through the deletion of effector genes. Some have speculated that the tendency towards a larger and TE-rich genome provides some plant pathogens with greater genetic potential to adapt to new environments and/or new hosts (Raffaele and Kamoun 2012). However, it remains unclear whether such expansions are sustainable over large evolutionary time scales.

Although TEs are an exciting topic of investigation for plant pathologists, new races of pathogens and evolution of pathogens with a more tractable genome can present significant challenges for practitioners (growers, breeders, and diagnosticians). The emergence of new races of a pathogen reduces the efficacy of cultivars resistant to races that previously dominated regions of production, and the potential need for new, diagnostically relevant DNA-based markers can complicate the capacity to detect some plant pathogens. Improving our understanding of TEs and their influence on the genomes of plant pathogens may make it possible to anticipate and track genomic changes in a timely manner, and address proactively the pending implications of such changes on disease management strategies.

4:10 pm | November 9<sup>th</sup>, 2020 | Plant Pathology 515, Fall 2020

Zoom Link and ID: <https://wsu.zoom.us/j/91621814000?pwd=MDVOY1prS0QybDRaMXNvTVNxTS82UT09>

Meeting ID: 916 2181 4000 Passcode: 5353 Call in number: 1 253 215 8782



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