
Plant Pathology Seminar Series

Retrospective and Prospective Look at Discoveries from Verticillium Comparative Genomics

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Abstract

Fungal pathogens in the genus *Verticillium* cause Verticillium wilt of high value crops, ornamentals, and trees worldwide. Today we recognize 10 species of *Verticillium*; the most notorious among these species is *V. dahliae*. Early comparative genomics focused on the comparisons of two species, *V. dahliae* and *V. alfalfae*, giving rise to valuable insights into their genome structures, predicted secretomes, and horizontal gene transfer. Next generation sequencing technologies and the increased availability of high-quality genome assemblies have rapidly yielded discoveries of avirulence genes, the genetic basis of the defoliating and nondefoliating phenotypes of *V. dahliae* and paved the way for additional comparative studies. In this talk, I will provide insights on the discoveries of early and two recent *Verticillium* comparative genomics projects and provide insights on *Verticillium* comparative genomics of the future.

