

Dothideomycetes Genetics workshop
33rd Fungal Genetics Conference at Asilomar
Nautilus Room, March 17, 2026

9:00-9:10	Steve Goodwin , <i>USDA-Agricultural Research Service, West Lafayette, Indiana</i>	Welcome and introductory remarks
9:10-9:30	Kona Swift , <i>University of Arkansas, Fayetteville</i>	<i>Cercospora</i> cf. <i>flagellaris</i> can infect <i>Nicotiana tabacum</i> and cause tobacco greenspot disease associated with latent <i>C. nicotianae</i> infections
9:30-9:50	Ashton Esco , <i>North Dakota State University, Fargo</i>	Measuring fitness penalties of fungicide resistance mutations via <i>in planta</i> competition assays
9:50-10:10	Burt Bluhm , <i>University of Arkansas, Fayetteville</i>	The polyketide synthase, Ctb1, is required for cercosporin biosynthesis but not virulence in the maize pathogen <i>Cercospora zea-maydis</i>
10:10-10:30	Nathan Wyatt , <i>USDA-ARS, Fargo, ND</i>	Identification and characterization of core <i>Cercospora beticola</i> biotrophic effectors through pan-genomic analysis
10:30-11:10	Break	
11:10-11:30	Rajdeep Jaswal , <i>North Dakota State University, Fargo</i>	Functional characterization of the HSP70 domain-containing core effector of <i>Cercospora beticola</i>
11:30-11:50	Si Qin , <i>University of California, Davis</i>	Unraveling the role of α -Glucan synthase (AGS) in the biology and virulence of <i>Cercospora beticola</i> and <i>Botrytis cinerea</i>
11:50-12:10	Md. Mukul Islam , <i>North Dakota State University, Fargo</i>	Distorted segregation and occurrence of non-parental allele type in a biparental population of wheat tan spot pathogen <i>Pyrenophora tritici-repentis</i>
12:10-12:30	Tim Friesen , <i>USDA-ARS, Fargo, ND</i>	A <i>Pyrenophora teres</i> f. <i>teres</i> effector defeats the broadly used barley net form net blotch resistance gene, <i>Rpt5</i>
12:30-14:00	Lunch	

14:00-14:20	Zhaohui Liu , <i>North Dakota State University, Fargo</i>	Molecular cloning of fungal genes required for Ptr ToxC production in <i>Pyrenophora tritici-repentis</i>
14:20-14:40	Alex Idnurm , <i>University of Melbourne, Australia</i>	Real-time evolution of fungicide resistance in <i>Leptosphaeria maculans</i>
14:40-15:00	Jesus Francisco Echaide Aquino , <i>Lincoln University, New Zealand</i>	Can the presence of a fungal volatile organic compound improve plant resilience to abiotic stress?
15:00-15:20	Julian Liber , <i>Duke University, Durham, NC</i>	<i>Aureobasidium pullulans</i> as a genetic model for phyllosphere commensalism and enhancing crop resilience
15:20-15:40	Lily Cooper , <i>University of Tennessee, Knoxville</i>	Telomere-to-telomere reference genome for <i>Septoria glycines</i> highlights shared and species-specific virulence factors among soybean foliar fungal pathogens
15:40-16:20	Break	
16:20-16:40	Richard Hamelin , <i>University of British Columbia, Vancouver</i>	Recent lineage diversification and gene flow shape climate adaptation in the Swiss needle cast pathogen of Douglas-fir
16:40-17:00	Alexandre Lassagne , <i>Oregon State University, Corvallis</i>	Comparative genomic approaches between cuticular wax composition of <i>Populus</i> species and germ tube length of <i>Sphaerulina musiva</i> enlightened promising genomic regions
17:00-17:20	Ioannis Stergiopoulos , <i>University of California, Davis</i>	Harnessing the potential of VHH antibodies for antifungal control: Progress, challenges, and opportunities ahead
17:20-17:40	Steve Goodwin , <i>USDA-ARS, West Lafayette, IN</i>	Progress on using CRISPR/Cas9 to knock out effector genes in <i>Zymoseptoria tritici</i>
17:40-18:00	Organizers	Additional questions and open discussion