



HAL
open science

Transposon analysis and comparative genomics of the *Leptosphaeria maculans*-*L. biglobosa* species complex.

Jonathan Grandaubert, C.L. Schoch, H. Bohran, Barbara Howlett,
Marie-Helene Balesdent, Thierry Rouxel

► To cite this version:

Jonathan Grandaubert, C.L. Schoch, H. Bohran, Barbara Howlett, Marie-Helene Balesdent, et al.. Transposon analysis and comparative genomics of the *Leptosphaeria maculans*-*L. biglobosa* species complex.. Dothideomycetes Comparative Genomics workshop 27th Fungal Genetics Conference at Asilomar, Mar 2013, Asilomar, United States. hal-01189707

HAL Id: hal-01189707

<https://hal.science/hal-01189707>

Submitted on 6 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Dothideomycetes Comparative Genomics workshop
27th Fungal Genetics Conference at Asilomar
March 12, 2013

Organizers:

Steve Goodwin, USDA-ARS/Purdue University (sgoodwin@purdue.edu)
Igor Grigoriev, US DOE Joint Genome Institute (ivgrigoriev@lbl.gov)

Agenda:

Dothideomycetes genome sequencing: status and future needs

9:00-9:15	Steve Goodwin, USDA-ARS/Purdue University	Opening, introductions and goals
9:15-9:30	Igor Grigoriev, JGI	Overview of the Fungal Genomics Program at the JGI and the next CSP
9:30-9:45	James Fountaine, SRUC, Scotland	Genome sequencing of the barley pathogen <i>Ramularia collo-cygni</i>
9:45-10:00	Jerome Collemare, Wageningen University, the Netherlands	The genome of <i>Cladosporium fulvum</i>
10:00-10:15	Chris Lawrence, Virginia Bioinformatics Institute	Comparative genomics of virulence factors, <i>Alternaria</i> species
10:15-10:45	<i>Break</i>	
10:45-11:00	Nada Krasevec, National Institute of Chemistry, Slovenia	Sequencing and analysis of cytochrome P450s in <i>Cochliobolus lunatus</i>
10:45-11:00	Jo Bowen/Kim Plummer, Australia and New Zealand	Update on genome sequences of <i>Venturia</i> species
11:00-11:15	Klaas Schotanus, Max Planck Institute, Germany	Centromeres of <i>Mycosphaerella graminicola</i>
11:15-11:30	Ronny Kellner, Max Planck Institute, Germany	Transcriptome profiling of <i>Mycosphaerella graminicola</i>
11:30-11:45	Stephen Poppe, Max Planck Institute, Germany	Effectors in the genome of <i>Mycosphaerella graminicola</i>
12:00-13:00	<i>Lunch</i>	

Comparative analyses of multiple genomes

13:15-13:30	Gert Kema lab, Wageningen, the Netherlands	Genomic analyses of <i>Mycosphaerella graminicola</i> and <i>M. fijiensis</i>
13:30-13:45	Richard Hamelin lab, University of British Columbia, Canada	Comparative genome-wide scan in poplar-infecting <i>Mycosphaerella</i>
13:45-14:00	Shaobin Zhong lab, North Dakota State University	Identification of virulence genes in <i>Cochliobolus sativus</i> by comparative genomics

14:00-14:15	Gillian Turgeon lab, Cornell University	<i>Cochliobolus</i> species and race variation
14:15-14:30	Rohan Lowe, University of Melbourne, Australia	<i>Leptosphaeria maculans</i> genomics in Australia
14:30-15:00	<i>Break</i>	
15:00-15:15	Jonathan Grandaubert, INRA, France	Transposon analysis and comparative genomics of the <i>Leptosphaeria maculans</i> - <i>L.</i> <i>biglobosa</i> species complex
15:15-15:30	Robin Ohm, JGI	Comparative genomics of 18 Dothideomycetes genomes
15:30-15:45	Steve Goodwin, USDA- ARS/Purdue University	Comparative analysis of mitochondrial genomes of the Dothideomycetes
15:45-16:00	Ben Horwitz, Technion IIT, Israel	Transcriptomics of <i>Cochliobolus</i> <i>heterostrophus</i>
<i>Future plans(open discussion)</i>		
16:00-17:00	Igor Grigoriev/Steve Goodwin	Publication plans, future collaborative grant opportunities and next CSP proposals