

Dothideomycetes Comparative Genomics workshop

28th Fungal Genetics Conference at Asilomar

Scripps Room, March 17, 2015

9:00-9:10	Steve Goodwin, USDA-ARS/Purdue University	Opening, introductions and goals
9:10-9:25	Sajeet Haridas, Joint Genome Institute, Walnut Creek, CA	Large-scale sequencing of Dothideomycetes provides insights into genome evolution and adaptation
9:25-9:35	Ben Horwitz, Technion - Israel Institute of Technology, Haifa, Israel	Prediction of G protein coupled receptor genes
9:35-9:50	Kim Plummer, La Trobe University, Melbourne, Australia	Comparison of effector candidates in apple and pear scab pathogens
9:50-10:05	Alex Idnurm, University of Melbourne, Australia	Gene expression analysis during biotrophic and necrotrophic phases of blackleg disease of canola
10:05-10:20	Shaobin Zhong, North Dakota State University	Nonribosomal peptide synthetase genes involved in virulence of <i>Cochiobolus sativus</i>
10:20-10:35	Break	
10:35-10:50	Jordi Muria Gonzalez, The Australian National University, Canberra	Broadening the approach to understand the role of secondary metabolites in <i>Parastagonospora nodorum</i>
10:50-11:05	Susan Breen, The Australian National University, Canberra	Understanding the <i>Parastagonospora nodorum</i> – wheat interaction; is it as simple as we think?
11:05-11:15	Kar-Chun Tan, Curtin University, Australia	Identification of novel effectors in <i>Parastagonospora nodorum</i>
11:15-11:30	Ioannis Stergiopoulos, University of California, Davis	Comparative evolutionary genomics of the Sigatoka disease complex on banana
11:30-11:45	Christophe Lemaire, Université d'Angers, France	Evolutionary history of gene duplications within the <i>Venturia</i> genus
11:45-11:55	Nicolas Feau, University of British Columbia, Canada	<i>Mycosphaerella populorum</i> and co.: the making of tree pathogens
12:00-13:00	Lunch	
13:05-13:20	Eli Thynne, The Australian National University, Canberra	Using next generation sequence to study the emergence of new wheat diseases
13:20-13:30	Anna Tiley, University of Bristol, UK	Investigating the sporulation pattern of <i>Zymoseptoria tritici</i> , a pathogen of wheat
13:30-13:45	Patrick Brunner, Institute	DMI resistance in <i>Zymoseptoria tritici</i> : a

	of Integrative Biology (IIB), Switzerland	history of gradual molecular evolution
13:45-14:00	Mark Lendenmann, IIB, Zurich, Switzerland	QTL mapping reveals novel fungicide resistance genes in the plant pathogenic fungus <i>Zymoseptoria tritici</i>
14:00-14:15	Ethan Stewart, IIB, Zurich, Switzerland	Elucidating the quantitative nature of virulence in <i>Zymoseptoria tritici</i> – A QTL mapping approach
14:15-14:25	Marc-Henri Lebrun, INRA, Versailles, France	Role of <i>Slr2</i> MAP kinase pathway in the biology of <i>Zymoseptoria tritici</i>
14:25-14:35	Janine Haueisen, Max Planck Institute for Evolutionary Biology, Plön, Germany	Comparative transcriptomics of <i>Zymoseptoria tritici</i> isolates
14:35-14:50	Break	
14:50-15:05	Steve Kelly, Swansea University, UK	DMI resistance and recent CYP51 enzymology in <i>Mycosphaerella</i>
15:05-15:20	Clémence Plissonneau, INRA, Thiverval-Grignon, France	Interplay between avirulence genes <i>AvrLm4-7</i> and <i>AvrLm3</i> in <i>Leptosphaeria maculans</i>
15:20-15:35	Thierry Rouxel, INRA, Thiverval-Grignon, France	Genomics (including optical mapping), high-density genome mapping and metatranscriptomics approaches in <i>Leptosphaeria maculans</i>
15:35-15:50	Megan McDonald, The Australian National University, Canberra	Characterizing chromosomal, inter and intragenic variation with whole genome re-sequencing of <i>Zymoseptoria tritici</i>
15:50-16:00	Jessica Soyer, Max Planck Institute for Evolutionary Biology, Plön, Germany	RNA-seq based gene annotation of <i>Zymoseptoria</i> species
16:00-16:15	Richard Oliver, Curtin University, Perth, Australia	Application of new gene calling and genome annotation software to Dothideomycete genomes
16:15-17:00	Igor Grigoriev/Steve Goodwin/Richard Oliver/anyone else	Re-annotating the genome of <i>Zymoseptoria tritici</i> (and potentially other species): Needs, possibilities and protocols

For genome re-annotations:

What is needed by the community?

How often should genomes be re-annotated?

By whom and how often should they be done?

Where should the new annotations be hosted?

What improvements are needed?

What kinds of tools are needed to make genome sequences more useful and accessible?

Other possible topics for annotation. Here is the list that was used for *A. nidulans*, provided by Nada Krasevic

List of annotation topics:

- Gene structure
- Genetic vs physical map
- RNA encoding genes
- Nutrient Transport
- Primary metabolism
- Nitrogen, a.a. metabolism
- Sulfur metabolism
- Secondary metabolism
- Cytochrome P450
- Polysaccharide degradation
- Transcription factors
- Signal transduction & stress responses
- Secretion
- Proteolysis & proteases
- Cell wall biosynthesis
- Endocytosis
- Morphology
- Cytoskeleton
- Cell cycle
- Transposable elements