Full Abstracts

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of non- or partially functional proteins. Little is known about pseudogenization in pathogenic fungi with different lifestyles. Here, we report the identification of DMs causing pseudogenes in the genomes of the fungal plant pathogens *Botrytis cinerea*, *Cladosporium fulvum*, *Dothistroma septosporum*, *Mycosphaerella fijiensis*, *Verticillium dahliae* and *Zymoseptoria tritici*. In these fungi, we identified 1740 gene models containing 2795 DMs obtained by an alignment-based gene prediction method. The contribution of sequencing errors to DMs was minimized by analyses of resequenced genomes to obtain a refined dataset of 924 gene models containing 1666 true DMs. The frequency of pseudogenes varied from 1% to 5% in the gene catalogues of these fungi, being the highest in the asexually reproducing fungus *C. fulvum* (4.9%), followed by *D. septosporum* (2.4%) and *V. dahliae* (2.1%). The majority of pseudogenes do not represent recent gene duplications, but members of multi-gene families and unitary genes. In general, there was no bias for pseudogenization of specific genes in the six fungi. Single exceptions were those encoding secreted proteins, including proteases, which appeared more frequently pseudogenized in *C. fulvum* than in *D. septosporum*. Most pseudogenes present in these two phylogenetically closely related fungi are not shared, suggesting that they are related to adaptation to a different host (tomato versus pine) and lifestyle (biotroph versus hemibiotroph).

612. Genealogical Concordance Phylogenetic Species Recognition in the *Fusarium oxysporum* Species Complex. Matthew Laurence[1], Brett Summerell[1], Lester Burgess[2], Edward Liew[1]. 1) The Royal Botanic Gardens and Domain Trust, Sydney, NSW, Australia; 2) Faculty of Agriculture and Environment, The University of Sydney, NSW 2006, Australia.

   Fusarium oxysporum is an important plant and human pathogenic ascomycetous group, with near ubiquity in agricultural and non-cultivated ecosystems. Phylogenetic evidence suggests that *F. oxysporum* is a complex of multiple morphologically cryptic species. Species boundaries and limits of genetic exchange within this complex are poorly defined, largely due to the absence of a sexual state and the paucity of morphological characters. This study determined species boundaries within the *F. oxysporum* species complex using Genealogical Concordance Phylogenetic Species Recognition (GCPSR) with eight protein coding loci. GCPSR criteria were used firstly to identify independent evolutionary lineages, which were subsequently collapsed into phylogenetic species. Seventeen independent evolutionary lineages were initially identified resulting in the recognition of two phylogenetic species. Further evidence supporting this delineation is discussed.

613. Host adaption in the plant pathogenic fungus *Mycosphaerella fijiensis*. Jean Carlier[1], Marie-Françoise Zapater[1], Daniel Bieysse[1], Yanetsy Montero[2], Veronique Roussel[1], Remy Habas[1], Luis Perez-Vicente[2], Catherine Abadie[3], Stephen Wright[4]. 1) CIRAD, UMR BGPI, Montpellier, France; 2) INISAV, Havana, Cuba; 3) CIRAD, UMR BGPI, Guadeloupe, France; 4) University of Toronto, Ontario, Canada.

   Plant pathogenic fungi are able to erode quantitative host resistance through changes in aggressiveness, thereby threatening the durability of host resistance. Such erosions are suspected in some areas in the fungus *Mycosphaerella fijiensis*, responsible for a recent and devastating banana pandemic, Black Leaf Streak Disease (BLSD). This study aims to test for the action of host-specific adaptation and to detect host-selected genes in *M. fijiensis*. We collected six samples in Cuba in three locations distributed throughout the banana production zones where resistant cultivars have been used for about 15 years. For each location, about 40 isolates were collected from two banana plots containing either a resistant variety or a susceptible variety located two to 10 km apart. We also included in the study three samples from Honduras where the disease was first introduced in the Latin America- Caribbean area. Some aggressiveness traits of a subsample of about 100 Cuban isolates coming from the three locations and the two cultivars were evaluated under controlled conditions on the same cultivars. A significant host effect was detected in some locations. A genome scan approach was conducted from whole-genome sequencing of pools of individuals (pool-seq). Differentiated genomic regions were detected between pathogen populations from the two cultivars in some locations. Further analyses have been undertaken to elucidate if these differentiated regions are due to either a host selective effect or demographic history.

614. Species composition of the genus *Saprolegnia* and intra-specific variability of the pathogenic oomycete *Saprolegnia parasitica* in fin-fish aquaculture systems. Paul de la Bastide, Cayla Naumann, Wai Lam Leung, William Hintz. Biology Department, Centre for Forest Biology, University of Victoria, Victoria, BC, Canada V8W 3N5.

   Saprolegniosis disease is a persistent problem in commercial fish aquaculture that contributes to significant losses in fish production. Despite its widespread occurrence, the genetic diversity of the causal agent(s) in these facilities is poorly understood. To determine the species composition of this genus, we examined sequence variability within the nuclear rDNA ITS region of *Saprolegnia* spp. for a collection of more than 400 isolates from fish aquaculture facilities. Sequence variation supported the designation of species identity based on ITS nucleotide sequence data, when compared to reference sequences. This approach identified at least 5 species in our study and confirmed the validity of using ITS sequence data to assign species identity to unknown isolates from water, fish and fish egg sources. The most common species detected was *Saprolegnia parasitica*, regarded as the primary pathogen of freshwater fish. A subset of the *S. parasitica* isolates, collected over a 21-month period, were evaluated for their intra-specific genetic variability. We used oligonucleotide primers that anneal to short simple repeat (microsatellite) sequences to amplify a set of variable-length products between annealing sites, thus generating a unique profile for each genotype. The presence or absence of these amplified characters was used to compare the *S. parasitica* isolates and evaluate patterns of genetic diversity over time, and among sample locations. Overall, the genetic diversity of *S. parasitica* isolates was determined to be low. However, there was sufficient variability for the isolates collected in the same time intervals to suggest that diversity was the result of a combination of asexual propagation and infrequent sexual reproduction. These genetic markers allow the monitoring of *S. parasitica* genotypes and facilitate the tracking of genotype origin in aquaculture production systems. Overall, our results demonstrate that *S. parasitica* is ubiquitous in aquaculture facilities and the management of saprolegniosis disease will be an ongoing concern in freshwater aquaculture.

615. Differences in fungal endophytes diversity in *citrus sinensis* (Orange) trees irrigated with fresh versus treated waste water. David Ezra, Noa sela, Lior Blank, Guy Haim, Yigal Elad, Maayan Grinberg-Baran. Plant Pathology, ARO The Volcani Ctr, Bet Dagan, Israel.

   Water has always been a resource in absence in the Middle East. Water for agriculture, of different origins and quality is used in the