30th Fungal Genetics Conference

March 12-17, 2019
Pacific Grove, California

Abstract Book

GENETICS

Genetics Society of America

G3 Genes | Genomes | Genetics

6120 Executive Boulevard, Suite 550, Rockville, MD 20852, (240) 880-2000
http://www.genetics-gsa.org

818W Epidemiosurveillance in the French West Indies of genotypes involved in the adaptation to varietal resistances in the fungus *Pseudocercospora fijiensis* causing the black leaf streak disease of banana. *T. Dumartinet*[1], S. Ravel[1], F. Bonnot[1], V. Roussel[1], N. Lubin[2], Y. Chilin-Charles[2], J. Aguayo[3], C. Abadie[2], J Carlier[1] 1) UMR BGPI, CIRAD, Montpellier, FR; 2) CIRAD, UMR BGPI, Guadeloupe, FR; 3) ANSES, Laboratoire de la Santé des Végétaux, Unité de Mycologie, Malzéville, FR.

The management of disease resistant varieties requires an epidemiosurveillance of pathogen genotypes that breakdown or erode them. This is the case of black leaf streak disease, a serious leaf disease caused by the fungus *Pseudocercospora fijiensis* which was recently introduced into the French West Indies (FWI). Very aggressive strains that breakdown the resistance of genitors and new resistant hybrids from breeding programs have been isolated in Guadeloupe. The mains goals of this work are to 1) elucidate the origin of these aggressive strains and 2) identify genes involved in adaptation to varietal resistances. Multiple introductions into the FWI from different Caribbean islands have been shown from population history study of the *P. fijiensis* in the geographic area and erosion of quantitative resistances have been observed in some Caribbean countries such as Cuba and Dominican Republic. These observations lead us to suspect introduction in the FWI of genotypes previously adapted to varietal resistance.

To test this hypothesis, we have first confirmed using cross inoculations that *P.fijiensis* populations have adapted to resistant cultivars in Cuba and Dominican Republic, countries where resistant cultivars have been first deployed in the Caribbean. Isolates from FWI will be tested the same way to compare their aggressiveness with Cuban and Dominican strains. A previous genome scan study showed that genomic region implicated in *P. fijiensis* adaptation to quantitative resistances can be identified using a genome scan approach based on genome sequencing from pools of isolates (pool seq). Such an approach will be broadened to more than 20 populations representing the genetic diversity in the Caribbean and including samples from the FWI. Genomic regions putatively implicated in adaptation to cultivars resistance will be then compared between samples of *P. fijiensis* to test whether adaptation genes have been introduced in the FWI.

819T Population structure and host specialization in *Botrytis cinerea*. *A. Mercier*[1,2], A. Simon[2], C. Duplaix[2], M. Cuel[2], J-M. Pradier[2], M. Viaud[2], A-S. Walker[2], P. Gladieux[3] 1) Paris Sud University, Orsay, FR; 2) Biology and Risk Management in Agriculture, INRA, Thiverval-Grignon, FR; 3) Biology and Genetics of Plant-Pathogen Interactions, INRA, Montpellier, FR.

Understanding the causes of population subdivision in pathogens is of fundamental importance, as studying barriers to gene flow between populations may reveal key aspects of the process of adaptation to host plants. The *Botrytis* genus encompasses more than 30 species, most of them being able to infect a narrow range of host plants. However, the *Botrytis cinerea* species is considered a generalist pathogen, found to infect more than 1600 plant species. This makes *B. cinerea* an interesting candidate to study ecological specialization. We investigated population structure and its genomic correlates in *B. cinerea* populations collected in France on tomato, grapevine, blackberry, strawberry and hydrangea. Population genetics analyses revealed a weak association between population structure and geography, but a clear differentiation according to the host plant of origin, and especially in populations infecting tomato and grapevine. Combining this observation with cross-inoculation experiments demonstrated the occurrence of partial host specialization. Genomes from strains associated with different hosts were Illumina-sequenced and phylogenetic analysis confirmed that population structure in the pathogen correlated with the host of origin, with one tomato-associated lineage and two well-differentiated grapevine-associated lineages. McDonald-Kreitman's tests were used to compare variation within lineages with variation against a common *Botrytis fabae* outgroup, and provided promising sets of genes under differential selective pressure between lineages. Three different genome scan approaches to detect selective sweeps events in lineages were also used to identify genomic regions relevant to host specialization. These candidates were selected using naïve (scores) and oriented (function annotation) approaches and their role in pathogenicity will be investigated by molecular genetics.

820F Quantification of syntenic relationships between fungal genomes. *M. Chi*, J. Choi, K. Craven Noble Research Institute, Ardmore, OK.

Dot plot is one of several visualization methods describing the syntenic relationship between two genomes. We have found that the dot pattern becomes more scattered as the evolutionary distance between two species increases. We calculated the level of scattering into a Shannon entropy equation. We considered a dot plot as a part of a matrix populated with two genomes. Syntenic area can then be measured as dots in a given plotting area. Unmatched regions (non-syntenic) remain empty in the dot plot. We then calculated the entropy of a total matrix by combining entropies of syntenic and empty clusters. For practical purposes, we assumed that a unit of entropy in the empty cluster would be identical with that of syntenic clusters. We have applied the equation to dot plots between *Agaricus bisporus* and various fungi belonging to different taxonomic clades. The value increased as taxonomic distance increased. We find that utilization of entropy between genome matrices has better power of discrimination than genetic distances calculated from ?1-tubulin gene alignment. Entropy of genome matrices can be a better scale for measuring evolutional time between two species, because homeostasis on coding sequences is higher than that on syntenic structure. We found that genome entropies between Serendipitaceae species are relatively high for their gene distances. This indicates that Serendipitaceae species kept their coding region intact during many genome rearrangements.

821W Q_{ST}/F_{ST} comparisons of quantitative traits in the *Parastagonospora nodorum* – wheat pathosystem. *D. dos Santos Pereira*[1], D. Croll[2], B. McDonald[1], P. Brunner[1] 1) Institute of Integrative Biology, Plant Pathology Group, Swiss Federal Institute of Technology, Zürich, Switzerland; 2) Laboratory of Evolutionary Genetics, Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland.

Populations are constantly under the influence of evolutionary forces such as mutation, genetic drift, recombination, gene flow and selection, which shape their genetic diversity and adaptive potential. Although phenotypic variation generated by environmental interactions are important for adaptability, information on the relative contribution of selection or genetic drift underlying the observed differences in phenotypes are often unknown. Determining the divergence between the differentiation for neutral genetic markers (F_{ST}) and for that of quantitative traits (Q_{ST}) is a powerful approach to elucidate the predominant evolutionary force.

Parastagonospora nodorum is a globally distributed necrotrophic fungal pathogen of wheat. We performed for the first time Q_{ST}/F_{ST} comparisons in this pathosystem including important traits related to agricultural practices (fungicide resistance), to environmental conditions (thermal performance) and to virulence (percentage of leaf area covered by lesions, PLACL). Our studied fungal collection comprised 164 distinct genotypes of *P. nodorum*, sampled from 8 geographically distant sites, representing different environmental and agricultural conditions. The F_{ST} index was calculated based on a set of 49374 neutral SNPs, identified by full genome sequencing of all isolates. To determine the Q_{ST} index, quantitative measurements were obtained for growth rate under different thermal conditions (18, 24 and 30°C) and fungicide stresses (0, 0.1, 0.5 and 1 ppm of propiconazole), and measurements of PLACL for infections on wheat leaves (Swiss variety CH Claro). Our results suggested that thermal performance at all tested temperatures and PLACL measurements are traits under stabilizing selection among the different populations ($Q_{ST} < F_{ST}$). In contrast, higher Q_{ST} than F_{ST} values ($Q_{ST} > F_{ST}$) indicated that growth rate under fungicide stress is under diversifying selection. This suggests that fungicide usage is acting as a strong selective pressure to local conditions, supressing the effects of genetic drift within and gene flow among populations.