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Abstract Book



between November and December 2013. Out of 37 isolates, the nitrate non-utilising auxotrophs (*nit* mutants) complementation test revealed 20 VCGs. KVCG14 and KVCG15 had highest distribution frequency ($n = 13$; 10.8%) while KVCG10 and KVCG20 ($n = 1$; 0.8%) the least. Analyses of VCG diversity using the Shannon Index (H) showed that Nandi ($H = 0.108$) and Kisumu ($H = 0.324$) counties recorded the lowest and highest VCG diversities respectively. Results also showed that, with a few exceptions, within-county isolates were self-compatible but they were incompatible across any two adjacent counties and across all the sampled counties. Heterokaryon incompatibility in Nandi ($n = 6$; 67%) and Makueni ($n = 3$; 33%) were the greatest and least respectively. Mycotoxin detection by coconut cream agar under UV light (365 nm) revealed blue fluorescence {(57%, $n = 21$) aflatoxin B} and green {(43%, $n = 16$) aflatoxin G}. The study further revealed L-, S- type strains (57%; $n = 21$ and 7%; $n = 2$) respectively. The findings of the study could provide reliable information in determining biocontrol strategies to mitigate aflatoxin contamination of maize by *A. flavus* in the studied counties.

333F Mycobiome in Anorexia Nervosa. K. Mueller¹, E. Huh¹, E. Bulik-Sullivan³, H. Zhang¹, Y. Wang¹, C. Bulik^{3,4,5}, I. Carroll³, S. Lee^{1,2} 1) Biology, The University of Texas at San Antonio, San Antonio, TX; 2) South Texas Center for Emerging Infectious Diseases, The University of Texas at San Antonio, San Antonio, TX; 3) Medicine, The University of North Carolina at Chapel Hill, NC; 4) Nutrition, The University of North Carolina at Chapel Hill, NC; 5) Psychiatry, The University of North Carolina at Chapel Hill, NC.

Anorexia nervosa (AN) is a mental illness characterized by a fear of gaining body weight, which results in severe weight loss and malnutrition. Persistent malnutrition, along with anxiety as a common comorbidity, contributes to AN having the highest mortality rate of mental illnesses. Typical treatment for AN involves re-nourishment of patients, which has proven to be insufficient in treating the disease, as relapse rates after treatment reach 50%. As such, finding new treatments for AN is of great importance.

Previous studies have shown an overall lowered bacterial diversity in AN patients, as well as a significant association between the bacterial diversity of AN patients and anxiety. However, these studies have overlooked the possible role of fungal diversity in the gut. Intestinal fungi have been implicated in diseases of the gastrointestinal tract, and previous studies have shown that disruption of normal gut bacteria may lead to enteric fungal dysbiosis. It then stands to reason that the fungal gut community, as well as an interplay between the fungal and bacterial communities, also plays a role in AN associated dysbiosis.

DNAs extracted from stool samples were used to analyze mycobiota in the guts of AN patients and healthy controls (HC). Utilizing fungal specific ITS1 primers and bacterial specific 16s rDNA primers, qPCR analysis demonstrated a significant increase in number of gut fungi relative to bacteria in the undernourished phase (T1) of AN patients as compared to the post-refeeding phase (T2) of the same patients. Furthermore, an increase in *C. albicans* was observed upon patients undergoing the refeeding treatment, providing a specific role of this fungus in lower weight phase of AN patients. Illumina sequencing of the ITS1 amplicons was performed to examine the dynamics of fungal species present in AN patients and HC. The obtained sequence data were filtered to identify taxa via IPITS pipeline. The OTU abundance from each sample was assessed with QIIME. Measurements of alpha diversity (T1 vs T2 vs HC) with the number of species and the Chao-1 index revealed less fungal species present in the gut of AN patients compared to that of HC. This result is similar to previous studies considering lower bacterial diversity in AN. Together, these findings suggest that fungal dysbiosis in the intestines may play a part in perpetuating microbiota in AN patients. Addressing this dysbiosis may then offer new methods for the treatment of AN.

334W *Nothophytophthora* prov. nom., a new sister genus of *Phytophthora*. T. Jung^{1,2,3}, B. Scanu⁴, J. Bakonyi⁵, D. Seress⁵, A. Durán⁶, E. Sanfuentes von Stowasser⁷, L. Schena⁸, S. Mosca⁸, P. Q. Thu⁹, C. N. Minh⁹, S. Fajardo⁷, M. González⁷, A. Pérez-Sierra¹⁰, H. Rees¹⁰, C. Maia¹, M. Horta Jung^{1,2} 1) Laboratory of Molecular Biotechnology and Phytopathology, Center for Mediterranean Bioresources and Food (MeditBio), University of Algarve, 8005-130 Faro, Portugal; 2) Phytophthora Research Centre, Mendel University, 613 00 Brno, Czech Republic; 3) Phytophthora Research and Consultancy, 83131 Nußdorf, Germany; 4) Dipartimento di Agraria, Sezione di Patologia vegetale ed Entomologia (SPaVE), Università degli Studi di Sassari, 07100 Sassari, Italy; 5) Plant Protection Institute, Centre for Agricultural Research, Hungarian Academy of Sciences, 1022 Budapest, Hungary; 6) Ontario Forest Research Institute, ?P6A 2E5 Sault Ste. Marie, Canada; 7) Laboratorio de Patología Forestal, Facultad Ciencias Forestales y Centro de Biotecnología, Universidad de Concepción, Concepción, Chile; 8) Dipartimento di Gestione dei Sistemi Agrari e Forestali, Università Mediterranea di Reggio Calabria, 89124 Reggio Calabria, Italy; 9) Forest Protection Research Centre, Vietnamese Academy of Forest Sciences, Duc Thang Ward, Northern Tu Liem District, Hanoi, Vietnam; 10) Forest Research, Alice Holt Lodge, Farnham, Surrey GU10 4LH, United Kingdom.

During various surveys of *Phytophthora* diversity in Europe, Chile and Vietnam slow growing oomycete isolates were obtained from soil samples and small streams in natural and planted forest stands. Phylogenetic analyses of ITS, β -tubulin, LSU and *cox1* sequences placed them into six new species belonging to a new genus, officially described as *Nothophytophthora* gen. nov., which clustered sister to *Phytophthora*. *Nothophytophthora* species share numerous morphological characters with *Phytophthora*: persistent (all *Nothophytophthora* spp.) and caducous (*N. caduca*, *N. chlamydospora*, *N. valdiviana*, *N. vietnamensis*) sporangia with variable shapes, internal differentiation of zoospores and internal, nested and extended (*N. chlamydospora*, *N. caduca*) and external (all *Nothophytophthora* spp.) sporangial proliferation; smooth-walled oogonia with amphigynous (*N. amphigynosa*) and paragynous (*N. amphigynosa*, *N. intricata*, *N. vietnamensis*) insertion of the antheridia; chlamydospores (*N. chlamydospora*) and hyphal swellings. Comparisons of morphological structures of both genera allow clues about the morphology and ecology of their common ancestor which are discussed. Including *Nothophytophthora* in coalescence analyses will give new insights into the evolutionary history of *Phytophthora*. Production of caducous sporangia by *N. caduca*, *N. valdiviana* and *N. chlamydospora* from Valdivian rainforests and *N. vietnamensis* from a wet mountain forest in Vietnam indicates a partially aerial lifestyle as adaptation to these humid habitats. Presence of tree dieback in all forests from which *Nothophytophthora* spp. were recovered and partial sporangial caducity of several *Nothophytophthora* species suggests they may be facultative pathogens. Pathogenicity tests are urgently required to clarify whether the individual *Nothophytophthora* species have a pathogenic or saprophytic lifestyle.

335T Diversity of *Phytophthora* species from natural and semi-natural ecosystems in Portugal, Chile and Vietnam. T. Jung^{1,2,3}, B. Scanu⁴, J. Bakonyi⁵, D. Seress⁵, A. Durán⁶, E. Sanfuentes von Stowasser⁷, L. Schena⁸, S. Mosca⁸, P. Q. Thu⁹, C. N. Minh⁹, S. Fajardo⁷, M. González⁷, A. Pérez-Sierra¹⁰, H. Rees¹⁰, C. Maia¹, B. Mora Sala¹¹, G. Carella¹², S. Moricca¹², A. Cravador¹, M. Horta Jung^{1,2} 1) Laboratory of Molecular Biotechnology and Phytopathology, Center for Mediterranean Bioresources and Food (MeditBio), University of Algarve, 8005-130 Faro, Portugal; 2) Phytophthora Research Centre, Mendel University, 613 00 Brno, Czech Republic; 3) Phytophthora Research and Consultancy, 83131 Nußdorf; 4) Dipartimento di Agraria, Sezione di Patologia vegetale ed Entomologia (SPaVE), Università

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Surveys of *Phytophthora* diversity were performed using baiting assays and direct plating of necrotic plant tissues. Isolates were identified using both classical identification and sequence analysis of ITS and *cox1*.

In Portugal, 68 forest stands, 12 forest nurseries, 38 river systems and 4 lagoon ecosystems were surveyed. The isolates obtained belonged to 29 known species, 3 informally designated taxa, and 1 previously unknown taxon of *Phytophthora*, nine new *Phytophthora* hybrid taxa from Clades 6 and 9, *Nothophytophthora homothallica* nom. prov., 1 known and 10 new *Halophytophthora* species, 7 known species and one new taxon of *Phytophythium*, and multiple *Pythium* species were isolated.

In Chile, the survey was performed in 13 natural forest stands and 20 forest streams located in two protected areas near Valdivia and in a temperate mountain forest in the Concepción area, and in each one planted stand of the introduced tree species *Castanea sativa* and *Fagus sylvatica*. Eight described species (including *P. kernoviae*) and 2 previously unknown taxa of *Phytophthora* were isolated. In addition, a diverse array of Clade 6 hybrids, and *Nothophytophthora caduca* nom. prov., *Nothophytophthora chlamyospora* nom. prov. and *Nothophytophthora valdiviana* nom. prov., were obtained.

In Vietnam the survey was performed in 23 natural forest stands and 10 forest streams and rivers in temperate montane and tropical lowland regions, and in 14 rubber plantations. Sixteen described species (including *P. ramorum*), 3 designated taxa and 23 previously unknown taxa of *Phytophthora*, amongst them 9 Clade 9 hybrid taxa, were isolated. In addition, *Nothophytophthora vietnamensis* nom. prov. and a diverse array of known and new taxa of *Phytophythium*, *Pythium* and *Elongisporangium* were recovered.

The implications of these findings for plant biosecurity and the development of a deeper understanding of the evolution and adaptability of the genus *Phytophthora* will be discussed

336F Fungi challenge global food security. Sarah Gurr, Dan Bebber, Helen Fones Biosciences, Exeter University, Exeter, GB.

Over the past centuries, crop diseases have led to the starvation of the people, the ruination of economies and the downfall of governments. Of the various challenges, the threat to plants of fungal infection outstrips that posed by bacterial and viral diseases combined. Indeed, fungal diseases have been increasing in severity and scale since the mid. 20th Century and now pose a serious threat to global food security and ecosystem health.

We face a future blighted by known adversaries, by new variants of old foes and by new diseases. Modern agricultural intensification practices have heightened the challenge - the planting of vast swathes of genetically uniform crops, guarded by one or two inbred resistance genes, and use of single target site antifungals has hastened emergence of new virulent and fungicide-resistant strains. Climate change compounds the saga as we see altered disease demographics - pathogens are on the move poleward in a warming world.

This presentation will highlight some current notable and persistent fungal diseases. It will highlight the evolutionary drivers underpinning emergence of new diseases and allude to the accelerators of spread. I will set these points in the context of recent disease modelling, which shows the global distributions of crop pathogens and their predicted movement and will discuss the concept of crop disease saturation.

I shall conclude with some thoughts on future threats and challenges, on fungal disease mitigation and of ways of enhancing global food security.

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337W Role of plant-endophyte interactions in shrub encroachment. M.I. Hutchinson, A.J. Robinson, D.O. Natvig Department of Biology, University of New Mexico, Albuquerque, NM.

Desertification is a significant global phenomenon, and in many dryland areas shrub encroachment is considered a primary factor. Shrub encroachment, the conversion of grasslands into shrublands, is a well-documented process but its causes are debated. Here, we