biontrophic stages. The genome comprises 5,245 contigs, an estimated size of 58Mbp with 96% BUSCO completeness. A deduced proteome of 12,051 proteins were used for downstream prediction of the secretome. In-silico analysis pipeline was used to predict the signal peptides, followed by the exclusion of membrane proteins and endoplasmic reticulum targets, to define a secretome of 1,185 proteins. These proteins were used to predict 224 CSEPs, of which 189 lacked Pfam domains. The candidates were further screened for known conserved motifs of effectors and similarity to known effectors. A total of 33 CSEPs with no orthologs in 19 related species and no Pfam domains, were presumed to be C. tanacetii-specific. These effector candidates can be utilized for investigating their biological function in pathogenesis and for breeding of pyrethrum for resistance.

Comparative genomic analysis of *Fusarium oxysporum* f. sp. *vasinfectum* isolates and their small secreted proteins
S. SEO, J. Coleman, Auburn University, Auburn, AL, USA

*Fusarium oxysporum* f. sp. *vasinfectum* (Fov) causing vascular wilt disease is one of the most devastating pathogens of cotton (*Gossypium spp*). To elucidate the molecular mechanisms responsible for host-specificity for pathogenicity on cotton, five Fov isolates were sequenced using PacBio SMRT sequencing and the genomes compared with 10 *F. oxysporum* genomes that are non-virulent on cotton. Genome analysis revealed that the highly virulent genotype race 4 had the largest genome size and coding genes and repetitive elements, compared to the other four Fov isolates. The genome of *F. oxysporum* comprises both core and accessory regions, and all the genomes of the Fov isolates were able to be divided into these two main architectures based on the genome of *F. oxysporum* f. sp. *lycoperdici* (Fol) as a reference. Comparative analysis among both cotton and non-cotton isolates of *F. oxysporum* focused on small secreted proteins (SSPs), which may function as virulence factors termed fungal effectors. The results showed that all isolates had similar proportions of SSPPs based on the whole genome following a universal effecter prediction pipeline. A total of 165 proteins were common to all the different *formae speciales* of *F. oxysporum*. Importantly, 56 SSPs are unique to the most virulent genotype and 17 SSPs existed only in the cotton Fov isolates. In summary, each Fov isolate genome reflects the diversity of pathogenesis-related genomic features, sharing or differing from each other, and may yield insights into the development of disease management strategies for cotton wilt.

Metabolome and transcriptome analyses to study plant-virus interaction: The case of study *Onion yellow dwarf virus* - 'rossa di tropea' onion

The -omics sciences are becoming a fundamental tool to better understand and investigate host-pathogen interactions, highlighting the complexity of plant responses. In this study, in the frame of the SIBORTO project (SIR-MIUR grant – SIBORTO-RBSI149L05), aimed to evaluate the effects of *Onion yellow dwarf virus* (OYDV, genus *Potyvirus*) on the accumulation of nutraceutical compounds in ‘Rossam di Tropea’ onion (IGP trademark), transcriptomic and metabolomic profiles were obtained using RNAseq and gas chromatometry-mass spectrometry (GC-MS)/high resolution angle magic spinning NMR (HR-NMR) respectively. Differentially expressed genes (DEGs) and metabolites (DEMs), in bulb onion samples, healthy versus OYDV-infected, showed, independently, an overall modulation of several metabolites connected to sugar and amino-acid metabolism, and the TCA cycle. Further, magnetic resonance micro-imaging (MRI) on whole bulbs, and determination of volatile organic compounds (VOCs) by GC-MS, highlighted a structural alteration and modulation of compounds related to flavor and organoleptic properties respectively in OYDV-infected bulbs. In agreement with metabolomic and transcriptomic profiling, preliminary results showed an actual OYDV modulation of important pathways. This research represents a first and multi-disciplinary study on metabolite interaction in a plant-virus pathosystem (’Rossa di Tropea’ onion–OYDV).

Genomic analysis of *Xanthomonas arboricola*: Pathogenicity and development of a real-time PCR protocol for bacterial spot disease of *Prunus* spp.
J. M. Garita-Cambronero (1), A. Palacio Bielsa (2), J. CUBERO (3), (1) Instituto Tecnológico Agrario de Castilla y León (ITACyL), Valladolid, SPAIN; (2) Centro Investigacion Y Tecnología Agroalimentaria Aragón, Zaragoza, SPAIN; (3) INIA, Madrid, SPAIN

*Xanthomonas arboricola* pv. *pruni* (Xap) causes bacterial spot of stone fruits. The bacteria produce lesions that reduce the marketability of fruit and the yield and vigor of the trees. Xap is within the interesting *Xanthomonas* genus, which has been intensively studied due its strain specialization and its host range complexity. Comparative genome analysis of *Xanthomonas arboricola* revealed the evolutionary history of the pathogenic bacteria of this species, as well as a characterization of factors involved in virulence. Phenotypic assays on *Xanthomonas*, isolated from *Prunus*, have revealed the coexistence of non-pathogenic strains phylogenetically different to those pathogenic ones. Taking advantage of the variation in genomic features, a real-time PCR protocol, based on the *xapE3* gene, has been developed to differentiate Prunus-pathogenic and non-pathogenic strains of *X. arboricola* and to refine the diagnosis of this quarantine pathogen. The use of this protocol in conjunction with a previous real-time PCR test based on the gen *ftsX*, showed a high specificity to differentiate pathovar pruni from the other groups of *X. arboricola*. The new real time protocol is a valuable molecular tool for the diagnosis of the bacterial spot of stone fruits and almond and the detection of its causal agent. This work was supported financially by the Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA) project RTA2014-00018.

Mining the *Penicillium expansum* proteome to unlock fungal virulence mechanisms during postharvest apple fruit decay
W. M. JURICK II PHD (1), H. Beard (2), W. Garrett (3), V. L. Gaskins (1), B. Cooper (2), (1) USDA-ARS Food Quality Laboratory, Beltsville, MD, USA; (2) USDA-ARS Soybean Genomics & Improvement Laboratory, Beltsville, MD, USA; (3) USDA-ARS Animal Biosciences & Biotechnology Laboratory, Beltsville, MD, USA

The blue mold fungus, *Penicillium expansum*, is one of the most globally important postharvest pathogens. The fungus reduces fruit quality, produces harmful mycotoxins, and contributes to food waste. It is a successful saprophyte, and is an aggressive necrotrophic wound pathogen that utilizes complex biochemical processes to overcome the host. To better understand fundamental mechanisms of *P. expansum* virulence, we compared the proteomes of an aggressive, wild-type strain (R19) and a lesser virulent mutant with a T-DNA insertion in the Heat Shock Protein 60 gene (*HSP60*). Proteins were extracted from mycelia, and peptides were labeled with isotopic tandem mass tags and analyzed by mass spectrometry. More than 3,500 proteins were quantified and mapped to known biochemical pathways in KEGG. In addition, proteins released into the culture medium were separately purified and analyzed. These included at least 100 secreted proteins (i.e. CAZymes) such as aspartic proteases, glucanases, invertases, and pectate lyases. It is likely that these enzymes contribute to decay by digesting host proteins and complex carbohydrates in apple. This study is the most detailed proteomic evaluation of this pathogen to date, and the results will provide a deeper understanding of how this pathogen causes disease. Our end goal is to translate these findings into new controls by interfering with fungal pathways, effectors and processes vital for blue mold decay development during storage.
Abstracts submitted for presentation at ICPP2018 in Boston, Massachusetts, U.S.A., July 29–August 3, 2018. The recommended format for citing congress abstracts, using the first abstract below as an example, is as follows:


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Comparative transcriptomic analysis of MAPK-mediated regulation of sectorization in Cryphonectria parasitica

D. H. KIM, Chonbuk National University, Jeonju, SOUTH KOREA

Fungal phenotypic sectorization is a complex trait and still not fully understood. The unique phenotypic change of sporadic sectorization in the mutants of \( \text{CpBck1} \), a MAPKKK gene, and \( \text{CpSlt2} \), a MAPK gene, in cell wall integrity pathway of the chestnut blight fungus \( \text{Cryphonectria parasitica} \) have been previously studied. Although there are several environmental and physiological factors causing this sectoring phenotype, genetic variants can also impact this complex morphogenesis. Therefore, transcriptome analysis was employed to discover candidate genes that are associated with the sectorization traits and to understand the genetic mechanism of this phenotype. Transcriptome analysis of the mutants of \( \text{CpBck1} \) and \( \text{CpSlt2} \), and their sectored progenies revealed a number of differentially expressed genes (DEG) related to various cellular processes. Functional description of DEG’s between the parental mutants and their corresponding sectored progenies revealed several key pathways including the biosynthesis of secondary metabolites, amino acid metabolism, and carbohydrate metabolism, among which the pathway for secondary metabolism appeared the most represented pathway. Our results of this comparative study provide better understanding the basis of genetic regulation of fungal sector formation and suggest a complex interplay between the secondary metabolites and morphogenesis.

Regulation of the Cryparin, Hydrophobin, by MAPK Signaling Pathways from the Chestnut Blight Fungus Cryphonectria parasitica

D. H. KIM, Chonbuk National University, Jeonju, SOUTH KOREA

We assessed the regulation of cryparin, a typical type II hydrophobin, by three representative mitogen-activated protein kinase (MAPK) pathways in \( \text{Cryphonectria parasitica} \). The mutation in the \( \text{CpSlt2} \) gene, an ortholog of the cell wall integrity (CWI) pathway of \( \text{Saccharomyces cerevisiae} \), showed dramatic decrease in the cryparin production. The mutant of \( \text{CpBck1} \) gene, a MAPKKK gene in CWI pathway, showed similar decreased cryparin production. In addition, the mutant of \( \text{cpmk} \) gene, an ortholog of yeast HOG1, showed the decreased cryparin production. However, the mutant of \( \text{cpm} \) gene, an ortholog of yeast \( \text{Kss1/Fus3} \), showed the increased cryparin production. Easy-wet phenotype and accumulation of cryparin transcript of corresponding mutants were in good agreement with the cryparin production. In silico analysis of the promoter region of cryparin gene revealed the presence of binding motifs related to the downstream transcription factors of CWI, HOG1, and pheromone responsive pathways including MADS box- and Ste12-binding domains. Real time RT-PCR analyses indicated that both \( \text{CpRlm1} \), an ortholog of yeast \( \text{RLM1} \) in CWI pathway, and \( \text{cpst12} \), an ortholog of yeast \( \text{STE12} \) in mating pathway, showed significantly reduced transcription level in the mutant strains showing the less production of cryparin. However, the transcription of \( \text{CpMcm1} \), an ortholog of yeast \( \text{MCM1} \), did not correlate with the mutant strains showing the down-regulation of cryparin. These results indicated all three representative MAPK pathways in filamentous fungi played a role in regulation of the cryparin production. In addition, protein expressions of \( \text{CpRlm1} \) and \( \text{cpst12} \) are underway to check the binding affinity of \( \text{CpRLM1} \) and \( \text{CpST12} \) into promoter region of cryparin.

Metagenomic signatures of bacteria harbored in sorghum leaf tissue

K. MASENYA (1), M. Tekere (2), G. Thompson (1), J. Rees (2,3), (1) Agricultural Research Council-Biotechnology Platform, Pretoria, SOUTH AFRICA; (2) University of South Africa, Johannesburg, SOUTH AFRICA; (3) University of South Africa, Pretoria, SOUTH AFRICA

Sorghum is a promising biofuel resource and one of the most important cereal crops globally. Large-scale planting would however require improved varieties that are tolerant to a range of stressors, including plant pathogens. This study aimed to extensively assess the bacterial diversity present in sorghum lines developed for cultivar breeding programs using 16S metagenomic sequencing. The observed patterns revealed a highly heterogeneous bacterial community and a link between the presence of plant pathogens and the composition of the endophytic bacterial community. Diseased plants...