



32<sup>nd</sup>

# Fungal

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**ABSTRACT BOOK**

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pathogenicity. In *A. nidulans*, AfFphA and AfFphB localized exclusively in nuclei, forming a heterodimer. Our results suggest that *A. fumigatus* FphA responds to red light and plays a role in stress responses, while the photoinactive FphB protein controls virulence.

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Igbalajobi, O., Yu, Z., and Fischer, R. (2019) Red- and blue-light sensing in the plant pathogen *Alternaria alternata* depends on phytochrome and the white-collar protein LreA. *mBio* **10**: e00371-00319.

Yu, Z., Streng, C., Seibeld, R., Igbalajobi, O.A., Leister, K., Ingelfinger, J., and Fischer, R. (2021) Genome-wide analyses of light-regulated genes in *Aspergillus nidulans* reveal a complex interplay between different photoreceptors and novel photoreceptor functions. *PLoS Genet* **17**: e1009845.

Fuller, K.K., Ringelberg, C.S., Loros, J.J., and Dunlap, J.C. (2013) The fungal pathogen *Aspergillus fumigatus* regulates growth, metabolism, and stress resistance in response to light. *mBio* **4**: e00142-00113.

**569A A multidisciplinary, cross-species approach to understanding woody plant declines: similarities between Kiwifruit Vine Decline Syndrome (KVDS) and Apple Replant Disease (ARD)** Micol Guaschino<sup>1,2</sup>, Tracey S Somera<sup>3</sup>, Davide Spadaro<sup>2,4</sup> <sup>1</sup>Dept of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, <sup>2</sup>AGROINNOVA, University of Torino, <sup>3</sup>Agricultural Research Service, USDA, <sup>4</sup>Dept of Agricultural, Forest and Food Sciences (DISAFA), University of Torino

Kiwifruit Vine Decline Syndrome (KVDS) and Apple Replant Disease (ARD) are both soil-borne diseases affecting fruit trees in perennial cropping systems. Both pathosystems are characterized by a similar complex of soilborne fungi and oomycetes which impact root development and soil health. ARD occurs in apple-producing regions worldwide. In the last decade, KVDS has severely compromised kiwifruit production in Italy and has also been reported in Turkey, Japan, and China. The contribution of similar biotic and abiotic factors to both pathosystems underlines the need for multidisciplinary and cross-species approaches to the management of woody plant diseases. This is of particular relevance in the framework of climate change where novel conditions may lead to shifts in microbial community composition and function. Root anoxia/flooding of the radical system is a key abiotic stress factor required for development of KVDS symptoms, together with infection by *Phytophthora vexans*. Preliminary gene expression analysis on kiwifruit roots revealed upregulation of ROS scavenging pathways and hormonal stress at specific time points in response to this dual stressor combination. Additional transcriptomic studies on inoculated *Actinidia* roots, with and without flooding, are currently underway. Results are expected to improve our understanding of how pathways associated with abiotic vs. biotic stress factors promote KVDS onset. In combination with this analysis, genes previously identified as exhibiting altered expression in apple roots in response to *Pythium ultimum* infection will serve as a foundation to explore potential similarities in KVDS and ARD pathosystems. Results are expected to provide new insights into oomycete pathogenesis in woody plants and improve disease management in both systems.

**570A Screening system based on growth defects due to unscheduled *brlA* expression to identify genes involved in the functional regulation of transcription factors in *Aspergilli*** Katsuya Gomi, Tomoko Shintani, Da-Min Jeong, Jikian Tokashiki Tohoku University

Pathway-specific transcription factors are involved in regulating the production of polysaccharide-degrading enzymes in filamentous fungi including *Aspergillus*, and to date a number of the Zn<sub>2</sub>Cys<sub>6</sub> binuclear cluster-type transcription factors unique to fungi have been identified by many studies. However, much remains to be elucidated about the transporters/sensors for inducing substrates, subsequent signal transduction, and regulation of transcription factor activation.

The aim of this study is to isolate unidentified genes involved in the functional regulation of transcription factors in *Aspergilli*. To this end, we first attempted to find the novel genes involved in the functional regulation of AmyR essential for amylolytic enzyme production as a model. We constructed an *Aspergillus nidulans* strain that overexpressed *brlA*, which is involved in conidiation, under the control of the  $\alpha$ -amylase gene promoter, and this strain showed a significantly restricted growth in the presence of isomaltose, an inducer of amylase production. By using this strain as a parent, spontaneous mutant strains that recovered growth were isolated on isomaltose-containing agar medium. Consequently, we successfully identified a putative sugar transporter gene involved in isomaltose transport/sensing through next-generation sequencing of the spontaneous mutants (see Jeong's presentation for details). Further, we are currently applying the screening system to find unidentified genes involved in the functional regulation of the transcription factor XlnR essential for xylolytic enzyme production.