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Transcriptional responses to white light in *Botrytis cinerea* involve the GATA transcription factors BcWCL1 and BcLTF1 and the MAP kinase BcSAK1

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CONCURRENT SESSION ABSTRACTS
CS3: Environmental sensing, stress response

Monday 4th April
16:20 - 16:40
Louis Armand Est

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Transcriptional responses to white light in *Botrytis cinerea* involve the GATA-transcription factors BcWCL1 and BcLTF1 and the MAP kinase BcSAK1

Botrytis cinerea is a necrotrophic plant pathogen that exhibits prominent light responses including the formation of the reproduction structures (photomorphogenesis), secondary metabolites/ pigments, and antioxidant enzymes. A complex regulatory network of photoreceptors, transcription factors (TFs) and chromatin modulates is supposed to initiate, transmit, and fine-tune the responses to different wavelengths of light on the transcriptional level that finally leads to the observable phenotypes. As the formation of the reproduction structures is strictly regulated by light in this fungus - conidia are formed in the light, sclerotia in the dark - the output can be easily monitored. The GATA-type TFs BcLTF1 and BcWCL1 are important regulators as their deletions resulted in conidiation in light and dark («always conidia») (Schumacher et al. 2014; PLoS Genet 10:e1004040, Canessa et al. 2013; PLoS One 8:e84223). Study of gene expression in both deletion mutants by microarray analyses highlighted the role of the TFs in mediating the transcriptional responses of the majority of light-responsive genes including a number of other transcriptional regulators. As the group of light-responsive genes also contained genes that are induced by oxidative and osmotic stress in a BcSAK1-dependent manner (Heller et al. 2012; MPMI 25:802-816), their expression levels were studied in the delta-Bcsak1 mutant. Indeed, light induction does not occur in the mutant background indicating that the MAP kinase cascade is another functional unit of the light regulatory network. More detailed expression analyses of chosen LTF-encoding genes showed that three major transcriptional profiles exist: genes that exhibit maximal expression after 15 min (early), 60 min (moderate) or 120 min (late) of light treatment. Expression levels of the majority of genes decrease after prolonged light exposure (photoadaptation); however, this is not observed for bcltf1. Eight LTFs have been functionally characterized by deletion and overexpression analyses so far: While BcLTF1 has various functions (growth in light, ROS homeostasis, virulence, differentiation), other LTFs specifically regulate certain developmental stages such as the initiation of conidiophore development or conidiogenesis.
