Regulation of the Primary and Secondary Metabolism in Fungi by a pair of Transcription Factors

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The fungal secondary metabolism is a source of a wide range of chemical compounds. Some of these compounds can be used in medicine and biotechnology applications and are potential sources for new therapeutic agents and drug leads. However, under laboratory conditions, the fungal secondary metabolism remains largely silent.

Previously, we have identified a pleiotropic regulator of the fungal secondary metabolism; the transcription factor Xpp1 is involved in the regulation of both, the primary and the secondary metabolism of *Trichoderma reesei*. Data from an RNA-Seq analysis suggest that Xpp1 is an activator of primary metabolism, as well as a repressor of the secondary metabolism. The deletion of *xpp1* leads to slower growth on a broad range of carbon sources and an enhanced production of low molecular weight compounds (presumably secondary metabolites) in the supernatant. The role of Xpp1 as a repressor of the secondary metabolism was determined by gene expression analyses of polyketide synthases and measurement of the secondary metabolites using an untargeted metabolomics approach.

Recently we identified a potential interaction partner of Xpp1, termed Xpp2. The deletion of Xpp2 led to a strongly reduced growth on a wide array of unrelated carbon sources. Notably, on some carbon sources no growth impairment was observed. Further, we investigated the influence of Xpp2 on the production of secondary metabolites by qPCR assays and an LC-HRMS based metabolite profiling, analogously to the studies of Xpp1. Moreover, we tested for the influence of Xpp1 and Xpp2 on stress responses in *T. reesei*.