



TRICHODERMA FOR BIOTECHNOLOGY

Trichoderma reesei is among the most potent producers for homologous and heterologous proteins, including plant cell wall degrading enzymes used in the biofuels industry. Additionally, several species of the genus *Trichoderma* are widely used biofungicides and enhance plant growth. AIT provides expertise on industrial strain improvement.

ENHANCING ENZYME PRODUCTION

Together with our clients we discover novel strategies for improving efficiency and stability of strains such as *Trichoderma reesei* used for biotechnological processes. We aim at exploiting reactions of *T. reesei* to its environment for optimization of enzyme production^[1]. We use screening methods for evaluation of transcription as well as activity and protein recovery (RT-qPCR, transcriptomics, enzymatic assays, Western blotting, etc.).

Environmental cues such as light and nutrients influence enzyme production. Besides testing candidate regulators in our functional genomics pipeline, we are also working to elucidate the exterior signaling mechanisms. We exploit the molecular regulatory processes like light dependent regulation, regulator phosphorylation and stability, transcript stability for strain improvement and more efficient enzyme production under industrial conditions. Thereby we include also epigenetic analyses in our approach.

KNOCK OUT STRAIN COLLECTION

Our knock out strain collection of the heterotrimeric G-protein pathway, cAMP signaling, protein kinases and protein phosphatases etc. serves as a valuable basis for research towards increased expression of target genes or gene groups. Flexible combination of mutations by crossing^[2] additionally increases our efficiency in identifying and optimizing regulation mechanisms.

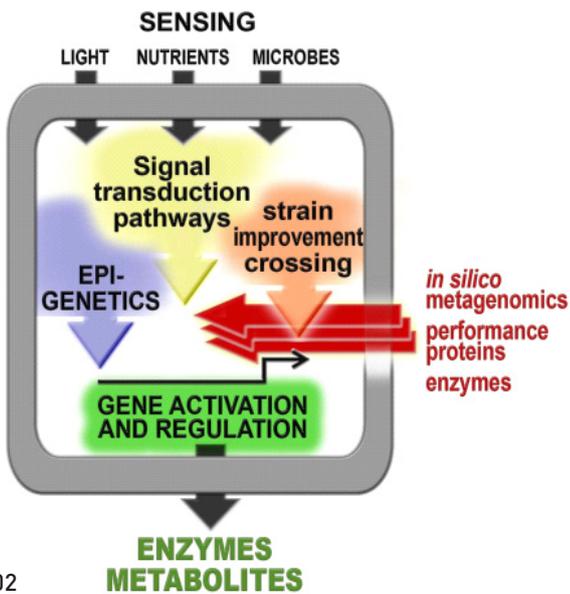
HETEROLOGOUS PROTEIN PRODUCTION

We provide expertise in optimization of heterologous protein production with *Trichoderma reesei*^[3] using different promoters and flexible vector construction. Our broad knowledge on fungal physiology enables us to select appropriate promoters, also for carbon source specific production of the protein, the use of inducible production and adjustment of expression.

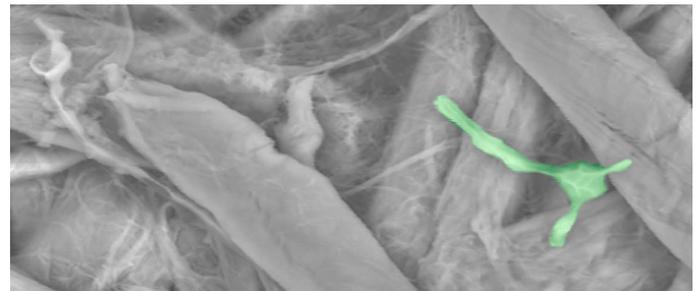
FUNGAL GENOME ANNOTATION

We are experienced in genome analysis of fungi of different genera^[4], including functional annotation of gene groups. These analyses provide a reliable basis for investigation of the biological meaning of differential gene expression^[5] under diverse conditions. Our functional genomics approach and our knock-out collection as well as the techniques we have available therefore are valuable resources for deeper investigation of fungal physiology. Our experience in fungal transformation, gene deletion and expression modification can be used to develop transformation systems and adapt analysis techniques for investigation of novel species.





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T. reesei growing on cellulosic substrate (electron microscopy)

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Target pathways and mechanisms for strain improvement

- [1] Eva Stappler, Christoph Dattenböck, Doris Tisch and Monika Schmoll (2017) Analysis of light and carbon specific transcriptomes implicates a class of G-protein coupled receptors in cellulose sensing; mSphere, 2 (3). pii:e00089-17 eCollection 2017 May-Jun.
- [2] Seidl, V., Seibel, C., Kubicek, C. P., & Schmoll, M. (2009) Sexual development in the industrial workhorse Trichoderma reesei. PNAS 106, 13909-13914
- [3] Schmoll M., Kotlowski, C., Seibel, C., Liebmann B., Kubicek, C. P. (2010) Recombinant production of an Aspergillus nidulans class I hydrophobin, [DewA] in Hypocrea jecorina [Trichoderma reesei] is promoter-dependent, Applied Microbiology and Biotechnology, 88(1):95-103.
- [4] M. Schmoll, C. Dattenböck, N. Carreras-Villaseñor, A. Mendoza-Mendoza, D. Tisch, M. I. Alemán, et al., (2016) The genomes of three uneven siblings – footprints of the lifestyle of three Trichoderma species, Microbiol Mol Biol Reviews, Vol. 80 (1): 205-327
- [5] Tisch, D. and Schmoll M. (2013) Targets of light signalling in Trichoderma reesei. BMC Genomics 14: 657

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