

New approaches in genome mining reveal conserved RiPPs in *Trichoderma reesei*

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Microorganisms can produce a diverse range of secondary metabolites (SM), also known as natural products. These have led to identification of new pharmacological effects and were crucial in the development of drugs to treat human disease. Ribosomally synthesized and post-translationally modified peptides (RiPPs) are a rapidly growing group of SMs that vary in the number of amino acids ~20-110. These chemically and structurally diverse groups have many different applications such as food preservatives or antibiotics. RiPPs are commonly produced by bacteria such as *Bacillus* and *Streptomyces*, on the other hand very few fungal RiPPs are known.

We developed a new procedure how to mine the genome of fungi with the specific focus on the identification of precursor peptides and the structural prediction of various RiPPs from the fungal genome with the use of existing tools, such as antiSMASH and RiPPMiner. To validate this procedure we mined the genomes of 4 different *Trichoderma ssp.* with most diverse average nucleotide identity (ANI) and could show that these genomes are a rich untapped source for various RiPPs some presumably only found in marine bacteria. Furthermore a phylogenetic analysis revealed highly conserved precursor peptides within the *Trichoderma* genus. Using RNAseq data and RT-qPCR analyses we could show that the predicted precursor peptides are transcribed in *T. reesei* QM6a. Concurrently we tested for the presence of the predicted RiPPs in the mycelium and the supernatant using HPLC-MS analysis.