

Unlocking fungal genomes by EPIGENETIC REMODELLING

Description:

Epigenetic remodelling of fungal genomes allows to unlock otherwise silenced genetic clusters which may provide access to novel “cryptic” metabolites with potential bioactive abilities. We established a knowledge base for different epigenetic approaches in fungal systems and have access to an extensive collection of natural fungal isolates and genetically modified model fungi.

From 2014 onwards, a high-throughput screening system, and technologies for substance isolation and chemical characterization will be available as a Research Service Core-Facility “BiMM”.

Background:

Fungi produce a wide range of bioactive metabolites comprising antibiotic, cytostatic or anti-cholesterol substances. **Our group** could show that genomic silencing mechanisms operate to lock secondary metabolite gene clusters and have set-up a rapid screening tool for „cryptic“ antimicrobial metabolites from epigenetic modified fungi. Screening fungal extracts of 56 strains epigenetic remodelled with 6 different chromatin modifiers for potential novel bioactive metabolites, revealed several bioactive fungal extracts. We now focus on the isolation and characterisation of these potential novel substances among them fungal extracts which show activities also against multi-resistant pathogens and having low cytotoxicity.

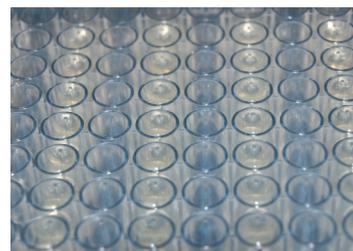
Current research focuses on the characterisation of these novel bioactive compounds and their mode-of-action.

Application:

- Large fungal collection including genetically modified strains and natural isolates
- New techniques for epigenetic modification
- Screening for compounds active against a variety of bacteria e.g. *S. aureus* including multi resistant strains.

Benefits:

- Discovery of novel bioactive substances with the potential of new mode-of-actions
- Great expertise in fungi, epigenetic regulation, and compound isolation and characterization in one team



IP status:

not patent protected yet

Type of cooperation:

Commercial partner to join the team and their activities.

See also:

Chromatin-level regulation of biosynthetic gene clusters (Nat Chem Biol. 2009 July; 5(7): 462–464)

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