**Chemical analysis of a genome wide polyketide synthase gene deletion library in *Aspergillus nidulans***

Thomas O. Larsen, Marie L. Klejnstrup, Jakob B. Nielsen, Dorte M. K. Holm, Lene Maj Petersen, Andreas Klitgaard, Kristian F. Nielsen, Mikael R. Andersen, Uffe H. Mortensen

Center for Microbial Biotechnology (CMB), Technical University of Denmark.

Filamentous fungi possess an advanced secondary metabolism that is regulated and coordinated in a complex manner depending on environmental challenges. The number of known and putative polyketide synthase genes greatly exceeds the number of polyketides (PKs) that these fungi are known to produce. This may reflect that many PKs are either produced in small amounts, under special conditions or in developmental stages that are rarely observed under laboratory conditions.

In order to trigger expression of “silent” genes we are currently pursuing several approaches; i) stimulation of *A. nidulans* wild type strains by culturing on different complex media to provoke induction of the secondary metabolism; ii) over expression of transcription factors encoding genes that are present in PKS gene clusters; iii) modification of chromatin structure regulation by knock out of histone H3 lysine methylation; iv) more random induction of secondary metabolism through heterologous expression of regulatory genes from other filamentous fungi using *A. niger* as test case.

To facilitate the linking of new compounds to genes we have made a collection of mutant strains where all thirty-two individual genes predicted to encode polyketide synthases have been individually been deleted. This presentation will highlight our recent linking of secondary metabolites in *A. nidulans* to genes, and in particular describe some recent work on characterization of *ANID\_6448* and associated genes responsible for biosynthesis of 3-methyl-orsellinic acid and derived products.