



## **A combined genetic and multi medium approach revels new secondary metabolites in *Aspergillus nidulans***

**Klejnstrup, Marie Louise; Nielsen, Morten Thrane; Frisvad, Jens Christian; Mortensen, Uffe Hasbro; Larsen, Thomas Ostenfeld**

*Publication date:*  
2011

*Document Version*  
Early version, also known as pre-print

[Link back to DTU Orbit](#)

*Citation (APA):*  
Klejnstrup, M. L., Nielsen, M. T., Frisvad, J. C., Mortensen, U. H., & Larsen, T. O. (2011). *A combined genetic and multi medium approach revels new secondary metabolites in Aspergillus nidulans*. Abstract from 26th Fungal Genetics Conference, Pacific Grove, CA, United States. <http://www.fgsc.net/26thFGC/>

---

### **General rights**

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

26th Fungal Genetics Conference, Asilomar, California, USA, 14/3-20/3 2011

Poster (abstract):

## A combined genetic and multi medium approach reveals new secondary metabolites in *Aspergillus nidulans*

Poster (abstract):

Marie Louise Klejnstrup\*, Morten Thrane Nielsen, Jens Christian Frisvad, Uffe Mortensen, Thomas Ostenfeld Larsen. Department of Systems Biology, Technical University of Denmark, Lyngby, Denmark, [\\*mark@bio.dtu.dk](mailto:*mark@bio.dtu.dk)

Secondary metabolites are a diverse group of metabolites which serve as important natural sources of drugs for treating diseases. The availability of full genome sequences of several filamentous fungi has revealed a large genetic potential for production of secondary metabolites that are not observed under standard laboratory conditions. Genetic approaches have proven a fruitful strategy towards the production and identification of these unknown metabolites. Examples include deletion of the *cclA*<sup>1</sup> and *laeA*<sup>2</sup> genes in *A. nidulans* which affects the expression of secondary metabolites including monodictyphenone and terrequinone A respectively. We have deleted the *cclA* gene in *A. nidulans* and grown the mutants on several complex media to provoke the production of secondary metabolites. This resulted in the production of several metabolites not previously reported from *A. nidulans*. Some of these have been reported from other *Emericella* spp or *Aspergillus terreus*.

<sup>1</sup> Bok, J.W. *et al*, Nat. Chem. Biol., 5, 462-464 (2009).

<sup>2</sup> Bok J.W. *et al*, Chem. Biol., 13, 31-37 (2006).