



The chemical heritage of *Aspergillus flavus* in *A. oryzae* RIB 40

Rank, Christian; Klejnstrup, Marie Louise; Petersen, Lene Maj; Frisvad, Jens Christian; Larsen, Thomas Ostenfeld

Publication date:
2011

Document Version
Early version, also known as pre-print

[Link back to DTU Orbit](#)

Citation (APA):

Rank, C., Klejnstrup, M. L., Petersen, L. M., Frisvad, J. C., & Larsen, T. O. (2011). *The chemical heritage of Aspergillus flavus in A. oryzae RIB 40*. Abstract from 26th Fungal Genetics Conference, Pacific Grove, CA, United States.

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.

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

Poster (abstract):

Authors

Christian Rank, Marie Louise Klejnstrup, Lene Maj Petersen, Jens Christian Frisvad, Thomas Ostenfeld Larsen.

Title

The chemical heritage of *A. flavus* in *A. oryzae* RIB40

Abstract

Aspergillus oryzae is a very important species in biotechnology and has been used for centuries in traditional Asian fermentation. The RIB40 strain is particularly interesting as it was one of the first genome sequenced Aspergilli together with *A. flavus*, a prominent food and feed contaminant capable of producing aflatoxin. These species can be perceived as ecotypes.

We have analyzed *A. oryzae* RIB40 and found that the chemical potential could be enhanced significantly under certain conditions. Delicate analysis of their metabolic profiles allow for chemical insight on the transcription level with indications to specific genetic changes. Several new metabolites and changes in biosynthetic routes have been found in *A. oryzae*, indicating subtle changes in the genomic heritage from *A. flavus*.