Friends and foes - comparative genomics of 23 Aspergillus Flavi species

Kjærbølling, Inge; Vesth, Tammi Camilla; Rasmussen, Jane Lind Nybo; Theobald, Sebastian; Frisvad, Jens Christian; Kogle, Martin Engelhard; Lyhne, Ellen Kirstine; Kuo, Allan; Salamov, Asaf; Riley, Robert; Larsen, Thomas Ostenfeld; Mortensen, Uffe Hasbro; Grigoriev, Igor V.; Baker, Scott E.; Andersen, Mikael Rørdam

Publication date: 2018

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):

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.
Friends and foes - comparative genomics of 23 Aspergillus Flavi species

Authors: Inge Kjærbølling1, Tammi C. Vesth1, Jane L. Nybo1, Sebastian Theobald1, Jens C. Frisvad1, Martin E. Kogle1, Ellen K. Lyhne1, Alan Kuo2, Asaf Salamov2, Robert Riley2, Thomas O. Larsen1, Uffe H. Mortensen,1 Igor V. Grigoriev2, Scott E. Baker3 and Mikael R. Andersen1.

(1) Department of Bioengineering, Technical University of Denmark, Kgs. Lyngby, Denmark
(2) DOE Joint Genome Institute, Walnut Creek, CA, USA
(3) Pacific Northwest National Laboratory, Richland, WA, USA

A. oryzae is widely used in food fermentation for the production of soy sauce, sake and miso in addition to enzyme production and it has GRAS status. A close relative A. flavus on the other hand produces some highly toxic compounds such as aflatoxin and is an opportunistic pathogen. Both species belong to section Flavi consisting of at least 29 species1.

In this study, we have whole genome-sequenced 19 novel Flavi species to examine the core of this section and the differences based on comparative genomics. The genomes reveal a highly diverse section with the number of predicted genes ranging from 9,078 to 14,216 in A. coremiiformis and A. transmontanensi respectively. We have identified 1,119 Flavi specific core protein families corresponding to approximately 9% of the proteome while the number of species specific protein families ranges from 395 for A. nomius NRRL 13137 to 2,219 for A. leporis.

Of particular interest is enzymes for degradation of carbohydrates, due to their essentiality both for food fermentation, plant pathogenicity, and biotechnology. Thus, the Carbohydrate-Active enZymes (CAZY) potential was investigated ranging from 353 to 617 identified proteins belonging to a CAzy family for A. coremiiformis and A. novoparasiticus respectively.

In addition, we have investigated the secondary metabolite (SM) potential of this section since it is vital for food safety but also represents potential useful bioactive compounds. The total number of predicted SM clusters in the Flavi section is 1,527 constituting 283 cluster families with an average of 73 clusters per species. No SM gene cluster family is shared between the all the Flavi species however 106 unique cluster families are only found in one species. Overall this investigation paints a picture of a highly diverse section encompassing friends and foes.

1 Varga et al. 2011 Studies in Mycology 69:57-80