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## Genetic diversity of 100+ Aspergillus species - the aspMine analysis resource

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*Publication date:*  
2017

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

[Link back to DTU Orbit](#)

*Citation (APA):*  
Vesth, T. C., Rasmussen, J. L. N., Theobald, S., De Vries, R. P., Grigoriev, I. V., Baker, S. E., & Andersen, M. R. (2017). Genetic diversity of 100+ Aspergillus species - the aspMine analysis resource. Abstract from 29th Fungal Genetics Conference, Pacific Grove, United States.

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## Fungi in Society

**Old collection, new discoveries.** *Kyria Boundy-Mills*<sup>1</sup>, Luis A. Garay<sup>1</sup>, Irnayuli R. Sitepu<sup>1,2</sup>, Tomas Cajka<sup>3</sup>, Oliver Fiehn<sup>3</sup> 1) Food Science, University of California Davis, One Shields Ave, Davis, CA USA 95616; 2) Department of Biotechnology, Indonesia International Institute for Life Sciences, Jalan Pulo Mas Barat Kav. 88, East Jakarta, DKI 10 Jakarta, Indonesia; 3) UC Davis Genome Center-Metabolomics, University of California, Davis, 451 Health Sciences Drive, Davis, California 95616 USA.

The Phaff Yeast Culture Collection at the University of California Davis is the fourth largest public collection of its kind in the world, containing over 7,500 strains belonging to over 800 different species. The yeasts were gathered, characterized and preserved over the last century by University of California personnel, primarily by Herman Phaff (1913-2001), from environmental sources such as plants, insects, and foods and beverages. The collection is expanding through rescue of over 3,000 yeasts from retiring professors W. T. Starmer (Syracuse University) and P. Ganter (Tennessee State University). Ribosomal sequences (partial 26S and ITS) have been generated for thousands of yeast strains. The yeasts are utilized by academic, government agency and industrial researchers around the world in a wide range of areas such as functional genomics, metabolomics, biogeography, ecology, food fermentations, and metabolomics. The yeast strains and associated data are available to the scientific community through the collection website, <http://phaffcollection.ucdavis.edu>. The broad diversity enables in-house research including studies of stress tolerance, yeast lipid accumulation, synthesis and secretion of glycolipids, and development of starter cultures for olive fermentations. Several yeast species were identified that are able to synthesize and secrete significant quantities of a class of glycolipids called polyol esters of fatty acids (PEFA), consisting of a 3-hydroxy fatty acid and either mannitol or arabinol, with varying degrees of acetylation. Because the molecule is amphipathic, it has biosurfactant activity. These discoveries are possible thanks to the accumulation, characterization and preservation of yeasts by forward-thinking scientists over many decades.

**Feeding fellow biologists their fungal vegetables.** *C. Adams* Plant and Microbial Biology, UC Berkeley, Oakland, CA.

Among eukaryotes, Kingdom Fungi is extremely diverse in terms of estimated species numbers, as well as ecologies, genetic systems, and more. Yet despite their comparable importance with, for example, animals and plants, the U. S. public knows very little about fungi. Though much remains to be learned about fungi, many aspects are well-understood, such as their importance in nutrient cycling and decomposition, heterothallic mating systems, and production of socially important compounds such as antibiotics. Then why are fungi relatively absent from primary education, and often even college-level biology? This illiteracy may be partially due to the fact biologists have historically understudied fungi, which were long mistaken for “lower plants” of little value or importance. This knowledge gap among biologists themselves hinders not only teaching mycology to the public, but conducting interdisciplinary research. In this talk, I will create a dialog to discuss the aspects of fungal biology that mycologists consider critical for other biologists to know. I will also present strategies that mycologists can use to better communicate with other biologists across a range of social media platforms.

**Diversity of spalting fungi in the Peruvian amazon.** *Sarath M. Vega Gutierrez, Sara C. Robinson* Wood Science & Engineering, Oregon State University, Corvallis, OR.

Most of the research related to fungi of the Peruvian Amazon is focused on edible mushrooms and pathogens. Other important fungi, such as spalting fungi, are not broadly studied because most of them do not produce fruiting bodies, are difficult to locate, and do not present an immediate value to the forager. Finding spalting fungi involves a complete sampling of downed trees and branches in a given area through the opening of the xylem to identify potential pigmented and zone line producing fungi. This methodology was employed in the district of Las Piedras, Madre de Dios, Peru. Fungi suspected of causing internal pigment and zone lines were collected, cultured, isolated, and sequenced. The species found belonged to the orders of the Helotiales, Xylariales, Hypocreales, Russulales, Polyporales, Botryosphaeriales and two specimens of the class Leotiomyces. Most of the fungi produced pigments or zone lines in wild conditions and all of them were part of the wood decomposing fungi. Findings from this research will benefit Amazonian communities as well as Peru as whole, through identification and location of value-added wood products that can widen the commercial wood market currently focused on dark, old growth trees. This also gives more inherent value to the forest, potentially saving the land from being converted to plantation or pasture.

**Improving STEM student retention via early research engagement: a pilot.** *Michael Watters, Patrice Bouyer* Dept Biol, Valparaiso Univ, Valparaiso, IN.

We describe here the results of a pilot study, the goal of which was to expose freshman to an ongoing research project during the academic year to promote student growth and improve retention in the STEM disciplines. Freshmen worked with a faculty mentor and were also chaperoned by a more senior student researcher in order that they learn lab techniques and the capacity to work independently. Participants were fully engaged in a research project (performing experiments, analyzing and discussing results), not a classic classroom projects, but discovery based projects. By bringing students into the research lab at this early stage, our aim was to improve retention by allowing science students to actually *act* as scientists, providing an enhanced experience over the usual freshman survey course content. Of the 6 students who joined the program as freshmen, 5 are still in their major, 4 are still actively engaged in research with a faculty member and have co-authored 11 different papers and conference presentations as of their junior year.

**Genetic diversity of 100+ *Aspergillus* species - the aspMine analysis resource.** *T. C. Vesth*<sup>1</sup>, J. L. Nybo<sup>1</sup>, S. THEOBALD<sup>1</sup>, R. P. DE VRIES<sup>4</sup>, I. V. GRIGORIEV<sup>3</sup>, S. E. BAKER<sup>2</sup>, M. R. ANDERSEN<sup>1</sup> 1) Department of Bioengineering, Technical University of Denmark, Lyngby, Denmark; 2) Joint Bioenergy Institute, Berkeley, CA, USA, Berkeley, CA, USA; 3) Joint Genome Institute, Walnut Creek, CA, USA, Walnut Creek, CA, USA; 4) Fungal Physiology, CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands, Utrecht, The Netherlands.

The filamentous fungal species of the *Aspergillus* genus are of broad interest to the scientific community including applied, medical and basic research. These fungi are prolific producers of native and heterologous proteins, organic acids, and secondary metabolites (including

bioactives and toxins such as ochratoxin A). Because of these abilities, they represent a substantial economic interests in pharmaceutical, biotechnology, and bioenergy applications. In a project collaboration with the US Joint Genome Institute and JBEI we are de novo sequencing 300 different species of *Aspergillus* and establishing an online analysis platform for the scientific community, aspMine. The goal of this project is to develop a targeted tool to expand and improve our knowledge and expertise about this versatile group of fungi. At time of writing, 200 genomes are in various stages of sequencing and a bioinformatic pipeline has been established to analyze and store the data. This project covers a wide range of biologically interesting ideas surrounding the concept of speciation, such as genetic diversity, primary and secondary metabolism and proteome diversity. Complementary to the tools offered by FungiDB and JGI, the aspMine analysis resource offers tools for tracking genes and functions across species, allowing for investigation of shared genes and clusters across the genus as well as species- and clade-specific genes. The online platform also offers comparative analysis of secondary metabolism gene clusters with focus on synteny and functional conservation across species. The aspMine is implemented as a number of web applications created in R shiny, a graphical interface for analysis. The different tools are collected on a webpage which also includes method descriptions and relevant literature. The webpage is available from the beginning of 2016 and will be continually expanded. It is our goal to provide a comprehensive analysis platform for the community for comparative analysis of *Aspergillus* species.

**PHI-base - the Pathogen-Host Interactions database.** Kim Hammond-Kosack<sup>1</sup>, Alayne Cuzick<sup>1</sup>, Kim Rutherford<sup>2</sup>, Helder Pedro<sup>3</sup>, Martin Urban<sup>1</sup> 1) Dept of Plant Biology and Crop Sciences, Rothamsted Research, Harpenden, Herts, AL5 2JQ, UK; 2) Cambridge Systems Biology and Department of Biochemistry, University of Cambridge, Sanger Building, 80 Tennis Court Road, Cambridge, Cambridgeshire CB2 1GA, UK; 3) The European Molecular Biology Laboratory, The European Bioinformatics Institute, Hinxton, Cambridgeshire, CB10 1SD, UK.

The pathogen-host interactions database PHI-base ([www.phi-base.org](http://www.phi-base.org)) is a knowledge database. It contains expertly curated molecular and biological information on genes proven to affect the outcome of pathogen-host interactions reported in peer reviewed research articles. Genes not affecting the disease interaction phenotype are also curated. Viruses are not included. Here we describe a revised PHI-base Version 4 data platform with improved search, filtering and extended data display functions. Also a BLAST search function is now provided. The database links to PHI-Canto, a new multi-species author self-curation tool adapted from PomBase-Canto. The recent release of PHI-base version 4 has an increased data content containing information from >2000 manually curated references. The data provide information on 4460 genes from 264 pathogens tested on 176 hosts in 8046 interactions. Pro- and eukaryotic pathogens are represented in almost equal numbers. Host species belong ~70% to plants and 30% to other species of medical and/or environmental importance. Additional data types included into PHI-base 4 are the direct targets of pathogen effector proteins in experimental and natural host organisms. The different use types and the future directions of PHI-base as a community database are discussed.

Urban et al., (2017) PHI-base: A new interface and further additions for the multi-species pathogen-host interactions database. *Nucleic Acids Research* (database issue Jan 2017)

This work is supported by the UK Biotechnology and Biological Sciences Research Council (BBSRC) (BB/I/001077/1, BB/K020056/1). PHI-base receives additional support from the BBSRC as a National Capability (BB/J/004383/1).

**Advances in chemical genetic tools and impact on the research and development of novel crop protection products.** Siân Deller, Helen Carter, Helen Clake, Eileen Scott, Michael Csukai Syngenta, Jealott's Hill, GB.

Chemical control agents are likely to remain a part of the mixture of control strategies open to farmers for the foreseeable future. In order to support the discovery and development of new active ingredients a wide range of chemical genetic tools are utilised and are under constant development. Historically many of these tools used the model organism *Saccharomyces cerevisiae*, but improvements in genomic information and tools make it possible to perform research directly in field-relevant plant pathogens. Some of the wide range of tools used in support of new fungicide discovery will be outlined, including:

- Forward genetic tools, which have long been the mainstay of mode of action diagnosis, provide an unbiased approach for the identification of the molecular target of a chemical inhibitor. If resistant mutants can be generated, the technique can now be applied to any pathogen, providing a reference genome is available and single nucleus cells/spores can be isolated.
- Libraries of engineered model organism strains. Chemistry with lower resistance risk is often associated with the inability to isolate resistant mutants in the plant pathogen of interest. In this case unbiased genetic tools are still of value and model organisms are employed. Haploinsufficiency or overexpression-induced resistance within a yeast library can provide information on proteins or protein families targeted by novel chemistry. Hypotheses can then be based on the mutations seen, and compared to information from additional phenotypes such as biochemical pathway inhibition and microscopic observations.

The improvements in transformation procedures, genetic engineering techniques and availability of multiple selectable markers make it possible to test hypotheses in fungal pathogens of economic importance such as *Zymoseptoria*. Additionally, genes from any species can be tested in a uniform host cell background, for instance, by heterologous expression. Furthermore, these tools can be used to assess the lifetime of a new fungicide product. Mutations induced in the lab or discovered in the field can be assessed for their importance in different genetic backgrounds and an assessment made of the impact on sensitivity and fitness. Advancing molecular biology tools and understanding of phytopathogens are helping to inform and support the development of ever safer and more effective chemical crop protection strategies. How these tools have been used to study *Zymoseptoria* will be shown.

**Evolutionary and population genetics of culture collections.** K. McCluskey Fungal Genetics Stock Center, Kansas State University, Manhattan, KS.

Living microbe collections are established for a number of reasons including biodiversity, genetics, genomics, industrial and agricultural applications, and in support of patents. The Fungal Genetics Stock Center has holdings in support of multiple areas including genetics, genomics, and biodiversity. Having developed to support researchers using *Neurospora* and *Aspergillus*, the FGSC is more of a research resource repository and this is reflected in its narrow taxonomic scope. Similar collections include the Coli Genetic Stock Center, the Bacillus Stock Center, and the Chlamydomonas Center. Other collections, such as the ATCC and the USDA NRRL have much broader