

1000 fungal genomes to be sequenced

fungi: 1000genomes

As diverse decomposers, pathogens, and mutualistic symbionts, fungi have an enormous impact on human affairs and ecosystem function. Perhaps more than any other group of non-photosynthetic eukaryotes, fungi are essential biological components of the global carbon cycle. Collectively, they are capable of degrading almost any naturally occurring and manmade biopolymers. As such, fungi hold considerable promise in the development of alternative fuels, carbon sequestration and bioremediation of contaminated ecosystems.

The use of fungi for the continued benefit of society requires an accurate understanding of how they interact in natural and synthetic communities. The ability to sample environments for complex fungal metagenomes is rapidly becoming a reality and will play an important part in harnessing fungi for industrial, energy, climate and ecosystem management purposes. Our ability to accurately analyze these data relies on well-characterized, foundational reference genome data of phylogenetically diverse fungi. With recent advancements in next generation sequencing technologies, the sequencing of fungal genomes is more tractable and less expensive than ever. The result is that sequencing of fungal genomes is becoming a relatively routine approach to data collection for all

areas of mycology. This growth in genomics is resulting in a more integrated approach to biological research with basic tools of evolutionary biology (e.g., phylogenetic tree reconstruction, tests for selection, etc.) being central to comparative genomics. There exists a need, however, for systematic sampling of the Fungal Tree of Life to fully leverage our knowledge of fungal evolution and its application to genome-enabled mycology.

To bridge this gap, an international research team in collaboration with the Joint Genome Institute (JGI) of the US Department of Energy has embarked on a five-year project to sequence 1000 fungal genomes from across the Fungal Tree of Life. The team comprises Joseph Spatafora (Oregon State University), Jason Stajich (University of California at Riverside), Kevin McCluskey (Fungal Genetics Stock Center), Pedro Crous (KNAW-CBS Fungal Diversity Centre), Gillian Turgeon (Cornell University), Daniel Lindner (USDA Forest Service), Kerry O'Donnell and Todd Ward (USDA Agricultural Research Service), Antonis Rokas (Vanderbilt University), N. Louise Glass (University of California at Berkeley), A. Elizabeth Arnold (University of Arizona), Francis Martin (INRA, France), and Igor Grigoriev (JGI). The overall plan is to fill gaps in the Fungal Tree

of Life through the sequencing of at least two reference genomes from every accepted fungal family. One hundred species from 27 orders and 55 families will be sequenced in the first year of sampling (Tier One) with ~225 additional species sequenced every year for the next four years. At the centre of this sampling effort are the unique biological resources that are housed in living culture collections, which provide access to high quality vouchered material.

This is an exciting time as we move into the genomic era of mycology. This project has the core goal of providing reference information to inform research on comparative genomics, evolution of development, plant-microbe interactions, industrial mycology, and environmental metagenomic sequencing. Close cooperation with other large-scale genomic sequencing projects is underway and we envision building a network for global participation in the project. More information can be found on the project website (<1000.fungalgenomes.org>).

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The Ug99 stem rust (*Puccinia graminis*) of wheat threatens global supplies



Ug99 is an aggressive race of stem rust of wheat (*Puccinia graminis*) first discovered in Uganda in 1998. The discovery was startling to pathologists and wheat breeders because the pathogen could potentially overcome the genetic resistance built into over half the world's wheat crop. Ug99 is more dangerous than other rusts

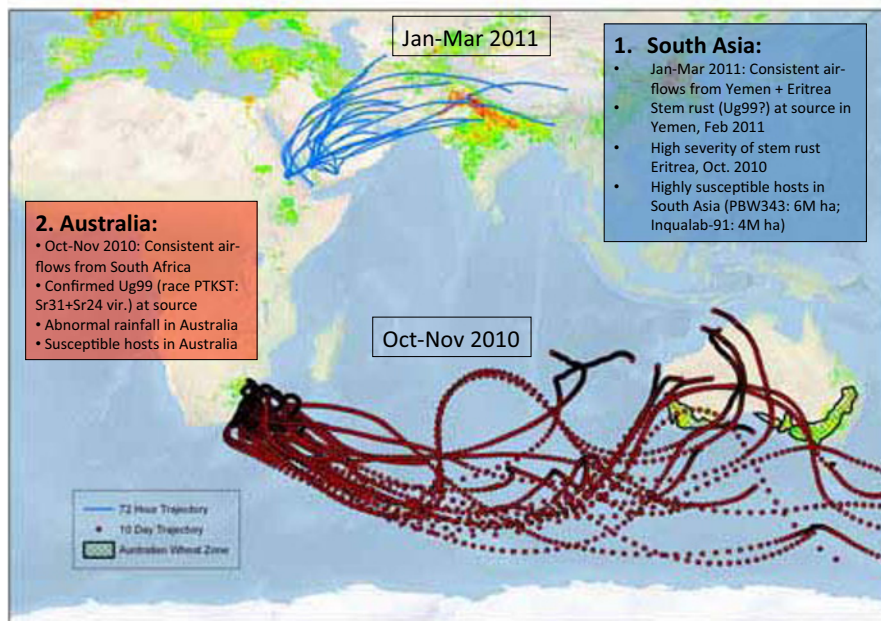
because of the number of resistance genes it is able to overcome.

The world is starting to take notice of this global threat to food security. For example, even though Ug99 has not reached the USA, the threat is so urgent that the United States Department of Agriculture (USDA) recently surveyed

Puccinia graminis race Ug99 on wheat. Photo Borlaug Global Rust Initiative.



World distribution of *Puccinia graminis* race Ug99 on wheat (November 2011). Courtesy Borlaug Global Rust Initiative.



Possible spread of *Puccinia graminis* race Ug99 on wheat. Prepared by David Hodson (CIMMYT).

and identified varieties of wheat that show Ug99 resistance in efforts to prepare for the possibility of a Ug99 outbreak in the USA. The Durable Rust Resistance in Wheat (DRRW) project, funded by the Bill & Melinda Gates Foundation and the UK Department for International Development, and administered at Cornell University, has been established with the mission to mitigate this threat to the world's wheat crop and avoid catastrophic losses. Two important DRRW objectives are pathogen surveillance and breeding wheat varieties that are resistant to the family of stem rust that includes Ug99, as well as stripe rust

(*P. striiformis*, syn. *P. glumarum*). New cultivated varieties must also improve farmers' yields to keep pace with a growing world population.

Ug99 is highly mobile, carried by wind or accidental human transmission. Because it does not recognize political boundaries, a surveillance system that is global in scope is necessary. The Global Cereal Rust Monitoring system is a coordinated network of national surveillance teams who collect standardized data from wheat fields in 20 countries in Africa and Asia. The surveyors note any instance of rust, collect a sample of the rust for genetic testing, and record

GPS data and other factors. These data are incorporated into a centralized database which allows researchers a bird's eye view of the track of the pathogen, which helps in predicting where it might go next.

Since its discovery in Uganda, Ug99 has spread north-easterly through Kenya, Ethiopia, crossed the Red Sea into Yemen and Iran, and is now currently threatening Pakistan (where 24 M tons of wheat were produced in 2009) and India (over 80 M tons). Both countries have large plantings of wheat that are known to be susceptible. Historical evidence of the movements of rust pathogens indicates that Pakistan and India are at-risk. Ug99 has also traveled south, down the eastern coast of Africa to South Africa. There is a chance it could travel via wind currents over the Indian Ocean into Australia.

Screening nurseries in Kenya and Ethiopia are key to the resistance breeding efforts. The nurseries are administered by CIMMYT (International Maize and Wheat Improvement Center), KARI (Kenya Agricultural Research Institute), and EIAR (Ethiopian Institute of Agricultural Research). Because Ug99 is present in east Africa, breeders from countries where Ug99 is not present send promising new wheat varieties to these nurseries for field testing. Wheat breeders at the nurseries plant the seeds, expose them to Ug99, and collect screening data based on the incidence and severity of infection. If a variety is not resistant to Ug99 it soon becomes apparent. Thirty countries have sent germplasm for screening to KARI and EIAR, and 225 000 lines of wheat have been screened since 2006.

Based on this screening process, 14 varieties of wheat that are resistant to Ug99 have been identified and are in testing with various national governments and seed programmes – and Ug99 resistant varieties have now been released in Ethiopia. Under an USAID (United States Agency for International Development) project, Ug99 resistant seed has been distributed to six countries. A total of 12 000 ha of resistant varieties of wheat have been sown in Nepal, Bangladesh, Afghanistan, Egypt, Ethiopia, and Pakistan.

Scientists on the DRRW project want to ensure that any new varieties released are not based on single gene resistance. Ug99, like any rust pathogen, has a great capability to

change and evolve through mutation or sexual recombination. In fact, eight variants of Ug99 have already been discovered. A wheat variety that only offers single gene resistance could be overwhelmed by Ug99 very quickly.

The DRRW project also supports the Borlaug Global Rust Initiative (BGRI), founded by Norman Borlaug in 2005. The

BGRI's mission is to reduce the world's vulnerability to rusts (stem, yellow, and leaf) and advocate for a sustainable international system for improving wheat yields and crop protection. The website for the BGRI (<globalrust.org>) is regularly updated and should be consulted for more information.

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A DNA barcode for *Fungi* proposed for adoption



although it is recognized that supplementary barcodes may need to be proposed for adoption in some circumscribed taxonomic groups.

The studies conducted involved the mitochondrial cytochrome c oxidase subunit 1, three regions from the nuclear ribosomal RNA cistron, regions of three representative protein coding genes (*RPB1*, *RPB2* and *MCM7*), nuclear ribosomal small subunit (SSU), and nuclear ribosomal large subunit (LSU) – but all were inferior to the ITS. A multiauthored paper, involving 148 researchers from 71 institutions, and describing the work carried out, is currently in revision in the *Proceedings of the National Academy of Sciences* of the USA, and is expected to appear shortly.

At a meeting of the Fungal Working Group of the Consortium for the Barcode of Life (CBOL) held in Amsterdam on 17–18 April 2011, it was agreed that a publication be prepared based on the studies carried out and which made a formal proposal to CBOL as to the barcode to be used for *Fungi* (see Schoch *et al.*, *IMA Fungus* 2: (5), June 2011). The results of an evaluation of six DNA regions by an international consortium using different groups of fungi, concluded that the internal transcribed spacer (ITS) region was the

most appropriate as it had the highest probability of successful identification of the regions within the ribosomal cistron across the broadest range of *Fungi*. This was particularly valuable as the region to adopt as while it was not successful in all cases, it was the region that most commonly provided a barcode gap between the levels of within-species and between-species sequence variation. This region is therefore now to be formally proposed for adoption by the Consortium for the Barcode of Life as the primary fungal barcode marker,

New world record for the largest fungal basidiome

A single basidiome of *Rigidoporus ulmarius* growing over the stump of an elm (*Ulmus* sp.) tree killed by *Ophiostoma novo-ulmi* in the grounds of the former International Mycological Institute at Kew (Surrey, UK) was accepted as the world's largest in the *Guinness Book of Records* for 1990. That specimen measured 1.56 × 1.37 m and had a circumference of 4.53 m in January 1993 (Aitchison & Hawksworth 1993). The basidiome continued to grow after that date, but it was never weighed, and subsequently deteriorated *in situ*.

Now, an even larger single basidiome has been discovered on Hainan Island in southern China which is described by Dai & Cui (2011). This is of another polyporaceous fungus, *Fomitiporia ellipsoidea*, found on the underside of a fallen trunk of *Cyclobalanopsis patelliformis* in virgin forest. This was judged to be 20 yr



A portion of the basidiome with Yu-Cheng Dai.

old and measured a massive 10.85 m long × 0.82–0.88 m wide and 4.6–5.5 cm thick, with a volume calculated as 409 000 – 525 000 cm³ and a fresh weight estimated at 400–500 kg. With some 452 million pores, in an editorial note at the end of the article Nick P. Money suggests that it would have been generating around one trillion spores per day!

Aitchison EM, Hawksworth DL (1993) *IMI: retrospect and prospect*. Wallingford: CAB International.

Dai Y-C, Cui B-K (2011) *Fomitiporia ellipsoidea* has the largest fruiting body among the fungi. *Fungal Biology* 115: 813–814.

A slice through a part of the basidiome showing the layers of pores.



International meetings planned to discuss fungal nomenclature

Following the dramatic revisions to nomenclatural rules for fungi enacted at the 2011 International Botanical Congress in Melbourne in July 2011 (Hawksworth 2011, McNeill *et al.* 2011, Norvell 2011), members of both the Nomenclature Committee for Fungi (NCF) and the International Commission for the Taxonomy of Fungi (ICTF) have received many questions about how mycologists should adapt to the changes. Precise responses must wait publication of the new *International Code of Nomenclature for algae, fungi, and plants* which is expected in mid-2012, but the need for coordinated action is clear. With that in mind, the executives of these two bodies have agreed to cooperate to ensure the efficient sharing of accurate and consistent information and to develop inclusive, open, and transparent procedures for acting on the changes.

Three major issues are:

- (1) the migration away from dual nomenclature, based upon nomenclatural priority, community consensus and the best interests of users, *via*
- (2) the development of 'Protected lists' of accepted names and their nomenclatural types, together with those competing synonyms (including sanctioned names), and in some cases lists of rejected names, *and*
- (3) the establishment of permanent subcommissions or temporary working groups focused on specific narrowly or broadly delimited taxa to develop and recommend names for the 'Protected' or 'Rejected' lists.

Logically, some of these working groups will be derived from the permanent Subcommissions or associated Commissions of the ICTF (*Aspergillus/Penicillium*, *Ceratocystis/Ophiostoma*, *Fusarium*, *Trichoderma/Hypocrea*). Others are yet to be formed, and we hope that many will self-organize among existing taxonomic communities, and identify themselves to the NCF and ICTF, who can then provide support and information.

As of this writing, four symposia are planned for 2012 to begin the process of sharing accurate information and formulate the expectations for the subcommissions and working groups:



CBS Symposium

CBS symposium: One Fungus = Which Name? 12–13 April 2012, Trippenhuis, Royal Netherlands Academy of Arts and Sciences (KNAW), Amsterdam, the Netherlands. This meeting, which will focus entirely on understanding the nomenclatural changes and developing plans for implementation, will be a mixture of keynote speakers, breakout sessions, and book launches. It is unclear whether there will be any side meetings among the ICTF Subcommissions or other working groups associated with this symposium, although both the IMA and the ICTF plan to hold general meetings. Check the CBS website (cbs.knaw.nl) for more information.



日本菌学会

The Mycological Society of Japan

Mycological Society of Japan, 56th Annual Meeting. 26–27 May 2012, Gifu University, Gifu. This meeting will include a 2 hour symposium, "The new nomenclature - what is going on and what should be done." Watch the MSJ website (mycology-jp.org) for more information. A subsequent "Forum on microbial databases for academia and industry," being organized by the Federation of Microbiology Societies, Japan (FEMS-Japan), is tentatively scheduled for 29 May 2012 in Tokyo and will include presentations on several mycological databases.



Mycological Society of America, Annual Meeting. 15–19 July 2012, Yale University, New Haven, CT, USA. This meeting will include a symposium, "The mycologist's guide to the new International Code of Nomenclature for algae, fungi, and plants." Preliminary plans are also underway for a satellite meeting of the ICTF Subcommission on *Fusarium* taxonomy (dgeiser@psu.edu) and a new *Hypocreales* working group to be held before or after the meeting (contact Amy Rossman, Amy.Rossman@ars.usda.gov). Watch the MSA website (msafungi.org) for more information.

Chinese Academy of Sciences, Institute of Microbiology Special Symposium: New era of fungal nomenclature. Tentative dates 9–10 August 2012, State Key Laboratory of Mycology, Beijing. Contact Dr. Cai Lei (mrcailei@gmail.com), and consult the June 2012 issue of *IMA Fungus* for more information.

We encourage organizers of other mycological meetings to consider adding sessions or symposia on nomenclature to their programs in 2012 in order to provide accurate information and encourage participation by mycologists in all countries.

The NCF and ICTF are interacting regularly with the curators of *Index Fungorum* and *MycoBank* to ensure that the data required for preparing Protected lists are available to working groups and the community as a whole. A nomenclatural database of connected anamorph and teleomorph genera should soon be placed on the IMA website (<IMA-Mycology.org>). We intend to develop a web-based mechanism so

that all mycologists can indicate their interest in specific taxonomic orders, in order to facilitate data sharing and the development of working groups.

The mandating of working groups, assurance of fair representation, avoidance of duplication of effort, and accommodation of overlapping areas of interest are a priority. Working groups are encouraged to identify themselves and to form preliminary working relationships. Subcommissions of the ICTF are expected to give these requirements top priority in their work plans, welcoming the participation of other interested mycologists who might not be formal members. Those interested in forming such groups or in sharing concerns should communicate with NCF Chair, Scott Redhead (scott.redhead@agr.gc.ca) and ICTF Chair, Keith Seifert (keith.seifert@agr.gc.ca).

Our goals are to ensure that all interested mycologists receive an accurate and complete understanding of the new nomenclatural rules so that anyone wishing to contribute may do so, and to define clearly the mechanisms and expectations for participation. The format, standardization and information requirements for the lists, and the approval of these final lists according to the requirements of the

Code is the mandate of the NCF. The ICTF, although focused primarily on fungi of economic importance, has an interest in facilitating the process for the broadest possible community. We welcome participation from all mycologists.

Hawksworth DL (2011) A new dawn for the naming of fungi: impacts of decisions made in Melbourne in July 2011 on the future publication and regulation of fungal names. *Mycologia* 1: 7–20; *IMA Fungus* 2: 155–162.

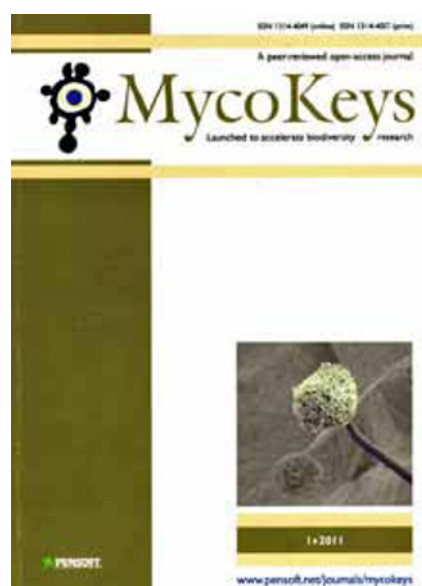
McNeill J, Turland N, Monro AM, Lepschi BJ (2011) XVIII International Botanical Congress: preliminary mail vote and report of Congress action on nomenclature proposals. *Taxon* 60: 1507–1520.

Norvell LL (2011) Melbourne approves a new *Code*. *Mycotaxon* 116: 481–490.

Scott Redhead (Chair) and
Lorelei Norvell (Secretary)
Nomenclature Committee for Fungi (NCF)

Keith Seifert (Chair) and
Andrew Miller (Secretary)
International Commission for the Taxonomy of Fungi (ICTF)

MycoKeys



The number of new mycological journals being produced continues to swell. *MycoKeys*¹ is a new open-access mycological journal

launched on 14 September 2011 with the aim of accelerating biodiversity research, swelling further the options open for mycologists to publish their research. A sister journal to the already launched *PhytoKeys* and *ZooKeys*, *MycoKeys* will consider works describing new taxa, taxonomic revisions, checklists and catalogues, phylogenetic analyses, biogeography, methodology, data mining and literature surveys, monographs, atlases, letters and points of view, conference proceedings and Festschriften, and data papers (manuscripts with large data sets). It is likely to be particularly attractive to authors of lengthy works or ones with many coloured illustrations. The philosophy of the journal is discussed further in a leading article (Lumbsch *et al.* 2011), which includes a vision of automated connections of included data to key global databases and repositories.

MycoKeys will be open-access and free

online to readers, though a few hard copies will be printed for archival purposes and deposited in key mycological libraries. Authors will, however, be able to purchase hard-copy offprints. There will normally be a fee of 15 € per page charge to authors, although this is being waived until September 2012 on articles of up to 20 pages, and for the first 20 pages of longer works. Thorsten H. Lumbsch has been appointed Editor-in-Chief, and the publisher is Pensoft Publishers of Sofia, Bulgaria. Further information can be found on the journal's website, <pensoft.net/journals/mycokeys>.

¹Not to be confused with the very successful *MycoKey* CD of keys to the genera of ascomycetes and basidiomycetes of Northern Europe produced by Thomas Læssøe & Jens H. Petersen (Version 2.1, 2006; Version 3.1 Funga Nordica Edition, 2008); see <www.mycokey.com>.

Lumbsch HT, Miller AN, Begerow D, Penev L (2011) *MycoKeys*, or why we need a new journal in mycology. *MycoKeys* 1: 1–6.