

# United States Culture Collections Network

2018 Meeting on collection Data | October 21-23, 2018 | Manassas, VA

*An NSF research coordination network for a community of ex situ microbial germplasm repositories*

**Meeting Location:** ATCC HQ | 10801 University Blvd. Manassas, VA 20110

**Hotel:** SpringHill Suites Centreville Chantilly, 5920 Trinity Parkway, Centreville, VA 20120-1915

## 2018 USCCN Meeting on Collection Data

**Tuesday, August 21, 2018**

9:30 AM Departure from Hotel to ATCC (for Steering Committee only)

10:00 AM **Steering Committee Meeting**

11:45 AM Departure from Hotel to ATCC (for attendees)

Noon **Lunch provided for all Attendees**

1:00 PM **Opening Session & Welcome**

Kevin McCluskey, USCCN  
Manzour Hazbon, ATCC

**Big Data and Culture Collections** (30 minutes each)

Public resources

Greg Riccardi **The NSF Initiative on Digitization: Advancing the Digitization of Biodiversity Collections and iDigBio**

Conrad Schoch **NCBI Taxonomy resources**

Persistent Identifiers

Anita Bandrowski, UCSD **Does the RRID initiative bring any value to stock centers?**

George Garrity, MSU **Making persistent connections between culture collections and research artifacts: the NamesforLife information architecture and web services**

Juncai Ma, IMCAS **A Global Catalog of Microbial Genome-Type Strain Sequencing Project of WDCM**

4:00 PM **American Type Culture Collection**  
Manzour Hazbón, ATCC **Overview of ATCC**

5:30 PM **Evening Dinner @ ATCC**

## Wednesday, August 22

8:45 AM Departure from Hotel to ATCC

9:00 AM Arrival at ATCC

9:30 AM **Implementing Data Standards** (30 minutes each)

Linhuan Wu, IM CAS

**A Proposed Specification on microbial data integration and publication in ISO TC 276**

David Nobles, UTEX

**Collection data in GBIF**

David Smith, CABI

**MIRRI data management and standards**

**Collection Updates** (20 minutes each)

Kimberly Webb,

**Backups at USDA NLGRP, Ft. Collins, CO**

Jessie Glaeser,

**US Forest Service Center for Forest Mycology Research, Madison WI**

Noon **Lunch**

1:00 PM Kyria Boundy-Mills,

**Positive impact of USCCN on the Phaff Yeast Culture Collection, UC Davis**

Hippokratis Kiaris,

**Peromyscus Stock Center, University of South Carolina, SC**

2:00 PM **Working Groups**

Posting data with iDigBio (and GBIF)

Implementing RRID Persistent identifiers

Support for generating genome DNA

Philanthropist support for USCCN

2019 CSBR RCN?

Evening Dinner on your own

## Thursday, August 23

8:45 AM Departure from Hotel to ATCC

9:00 AM Arrival at ATCC

9:30 AM **Collection Updates** (20 minutes each)

James Scott,

**UAMH update**

Todd Ward,

**An Update on the ARS Culture Collection (NRRL) and International Depository Authority**

Jennifer Normanly,

**Update on the UMass Amherst Plant Cell Culture Library: A "Biological Gold Mine" of plant natural products and pathways for biochemical and evolutionary studies**

Kevin McCluskey,

**FGSC update**

Catharina Alves-de-Souza,

**The Algal Resources Collection: an asset for the in the cultivation, maintenance, and identification of toxic microalgae**

David Smith, CABI, UK,

**CABI training for collection management and fungal recognition**

## Thursday, August 23, continued

Noon	Lunch
1:00 PM	<b>Reports from the Working Groups/Discussion</b> Posting data with iDigBio (and GBIF) Implementing RRID Persistent identifiers Support for generating genome DNA Philanthropist support for USCCN 2019 CSBR RCN?
3:00 PM	Adjournment

## Abstracts

### **The NSF Initiative on Digitization: Advancing the Digitization of Biodiversity Collections and iDigBio**

Greg Riccardi, Florida State University and iDigBio

The National Science Foundation committed \$10 million to Advancing the Digitization of Biodiversity Collections (ADBC) program from 2011-2021. The iDigBio project at the University of Florida and Florida State University serves as the hub of ADBC, with commitments to improving digitization practices, creating and sustaining communities, mobilizing data, and providing portal access to data. Digitization projects are funded through the Thematic Collection Networks (TCN). 20 TCNs have been funded so far. This talk will focus on the activities of iDigBio and the TCNs, the process of digitization and mobilization of biodiversity data, data standards, and the unique issues, challenges and opportunities for culture collections. Of particular interest is identifying strategies for culture collections to organize and mobilize data and to compete for ADBC funding.

### **NCBI Taxonomy Resources**

Conrad L. Schoch & Sharma Shobha NCBI/NLM/NIH

The International Nucleotide Sequence Database Collaboration (INSDC), is now more than 30 years old and comprise of three partners. These are the DNA Data Bank of Japan (DDBJ) at the National Institute for Genetics in Mishima, Japan; the European Nucleotide Archive (ENA) at the European Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI) in Hinxton, UK; and GenBank at the National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), National Institutes of Health (NIH) in Bethesda, Maryland, USA. A 1997 agreement to resolve taxonomic issues prior to the release of new data paved the way for the NCBI Taxonomy database to serve as a central organizing hub for the INSDC members. This database was thus intended for a specific, practical purpose - to provide nomenclature and classification information for the source organisms in the public sequence databases. This presentation will highlight and clarify recent improvements introduced to attain this goal.

### **Does the RRID initiative bring any value to stock centers?**

Anita Bandrowski, Ph.D., UCSD / SciCrunch Inc

The RRID is a persistent unique identifier that is based on the model organism database identifier for the animal or the stock center catalog number. The RRID initiative and associated infrastructure ensures the following: 1. persistence, i.e., making sure that the catalog data is backed up; 2. findability i.e., ability of authors prior to publication to search the SciCrunch website and find the RRID information, and 3. resolution of the RRID information whether or not the organism is available at the stock center. RRIDs include most of the standard vertebrate model organism stock centers (mouse, rat, zebrafish) as well as commonly used invertebrates (fly, worm) and cell lines, which are governed by ExPASy Cellosaurus database. Currently the RRID portal is pointed to by the instructions to authors for multiple journals across several of the major publishing groups including Cell Press, Society for Neuroscience, Wiley, Society for Endocrinology, eLife, the American Association for Cancer Research, Frontiers (Springer Nature), and BMC. RRIDs are found and curated by SciCrunch staff and made available as linked open data. RRIDs themselves, as they are used by authors substantially improve the "findability" of animals and other resource types (Bandrowski et al, 2016) and in several publishers they are routinely typeset so that the RRIDs are one click away from the stock center.

## **Making persistent connections between culture collections and research artifacts: the NamesforLife information architecture and web services**

George M. Garrity and Charles T. Parker, Michigan State University and NamesforLife, LLC, East Lansing, MI

A common problem in the life sciences is understanding the correct application of a name to an organism or higher taxon, especially in microbiology. Names provide a primary means of accessing the scientific, technical and medical (STM) literature, databases and other resources ranging from analytical platforms to culture collections. Names also serve as a concise way to summarize all that is known about a particular strain, a species or a higher taxon at a specific point in time, including revisions and emendations of prior taxonomies and names. Historically, taxonomists were affiliated with biological collections or other centers of excellence, but over the last 25 years, sequenced based methodologies significantly changed the way the science is practiced. Today, taxonomic revisions occur on a near daily basis and have outstripped the ability of end users, information and service providers and device manufacturers to keep pace. This has prompted calls from the end user communities to provide support for curation of taxonomic databases to ensure reproducibility to ensure reproducibility and replicability of results. But those calls fail to recognize the much larger need that extends across the entire field, from publishers to biological repositories and culture collections. Taxonomy has evolved a highly dynamic field and changes in our understanding must flow back into all of the resources from which our knowledge is derived. This is particularly challenging when much of that knowledge is captured in static form. NamesforLife is a unique information architecture and a proprietary system and method that was developed to resolve ambiguity in nomenclature that arises as a result of taxonomic revisions. This information architecture provides way to continuously monitor and track changes in a taxonomy and nomenclature to ensure that all of the underlying data are properly annotated and are persistently accessible, whether the current name or an earlier synonym is used in queries. NamesforLife services provide a means of continuously and effortlessly refreshing the published literature, databases and other resources via Digital Object Identifiers (DOIs) as part of a middle layer that correctly links together all of the key information. These services not only help to prevent a loss of knowledge, they also provide a way of reducing duplicated curatorial costs while improving overall information quality. In this presentation, I will discuss the NamesforLife Information Architecture, web services that are built on top of this architecture that were developed for the publishing industry, curated data resources (aka research artifacts) that are now created automatically through our information harvesting efforts, and derivative web services of relevance to culture collections. Those include a strain resolution service and web-analytical that allow monitoring of research artifacts (e.g., strains, sequences, other concrete and abstract research products), by individual and by institution, in real time. These latter services provide a novel and direct means of assessing the impact of research products by individuals and research institutions that are used by the community but rarely cited. NamesforLife provides a way to correct this deficiency and objectively assess the impact of curators and resource providers.

## **A Global Catalog of Microbial Genome-Type Strain Sequencing Project of WDCM**

Juncai Ma, World Data Center for Microorganism (WDCM), Institute of microbiology, Chinese Academy of Sciences (IMCAS), NO.1 Beichen West Road, Chaoyang District, Beijing 100101, China, +86-64807422, ma@im.ac.cn  
WFCC-MIRCEN World Data Center for Microorganisms (WDCM, <http://www.wdcn.org/>) has long been committed to facilitating the application of cutting-edge information technology to improve the interoperability of microbial data, promote the access and use of data and information, and coordinate international co-operation between culture collections, scientists and other user communities. To help plenty of culture collections that cannot make their data available online, WDCM launched the Global Catalogue of Microorganisms (GCM) (<http://gcm.wdcn.org/>) project in 2012. Up to now, GCM (<http://gcm.wdcn.org/>) has become one of the largest data portals for public service microbial collections and several international culture collection networks, providing data retrieval, analysis, and visualization system for microbial resources. Furthermore, GCM gradually developed into a knowledge base linking taxonomy, phenotype, omics data as well as relative scientific papers and patents with its catalogue information, which currently has aggregated 406,260 strains and other holdings (plasmids and antibodies) deposited in 120 collections from 46 countries and regions. Recently, WDCM announced the launching of Global Microbial Type Strain Genome and Microbiome Sequencing Project in the 7th WDCM Symposium, marking the GCM project has begun to enter a new stage (GCM 2.0). Focused on exploring the genomic information of microorganisms, this project has planned to sequence all uncovered prokaryotic type strains together with select eukaryotic type strains, construct a database for genomics data sharing, and also provide online data mining environment. Working groups responsible for selecting bacteria and fungal strains, drafting SOP, managing intellectual property right and legal issues and constructing database have already embarked on the the pioneer stage of GCM 2.0, scheduled to last until May 2018. The project will establish a cooperation network for type strain sequencing and functional mining, covering more than 30 major culture collections of 20 countries, and complete genome sequencing of over 10000 species of microbial type strains in five years.

## **A proposed Specification on microbial data integration and publication in ISO TC 276**

Linhuan Wu, World Data Center for Microorganism (WDCM), Institute of microbiology, Chinese Academy of Sciences (IMCAS), NO.1 Beichen West Road, Chaoyang District, Beijing 100101, China, +86-64807422, wulh@im.ac.cn

Different culture collections use their own data form for in-house data management and also online data sharing, which greatly hinder the further data exchange and integration globally. As a result, it is difficult for all the clients and potential users to access the information of microbes preserved in mBRCs, which severely impedes the further exploitation of the microbial resources in academia and bioindustries. This is especially true for the biotechnology companies focusing on microbial resource development that depend to a great part on the deep utilization of their own and external resources by tapping into the huge body of data. Therefore, our team proposed an international standard project “Biotechnology — Data management and publication in microbial biological resource centers” in ISO technical committee 276 Biotechnology, which aims at realize accurate, reliable and cost-efficiency data access, exchanges and integrations between mBRCs and between mBRCs and the users. It specifies requirements for the data management workflow and information which should be recorded in the in-house database of a microbial resource centre, and also specifies criteria for the data sharing of online catalogue, including minimum dataset and recommended dataset which will be used for the data publication. With the joint efforts of our project team with experts from both WDCM and ISO/TC 276 WG2 and WG5, this new project was proved unanimously in a 2-month CIB ballot of ISO/TC276 and registered into its work programme in July 2017. And this project is scheduled to develop into an ISO standard in a 3-year period and it has been registered as ISO/WD 21710 in June 2018.

## **MIRRI data management and standards**

David Smith, CABI, UK

The Microbial Resource Research Infrastructure (MIRRI) stresses the importance of access to microbial data as well as to high quality microorganisms in the execution of sound science and innovative research and development. MIRRI’s mission is to remove fragmentation in resource and service availability and focus on fundamental needs and challenges that face the microbial domain Biological Resource Centres (mBRCs) and the user of microorganisms. MIRRI aims to provide a single access entry point to state-of-the-art microbial biological services and to expert and technical platforms to enable researchers to carry out in-house research on mBRC holdings. This requires improvement in the interoperability between mBRCs and overarching, as well as complementary data offers and the implementation of quality management including standardised procedures, best practices and appropriate tools to increase the quality of the resources collected and their associated data as well as performed services. MIRRI is currently establishing its legal entity through a European Research Infrastructure Consortium (ERIC). Portugal and Spain will be the host countries of MIRRI’s headquarters. MIRRI will be established as a not-for-profit legal entity following a distributed model with a Central Coordination Unit (CCU) accommodating the operational headquarters and the national nodes bringing together the partners and stakeholders in each member country. MIRRI Statutory Seat will be located in Portugal (University of Minho, Braga) and the Collaborative Working Environment hub operated from Spain (University of Valencia, Paterna) and supported by LifeWatch-Spain, a closely related e-infrastructure. Seven prospective countries are establishing the ERIC (Belgium, France, Greece, Latvia, Poland, Portugal and Spain). MIRRI partners follow common protocols on data management for mBRC holdings that will enable users to access the microorganisms’ yet unrecognised potential, deliver regulatory compliance and facilitate knowledge and technology transfer. One of the most fundamental problems of managing a collection of microorganisms is keeping pace with the taxonomy and resultant name changes being introduced for species. To overcome such problems MIRRI has produced a data policy and strategy in order to establish an integrated portal for mBRCs (Smith et al. 2017). A prime objective of MIRRI is to unite and provide universal access to the information available in European public collections of microorganisms through a dynamic Information system. In this context, the desired outcome would include a repository for microbial domain Biological Resource Centre (mBRC) catalogues in a common format, the validation of catalogue contents to provide quality data, the interconnection of domain information systems for data extension, a unique portal for catalogues and associated data and an interoperable system based on Application Programming Interfaces (APIs) and service based interfaces and workflows. The architectural design of the system foresees the adoption of a standard format for exchanging data between CCs, a Minimum Data Set for essential data, to evolve into Minimum Information about Biological Resources, a user-friendly interface, as well as APIs and services/workflows for integration software. A five-year plan for the implementation of the MIRRI information system has been defined. The four main lines included in the plan are data curation, interoperability, applications development and IT competence. Data curation is meant to be developed by the progressive adoption of Standard Operating Procedures, able to lead user catalogues from the current Minimum Data Set to a structured extended data set and finally to data sets fully compliant with Minimum Information about Biological Resources guidelines, still under definition. Interoperability

will lead current separated catalogues to interact with an integrated repository of reference data which will finally allow user access to all catalogues through a common portal (Romano et al. 2017).

Romano, P., Smith, D., Bunk, B., Vasilenko, a & Glöckner, F.O. (2017). PeerJ Preprints |

<https://doi.org/10.7287/peerj.preprints.2815v1> | CC BY 4.0 Open Access | rec: 17 Feb 2017, publ: 17 Feb 2017

Smith D, Stackebrandt E, Casaregola S, Romano P, Glöckner FO (2017) MIRRI Recommendations for Exploiting the Full Potential of Microorganism Data. *Ann Biom Biostat* 4(1): 1027.

### **An update on the Center for Forest Mycology Research (USDA – Forest Service) culture collection and herbarium.**

Jessie A. Glaeser, US Forest Service, Forest Products Laboratory, Madison, WI

The Center for Forest Mycology (CFMR) herbarium and culture collection constitute a library of the fungal kingdom that is used by researchers throughout the world as reference specimens. The culture collection includes approximately 20,000 living cultures representing 1,600 species of fungi. The associated herbarium contains approximately 50,000 dried specimens representing 3,500 species, including about 300 type specimens, with many dating back to the early 1900's. Many of the cultures have their associated dried fruiting bodies housed in the herbarium. While many of these fungi are wood-decay fungi, the collection also contains mycorrhizal species, litter decay fungi, soil inhabiting fungi, fungi associated with bats and other wildlife, as well as representatives from many other ecological groups. Since most of these fungi do not produce large numbers of spores, they are kept in liquid nitrogen. The working collection is kept at 4°C in sterile, distilled water and transferred approximately every seven years. The database for the collections has recently been updated with a newly redesigned web page that will be released shortly. It is also now listed with the Mycobank portal:

(<http://mycoportal.org/portal/collections/misc/collprofiles.php?collid=47&stat=geography#geographystats>). In

August, 2018, Dr. Daniel Lindner ([dlindner@fs.fed.us](mailto:dlindner@fs.fed.us)) became the Project Leader of research work unit,

“Restoration and Conservation of Rural and Urban Forests,” the larger unit through which CFMR is administered.

Dr. Lindner has a long commitment to mycology and to maintaining the integrity of the collections. Dr. Beatriz

Ortiz-Santana ([bortizsantana@fs.fed.us](mailto:bortizsantana@fs.fed.us)) has recently become the CFMR Team Leader and is the contact person for both the culture collection and the herbarium. The future of the collection is in good hands.

### **Positive impact of USCCN on the Phaff Yeast Culture Collection, UC Davis**

Kyria Boundy-Mills, Curator, Phaff Yeast Culture Collection

The US Culture Collection Network has positively impacted numerous microbe culture collections since its inception in 2012. The Phaff Yeast Culture Collection at the University of California Davis is among the many beneficiaries of this organization. This yeast collection, curated by Dr. Kyria Boundy-Mills, is the fourth largest of its kind in the world, with over 7,500 strains belonging to over 1,000 different yeast species. The collection is more stable, more efficient and more visible thanks to USCCN. Discussions with other curators have helped shape Phaff collection pricing structures, acquisition and distribution policies, database management, and publicity and outreach practices. Curators shared strategies for engagement of undergraduate students in the first USCCN meeting in 2012 in Kansas City. Learning of quality control practices and ISO certification steps were a particularly useful outcome of participation in the 2012 MIRRI Kickoff Meeting in Braunschweig, Germany, arranged through USCCN. In 2013, Phaff collection curator Kyria Boundy-Mills was elected to the executive board of the World Federation for Culture Collections, thanks to connections made through USCCN. Also thanks to these connections, the Phaff collection public catalog was incorporated into the Global Catalog of Microorganisms, bringing worldwide visibility of the holdings of the Phaff collection. In 2014, the USCCN meeting connecting culture collections to genome sequences was hosted at UC Davis. The Phaff collection is providing yeasts and data for two 2018 applications to the JGI Community Sequencing Program. Thousands of Phaff collection yeasts are now cryopreserved off-site at the site of the 2015 USCCN meeting at the USDA National Laboratory for Genetic Resource Preservation in Fort Collins, Colorado. Remote storage of the yeast collection is reassuring as the curator watches the ashes from nearby wildfires land on the UC Davis campus. Exploration of the complexities of the Nagoya Protocol at the USCCN meeting in DC in 2017 led to a manuscript co-authored by Boundy-Mills and other meeting participants that was published in *Microbe Magazine* of the American Society for Microbiology, the largest life science professional society in the world, as well as a presentation at the ASM annual meeting in 2017. The geographic origin and year of isolation of most Phaff collection yeasts has now been updated in the database, allowing users to determine restrictions on use. The Phaff collection is grateful for all of these benefits and hopes they can continue into the future.

### **The Peromyscus Genetic Stock Center at the University of South Carolina**

Hippokratis Kiaris, Peromyscus Genetic Stock Center, University of South Carolina, SC, USA.

The University of South Carolina hosts for more than 30 years the Peromyscus Genetic Stock Center (PGSC). The major mission of the PGSC is to supply animals of the genus *Peromyscus* to external investigators worldwide, to be used in research. Research areas at which *Peromyscus* finds great utility are speciation, stress response, altitude adaptation, behavior adaptation in the context of physiology and evolution, host-parasite interactions, microbiome-associated studies and others. In addition, the PGSC's-associated personnel consults with external users and performs as "work for hire" simple research tasks such as tissue harvesting, administration of special diets, selective breeding of particular species, and others. In addition, several undergraduate students, graduate students and postdocs, as well as junior and more senior faculty are being trained in the PGSC in rodent research in general and *Peromyscus* research in particular. Most of the users are academic institutions-based investigators while private companies and other government organizations occasionally request and receive *Peromyscus* animals. The major *Peromyscus* species that are held and supplied by the PGSC are *P. leucopus*, *P. maniculatus* (both low and altitude populations), *P. eremicus*, *P. polionotus* and *P. californicus*, all of which are maintained as outbred stocks. In addition, the Center maintains a number of coat color and neurological mutants. The Center communicates with the communities of interest via its web site, a newsletter it publishes twice per year and more recently by the yearly *Peromyscus* Symposium it organizes. The operation of the PGSC is facilitated by grants from the National Science Foundation, as well as by the income generated from the animals provided to the users.

### **An Update on the ARS Culture Collection (NRRL) and International Depository Authority**

Todd Ward, USDA ARS, NCUAR, Peoria, IL

The USDA's Agricultural Research Service Culture Collection, also known by the original acronym for the Northern Regional Research Lab (NRRL) in Peoria, IL, is one of the largest public collections of microorganisms in the world, and currently maintains more than 98,000 strains of bacteria and fungi. This includes more than 7,000 strains held in the ARS Patent Culture Collection, an international depository authority under article 7 of the Budapest Treaty. This collection facilitates technological innovation by enabling scientists to simultaneously fulfill microbial culture deposition requirements in association with patent applications in the United States and internationally. The major goals of the ARS Culture Collection are to conduct and support microbiological research that advances agricultural production, food safety, public health, and economic development. These goals are pursued through in-house research that improves understanding and utilization of microbiological diversity and through efforts to enhance the value and accessibility of microbial germplasm in the Agricultural Research Service Culture Collection (NRRL). NRRL cultures have contributed to scientific advances reported in more than 65,000 scientific publications and patents.

### **Update on the UMass Amherst Plant Cell Culture Library: A "Biological Gold Mine" of plant natural products and pathways for biochemical and evolutionary studies**

Jennifer Normanly, Principal Investigator Li Jun Ma, Co Principal Investigator Tristram Seidler, Co Principal Investigator  
The University of Massachusetts Amherst (UMass) seeks improve a large Plant Cell Culture Library (PCCL), which was donated to the university from industry, and to make the PCCL available to the research community. The PCCL includes over 2200 unique plant species--the largest and most diverse collection of plant cell cultures in the world, and the only such collection in the western hemisphere. The specific aims of the project are 1) to streamline culture maintenance protocols and optimize procedures for rapid culture scale-up and dissemination to the research community, 2) to modernize the PCCL computer database and develop a web interface for the research community, and 3) to develop a sustainable model for maintaining and distributing PCCL materials. It is a critical to accomplish these goals now in order to insure its broad availability to the research community.

### **An update on the status of the FGSC**

Kevin McCluskey, Fungal Genetics Stock Center, Department of Plant Pathology, Kansas State University, Manhattan, KS  
After over 60 years of continuous support by the US National Science Foundation, the Fungal Genetics Stock Center has transitioned to University support. That support has been contingent on continued revenue generation and impact. Originally, including salary for a professional curator and research assistant, fiscal limits meant that the research assistant was only supported for two years and is no longer available to the center. Because the collection needs to generate revenue on a cost recovery basis, fees were raised. As an experiment in micro-economics, this had the predictable outcome of encouraging peer-to-peer exchange and distribution of individual wild-type, classical mutant, and gene deletion mutant strains from the FGSC collection dropped precipitously. Because the FGSC had engaged new communities since 2007, revenue for distribution of arrayed sets of gene deletion mutants of *Cryptococcus neoformans* and *Candida albicans* has supported a modest revenue stream, although not enough to support any full-time staff.

## **The Algal Resources Collection: an asset for the in the cultivation, maintenance, and identification of toxic microalgae**

Catharina Alves-de-Souza, Algal Resources Collection, MARBIONC at Crest Research Park, University of North Carolina Wilmington, 5600 Marvin Moss K. Lane, Wilmington, NC 28403

The Algal Resources Collection (ARC) was formally established as a public service collection in September 2016, although it had been operating as a private research collection since its initial inception in 1987. Our main goal is to be a resource to both the HAB research community and to biotechnology endeavors. Presently, the collection is a major supplier of toxic algal strains for researchers all over the world, with many collaborations, loans and exchanges initiated each year. Focused on the growth and maintenance of toxic microalgae, the ARC currently houses 412 strains distributed across 10 taxonomic groups, 50 genera, and 102 species. Although the majority of the collection is comprised of Dinoflagellates (63%) and Raphidophytes (23%), other taxonomic groups are also represented, including Haptophytes (7%), Cryptophytes (2%), Dictyochophyceans (1%), Diatoms (1%), Cyanobacteria (1%), Eustigmatophyceans (1%) and a few others (1%). About 80% of our cultures have been classified as harmful taxa with known toxin production, found in association with toxic species, or related to known toxin producers. ARC strains originate from diverse locations around the globe, from tropical and temperate climates. These include type cultures used in the description of new species and a new algal class currently under description. ARC strains have been used in various applied research studies, some of which led to the development of advanced bioassays, used for detecting and quantifying marine algal toxins. ARC strains have also been the source from which new bioactive compounds have been discovered and utilized to produce new pharmaceuticals that now treat or cure a variety of diseases. The collection was recently awarded a National Science Foundation (NSF) award that will facilitate the necessary adjustments to take the final step towards its consolidation as a research resource and to achieve the self-sustainability necessary for its maintenance and expansion. An overview of the species diversity, bioreactor culturing, and collaborative opportunities will be presented.

## **CABI training for collection management and fungal recognition**

David Smith, CABI, UK

CABI scientists provide training in molecular identification of microorganisms, morphological identification of fungi, microbial techniques, isolation methods for fungi and bacteria, plant pathology, biological control and preservation of microorganisms. A course entitled Isolation and identification of environmental fungi will be run 13 - 15 November 2018. This course provides expert tuition in isolating and culturing fungi from environmental sources, identifying at least 20 common fungal genera by morphology and providing information on hazard status of key environmental and laboratory species. It is targeted to those working in the pharmaceutical, food and biotechnology industries; laboratory personnel involved in quality control of clean rooms, products and industrial processes; technical staff working in environmental mycology and conservation personnel in the heritage sector. Participants will receive, a comprehensive course manual, powerpoint lectures, authoritatively named cultures and practical demonstrations. Free slide boxes will be provided to take away labelled slides prepared during the course. Lectures and digital images will be provided on a memory stick. CABI has developed e-learning tools to enable courses to be followed in the participants own surroundings to reduce travel costs but also to be used in conjunction with the laboratory training. For example Managing Microbes was produced to ensure participants arrive at CABI for the course on collection management and preservation of fungi with a similar level of background knowledge so that the course can focus on laboratory based work to give best value for the time spent at the CABI facilities. Another e-learning experience is given through the PestSmart Diagnostic Course which takes the participant through a learning experience of plant disease symptoms and shows how these differ according to causative organism and from plant nutritional deficiencies as causes of symptoms. Once a practitioner has an idea of what causative organism they are looking for the plant specimen can be examined, obligate pathogens can be observed and their characteristics used to identify them or organisms can be isolated and grown and then identified. CABI courses link together to enable basic techniques and basic identification skills to be learned. CABI provides a vast range of information products to provide further information and allow participants to extend their knowledge. The Plantwise knowledge bank is a global resource that provides country- or region-specific plant health information. Through this you can use the diagnostic tool to find out what problem might be affecting your crop; use the site search to find information on management of pests and diseases and use the map to view the distribution of up to three pest or crop species at a time <https://www.plantwise.org/KnowledgeBank/home.aspx>. CABI's bibliographic databases, including CAB Abstracts and Global Health with over 11.4 million records can be accessed to provide relevant information as can the 70 data resources available at <http://www.cabi.org/publishing-products/online-information-resources/>