

Keynote speech

Omics-driven Synthetic Biology Power for Reviving the Natural Products

Legend

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Abstract

Current knowledge on natural and engineered biosynthesis of diverse classes of natural products like antibiotics at levels of genomics, proteomics, metabolomics, metabolic engineering, combinatorial biosynthesis and synthetic biology are now providing the wonderful new opportunities for generating novel antibiotic compounds or optimized biopharmaceutical derivatives. By focusing on the representative and well-studied antibiotics from our labs as examples, I will summarize some of the recent mechanistic and technical advances, ranging from using traditional approaches toward the concept of synthetic biology for natural products research. The great potential of Omics-driven synthetic biology approaches for creative structural modification and innovative production of fine chemicals and natural products will be demonstrated.

Keynote speech

WDCM, past and another 50 years to come

Sugawara Hideaki

Professor of National institute of Genetics, Japan

Abstract

Microbial culture collections (MCCs) and the World Data Center for Microorganisms (WDCM) together had trod through a long and winding road.

In 1966, UNESCO organized a meeting of experts to promote MCCs. The participants immediately recognized that they were not able to develop a strategic plan for MCCs without comprehensive information on existing MCCs and their holdings. The International Association of Microbiological Societies (IAMS) Section on Culture Collections agreed to prepare a World Directory of Cultures of Microorganisms. The first edition of the World Directory was actually compiled by Professor V. B. D. Skerman and his staffs at the University of Queensland in Brisbane, Australia and the second edition of the World Directory followed on 1982. Thus the Brisbane team established the World Data Centre for Microorganisms (WDCM). In the meantime, the IAMS Section on Culture Collections became the World Federation for Culture Collections (WFCC).

In 1984 at the 5th International Congress of Culture Collections (ICCC) in Bangkok, WFCC advertised for a new host institute to sustain WDCM after the coming retirement of Professor Skerman. WFCC chose via open bidding the Institute of Physical and Chemical Research (RIKEN), Japan to be the new host. In 1986, WDCM was relocated to RIKEN and managed by Professor Kazuo Komagata and subsequently by the author. In 1997, WDCM at RIKEN was further transferred to the National Institute of Genetics (NIG), Japan shortly after the author moved from RIKEN to NIG. The transfer was carried out based on agreements among WFCC, RIKEN, NIG and Japan Society for Culture Collections (JSCC). WDCM in Japan created and maintained an online system for the registration and dissemination of information on MCCs and their holdings, and Web site as well.

In addition to the computerization of WDCM, the author contributed as a chair of a Task

Force on Biological Resource Centres in OECD to the development of the Microbial Resources Centres (MRCs) concept, taking into consideration of three major factors that would impact MCCs in the 21st century, namely, biodiversity, genomics and informatics. The OECD finally published two reports of “Biological Resource Centres – underpinning the future of life sciences and biotechnology” in 2001 and “OECD Best Practice Guidelines for Biological Resource Centres” in 2007.

In 2011, WDCM found a new home in the Institute of Microorganism, Chinese Academy of Sciences (IMCAS) based on another open bidding when the author retired from NIG. It was Déjà vu. The 3rd generation of WDCM at IMCAS has already created innovative services such as Analyzer of Bio-resource Citations (ABC) and Global Catalogue of Microorganisms (GCM).

Then, what will be the 4th generation of WDCM (WDCM 4G)? Databases essentially mirror the real world. WDCM is expected to evolve as MRCs evolve and vice versa. It is still true that the three factors, biodiversity, genomics and informatics, impact WDCM and MRCs, but the scale and diversity of the impact will surpass our imagination in 50 years to come. We have already observed sequencing of thousands of strains from a single species, researches on metagenomics and unculturable strains, development of synthetic microbial genomes and their application to biotechnology, and elucidation of architecture and functions of microbial communities for human health. Whatever the impact is, WDCM 4G will be the information hub of heterogeneous multi-layer real world to support MRCs and their users.

Keynote speech

WDCM in new era

Juncai Ma

Director of World Data Center for Microorganisms

Institute of Microbiology, Chinese Academy of Sciences, China

Abstract

Microbial resources are one of the most important natural resources in the world, which is the scientific basis to support the development of biotechnology and life sciences. WFCC-MIRCEN World Data Centre of Microorganisms (WDCM), which once hosted in Australia and Japan and then moved to China in 2010, plays a crucial role in providing a database of microorganisms, analysis of the function and establishing a platform of international communication.

WDCM launches the international project Global Catalogue of Microorganisms (GCM) to construct a data management system and a global catalogue to help organize, unveil and explore the data resources of culture collection worldwide. GCM provides a comprehensive view on the microbiological material made accessible online by public collections, and the function of Analyzer of Bio-resources Citation.

Future developments such as “BIG DATA” technology including semantic web or linked data will allow the system to provide more flexible data integration broader data sources. Linking WDCM strain data to broader data sets such as environmental, chemistry and research literature can add value to data mining and targeting microorganisms as potential sources of new drugs or industrial products.

Cooperation with other organizations and institutions promoted broad utilization of WDCM data platform. The WDCM is exploring collaboration with the World Health Organization (WHO) for the establishment of a database allowing influenza virus information integration. Moreover, the WDCM database is able to provide services for the implementation of the TRUST code of conduct to allow culture collections to comply with the Convention on Biological Diversity and Nagoya protocol for Access and Benefit Sharing. The unique strain

identifier available through the WDCM will and the further utilization of information extracted by ABC implements key provisions of the Nagoya Protocol and provides required transparency, legal certainty while lowering transaction costs and reducing administrative and governance burdens.

The WDCM will work with Research Infrastructures, Publishers, Research funders, Data holders and individual collections and scientists to ensure data interoperability and provide the environment for enhanced tools for research and development. WDCM is prone to evolve and continue.

Keynote Speech

WDCM: the sum of all efforts and much more Get the right information at any time

Philippe Desmeth

*President of World Federation for Culture Collections (WFCC),
Belgian Science Policy Office, Belgium*

Abstract

In 1966, when Professor Victor B. D. Skerman (University of Queensland, Australia) and his colleagues started the World Data Centre for Microorganisms (WDCM), they had in mind to help their fellow scientists find the right microbiological material and related information in due time.

The World Federation for Culture Collections (WFCC) needed comprehensive information on culture collections and their holdings worldwide. WDCM started the development of an international database on culture resources and the first edition of the World Directory of Collections of Cultures of Microorganisms (CCINFO) was published in 1972. It was about facilitating access to the culture collections. Floppy disks had just been introduced commercially in 1971; the IBM System 370 performed 0.64 Million of Instruction per Second at 8.696 MHz; nowadays, personal computer Central Power Units give us a speed of about 4 GHz, 4 billion calculations per second.

In the 1980's, WDCM was again on the frontline, aiming at facilitating access to microorganisms and related data. Data storage and data management had to be optimized to allow publication of users-friendly catalogues where scientists could retrieve both raw materials for their research and related data. Projects such as Microbial Information Network Europe (MINE) contributed to define the database structure and catalogue standards in microbiology.

When Professor Skerman retired in 1986, WDCM moved to the Japan Institute of Physical and Chemical Research (RIKEN) under leadership of Professor Kazuo Komagata and later of Dr. Hideaki Sugawara. In 1987, the most common formatted capacity was advertised as "1.44

MB" and displayed as "HD" for High-Density" format. Today, Terabyte hard disks are marketed for less than 100 USD.

In the 1990's, it was about data publishing and data sharing. WDCM was next to the cradle of Internet and ready for it when Tim Berners-Lee of CERN (European Organization for Nuclear Research) started the World Wide Web in 1989. The WDCM at RIKEN made the World Directory CCINFO database open to the public via a Packet Switching System and then via the Internet using a Gopher system.

In April 1997, it was agreed to transfer WDCM from RIKEN to the National Institute of Genetics (NIG), when Dr. Hideaki Sugawara moved to the Center for Information Biology and DNA Data Bank of Japan, NIG. WDCM at NIG dropped the Gopher service and concentrated on providing Web-based services.

In the year 2000, internet got mature. When Professor Sugawara retired he looked to instill new life to WDCM, he handed the destiny of WDCM over to Dr. Juncai MA, present Director of WDCM and of the Information Center at the Institute of Microbiology, Chinese Academy of Sciences (IMCAS).

At present, well into the 21st century, it is about big data, dealing with volume exceeding Exabyte (10^{18}) of data, real-time accessibility, merging of a variety of data, and ensuring the accuracy of these huge pools of data, many of importance for advancement of science and production of socio-economic value.

Dr Ma and his team launched the Global Catalogue of Microorganisms; they want to involve as many partners as possible into this worldwide action, not only people from culture collections but the entire microbiologists' community, not only academics but also companies' research teams. WDCM is connecting upstream and downstream research, underpinning cumulative research, providing secured access to reliable, valuable, relevant data related to microbiological material, contributing to build a sustainable and equitable knowledge based bio-economy.

Fifty years ago, WDCM was ready for databases structuring and management. In the 1990's, WDCM went online at the very beginning of Internet. Now and in the future WFCC rely on WDCM and its host institute to meet the challenges, to strive in the big data and beyond. WDCM is much more than the sum of a succession of efforts; it is a driving force, a source of innovation in bioinformatics, at the frontline of ICT development.

Keynote speech

Dynamic Changes of Marine Microbial Communities over Time

Takashi Gojobori

Vice President of CODATA,

King Abdullah University of Science and Technology, Japan

Abstract

Marine metagenomics is a study of examining microbial communities in the sea of interest by directly sequencing genomic DNA fragments from seawater samples. The so-called NGS (Next-Generation Sequencing) technologies have enabled us to sequence a tremendously large amount of DNAs that have been isolated from the sea periodically, say every two weeks or every month. When we focus upon the sea surrounding Japan islands and the Red Sea in the Middle East, our marine metagenomics studies revealed very interesting features of time-changes of microbial diversities in the two different sea regions. In particular, the Red Sea is regarded as a model of the global warming sea because of high water temperature and salinity. A comparison of the time-changes in microbial diversities between the two seas gives us a significant hint of possible influences of the global warming effect to marine microbial communities.

Keynote speech

Identifying the micro from the peta: tales of big data in the micro world

Nikolaos C. Kyrpides

Prokaryote Super Program Head, U.S.

Department of Energy Joint Genome Institute (DOE JGI), USA

Abstract

Shotgun sequencing of environmental samples has revealed a new universe of microbial communities (metagenomes) involving previously uncultured organisms, which is expected to further advance our understanding the structure and function of entire microbial communities and expand our current knowledge of genetic and functional diversity of individual microorganisms. Although most metagenomic studies aim to unveil the genetic and functional novelty present in various environments, current best practices in metagenome analysis tools, and workflows, are suffering from a number of pitfalls, impairing the fulfillment of this objective. I will present some of our approaches enabling the exploration of large metagenomic datasets and the discovery of novelty.

Keynote speech

Beyond sequencing

Ye Yin

CEO of BGI Genomics Co. Ltd., China

Abstract

As gene technology develops very rapidly these years, people are beginning to realize how it's going to influence their life, and somehow it becomes a Hi-Tech fashion. Ever since President Obama announced Precision Medicine as a new focus, public healthcare is undergoing an unprecedented change, coming with a burst of big data processing. Now that sequencing is just a piece of cake, what would be the next challenge in the industry? If we can “read” through a book, can we “write” one by ourselves? If we can “read” through a genome, can we just “write” one? In the speech, Ye will make a brief introduction on what BGI is doing, then review back to the history of genome sequencing, and look forward to next stars like synthetic biology, metagenome, etc. in the industry.

Keynote Speech

Polymorphisms in microbial whole genome sequence identify classical mutations and may establish geographic origin for the Nagoya Protocol

Kevin McCluskey

WFCC Executive Board member, Fungal Genetics Stock Center, USA

Abstract

Eukaryotic microbes such as fungi have been important research organisms and were foundational in the development of molecular genetics. *Neurospora* was the specific organism used to demonstrate the central paradigm of molecular biology which is "one gene, one enzyme." While this has been modified to accommodate multi-subunit enzymes, and post-transcriptional and post translational processing, it remains at the center of modern biology and biotechnology.

Extensive mutagenesis and analysis identified over 1,200 genetic phenotypes in *Neurospora crassa*. These are defined by the ability to follow a trait through a genetic cross and include both nuclear and mitochondrial traits. Whole genome analysis has demonstrated that *N. crassa* has nearly 10,000 genes and a nearly complete set of gene deletion mutants has been generated and deposited at the Fungal Genetics Stock Center. Not surprisingly, nearly 8,500 of these directed mutants have no visible phenotype.

Among the mutant strains in the FGSC collection 330 classical mutant loci exist with no direct relationship with a gene sequence. To identify the open reading frame mutated in these strains, a gene complementation approach was used but it was very labor intensive. To simplify classic mutation identification whole genome resequencing approach was undertaken. Based on the simple logic that a sequence polymorphism that is present in multiple strains should not cause a phenotype in only one strain, a multiple strain analysis pipeline was established that allowed rapid identification of the causal mutation in many strains. Examples of the analysis and validation by comparison with the targeted gene deletion mutant will be described.

**NIEMA: a transfer and exchange system of microbes for microbial
resource centers for non-commercial purposes according to the CBD and
the Nagoya protocol**

Ando-katsuhiko

Acting Director-General, NITE Biological Resource Center,

National Institute of Technology and Evaluation, Japan

Abstract

The Asian Consortium for the Conservation and Sustainable Use of Microbial Resources (ACM) was established in 2004 with currently 23 organisations from 13 countries (Cambodia, China, India, Indonesia, Japan, Korea, Lao, Malaysia, Mongolia, Myanmar, Philippines, Thailand, and Vietnam). The objective of the ACM is to promote collaboration among governments and public organisations in Asian countries to enhance conservation and sustainable use of microbial resources in Asia.

Microbial Resource Centres (MRCs) are fundamental for *ex-situ* preservation to safely maintain the world's biodiversity and genetic resources of microbes, and for the development of microbiology. Having recognized the importance of MRCs, a new scheme titled the 'Network of International Exchange of Microbes under the ACM (NIEMA)' has been developed by the Task Force of Management of Material Transfer (MMT-TF) in the ACM. The basis of the NIEMA is the common policy for all NIEMA MRCs: the NIEMA Code of Conduct for Microbial Resource Centres. The Code of Conduct consists of four obligations: 1. Acquisition and entering of microbes into the NIEMA framework; 2. Transfer of NIEMA strains from a Primary-MRC to a NIEMA MRC; 3. Distribution of NIEMA strains from a NIEMA MRC to third parties; and 4. Maintaining a NIEMA Clearing-House Mechanism (NIEMA-CH), which would store and make available any information related to the transfer of NIEMA microbial strains between NIEMA MRCs. The Code of Conduct covers the transfer of microbial strains for non-commercial research purposes and complies with the provisions of the Convention on Biological Diversity (CBD) and the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from Their Utilization to the

Convention on Biological Diversity (NP). The NIEMA scheme proposes a legitimate and streamlined way of transferring and utilizing microbial resources in line with the principles of the CBD and the NP.

Ref.: Katsuhiko Ando, Tae Eun Jin, Rie Funabiki, Linhuan Wu, Honglada Thoetkiattikul, Jung-Sook Lee, Bubpha Techapattaraporn, and Tanit Changthavorn. (2014) Network of International Exchange of Microbes under the ACM (NIEMA) - A transfer and exchange system of microbes for microbial resource centres for non-commercial purposes according to the CBD and the Nagoya Protocol. *Microbiol. Cult. Coll.* 30(2): 85-96.

Implementation of the Nagoya Protocol in the EU - Guidance on scope and utilization

Axel Braun

Law Department Officer, F.HOFFMANN – LA ROCHE Ltd., Switzerland

Abstract

EU Regulation No. 511/2014 and Implementing Regulation 2015/1866 implementing the provisions of the Nagoya Protocol are now in force in the EU. National law in EU Member States further providing detailed ruling on either access and/or monitoring and sanctions are also in place in some but not all EU Member States, including National Competent Authorities. On the request of users of genetic resources and/or associated TK in the EU the Commission together with EU Member States and users has developed "Horizontal Guidance" on the interpretation of the scope of its respective regulations, specifically on the aspects of temporal, material and geographical scope, user's obligations, events which trigger due diligence obligations and sector specific issues in relation to health and food and agriculture. In addition, together with users from sept different sectors, sector specific guidance on how the term "utilization", which is a key term under EU law, is to be applied to research and development activities of these sectors is under preparation. Short explanations of these topics will be given and challenges for users in the industry, especially the pharmaceutical industry, but also for culture collections will be illustrated.

Keynote Speech

Standardizing Data in Biotechnology: From Community to ISO Standards

Martin Golebiewski

Convener of ISO/TC 276 Biotechnology WG5 'Data Processing and Integration',

Heidelberg Institute for Theoretical Studies, Germany

Abstract

The complexity and interdisciplinarity of modern biotechnology and the whole field of the life sciences require a high degree of standardization of processes, as well as standardized formats for data, computer models and their descriptions. It is crucial to standardize the acquisition and description of the data and the documentation of its origin and context. This comprises the standardized description of the applied methods and biological material (stored in biobanks) and workflows for data processing, analysis, exchange and integration, as well as for the incorporation of the data into computational models. Also the setup, handling and simulation of the resulting computer models have to follow dedicated standards. To this end many grassroots community standards for formatting and exchanging data, models and metadata (data describing the data) have been defined by different scientific communities in the field. However, it often is confusing and cumbersome for the potential users to find the appropriate standards for their tasks and apply them in their workflows.

In light of its rapid growth and market relevance, the International Organization for Standardization (ISO) has identified biotechnology as an area of major potential for standardization. In December 2013 the technical committee of ISO for biotechnology standards (ISO/TC 276) had its inauguration meeting. Where is the journey of ISO/TC 276 Biotechnology heading? How could existing scientific community standards be of use for the definition of official ISO standards? What are the benefits for the grassroots communities in doing so? In my talk I will outline options for classifying and integrating existing community standards into official norms and how that might help in defining a framework and guideline for community standards and their application in different biotechnological use cases.

Keynote Speech

Progress in ISO/TC 276 Biotechnology/WG 2 Biobanks and Bioresources

Yong Zhang

Convenor of ISO/TC 276 Biotechnology WG2 & WG5

'Data processing and integration', China

Abstract

ISO/TC 276 Biotechnology was created in 2013. TC 276's Scope is Standardization in the field of biotechnology processes that includes the following topics: 1) Terms and definitions; 2) biobanks and bioresources; 3) analytical methods; 4) bioprocessing; 5) data processing including annotation, analysis, validation, comparability and integration; 6) metrology. In this talk, as the co-convenor of WG 2, I am going to give a short introduction about WG 2 (biobanks and bioresources). Also, I would like to share some progress in China.

Quality by Testing and Quality by Design in microbial Biobanks

Anabela Martins

Quality Manager of Micoteca da Universidade do Minho, Portugal

Abstract

Throughout its existence, Biobanks on the microbial domain (mBb) have embraced this endeavour of preserving authentic microorganisms and its related data for future purposes. A microbial Biobank should have a high degree of assurance in the performance of its preservation processes so that it will, on one hand, consistently supply authentic microbiological material, and on the other, ensure an effective preservation of authentic microorganisms avoiding its loss. Current mBb approaches to quality management are mainly based in controlling quality which does not ensure process consistency. A modern approach to quality management and process validation which can lead mBbs to attain a high degree of quality assurance is proposed. Besides the quality assurance, the proposed approach is also a source of process and microorganism enhanced knowledge including different kind of data such as the microorganism critical quality characteristics, how they are affected by the process variables and the *control space* (concept related to the robustness of the process) for a given preservation process. This acquired enhanced knowledge encloses new challenges as it includes data that needs to be captured, managed, disseminated and used to promote the effective and consistent microorganism preservation.

The importance of standardization in biobanking and introduction of

KNNRC

Ki Hyun RYU

President of Korea National Research Resource Center (KNNRC), Korea

Abstract

In recent years, revenue from biotechnology industry and investment for biotechnology R&D has both shown continuous growth globally. Korean bioindustry also has demonstrated the remarkable annual growth rate, reaching almost 14% in 2013. As the bioindustry expands, international standards concerning biobanks and bioresources will have profound implication on the field of biotechnology as a blueprint establishing its overall landscape. International Organization for Standardization (ISO) Technical Committee (TC) 276 is currently working on creating standardized guidelines of human, animal, plant, and microorganism biobanks¹. These standards will ensure the quality of bioresources and establish standard operating procedures for handling various types of bioresources.

ISO/TC 276 was created at Berlin, Germany on December 13, 2013. With objectives for conservation of resources and sustainable development of bioresource technology through information sharing, four Working Groups (WGs) – Terminology, Biobanks and Bioresources, Analytical Methods, and Bioprocessing – were initially created with later addition of a fifth WG, Data Processing and Integration. Participating members of TC 276 are 25 countries, including Germany, the secretariat, China, Japan, and Korea. TC 276 also has 14 observing members, 14 internal liaisons and 5 Category A liaisons which includes ANRRC, Asian Network of Research Resource Centers. The Korea National Research Resource Center (KNRRC) has administered the activities of ANRRC as the permanent secretariat.

KNRRC has been actively participated in domestic and international standardization efforts. The Center has published 16 best practice guidelines which thoroughly cover diverse organisms and fusion

¹ Resources for research and development (R&D) aspects, but excluding therapeutics and highly regulated agricultural productions

materials. They are utilized as practical manuals for the operation of numerous biobanks. Based on these expertise, KNRRC participates in the activities of TC 276 to contribute in the process of international standardization.

In October 2016, experts of TC 276 will convene at Dublin, Ireland for working group meetings. Next general meeting of TC 276 will be held in Korea during the week of 8th to 12th of May 2017.

Keynote Speech

The collaborative working environment – a new level of knowledge transfer and Innovative collaboration

Erko Stackebrandt

Coordinator of MIRRI, Leibniz-Institut DSMZ-

German Collection of Microorganisms and cell cultures Germany, Germany

Abstract

Each of us, being confronted to search the literature and/or the internet for specific data on a given taxon, is confronted with the tedious task to collect information from various sources. If the search is restricted to a recent species description which is based on a single strain, the type strain, the search is easy as the original description is all there is. If however, the search relates to a strain of importance to food and agriculture, health or basic science, the task is highly laborious or one turns textbooks such as ‘The Prokaryotes’, ‘Bergey’s Manual’ or topic-specific essays. The search is even more complicated if extended to comparative surveys on specific physiological properties, constituents, habitats, applications and so on. Most properties generated in public culture collections are not included in their strain catalogues and data on the composition of chemotaxonomic properties and commercial test kits are not routinely available. Other databases need the purchase of a commercial system, such as BIOLOG, MIDI-System for fatty acid data or Biotyper for MALDI-TOF spectra. The time-consuming search for published data on a given strain is well known to any researcher. An exception is the situation for sequence data as their deposition in public databases is mandatory and availability of data is now high on the agenda of scientific journals.

The ESFRI project Microbial Resource Research Infrastructure (MIRRI) is trying to change this dismal situation. MIRRI has identified its present offer to the users which, in the future, will be managed through a single access entry point. The underlying knowledge-based platform, the Collaborative Working Environment (CWE), to be established in the MIRRI Transition Phase (2017-2020), will guide the user to state-of-the-art microbial biological services, to

experts and training and this technical platform will enable researchers to carry out in-house research on mBRC holdings. Through individual gateways the platform provides the core knowledge base to enhance:

- The data offer (interoperability to facilitate data mining)
- Legal certainty on use in use of microbial resources
- Innovative business models for operations
- Broader access to materials
- Improved quality and data in science
- Better resources and services to meet stakeholder needs

Through the “Gate to Data & Resources”, MIRRI will offer catalogue(s), advanced search functions and all required facilities to meet the user demands for efficient access to resources and related data. Access to propriety information on published data will also available via this gateway, but it may be dependent on fees imposed by publishers.

The MIRRI-CWE will be designed as a sophisticated Information System (IS), which will be the central entry point for users, curators and developers that need access to the data and resources of mBRCs and selected third party databases. The MIRRI-IS is integrated as a tool and will focus on smaller datasets, but very well curated and expected to be highly appreciated by the users; they will serve as a reference for academia and industry stakeholders.

The ultimate goal of a functional platform includes access to all of its areas, no matter from which individual point of interest a user approaches. Moreover, based upon certain query key words the

users have the option to retrieve information on related topics beyond which they had originally anticipated.

Actinomycetes and bacteriophages: powerful tools for biotechnology and biodiscovery

Dilber Ipek Kurtboke

WFCC-(ex-officio) EB Member, University of the Sunshine Coast, Australia

Abstract

Following the discovery and medicinal applications of the first antibiotics global research provided a wide range of structurally diverse and effective agents to treat microbial infections. The “golden era” of antibiotics lasting from the 1940s to the late 1960s revealed the true potential of a particular group of bacteria belonging to the order *Actinomycetales* within the class of Actinobacteria. These bacteria provided the 45% of the currently known antibiotics including the first antituberculosis antibiotic streptomycin followed by other potent antimicrobials like gentamicin, tetracycline and vancomycin. However, antibiotic resistance has developed steadily as these antimicrobial agents were introduced in the recent years resulting in severe and fatal infections and there has been a dramatic increase in the occurrence of resistant pathogenic organisms such as Methicillin-resistant *S. aureus* (MRSA) and Vancomycin resistant enterococci (VRE). Moreover, the detection of vancomycin-intermediate-resistant *S. aureus* strains again stressed the importance of discovery of novel classes of antibiotics with new mode of actions to combat multiple drug resistant bacteria.

Different strategies have to be implemented to supply new chemical diversity for natural product discovery, particularly from previously undetected members of the order *Actinomycetales*. However, recovery of these bioactive taxa requires highly selective isolation techniques stemming from in-depth understanding of their eco-physiology. In this context, bacteriophages can be useful tools as naturally-present indicators rare actinobacterial taxa in environmental samples; and/or they can be used to deselect unwanted taxa on the isolation plates in the process of target specific isolation of rare taxa.

CGMCC-Promoting the Utilization of Microbial Resources

Yuguang Zhou

*Director of China General Microbiological Culture Collection Center (CGMCC),
Institution of Microbiology, Chinese Academy of Sciences, China*

Abstract

China General Microbiological Culture Collection Center (CGMCC) is a non-profit organization established in 1979 as the central culture collection in the cooperative network of various collections in china. The CGMCC has started to carry out its tasks as a depository organization designated by Patent Bureau of China since 1985 and as an International Depository Authority (IDA) under the regulations of the Budapest Treaty since 1995. In 1996, CGMCC has registered as a member of the Committee for Type Culture Collection of CAS and became a member of the Platform of National Science & Technology Infrastructure in 2003.

In 2010, the quality management system of CGMCC was audited and issued compliant with ISO 9001:2008 requirements, WFCC Guideline and OECD's standard for BRC.

The main focus of CGMCC is to collect, preserve, distribute and maintain living microbiological resources. The CGMCC has, at present, more than 54000 microbial cultures including biological material for patent purpose. CGMCC has providing microbiological cultures, gene resources and relevant technical services for various areas such as: industrial and agricultural production, health, environmental protection, scientific investigation and education accord with the national and international laws of bio-safety and intellectual property.

In the future, CGMCC will continue to provide high quality microbial resources, information and techniques to support and promote the development of bio-industry in china.

The European Culture Collections' Organisation: How to promote training and education innovative approaches

Nelson Lima

President of European Culture Collections' Organization (ECCO), Portugal

Abstract

The European Culture Collections' Organisation (ECCO) was established in 1981. The aim of the organisation is to promote collaboration and exchange of ideas and information about all aspects of culture collection activity. ECCO meetings are held annually and are a valuable forum for discussion and innovation on the future development of member culture collection activities. The organization has evolved for an important think tank with important contributions through collaborative projects like the MINE EU in the mid-1980s to bundle the common interests of microbial service collections and their users. In the subsequent CABRI EU project, some of the leading collections in Europe made available the contents of their individual catalogues for comparison via a search engine which provides access to a common Catalogue. Later on, the EBRCN EU project focused on guidelines for best practice towards an ISO-compliant quality management. These outputs were key-elements for the OECD initiative related with the BRCs task-force and the current OECD guidelines for BRCs. More recently, the EMbaRC (2009-2012) project enlarged the spectrum of activities and dealt with contemporary topics such as biological safety, improved identification methods and the development new concepts on training and education. Finally, inside of ECCO organisation another important developed project is the current MIRRI (2012-2016). Currently, MIRRI is involved on the Ritrain (<http://ritrain.eu/>) and CORBEL (www.corbel-project.eu) Horizon 2020 projects. This cascade of projects has had ECCO as incubator and several Culture Collections as lead partners. Moreover, documents that have addressed legal framework of Culture Collection operation, like MTA were also developed inside ECCO and a core MTA is now available to all Culture Collections that want adhere. Certainly that many other topics are in

discussion inside of ECCO, like the implications of Nagoya Protocol and the relate EU regulation 511/2014 with a fully entry into force on last 12 October 2015. Other topic is long tradition that culture collections have in training people that directly, or indirectly, are interested in microbial taxonomy and in microbial preservation and management. Academic (PhD and Master), advanced as well as bespoke courses on related topics in this field are regarded of true added value for the educational and microbial research community in Europe. In addition, only with modern and appealing approaches we can reverse the strong decline in numbers of trained microbial taxonomists in Europe that has been observed over the last decades. Gaps in microbial resource management training and potential synergies have been identified and the establishment of an educational community to create a knowledge-based training network and implement lifelong educational and continuing professional development courses for people working within culture collections have been developed. Training courses involved both theoretical and wet laboratory experiences in microbiology not only covering elements of taxonomy and identification of microorganisms but also isolation, characterisation, preservation and use of microbial resources are of the importance. To support these actions e-learning materials for training activities and distance courses need to be implemented with innovative approaches.

Data associated with yeast culture collections: Challenges and opportunities

Kyria Boundy-Mills

WFCC Executive Board member, Phaff Yeast Culture Collection, USA

Abstract

Yeasts, especially *Saccharomyces cerevisiae*, are important model organisms for basic life science research, and are also important for industrial fermentations including chemicals, therapeutics, foods and beverages. The importance of maintaining culture collections of yeast strains, and databases of their associated data, have been recognized for several decades. Recent advances have presented opportunities and challenges for culture collections and their users. Globally, there are over 40 public culture collections with over 500 yeast strains in their public catalogs, many of which have detailed listings in WDCM resources including CCINFO and the Global Catalogue of Microorganisms. The data associated with these strains vary depending on the strain and its intended use, such as whether the strain is a lab strain or wild-type strain. Data that are useful to users of yeast collections may include genetic markers, phenotypic characteristics, source, provenance, literature references, DNA sequences, and photos of cells and colonies. Source information including location of origin of the yeast strain and the date isolated are due to requirements of the Nagoya Protocol. Users also need access to ribosomal DNA sequences for taxonomic and identification activities. This is especially important at this time due to major taxonomic revisions underway: the genus or species names of a significant portion of the 1600 known yeast species are being changed to conform to the 2011 Melbourne Code. Public resources such as the Global Catalog of Microorganisms help to ensure that yeast researchers have access to information and strains from over 90 culture collections, so they can continue the long history of discoveries made using yeasts.

Bioinformatics for culture collections at the era of Big Data

Vincent Robert

Head of Bioinformatics,

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Abstract

Incredible challenges are facing culture collections with the rise of big data and next generation sequencing. While new technologies can be seen as major threads or hurdles, we strongly believe that they are great opportunities for collections and a few examples of the use of culture collections data will be provided.

Co-creating IT innovation to unlock microbial Big data

Lily Eurwilaichitr

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Director of Thailand Bioresource Research Center (TBRC), Thailand

Abstract

Microbes are everywhere and they affect everything around them, yet we know little about them. Only 1% of them can grow in the lab, leaving 99% of them unexplored. With increase knowledge of microbes, more benefits to mankind could be achieved in several areas, including health and medicine, industrial and environment and food and agriculture. Therefore, with the advancement of sequencing technology and big data analysis, more insights of microbes, including genomics, functional, and ecological information, could be rapidly obtained. However, the challenge of research in big data analysis of microbes, including, the storage capacity, the accuracy and completeness of data, and the complexity of heterogeneous data, need to be solved for sustainable development of big data exploration and utilization. In the data-driven science era, the role of Biological Resource Center (BRC) in providing associated high-quality Big Data of microbes is crucial for expedite the discovery of useful microbes for modern industry. Thailand Bioresource Research Center (TBRC) realizes the importance of collaboration to harness the power of Big Data. For instance, by automating data integration and governance at the point of data creation, the quality and trustworthy in the data can be boosted to ensure the power of Big Data. A tool called iCollect has been developed and shared to TBRC partners for data management and integration with the Global Catalog of Microorganisms (GCM). This will lead to the co-creation of high-quality microbe data in TBRC, TBRC partner collection and GCM. In addition, TBRC collaborates with the World Data Center for Microorganisms (WDCM) in term of infrastructure and tools for big data analysis which will be described in this presentation.

Life science databases and possible interconnection with mBRC Data

Alexander VASILENKO

IT specialist in All-Russian Collection of Microorganisms - VKM, Russia

Abstract

The aim of the project is to analyze perspective for establishing a network allowing efficient data integration for two mostly disconnected communities:

- 1) Life Science databases containing data on microorganisms,
- 2) mBRC and Culture Collections (CC) catalogues, WDCM, regional CC and mBRC networks, StrainInfo, CABRI.

We consider opportunities for network interconnection

1. in two directions:
 - a. to make mBRC and CC catalogue data visible and accessible from partner Life Science databases,
 - b. to make partner database records visible and accessible from aggregated catalogues of CC and mBRC;
2. in two formats – available for human access and for computer programs.

On the way we studied the most popular database holdings (MetaBase, Biosharing, BioMedBrigeds list, Elixir databases, ExPASy) and additional sources, more than 5500 database references in total. More than 2000 Life Science databases available in Internet were collected. In more than 800 data bases we found information on microorganisms (bacteria, archaea, fungi, yeasts, microalgae) and viruses, that could match the data presented in mBRC or CC catalogues.

The report presents system of Life Science databases, the information structures discovered and some technical details for a desirable data integration schema.

Industrial microbial resources informatization and sharing platform in

China

YAO Su

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Director of R&D department of fermentation

China National Research Institute of Food & Fermentation Industries, China

Abstract

Industrial microbial resources include microbial strains and their related information, which are valuable in fields like food, fermentation, light industry, bio-transformation, oil, environmental protection, etc., as well as in research. China Center of Industrial Culture Collection (CICC) is a core member of National Infrastructure of Microbiology Resource, and also a member of World Federation for Culture Collections. CICC holds a collection of 11434 industrial microbial strains, including production strains for traditional food fermentation of white spirit, yellow wine, soy sauce, vinegar, tea, fermented bean curd, pickled vegetable, natto and etc., production strains for modern bio-fermentation of erythritol, astaxanthin, itaconic acid, lactic acid, butanedioic acid and etc., and also reference strains for industrial safety control. The information management system has been established to manage the general and unique functional information of industrial microbial resources. According to the regulation of microbial resources data, the information have been standardized collected, arranged and digitally expressed. The basic industrial microbial resources database, quality control database and featured resources database have been established. Meanwhile, the information could be shared via www.china-cicc.org. Every year, more than 6000 microbial strains were distributed and over one million IP visits browse online through industrial sharing platform. In the future, CICC will continue to promote and develop the construction of shared system of the industrial microbial resources.

Keynote Speech

Challenges of a new era for culture collections: a curator's view

Takashi Itoh

*WFCC Executive Board member, Japan Collection of Microorganisms,
RIKEN BioResource Center, Japan*

Abstract

In the era of the CBD, the major principles for general culture collections and microbial resource center including JCM would be 1) increasing capacity of ex situ preservation, 2) promotion of use of microbial resources in the research and development environments, and 3) support of the ABS practices to depositors and users. Curators of culture collections, who work with microbial strains on a daily basis and communicate with depositors and users when necessary, also confront challenges in line with these principles. As a curator of the JCM, I would like to deal with two issues in my talk: acceptance of fastidious microorganisms for deposition and improvement of usability of the online catalogue.

Chilean Network of Microbial Culture Collections: Construction and Operation

Cledir Santos

*Interim Representative of the Chilean Network of Microbial Culture Collections,
the Universidad de La Frontera, Chile*

Abstract

According to the data available at the World Data Center for Microorganism-WDCM of the World Federation for Culture Collection-WFCC, Chile has four registered Culture Collections (CCs) that preserve a total of 2064 microbial strains (<http://www.wfcc.info/ccinfo/>, access on 08/07/2016). In addition, according to a recent publication by Overmann (2015), Andean countries, which includes Chile, are recognised as little capacity building states, where only eleven CCs are available with the focus on microbiological strains from the Andean Region.

Taking into consideration that a) Chile is already a full member country of Organisation for Economic Cooperation and Development-OECD and that b) Chile has already an economic and societal development which ranks it in a international position together with European Union countries, the information previously published about the little capacity building of Chile is not totally through (Human Development Report 2015, United Nations, <http://hdr.undp.org/en/countries>).

Expertise and infrastructure on microbial ex situ preservation are already available across Chile. In contrast, it is through that some limitations regarding low availability rate of microbial resources preserved in the country as well as the its associated information are observed. Moreover, at the global point of view, the current existing CCs in Chile are in different level of quality regarding its own infrastructure, the quality standards of culture preservation and the provided services.

Taking into consideration both the already existing expertise and know-how in each CC and the infrastructural limitation nationally faced by the different CCs, Chilean researchers started

working together to establish the Chilean Network of Microbial Culture Collections (RCCCM, acronym in Spanish). The main goal of RCCCM is to implement in the Chilean CCs the international recommendations for the Microbial Resources Centres as those defined by the OECD (Best Practice Guidelines for Biological Resource Centres).

In this communication, the effort in the Construction and Operation of the Chilean Network of Microbial Culture Collections will be presented and discussed.

The UK's National Collection of Type Cultures – answers to 21st century public health questions

Julie E. Russell

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Abstract

The UK's National Collection of Type Cultures (NCTC), established in 1920, includes more than 5000 type and reference bacterial strains of medical and veterinary importance. This dynamic collection provides bacterial strains to the biomedical community that have been implicated in recent challenges to people's health such as strains that are resistant to antibiotics. It is also a source of strains of historical importance, some of which were isolated in the 19th century, that help to improve our understanding of bacterial evolution, particularly the emergence of virulence factors and pathogenicity. It is important to continuously review and update the technologies used to authenticate and characterise NCTC bacteria. As part of a project funded by a Wellcome Trust grant, NCTC scientists are working in partnership with the Wellcome Trust Sanger Institute to provide whole genome sequences using long read technology for 3000 bacteria, thereby providing reference genomes that will become of increasing importance as next generation sequences are adopted in clinical diagnostic, reference and specialist microbiology laboratories over the coming year. The sequences (raw data and annotated sequences) are already in the public domain. The presentation will provide a brief introduction to the project, progress to date and the next steps being taken to design an eResource that will deliver access to the NCTC strains and their associated metadata and the use of WGS in Salmonella reference microbiology.

WDCM serves as an information infrastructure for the exploration and utilization of microbial strains preserved worldwide

Linhuan Wu

World data centers of Microorganisms

Institute of Microbiology, Chinese Academy of Sciences, China

Abstract

The World Data Centre for Microorganisms (WDCM) was established 50 years ago as the data center of the World Federation for Culture Collection (WFCC)-Microbial Resource Center (MIRCEN). It aims to provide integrated information services by fully utilizing hyperlinked big data technology for microbial resource centers and microbiologists all over the world. In this report, we provide an overview of WDCM information platform and services. CCINFO (Culture Collections Information Worldwide) provides metadata information on 708 culture collections from 72 countries and regions. The GCM (Global Catalogue of Microorganism) gathers strain catalogue information and provides a data retrieval, analysis, and visualization system for microbial resources. Now it includes more than 368,000 strains from 103 culture collections in 43 countries and regions. The ABC (Analyzer of Bio-resource Citation) is a data mining tool extracting strain related publications, patents, nucleotide sequences and genomes information from public data sources to form a knowledge base. The RSC (Reference Strain Catalogue) maintains an online database of strains listed in ISO and other international or regional standards. It allocates a unique identifier to strains recommended for use in diagnosis and quality control and hence serves as a valuable cross-platform reference. WDCM hope to further develop these platforms to be an integrated data server by cutting-edge information technology for culture collections and microbiologists all over the world.