

WDCM Training Course for Microbial Data Analysis

Institute of Microbiology, China Academy of Sciences (IMCAS)

Report of the training course

By

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Personal introduction

My name Carla Santos and I work as a researcher in the Biological Engineering Center (CEB), University of Minho, Braga, Portugal; and for the Micoteca da Universidade do Minho (MUM). I am a professional, highly motivated and interested Biologist with a strong desire for Molecular Biology applications. I have extensive experience in DNA analysis, including the development and optimization of new assays using several techniques such as fragment analysis, SNP analysis by single base extension and massively parallel sequencing. My main research line is the molecular identification of filamentous fungal strains isolated from diverse substrates and of different geographical regions.

Name of the culture collection

Micoteca da Universidade do Minho (MUM), Braga, Portugal

ABSTRACT

This is a report for the WDCM Training Course for Microbial Data Analysis where 15 participants from several international culture collections participated. This course gave valuable insights on WDCM activities, particularly on the works developed by the Chinese Academy of Sciences and the Global Catalogue of Microorganisms, and several databases and analysis tools of interest were described. This report includes a description of what I believe were the main benefits for me and the culture collection I represent (MUM) and also suggestions for the future editions of this training course.

I would like to thank WDCM and ICMAS for the opportunity to participate in this course.

Key words: MUM, Culture collection, Fungi, Database, Annotation, Microorganisms, WDCM, GCM.

Contents

1. Brief introduction of your Culture Collection.....	4
2. Benefits from the training course.....	5
3. Suggestions on WDCM work.....	6
4. Comments or suggestions on the training course.....	7
5. Suggestions on further cooperation between WDCM and your collection.....	8

1. Brief introduction of your Culture Collection.

Micoteca da Universidade do Minho (MUM) is a filamentous fungi culture collection based at the Biological Engineering Center of University of Minho (Portugal) since 1996. In 2011 MUM obtained the ISO 9001 certification for deposit, conservation and supply of filamentous fungi. MUM aims to be a resource center for the preservation of fungal diversity and its associated information and to create solutions for the sustainable development and the well-being of man.

MUM's quality policy is based on stimulating the motivation and involvement of all stakeholders in quality processes with a view to internalizing a culture of excellence and applied to all products and services. In this process, ongoing evaluation is seen as an element of continuous improvement that enhances the achievement of the MUM mission.

MUM is a member of the European Culture Collections Organization (ECCO), which it chairs since 2013. It is also a member of the World Federation for Culture Collections (WFCC) and is registered in the World Data Center of Microorganisms (WDCM) data center with the number 816. Additionally, it is registered in the BioCase (The Biological Collection Access Service for Europe) and StrainInfo.net networks. MUM has been involved in several european projects such as the European Consortium Microbial Resources Centers (EMbaRC) and is a

partner of the european research infrastructures project Microbial Resource Research Infrastructure (MIRRI; co-joint coordination by Portugal and Spain; statutory headquarters located at University of Minho, Braga, Portugal) and of the H2020 Research Infrastructure Training Programme (RItrain) project.

2. Benefits from the training course.

The WDCM training course covered several topics in detail and several benefits from attending it can be described:

- networking with members of several international culture collections and with different divisions of the Chinese Academy of Sciences allowed a better knowledge of the works being developed and resources available in each one as a way of establishing common ground for future collaborations;
- extensive information about databases and platforms useful for research lines based on microorganisms;
- information about several software and programs to perform data analysis, especially those related with annotation of complete genomes;
- discussion of topics regarding management such ISO standards and the implications of the Nagoya Protocol.

In conclusion, I believe that the knowledge acquired during the training

course will be helpful for the future development of my culture collection, specially in the fields of identification and characterization of fungal strains isolated from diverse matrices. Furthermore, I consider that the contact with IMCAS and other international culture collections, together with the established communication channels, will be translated in fruitful collaborations.

3. Suggestions on WDCM work.

WDCM work is very impressive and has originated tools of interest for microbiologists around the world, including a database of microorganisms and a platform of communication. It was also responsible for the Global Catalogue of Microorganisms, which is a landmark project when it comes to genomic generation of data from microbiological resources.

I believe that WDCM should continue to stimulate communication and cooperation between its members through the organization of meetings such as the one that preceded the training course (World Data Center for Microorganisms 8th Symposium). It should also continue to invest in the training of its members by supporting courses as the one that this report refers to. The next International Conference on Culture Collections (ICCC 15) meeting will be held in Temuco, Chile; and it can represent an excellent opportunity to offer pre- and/or post-courses on these issues.

4. Comments or suggestions on the training course.

This was a very helpful course as it gave good insights to various databases and tools available and being used in the Global Catalogue of Microorganisms (GCM) 2.0 project. The opportunity to interact with other members of the WDCM was also of great importance.

As a suggestion, I believe it could be interesting to include more practical exercises for the students. As not all participants might have access to their own sequences, lecturers could provide example files (from publicly available sequences) for students to work with using the platforms and pipelines described during the lectures. A good example is the talk and practice imparted by Dr. Jun Wang and his scientific collaborators. In this a tutorial file and a link to 16S metagenomic data were provided to the students to practice using *R* software. In fact, this was a good experience since any doubts that arose during the exercises could be solved *in situ* with the teacher. Following this idea, it could be beneficial if a list of software and databases to be used is shared with the participants in advanced so that everyone involved has the necessary tools to make out the most out of the course.

Considering that MUM is a fungal collection, I would also like to suggest the inclusion of tools specific to the analysis of fungal genomes. Although we expect those to be very similar to the ones used in the analysis of bacterial genomes, it could be interesting to see a comparison

where main differences between both pipelines are pointed out in order to defined cooperative strategies for data analysis.

5. Suggestions on further cooperation between WDCM and your collection.

Future work plans of MUM include the participation in the GCM 2.0 project, where we hope to play a role in the generation of data on strains that are of scientific and industrial importance, and the comparative study of complete genomes of fungal species of interest, particularly those useful in biotechnological applications. Alongside with molecular biology applications, MUM is also keen to share with WDCM members its knowledge and capacity regarding topics such as fungal classification/identification using morphological/phenotypical (including MALDI-TOF MS), secondary metabolites analyses, certification and ISO standards, and fungal *ex situ* preservation.