BCCM GEN-ERA

BCCM collections in the genomic era

DURATION
15/03/2020 – 15/03/2022

BUDGET
297.545 €

PROJECT DESCRIPTION

Context & general objectives

BCCM (Belgian Coordinated Collections of Microorganisms) is a consortium of Belgian public culture Collections that aims at preserving, distributing and study microbial diversity.

Prokaryotic and eukaryotic microorganisms play a major role in ecosystems and human activities. Research in microbiology, fundamental or applied, is therefore essential. Culture Collections actively participate in this research by analyzing their biological resources or by making them available to the scientific community. Technological advances allow to unravel in an easier and faster way the secrets of the microorganisms. Among these technologies, sequencing and functional analysis of their genome offer remarkable perspectives.

Through specific research questions on a selection of microorganisms associated notably with human health, pollinating insects and extreme environments, the BCCM GEN-ERA project aims at implementing genomic analyses tools in BCCM Collections. This will result in a greater valorisation of their microbial resources while enabling future investigations on other species and strains of interest.

Methodology

The methodology is based on the acquisition and annotation of genomic sequences on a selection of different types of microorganisms (i.e. bacteria, mycobacteria, cyanobacteria, yeasts and moulds). The sequencing strategy, re-sequencing or *de novo* sequencing, will depend on the availability of reference genomes in public databases. Annotation is based on two approaches: *ab initio* (« Hidden Markov Models » prediction) or by homology (comparison with databases of genes with known functions). The project also foresee the training of the BCCM scientists on the utilisation of these tools to ensure their use in the long term.

Research questions and impact

Genome-based microbial taxonomy is offering a new approach to delineate species and improve classification. The present proposal will bring modern state-of-the-art methodologies to analyse the gene repertoire of strains, allowing many developments, notably in molecular taxonomy, understanding of the metabolism, or evolutionary processes. More specifically, the project will contribute to: (1) the functional analysis of the genomes of bumblebees gut bacteria, providing novel insights into their roles and the interactions with their hosts, (2) expand the current mycobacteria phylogenomic investigations and identify phages, mobile elements and large repetitive regions, implicated in the virulence and immune stimulation/escape within the Mycobacterium tuberculosis complex, (3) improve the phylogenomic framework of cyanobacteria, as well as the understanding of the genomic adaptations related to the tolerance of extreme environmental conditions and to the synthesis of bioactive compounds, (4) the prediction of gene functions in bees gut yeasts that could be meaningful in nutrition, metabolism of pesticides, and pathogen defense of bees, (5) resolve the taxonomy of highly prevalent fungal pathogens, hence facilitating their (clinical) identification and epidemiology.

These research questions and the investigated microorganisms were thus especially selected for their added value for the society. Targeted species and strains include human and animal pathogens, microorganisms associated with pollinating insects as well as microbial strains producing bioactive compounds or adapted to extreme environments.

Valorization

The BCCM GEN-ERA project will result in the publication of assembled and annotated genomic sequences originating from diverse microbial strains of the BCCM collections. It will also allow the implementation, within the collections, of bio-informatics pipelines dedicated to the analysis of genomic data. The maintenance of a long-term expertise in the use of these data and pipelines by the BCCM scientists is also foreseen through trainings. Finally, results linked to the research questions (functionality and phylogenomics) will be published in peer-reviewed articles and communicated during (inter)national conferences.

CONTACT INFORMATION

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