Introduction

The Blue Biotechnology and Ecotoxicology group (CIMMAR, University of Porto) has undertaken a process of organizing its cyanobacterial isolates by creating a culture collection. This led to the recently membership of LEGE CC in the World Federation for Culture Collections (WFCC). The collection is also part of the Research Infrastructure EMBOPT. At present it comprises more than 350 different cyanobacterial strains, several of them unique among the phylogenetically diverse group. These isolates have been obtained since 1991, from samples collected in different environments and locations mainly in Portugal (including Madeira and Azores Islands), but also elsewhere (e.g. Australia, Brazil, Colombia, Morocco, Mexico). As in other collections worldwide, LEGE CC seeks to provide standards cultures for a wide range of aims (R&D, science education & dissemination). In fact, this has being done with local, national and international entities, under different types of partnerships. Several studies, most of them from BBE group’s own research, have shown the potential or the effective capacity of different LEGE strains to produce a myriad of chemical compounds, including toxins or newly discovered bioactive molecules. Soon, a number of strains (at least three) will have their genomes sequenced and annotated. Others studies revealed that some strains are phylogenetically distinct, and thus taxonomic challenging. In this work, while presenting the Culture Collection, the main findings from a survey of published and unpublished data available on the total LEGE strains are given. The methodological approach followed for this meta-data survey is summarized and presented in a systematic manner. Preliminary results are presented, linking the phylogenetic placement of LEGE strains in the “cyanobacterial Tree of Life” (based on 16S rRNA gene sequences), along with relevant information retrieved from the data compilation process (i.e. morphological features and identification, geographic and ecological origin, ecophysiological data, toxicity and bioactivity (bioassays, molecular, analytical) analyses performed; production/ type of secondary metabolites, publications, year of publication, etc.). It is believed that connecting the phylogeny of each LEGE strain to the aforementioned data creates awareness and capture interest of the scientific community and of members of the general public, such as pharmaceutical and biotechnological enterprises. Full information about each LEGE strain will be made available through the online version (currently under construction) of the collection.

Material & Methods

- Workflow diagram for the data survey and/or data collection process, and analysis.

References


Results

There are many strains and cultures (e.g.[3]) A of them, by data, for available geographic regions. It was led and it shown by CASTENHOLZ et al. (1993) and Le GALL et al. (1995) for the results obtained and process. The results were done to studies of toxins and analyses of taxa. LEGE toxicology data were supported for this study. Relevant data is also provided for some taxa, for example (bioassays, and/or bioassays, and/or the 16S rRNA sequences). The data were collected in Portugal, and are available from the survey (see M&M and Fig. 3) will capture interest from the scientific community and/or bioenterprises. Data gathered from this process (e.g. Fig. 3) will be made available in the website of LEGE CC (www.cimmar.up.pt/legeculturecollection), aiming to give awareness and visibility to the Collection.

Conclusion

LEGECs strains (see Fig. 2 for some statistics) are phylogenetically diverse and widespread across the tree (Fig. 1). It is believed that linking their phylogenetic placement along with relevant data being retrieved from the survey (see M&M and Fig. 3) will capture interest from the scientific community and/or bioenterprises. Data gathered from this process (e.g. Fig. 3) will be made available in the website of LEGE CC (www.cimmar.up.pt/legeculturecollection), aiming to give awareness and visibility to the Collection.

Future work

- To finish the sequencing of 16S rRNA genes from all LEGE CC strains.
- To identify the cyanobacterial taxa according to the most recent (polyphasic) taxonomy (e.g.[3]).
- To populate the site’s database.

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