Project SUS-MIRRI.IT
“Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy”
Area ESFRI “Health and Food”, granted by the European Commission – NextGenerationEU
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Services offered by OU08 at CNR-IRSA, Verbania

Morphological and Molecular Identification of Ascomycetes

The UO08 has expertise in identification of marine and freshwater Ascomycetes, cave microfungi including pathogenic micr④organisms as *Pseudogymnoasus destructans*, and the plant pathogen *Pyricularia oryzae*. Taxonomic and phylogenetic assignment based on morphological features and analyses of barcode marker and genes specific to each fungal class.

Reference: Laura Garzoli

Molecular Identification and Genome Analysis of Prokaryotes

Expertise in identification of prokaryotes with genetic markers. Taxonomic and phylogenic placement of prokaryotes based on single marker genes of whole genome analysis. Optimization of DNA extraction for specific strains. Analysis of prokaryotic genomes with focus on antibiotic and other resistance genes.

Reference: Ester M. Eckert

DNA Taxonomy

In the last two decades, the use of DNA sequence data for the identification and delimitation of taxa, namely DNA taxonomy, has found consensus and applications in various fields. After the advent of DNA barcoding, which showed the potential of using short DNA sequences for species identification across multiple groups of organisms, different methods and approaches made DNA taxonomy flourishing as a mature discipline. The UO08 can provide expertise in DNA-based delimitation of independent evolutionary units, akin to species. Such approach on DNA taxonomy can be used for performing taxonomic revisions and combined with morphology and ecology in the description of new species covering all groups of organisms, including prokaryotes and microscopic eukaryotes.

Reference: Diego Fontaneto

Sample Preparation for LC-MS-based Proteomics

In the last years, proteomics become increasingly important in different topics: drug discovery, biomarker discovery, analysis of microbial community (e.g. metaproteomics on human microbiome or environmental samples). Proteomics relies on data obtained from high resolution Mass Spectrometer coupled with Liquid Chromatography (LC-MS). To obtain reliable and reproducible results, an effective preparation of the samples is crucial. The OU08 can provide support in set up the experimental design for proteomics experiments and the protocol for the preparation of samples. In particular, our expertise could be useful in protein isolation from different matrixes and their digestion and purification.

Reference: Emanuele Ferrari

Bioinformatic Analysis of Proteomics and Metaproteomics Data

The increasing amount of LC-MS-based proteomics experiments poses the issue of how to handle the great amount of data that is being generated. A careful and precise analysis workflow has to be set up in order to have consistent and reliable data. In this context, OU08 can support and perform the identification of proteins from raw data coming from LC-MS-based proteomics experiments. Furthermore, we can assist and perform statistics and bioinformatic analysis of proteomics and metaproteomics data, in order to evaluate the biological significance of these data.

Reference: Emanuele Ferrari

Bioinformatic Analysis of Metagenomics Data

The increasing quality and amount of data produced by Illumina and other sequencing platforms has set in past decade the need of a range of bioinformatic tools and pipelines to treat such data and obtain the required information out of it which can vary dependently on the research topic. We can assist in developing and curate a pipeline that accommodates the researcher needs, we are specialized in the topic of antimicrobial resistance and functional annotation. We also work with WGS (Whole Genome Sequencing) data deriving from microbial isolates. We can further assist with the data analysis of the bioinformatic outcome.

Reference: Tomasa Sbaffi

Costs and duration of offered services and protocols

- Freshwater microbial biodiversity assessment

CNR-IRSA Verbania MEGic Culture Collection offers to users the possibility to characterize freshwater environmental samples to assess bacterial microbial biodiversity. The service includes DNA extraction, high-throughput amplicon libraries preparation and sequencing of 16S rRNA gene through Illumina platform (external service), and community analysis in term of diversity and composition based on OTUs taxonomic assignment.

Potential users: Research Centers, SMEs, public

Access to the service (physical, remote, virtual): virtual

Cost of the service: 200€

Duration of the service: (tentative) 4 months from sample acquisition to data delivery

- Bacterial and fungal strain identification

CNR-IRSA Verbania MEGic Culture Collection offers to users the service of strain identification of enivronmental bactarial and fungal strain. In particular, the CC is specialized in the identification of freshwater bacteria, and marine fungi. The service includes the verification of strain purity, DNA extraction, Sanger sequencing of appropriate gene markers (16S rRNA gene for bacteria, ITS rRNA gene and, in case, additional markers such as LSU, SSU, *ACT*, *TUB*, etc.), taxonomic assignment based on comparison with available datasets (GenBank, Mycobank) and, eventually, phylogenetic analyses for strains of difficult identification.

Potential users: Research Centers, SMEs, industries, public

Access to the service (physical, remote, virtual): virtual

Cost of the service: 50€ *per* strain

Duration of the service: max 1 month from sample aquisition to data delivery

- Bacterial strain characterization

CNR-IRSA Verbania MEGic Culture Collection offers to users whole genome sequencing of environmental bacterial strain. The service includes the verification of strain purity, DNA extraction, whole genome shotgun sequencing through Illumina or Nanopore technologies, genome assembly (and annotation).

Potential users: Research Centers, SMEs, industries, public

Access to the service (physical, remote, virtual): virtual

Cost of the service: 1500€ *per* strain

Duration of the service: 6 months from sample acquisition to data delivery

- Bacterial and fungal strains pigments production and protein expression

CNR-IRSA Verbania MEGic Culture Collection offers to users the proteomic characterization of bacterial and fungal strains. The service includes the verification of strain purity (including DNA-based confirmation), incubation and growth at required temperature and dedicated media, secretome and biomass extraction, analysis of pigments production through HPLC, preparation of samples for protein characterization through liquid chromatography-mass spectrometry, bioinformatic analysis of the identified proteins.

Potential users: Research Centers, SMEs, industries, public

Access to the service (physical, remote, virtual): virtual

Cost of the service: 1500€ *per* strain

Duration of the service: 6 months from sample acquisition to data delivery