



ABSTRACT

Title:

The Italian Microbial Research Platform: A Model for Collaborative, FAIR, and Sustainable Data Infrastructure.

Authors:

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Presenting:

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Abstract content:

In microbial research, sustainable and interoperable data sharing is essential for collaboration and reproducibility. In Europe, these efforts are led by MIRRI-ERIC, with Italy's integration driven by the SUS-MIRRI.IT project. Coordinated by the Turin University Culture Collection (TUCC), the project aims to develop research, services, and training within the Italian network of culture collections (MIRRI-IT). Through the project, a considerable amount of genomic and metabolic data has been added to the stored bioresources, unlocking their potential and increasing their relevance for the bioindustry. These activities lead to the creation of a national catalog, thereby strengthening the national and EU network of microbial biobanks.

Beyond catalog development, the initiative achieved two additional outcomes. First, it defined standardized operating procedures for microbial wet-lab analyses and supported the sequencing of 390 microbial genomes generated according to high-quality standards. These resources were contributed by multiple collections with specialized objectives focused on addressing critical knowledge gaps in fungal genomics in plant and animal pathogens, including human beings, food, and environmental niches.

Second, the project developed a high-performance bioinformatics service hosted at the University of Turin. The platform currently provides two workflows. The Microbial Genome Assembly workflow is optimized for long-read data and integrates multiple assembly tools to ensure high-quality genome reconstructions and enable protein prediction. The Metagenomic Analysis workflow is designed for taxonomic annotation and characterization of microbial communities and is organized into three



main stages: (i) quality control and preprocessing of sequencing data, (ii) taxonomic classification, and (iii) downstream functional and diversity analyses.