

ABRomics: An integrated multi-omics platform for antibiotic resistance research and public health

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Antibiotic resistance (ABR) is a major public health issue prioritized for mitigation by international institutions. Multidrug resistant bacteria (MDRB) and Antibiotic Resistance Genes (ARGs) carried by mobile genetic elements spread between the human, animal, and environmental sectors. Whole Genome Sequencing (WGS) is used for molecular typing purposes at the highest resolution. It provides identification of ARGs and their genetic supports as well as mutations leading to a decrease in antibiotic susceptibility. Epidemiological and WGS data are used for tracking MDRB in hospital outbreaks but also across the animal and environmental sectors. Sharing and interoperability of high-quality data (sequence and metadata) are key requirements for addressing the spatio-temporal dissemination of MDRB. To this aim, the French Priority Plan on ABR has funded the development of an online, open platform dedicated to antibiotic resistance.

We are establishing a repository of structured, interoperable, standardized, and well-annotated multi-omics data with tailored mathematical and bioinformatics tools to answer generic and specific research questions related to ABR. The ABRomics platform includes standardized pipelines to run ABR analyses of WGS from pathogenic strains supported with integrated databases (ARG, sequence types [ST], virulence factors [VF]). Uploading data, launching pipelines, viewing and cross-referencing enriched results will be achieved through easy-to-use web interfaces. ABRomics β -version integrating the ABR detection genomic pipeline and other markers such as ST, and VF will be available to the consortium in summer 2023 and to the whole microbial research community by the end of 2023. Core-genome multi-locus sequence typing, relationships between strains and metagenomics pipelines will next be made available.

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The ABRomics aims at developing a secure One Health cross-sectorial online platform to make accessible bacterial infectious disease (meta)genomics data and their associated clinical and epidemiological metadata to epidemiologists, clinical microbiologists, and the broader research community. ABRomics will offer a repository of structured, interoperable, standardized and well-annotated multi-omics microbiological data, with tailored mathematical and bioinformatic tools, that can be used to answer specific research questions related to antibioresistance (ABR). We will present the current status of the ABRomics developments: its infrastructure for the storage and management of heterogeneous data, the implemented “standards” workflow analysis, the database model allowing to store metadata and analysis results, and the web interfaces.