

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

Julie LAO^{1,3}, Pierre MARIN^{1,2}, Romain DALLET^{1,4}, Fabien MAREUIL⁷, Alix DE TOISY⁷, Kenzo-Hugo HILLION⁵, Aurélien BIRER⁶, Nadia GOUE², Richard BONNET⁶, Etienne RUPPE³, Gildas LE CORGUILLE^{1,4}, Philippe GLASER⁸, Claudine MEDIGUE^{1,9}

¹CNRS, Institut Français de Bioinformatique, IFB-core, UAR 3601 - Évry (France)

²AuBi platform, Mésocentre, Université Clermont-Auvergne - Aubière (France)

³Université Paris Cité and Université Sorbonne Paris Nord, Inserm, IAME - Paris (France) ⁴Sorbonne Université, CNRS, FR2424, ABiMS, Station Biologique - Roscoff (France) ⁵Faculté des Sciences Techniques, Université de Nantes, F- 44000 - Nantes (France)

⁶CHRU Clermont-Ferrand Gabriel-Montpied - Clermont-Ferrand (France)

⁷Institut Pasteur, Université Paris Cité, Bioinformatics and Biostatistics Hub, F-75015 – Paris (France)

⁸Institut Pasteur, Unité EERA, CNRS UMR604, F-75015 - Paris (France)

⁹CNRS UMR8030, Université Evry-Val-d'Essonne, CEA, Genoscope, LABGeM - Évry (France)

Introduction and objectives

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 research and public health.

Methods

We are establishing a repository of structured, interoperable, standardized, and well-annotated multi-omics data with standard workflow analysis (Galaxy pipelines) to answer generic questions related to ABR, and tailored mathematical and bioinformatics tools to address more specific research questions. To access the platform, we are designing a web interface to also facilitate and combine the surveillance of ABR in the three sectors. FAIR (Findable, Accessible, Interoperable and Reusable) data management procedures will enable retrospective studies.

The ABRomics platform is hosted at the French Bioinformatics Institute (www.francebioinformatique.fr) with a high capacity of analysis and 2 petabytes data storage.

Results and conclusions

The ABRomics platform includes standardized pipelines to run ABR analyses of WGS from pathogenic strains of interest for ABR, with integrated databases (ARG, sequence types [ST], virulence factors [VF]). Uploading data, launching pipelines, viewing and cross-referencing enriched results is 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 made available to the consortium in autumn 2023 and to the whole microbial research community in the beginning of 2024. Core-genome multi-locus sequence typing, relationships between strains and metagenomics pipelines will next be made available.

Acknowledgement of grants and fundings:

This work is financially supported by the French Priority Research Programme on Antimicrobial Resistance (PPR antibioresistance), coordinated by Inserm and funded by the Secretaire General Pour L'investissement (SGPI)

