Mycobacterium tuberculosis (TB) topic research

The Emerging Bacterial Pathogens Unit (EBPU) is recognised as a Supranational reference Laboratory and WHO Collaborating Centre ITA-98 for Tuberculosis Laboratory Strengthening and Italian Reference Centre. The Unit also actively participates to the international training courses in TB management and organizes annual trainings on WGS technologies to detect drug resistance and cluster analysis. The Unit has the role of technical partner for the National Subgroup on Tuberculosis of the Ministry of Health, and actively contributed to the preparation of the National Mycobacteriology Manual within the working group for national TB recommendations. The Unit performs molecular typing of relevant bacterial isolates including TB for infection control and epidemiology purposes.

Main Activities:
- Molecular mapping of mutations conferring resistance to first and second line drugs in M. tuberculosis.
- Detection of TB latent infection in immunocompetent and immunosuppressed hosts and identification of virulence markers in TB strains.
- Identification of gene and mutations panels associated to resistance to specific classes of antibiotics, by Next Generation Sequencing (NGS) of a large collection of TB strains.
- Identification and validation of specific signature based on circulating miRNAs able to discriminate people with active TB from healthy controls. RNAseq approach has been used to provide novel insights in mycobacterial transcriptomic networks (sRNA + mRNA) and showed that selective sRNAs are expressed during exposure to ofloxacin.

Research Projects:
- TB in migrants (E-Detect TB, RF of the Ministry of Health)
- New Tools for TB diagnosis (CAP-TB)
- WGS for TB (EUSeq my TB)
- Genotype vs phenotype (Reseq, Cryptic)
- Determinants of virulence and markers of drug resistance (Trans-TB-Trans)
- Development of mycobacterial small regulatory RNAs for attenuating virulence of Mycobacterium tuberculosis (RF of the Ministry of Health)
- Evaluation of the host-pathogen interactions in in vitro/vivo infection models with MtB strains (OSR Pilot & SEED Grant)

Sequencing multidrug resistant bacterial pathogens for next generation therapy and public health interventions

- Develop new typing tools or new algorithms allowing a better interpretation of data obtained with the existing ones in order to minimize health care associated infections trough prompt intervention after recognition of nosocomial transmission of pathogens.
- OSR surveillance protocols in multidrug resistant bacterial pathogens.
- Snapshot of clones circulating in Italy and in OSR
- PFGE/WGS for MRSA (methicillin-resistant S. aureus) and KPC-Klebsiella pneumoniae surveillance
- Cluster analysis and cgMLST were performed using the SeqSphere+ software exploiting a genome-wide allelic numbering schema named core genome Multilocus Sequence Typing (cgMLST).

Mouse model of chronic respiratory infection: Nontuberculous mycobacterial and MDR pathogens

- Screening and clinical significance of a large collection of a large NTM strains in cystic fibrosis (CF) patients
- To characterize a murine model of chronic lung infection in immunocompetent mice to investigate the pathogenesis of different MA subspecies
- To perform longitudinal studies with magnetic resonance imaging (MRI).