Main Activites

Figure 1

Nucleic acid extraction

- Samples collection
- Nucleic acid extraction
- Quality Control

Library preparation

- Adaptor ligation/barcoding
- Size selection
- Amplification/purification
- Quality control

Sequencing and analysis

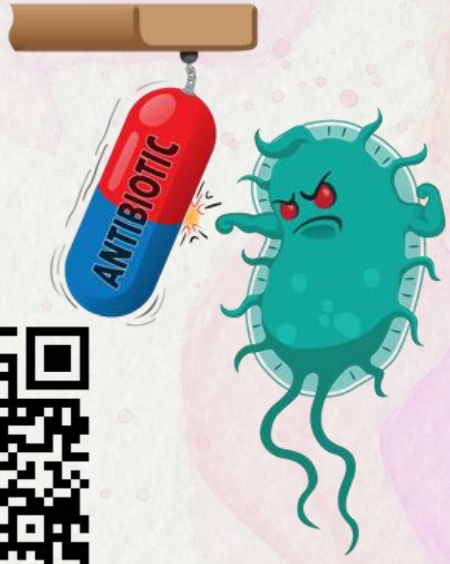
- Sequencing
- Data analysis
  - Base calling
  - Read alignment
  - Variant calling
  - Variant annotation

Impact & Outcomes

Improve our knowledge on multidrug-resistant microbes and their transfer to humans.

Improve service provided at Mater Dei Hospital.

One Health approach - this aims to achieve the best possible health outcomes whilst taking into account the relationship between humans, plants, animals and their surrounding environment.



Please visit our website for more information on:

www.amr-wgs-malta.com

ANTIMICROBIAL RESISTANCE SURVEILLANCE IN MALTA

INTEGRATING WHOLE GENOME SEQUENCING FOR THE MOLECULAR CHARACTERISATION OF CLINICALLY ISOLATED CARBAPENEM / COLISTIN RESISTANCE ENTEROBACTERIACEAE

AMR-MT-WGS

Funded through:
EU4H-2022-06A-MS-IBA-01-02



Contact Number: +356 25456425

SPTAR MATER DEI

Molecular Diagnostics
Infectious Diseases

What is Antimicrobial Resistance?

Antimicrobial Resistance (AMR) is a global health crisis where microbes, like bacteria and viruses, evolve to resist the drugs designed to treat them.

This development of resistance to antibiotics makes infections harder to treat, leading to longer illnesses, higher mortality rates, and increased healthcare costs.

Effects, causes & why it is a problem

This resistance is primarily driven by the overuse and misuse of antimicrobial drugs in human and animal health, as well as in agriculture. As a result, treatable infections can become untreatable.

Patients undergoing certain medical procedures such as organ transplantation and cancer chemotherapy are prone to infection. If antibiotics are no longer effective, the risk of infection following these types of interventions would be extremely high.



Addressing AMR requires an effort to preserve the effectiveness of existing antibiotics, promote responsible use, and invest in research for new treatments.

The first step in combatting this global threat requires a thorough understanding of these microbes' genetic make up and patterns leading to resistance

Ways to prevent AMR

- Use antimicrobials responsibly to slow down the development of AMR.
- Follow your doctor's advice when taking antibiotics.
- Prevent infections by practicing hand hygiene and keeping vaccinations up to date.
- Antibiotics should be prescribed in order to treat bacterial infections only and not viral infections.



OUR PROJECT

Malta has observed a steady increase in bacterial resistance rates for several antibiotics, including carbapenem/colistin. Currently we screen for AMR bacteria by conventional methods which include growing bacteria on culture plates which is followed by drug susceptibility testing. However, the value of using next generation sequencing technologies to detect and monitor infectious diseases was brought to the forefront of the COVID-19 pandemic. The Ministry of Health has an ongoing campaign called 'A Strategy and Action Plan for the Prevention and Containment of Antimicrobial Resistance in Malta (2020 – 2028)' which deals with prevention and containment of AMR in Malta.

The laboratory's role in this strategy is to use molecular typing to identify specific strains of bacteria resistant to antibiotics. Our project aims to do that! The project is called Antimicrobial Resistance Surveillance in Malta: Integrating Whole Genome Sequencing for the molecular characterisation of clinically isolated carbapenem /colistin resistance Enterobacteriaceae or AMR-MT-WGS in short. We aim to strengthen the AMR surveillance in Malta by implementing WGS of carbapenem/colistin resistant Enterobacteriaceae. This will help us contribute to enhance readiness for cross-border outbreaks of infectious diseases and pandemics.



Project Components

Figure 1 depicts the workflow implemented during NGS. This includes extracting the genetic material (DNA) which then undergoes a number of amplification and purification steps during library preparation. The samples are then loaded on a sequencing analyser where the raw data is collected and studied in a process called bioinformatics.

