



qMAR – MSCA-IF-2017

The gut microbiome is involved in numerous processes that include protection against colonization and infection by harmful microorganisms. The extensive use of antibiotics could result in an imbalance between the helpful and harmful bacteria, leading to detrimental effects on the health of an individual and increasing the risk having multi-drug resistant organisms in the intestines. This is especially concerning for paediatric transplant patients that have special needs and are heavily reliant on antibiotics.

Previous studies showed that determining the load of resistance genes among the gut microbial organisms could be a predictive factor for the development of harmful infections. Along these lines, qMAR main objective is to evaluate the use of qPCR, a sensitive and accurate test, for monitoring biomarkers. The biomarkers that are expected to be found are in terms of the intestinal load of selected antibiotic resistance genes over time. Ultimately, our objective is identifying tools that could be used in personalized medicine approaches for paediatric transplant patients in order to improve on their course of treatment.

In order to achieve our objective, faecal samples and medical records will be collected from each paediatric transplant patient over a period of 12 months. Antibiotic susceptibility testing will be performed for the isolated bacteria in order to determine the presence of resistance. qPCR will then be performed directly on the samples in order to determine the load of epidemiologically relevant resistant genes over time. Multi-locus sequence typing will also be performed for determining the clonality of the isolates encountered in this study, allowing us to trace the origin and dissemination of resistant bacteria. Finally, statistical analyses will be performed in order to determine associations between clinical interventions, the load of resistance genes, and clinical outcomes.

The main expected results are determining a threshold of resistance genes after which adverse clinical outcomes would be expected, and determining how clinical interventions are affecting the load of resistance genes and the microbiome. At least three main articles are expected to be published in this study, and they are:

- The Use of qPCR as a Tool for Monitoring the Resistome among Paediatric Transplant Patients
- The Effect of “X” on the Resistome among Paediatric Transplant Patients (where X represents a specific medical intervention)
- The “X” Load of “Y” in the Gut Microbiome of Paediatric Transplant Patients increases the Chances of “Z” (where X is the load quantified by qPCR, Y is a specific gene(s), and Z is a specific adverse effect)

The results of this project will also be freely disseminated to the general public and to the scientific community in order to ensure maximal exploitation of the data obtained, contributing to the ultimate objective of improving on the quality of life of paediatric transplant patients.