

CAF/20/03 - Unravelling the role of host microenvironment in the development of phenotypic resistance in Mycobacterium Tuberculosis

Tuberculosis (TB) is the biggest infectious killer in the world, with a person dying from it every twenty seconds. It is caused by a bacterium called Mycobacterium tuberculosis (Mtb). Over the next 10 years, the number of patients with diabetes will double, and more than 600 million individuals will be living with diabetes worldwide. This is a major concern as it has been shown that patients with diabetes are at higher risk of TB disease return (relapse) and more likely to die of TB disease. This project aims to understand why diabetic patients have poor response to TB treatment. The cause of relapse is thought to be the significant number of Mtb bacteria that transform into a slower and fatty form and survive despite antibiotics. These fatty Mtb bacteria is difficult to identify with current laboratory techniques, but we have established one smart way to identify them. Using fluorescent microscopy, we can detect fatty droplets inside the Mtb. By counting these fat and lazy bacteria, I aim to rapidly identify patients who may not respond to treatment as well as others. Through the project, I aim to develop effective interventions, tailored to the individual needs.