Imperial College London

Natural Environment Research Council

2024_42_DoLS_TD: The impact of environmental cues in antimicrobial resistance spreading

Supervisors: Dr Tiago Dias da Costa (mailto:t.costa@imperial.ac.uk)

Department: Department of Life Sciences

The outlook is bleak. In the next 35 years, 300 million people are predicted to die prematurely due to antimicrobial resistant infections. By 2050, antimicrobial resistance (AMR) infections will be the leading cause of death, accounting for an estimated 10 million deaths per year and a cost of $100 trillion globally. The “golden era” of antibiotics has fallen away to reveal the immense threat of the impending “post antibiotic” era. Continual consumption and misuse, over several decades, has driven bacterial natural selection at a phenomenal rate culminating in the rapid emergence of AMR bacteria. The AMR situation has continued to escalate. In 2016, the first case of a bacterial infection resistant to every available antimicrobial drug was reported while bacterial plasmids such as the NDM-1 plasmid confer resistance to even last resort antibiotics. Alarmingly, the discovery and development of new antibiotics has also rapidly declined. Antibiotic classes discovered in the 1940’s and 1960’s still remain our primary means of treatment, further exacerbating the threat of AMR bacteria given that widespread antibiotic resistance typically occurs within three years of introducing a new antibiotic. The impending catastrophe of the “post antibiotic” era indicates that a drastic change in strategy is urgently required to tackle the threat.

The spread of antibiotic resistance is clearly outpacing the development of new antibiotics. This became a pressing medical challenge and a global health crisis highlighted by World Health Organization. Horizontal gene transfer (HGT) is the main process whereby bacteria can rapidly and robustly transfer plasmids encoding antibiotic resistance genes and accessory genetic traits among a bacterial population. This important process occurs in a wide variety of environmental niches and allows the sharing of ecologically important traits that can rapidly drive the generation of genomic innovation and diversification in the environment. Importantly, such beneficial traits provide bacteria with unique genes that accelerate adaptation to novel or fluctuating environments entailed by a variety of factors ranging from antibiotic exposure to climate change.

The PhD project will focus on identifying and understanding the effect of specific environmental cues in the process of bacterial HGT. The student will obtain solid training in a wide variety of microbiology and molecular biology techniques