Antimicrobial Resistance in Biofilms: Introduction

Antimicrobial Resistance (AMR) is increasingly recognised as a vitally important, global public health concern [1], potentially causing untreatable infectious diseases and making recent medical advances (e.g. chemotherapy, organ transplant) very high risk. This is especially important when considering the emergence of resistance to so called critically important antimicrobials (CIAs) (for example [2]), which can be the last line of defence against bacteria already resistant to frontline antibiotics. The use of antimicrobials in the agrifood chain is known to lead to the evolution of AMR, which may be transmitted to human pathogens or the human commensal microbiota [3, 4].

Biofilms are bacteria with extracellularly secreted matrices, and they are a potentially important source of AMR genes in the food processing environment. Biofilms protect bacteria from the action of sanitizers and mechanical cleaning, leading to persistence in the environment [5]. These biofilm populations can then act as a source of future contamination of foodstuffs. The reduced exposure to antimicrobials that bacteria experience in biofilms can also increase the likelihood of the evolution of AMR [6], including from routes such as co-selection of antibiotic and biocide resistance [7, 8]. Biofilms also lead to bacterial cells being in close physical proximity, which can increase the likelihood of AMR genes being exchanged between taxa by conjugation [9].

An evidence gap exists regarding the extent to which bacteria in biofilms contribute to the AMR burden of foodstuffs and the population in general. This project sampled biofilms from environments where biofilms were most likely to be present, from four secondary meat processing facilities. These samples underwent DNA extraction, metagenomic sequencing and qPCR (quantitative Polymerase Chain Reaction) analyses to determine the AMR gene content of the samples. Due to a paucity of publicly available comparable data, determining whether or not the AMR gene content that we found is significant compared with the AMR content of products is challenging. However, data from two relevant studies were compared to the results of the current report, to attempt to contextualise these results.

This research also provided insights into the application of metagenomic sequencing for AMR surveillance in this context, and contributes to FSA's mission to ensure food is safe to eat. The evidence generated in this project will also help to elucidate the routes by which food can become contaminated with AMR genes and bacteria, which the FSA have a remit to study based on the UK's five-year national action plan on tackling antimicrobial resistance, 2019-24.

It is worth noting that this project took place during the most severe phase of the global SARS-CoV-2 pandemic, which had a significant impact on several aspects of the work (notably the sampling method development, due to limitations on face-to-face collaborative work between institutions, and the sampling itself, as project team members could not access the facilities to perform sampling themselves). The project was able to overcome these limitations by making increased use of remote collaboration techniques, and by relying on the expertise and willingness of the factories to perform sampling themselves.