

What is the burden of antimicrobial resistance genes in selected ready-to-eat foods?

Area of research interest: [Antimicrobial resistance](#)

Study duration: 2019-02-04

Project code: FS301050

Conducted by: Fera Science Ltd

Background

AMR is a high priority area for the UK government and a worldwide concern. There has been a focus on the prevalence of AMR genes in raw meats due to concerns about carryover from agriculture. There is however an evidence gap concerning the presence of AMR genes in RTE foods. As RTE foods are generally consumed without further processing, any bacteria and AMR genes present have an increased chance of coming into contact with the human gut microbiome. This could be an important dietary driver of AMR and evidence is needed to assess the contribution from this source. The data gathered will also inform future risk assessments on AMR and RTE foods.

Objectives and Approach

An evidence gap has been identified on the prevalence of AMR genes in RTE foods, as much of the surveillance is currently in raw retail meats.

This study aims to sample RTE foods at retail to determine the prevalence of AMR genes. The work should provide data on the relative abundance of AMR genes and allow an estimate to be made of consumer exposure.

A brief literature review of existing prevalence data will guide the sampling strategy. Samples will be selected from four broad categories; cooked meats, dairy products, seafood and fresh produce, and will be representative of UK consumption.

All 1000 samples will be screened to determine presence of bacteria and suitability for sequencing. 256 samples will be selected for full metagenomic sequencing to determine the prevalence of AMR genes.

A small subset will also be sequenced using the emerging PromethION platform from Oxford Nanopore Technologies. The PromethION may provide additional information such as the genomic location and hosts of the AMR genes, which may be relevant for assessment of multidrug resistance.