

# Antimicrobial Resistance in Biofilms: Recommendations for work

In order to produce a more reliable estimate of burden, suggestions to address knowledge gaps are:

- more consistent coding of processed food types that are linked to biofilms (determined from samples or expert judgments). Where possible these should also consider the food types with food codes as used in the NDNS
- larger samples from processing plants representative of UK consumption. The summaries showing the main meat products (by numbers of consumers) could be used to target individual production lines. Processing of minced beef products should also be included. However, we have found this may be limited due to practical constraints
- sampling of processed food items and intake carcasses in addition to the biofilms on the production lines. This would potentially allow a direct comparison to understand the level of ARGs transferred to the product. This could include isolation, phenotypic testing and WGS of indicator organisms, which would remove the difficulties of dealing with the “kitome”. It would also give clear evidence of phenotypic AMR burden (instead of inference from presence of genes) and possibly allow comparison of strains (or even plasmids) to identify transmission pathways.

## Acknowledgements

We gratefully acknowledge the participation of the companies and factories involved in this project, without whom the work could not have been performed.

We acknowledge the help and guidance of the FSA, especially Dr Iulia Gherman and Dr Erin Lewis.

NovaSeq 6000 sequencing of libraries prepared at Fera was performed at Newcastle University Genomics Core Facility, under the direction Dr Jonathan Coxhead.

Thanks to Paul Browning (Freedom Hygiene) and Rob Limburn (Campden BRI) for discussions around biofilm sampling and the use of Biofinder spray.