# Annex A: Overview of PATH-SAFE WSs and Projects

## Table 5 Overview of PATH-SAFE WS activity

| Responsible government department | Work Stream (WS) | Target pathogen | WS project | Summary of project |
|---|---|---|---|---|
| FSA | WS1 - Establish a curated and national foodborne disease genomic data platform | *Salmonella* | 1a | The flagship project of PATH-SAFE. Providing recommendations for building an end-user organisation-independent, interoperable system that will collate raw Salmonella WGS data, post-processed and analysed WGS data, and a small subset of related isolate or sample metadata to predict, detect, and proactively mitigate Salmonella outbreaks through generating comprehensive low-level and high-level reports. |
| FSS | WS1 - Establish a curated and national foodborne disease genomic data platform | *E.coli* | 1b | Known as 'the Scottish pilot'. Understanding source attribution, infection threat and level of AMR of E. coli. isolated from a range of different reservoirs in Scotland, including animal hosts, wastewater, shellfish, food and humans (i.e., determining which E. coli (and their resistance genes) are present in food and how these relate to those that can be associated with serious disease in humans). |

| Responsible government department | Work Stream (WS) | Target pathogen | WS project | Summary of project |
|---|---|---|---|---|
| DEFRA | WS2 - Pilot new FBP and AMR surveillance tools using novel technologies (for example, WGS) based on regular, multi-location sampling in a range of settings. | *Salmonella, Listeria, Norovirus, E. coli* | 2a Study A | Providing evidence to support integrated, effective and cost-efficient targeting of surveillance measures that will aid the prevention and/or mitigation of FBP outbreaks and increase understanding of transmission routes for AMR genes.<br><br>Comparing pathogen prevalence and diversity in two river catchments and assessing onward pathogen transport. Focus on Salmonella, Listeria, and E.coli. |
| DEFRA | WS2 | *Salmonella, Listeria, Norovirus, E. coli* | 2a Study B | Providing evidence to support integrated, effective and cost-efficient targeting of surveillance measures that will aid the prevention and/or mitigation of FBP outbreaks and increase understanding of transmission routes for AMR genes.<br><br>1. Understanding the temporal and spatial distribution of Norovirus in England and evaluating the effectiveness of wastewater-based epidemiology (WBE) for Norovirus surveillance. Focus on Norovirus.<br><br>2. Assessing the effectiveness of wastewater surveillance for Salmonella and providing genomic sequence data on the diversity of Salmonella to feed into the WS1 database. Focus on Salmonella. |

| Responsible government department | Work Stream (WS) | Target pathogen | WS project | Summary of project |
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| DEFRA | WS2 | *Salmonella, Listeria, Norovirus, E. coli* | 2a Study C | Providing evidence to support integrated, effective and cost-efficient targeting of surveillance measures that will aid the prevention and/or mitigation of FBP outbreaks and increase understanding of transmission routes for AMR genes.<br><br>Known as 'the Bangor study'. Investigating the potential use of data-driven 'active management' approaches to monitor, predict and limit the spread of microbial pathogens and the resistome in the context of recreational waters (for example, rivers, coastal zone) and shellfisheries in Wales. Focus on AMR and Norovirus. |
| FSA | WS2 - Pilot new FBP and AMR surveillance tools using novel technologies (for example, WGS) based on regular, multi-location sampling in a range of settings. | *E. coli, salmonella, listeria, campylobacter, enterococci, S. aureus,* ESBL producing *E. coli,* ESBLs, Carbapenemase | 2b.1 | Focus on determining impacts on agri-food system.<br><br>Investigating AMR genotypes of ESBL/ampC/carbapenem/colistin isolates being collected through AMR monitoring of raw retail meat in 2021 (beef and pork) and 2022 (turkey and chicken) in GB, and from livestock caeca (poultry and pigs) from Northern Ireland (NI) since 2015, to help determine any changes in the AMR trends within UK. Focus on E. coli. |

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| FSA | WS2 (as above) | *E. coli, salmonella, listeria, campylobacter, enterococci, S. aureus,* ESBL producing *E. coli,* ESBLs, Carbapenemase | 2b.2 | Focus on determining impacts on agri-food system.<br><br>Piloting a novel approach for AMR surveillance in livestock (using sheep) with whole genome sequencing (WGS) and metagenomics approaches alongside phenotypic testing in the abattoir environment and wastewater. Focus on *Salmonella*, *E. coli, Enterococci,* and *Campylobacter*. |
| FSA | WS2 (as above) | *E. coli, salmonella, listeria, campylobacter, enterococci, S. aureus,* ESBL producing *E. coli,* ESBLs, Carbapenemase | 2b.3 | Focus on determining impacts on agri-food system.<br><br>Establishing the prevalence of AMR in indicator organisms and foodborne pathogens in UK cattle at slaughter and comparing the results to existing surveys of beef at retail. Focus on E. coli, ESBLs, Carbapenemase, *Enterococci, Campylobacter.* |
| FSA | WS2 (as above) | *E. coli, salmonella, listeria, campylobacter, enterococci, S. aureus,* ESBL producing *E. coli,* ESBLs, Carbapenemase | 2b.4 | Focus on determining impacts on agri-food system.<br><br>Providing an overview of AMR genes and AMR bacteria in raw milk. Focus on *E. coli*, ESBL producing *E. coli, Enterococcus, S. aureus* |

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| FSA | WS2 (as above) | *E. coli, salmonella, listeria, campylobacter, enterococci, S. aureus,* ESBL producing *E. coli,* ESBLs, Carbapenemase | 2b.5 | Focus on determining impacts on agri-food system.<br><br>Identifying raw animal feed ingredients and countries of origin presenting the greatest risk of introducing AMR into UK agri-food chains. Focus on *Salmonella*. |
| FSA | WS2 (as above) | Norovirus, influenza, SARS-CoV-2 | 2c | Known as 'the NI pilot'. Determining if building-level wastewater sampling can be used to detect AMR and screen for Norovirus in 2 care homes in NI. |
| FSA | WS2 (as above) | *Campylobacter* | 2d | Investigating routes of transmission and levels of AMR amongst *Campylobacter* isolates from UK Agri-Food sources. |
| FSA | WS2 (as above) | *Salmonella* | 2e | Identify appropriate pathogen isolate collections that could be whole genome sequenced to generate background data on the genomic diversity of foodborne pathogens in the UK, and to feed into the WS 1a data system. Small piece of work. |
| FSA | WS3 - Map and test new and repurposed technologies for rapid onsite FBP testing in collaboration with end users | Norovirus, *Campylobacter, Salmonella, Listeria, Clostridium* | 3a | Landscaping and TRL study. Testing the feasibility of using portable diagnostics as inspection tools for FBP. The results will inform a pilot in-field testing study to create a legacy output which can then be used to prime future studies. |

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| UKHSA | WS3 - Map and test new and repurposed technologies for rapid onsite FBP testing in collaboration with end users | Norovirus, *Listeria*, *Salmonella*, Adenovirus, Astrovirus, Rotavirus, Sapovirus | 3b | Repurposing rapid, in-field wastewater diagnostic technology that were developed in response to the COVID-19 pandemic for detection of foodborne pathogens and demonstrating its viability, economic and informational value, and versatility in one or more agri-food settings.<br>[Linked to WS3a (results may have an impact on the technology readiness level assigned to loop-mediated isothermal amplification (LAMP) for FBP detection) and the other wastewater work (WS1b, WS2a, WS2b, WS2c, WS4)] |

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|---|---|---|---|---|
| DEFRA and UKHSA | WS4 - Develop a pilot AMR surveillance system based on mechanisms of AMR spread in the environment | Applied methodology:<br><br>Testing comprehensive range of methodologies to examine AMR in a range of environmental media (river water, bioaerosols and shellfish)<br>Applied methodologies include:<br><br>Surface (river) waters:<br>- Phenotypic testing of total and ESBL-E. coli, total and vancomycin-resistant Enterococcus sp., yeast and mould species<br>- Antimicrobial Susceptibility testing of bacterial and fungal isolates<br>- Whole Genome Sequencing of bacterial isolates<br>- Metagenomic Sequencing<br>- High-Throughput detecting and quantification of 248-384 Antimicrobial Resistance Genes<br>- Chemical analysis of 41 antimicrobial substances<br><br>Bioaerosols: trial | N/A | Testing a comprehensive range of methodologies to assess the role and impact of AMR in the natural environment (for example, river water, bioaerosols and shellfish). Environment focus (impact on anything outside of agri-food system). |