

Title: Whole Genome Sequencing *Salmonella* for typing and epidemiological investigation

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Background:

The Animal and Plant Health Agency (APHA) is the UK National Reference Laboratory for *Salmonella* in animals. All isolates from livestock species, animal feed and dogs in England and Wales (and the statutory isolates from poultry from Scotland) are sent for typing to the APHA Weybridge laboratory. Typing was traditionally carried out by phenotypic serotyping of *Salmonella* using agglutination tests. Serovars are derived by reference to the White Kauffmann-Le Minor Scheme (WKLM).

The UK Health Security Agency (UKHSA) is responsible for typing isolates obtained from people. Since 2014, UKHSA has been characterising *Salmonella* isolates through whole genome sequencing (WGS). To enable effective One Health working, surveillance, cluster identification and outbreak response, APHA has implemented WGS-based typing for *Salmonella* as its primary method of characterisation. Here I reflect on the steps that were taken to operationalise this process, offer lessons learnt and demonstrate impact of this new approach in a veterinary and One Health setting.

Methods:

Salmonella control and hygiene regulations in the veterinary sector impose the use of the conventional WKLM serotyping scheme. However, alternative methods may be used if they have been validated in accordance with internationally recognised standards and offer equivalent results to those obtained by the reference method.

Firstly, a *Salmonella in-silico* typing platform was designed, incorporating free and open-source software and bespoke differentiation of strains important for veterinary surveillance (<https://github.com/APHA-BAC/NextflowSerotypingPipeline>). The performance of the pipeline was validated against the reference method in accordance with the requirements of ISO 16140-6:2019. Once validation was complete, expert rules were designed and the pipeline was linked to the laboratory management information system. An application was then made to the UK Accreditation Service for ISO 17025:2017 accreditation. Once this was granted, a soft launch period was followed by implementation in 2023.

The implementation process was managed through a project board approach.

Results and discussion:

Salmonella typing through WGS has been implemented for all isolates of *Salmonella* typed at APHA in 2024, approximately 10 years after the process of shifting from phenotypic to WGS-based typing began. The reasons for this prolonged timeline are many, mostly relating to the quality requirements necessary to adhere to *Salmonella* legislation relevant to the veterinary sector. Furthermore, interaction between bioinformatic pipelines and standard laboratory management systems required intensive coding and troubleshooting. Although the journey was complex, implementation has allowed more efficient and prompt outbreak identification and a One Health approach to investigation and control.