Surveillance programmes based on active and harmonised sampling are considered the most suitable for food-borne outbreak investigations, hypothesis generation, early detection of emerging pathogen subtypes, attribution modelling and genetic studies of bacterial populations. Currently, prototype molecular databases are not widely linked and contain limited epidemiological data, therefore development of linkage mechanisms is a priority. A key technical requirement is determination of an agreed threshold value for the level of genetic variation amongst isolates that can still be regarded as epidemiologically-related. Molecular typing data should be coupled with a minimum required set of epidemiological data and datasets should be comparable to facilitate joint analyses in conjunction with human case data. Rules for assembling strain collections and associated provenance data should be agreed and introduced as EU standards. The data collection process and the characteristics of the data repository should ensure reproducibility and maximise compatibility and interoperability between different datasets. Molecular bacterial characterisation developments, particularly Whole Genome Sequencing (WGS), should be harmonised with those used for surveillance in the human population and food industry. Reference methods and materials, including sequence data, should be adopted for typing of food-borne pathogens. Upload of molecular data should only be allowed for approved laboratories and should be subject to External Quality Assessment. Ongoing international oversight is required to ensure a consensual ‘one-health’ approach. The establishment of a joint EFSA-ECDC-EU-RLs committee for the support of cross-sectoral molecular surveillance, with a balance of public health and veterinary expertise and including both epidemiologists and microbiologists is strongly recommended. Revision of the legal basis of programmes for pathogen reduction based on historic organism nomenclature may be necessary following the increased use of WGS and the subsequent identification of more biologically relevant groupings of organisms.

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