

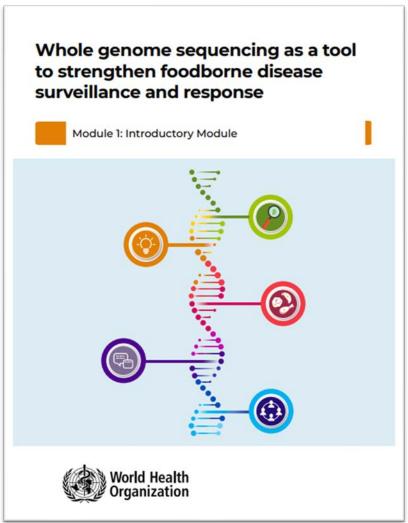
Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response

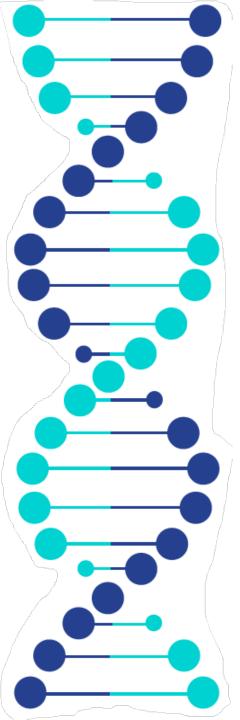
Dr Kirsty Hope

WHO Health Talks Friday 9 June 2023

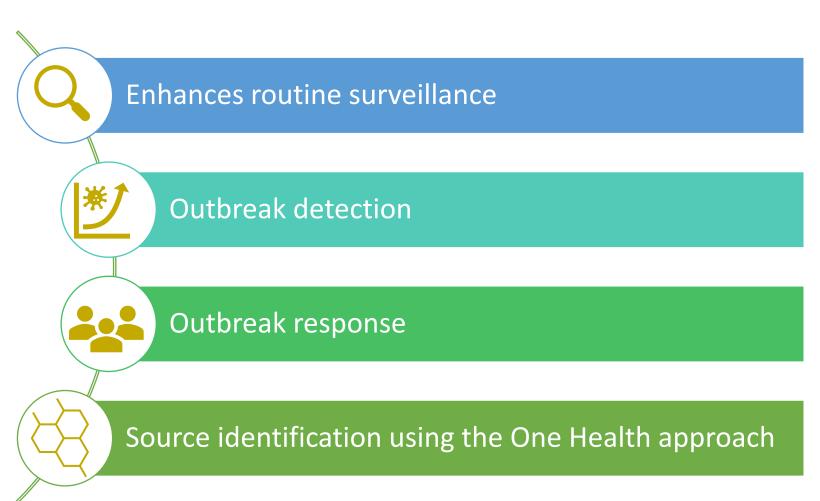
# Whole genome sequencing (WGS) as a tool to strengthen foodborne disease surveillance and response

- Introduction and objectives
- Why is WGS for foodborne pathogens important?
- How the results from WGS be used for surveillance and outbreaks of foodborne diseases?



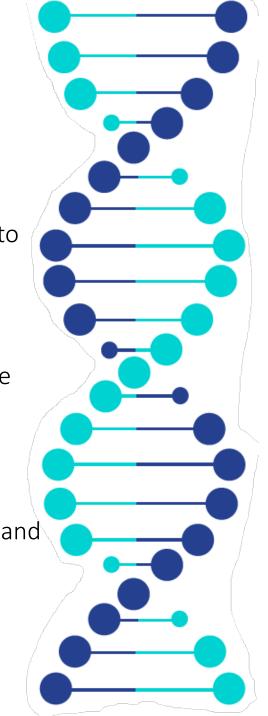


## How is WGS useful for response to foodborne diseases?



### **Guiding principles**

- 1. Focus is on building on existing national surveillance and response systems
- 2. Surveillance is needed to detect and respond effectively to acute public health events to minimize the adverse impact on public health and the economy.
- 3. National surveillance and response systems in countries are at different levels of development and complexity, with different requirements and priorities
- 4. Developments outside the health sector can strengthen foodborne disease surveillance and response systems
- 5. Commitment at the senior policy and decision maker-level to using WGS is vital
- 6. Introducing and using WGS requires sufficient human and financial resources
- Existing international networks can have resources to strengthen national surveillance and response systems.

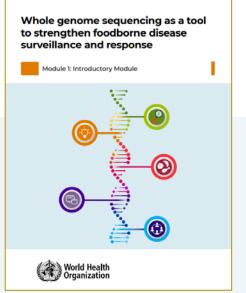


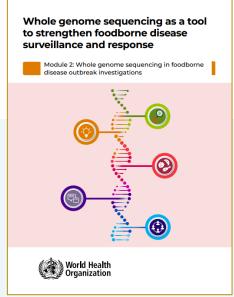
#### WHO's new guidance document:

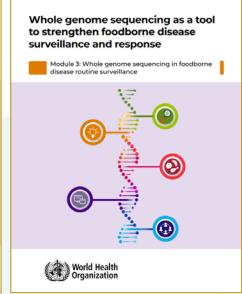
#### Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response

- Motivation
- Development

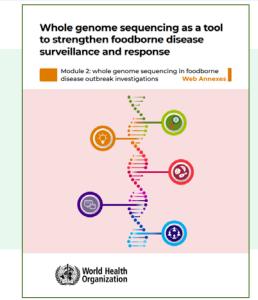
Modules 1, 2, and 3

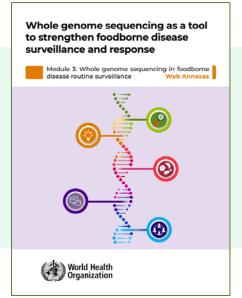






Web Annexes 1 and 2



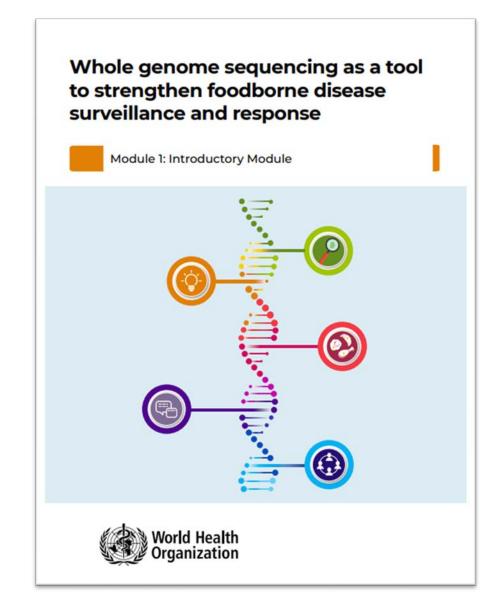


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### Introductory module

It is not necessary to read all three modules. The purpose of the first module is to:

- introduce WGS and its relevance to foodborne diseases
- define the minimum capacities needed before a country can implement WGS for outbreak investigations and routine surveillance
- assist countries in selecting an option for implementing WGS within their existing surveillance and response system



### **Outbreak module**

This module discusses how WGS can be used to support foodborne disease outbreak investigations.

It is meant for countries in the initial stages of laboratory-based surveillance for selected foodborne pathogens.

The module describes how WGS can be used in the investigation of outbreaks detected by existing surveillance systems.





### Surveillance module

This module is about using WGS in routine surveillance of foodborne diseases.

It is meant for countries experienced in laboratory-based surveillance of foodborne pathogens.

WGS can be implemented where subtyping foodborne pathogens or replacing traditional typing methods is being considered.

Routine surveillance includes outbreak detection, monitoring trends over time, and using WGS for AMR and virulence factor monitoring.

### Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response

Module 3: Whole genome sequencing in foodborne disease routine surveillance







## Annex 2: Outbreak investigations

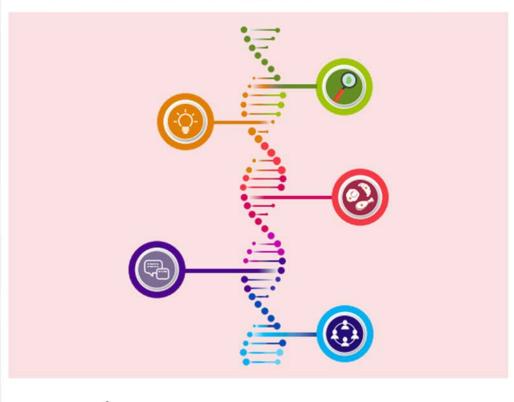
- Working group terms of reference
- Mapping, outsourcing and establishing wet lab sequencing capabilities and the bioinformatics component in the public health laboratory
- Epidemiologists and WGS during outbreak investigations
- The role of key stakeholders
- Points to communicate to decision makers
- Templates:
  - System description
  - Requirements document
  - Mapping wet and dry lab sequencing capacities
  - Business case
  - Cost estimates
  - Pilot study plan
  - Managing implementation

### Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response



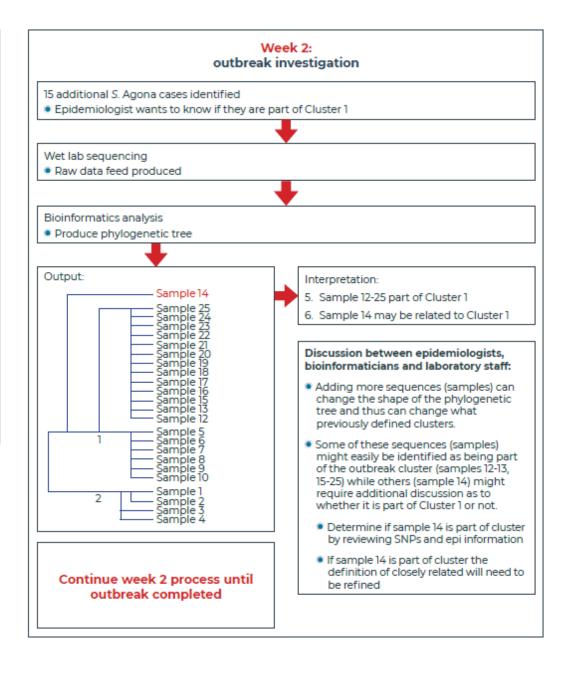
Module 2: whole genome sequencing in foodborne disease outbreak investigations

Web Annexe





#### Week 1: WGS of initial case 10 Salmonella Agona cases identified in one week Possible outbreak • As S. Agona is a common pathogen, we need to know if any of the 10 cases are closely related Wet lab sequencing Raw data feed produced Bioinformatics analysis Produce phylogenetic tree Interpretation: Output: Sample 5-10 closely related\* Sample 5 Sample 6 Sample 7 2. Sample 1-2 may be closely related to Sample 8 each other Sample 9 Sample 10 3. Samples 1-4 are different from samples Sample 2 Sample 3 Sample 4 4. Samples 5-10 defined as 'Cluster 1' and for further investigation



<sup>\*</sup>Closely related can mean different things depending on the organism, time between sample collection, and possible source, etc.



## Annex 3: Routine surveillance

- Working group terms of reference
- Establishing wet lab sequencing capabilities and the bioinformatics component in the public health laboratory
- Case studies
- The role of key stakeholders
- Points to communicate to decision makers
- Templates:
  - System description
  - Requirements document
  - Mapping wet and dry lab sequencing capacities
  - Business case
  - Cost estimates
  - Pilot study plan
  - Managing implementation

## Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response



Module 3: Whole genome sequencing in foodborne disease routine surveillance

Web Annexes







## Annex 3: Routine surveillance

#### • Case studies:

- US Centers for Disease Control and Prevention
  - PulseNet USA
- Public Health England (PHE)
- Public Health Agency of Canada
- Malbran Institute in Argentina
- PulseNet international





### Thank you

For questions, please email <a href="mailto:fbd-burden@who.int">fbd-burden@who.int</a>

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