**ODIN Project – Tanzania**

**Co-organizers: National Public Health Laboratory (NPHL) &National Institute for Medical Research (NIMR)**

# REPORT

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**Workshop Title:**

## Strengthening Next Generation Sequencing Capacity for Wastewater Surveillance of Waterborne Pathogens and Emerging Threats in Tanzania

**Dates:** 21st – 29th July 2025
**Venues:**

*Wet-Lab Genomics and Bioinformatics Training:* National Public Health Laboratory (NPHL), Mabibo, Dar es Salaam

**Co-hosting Institutions:** National Public Health Laboratory (NPHL) and National Institute for Medical Research (NIMR), Tanga

## Background

Access to clean water remains a critical public health challenge across low- and middle-income countries (LMICs). Contaminated water sources contribute significantly to the global burden of waterborne diseases, leading to approximately 1.7 million deaths and widespread morbidities annually. In sub-Saharan Africa, recurrent outbreaks of cholera and other diarrheal diseases caused by pathogens such as *Vibrio cholerae*, *E. coli*, and other emerging pathogens are frequent and worsened by inadequate sanitation, climate change, and fragile healthcare systems.

Additionally, the emergence and spread of antimicrobial resistance (AMR) in waterborne pathogens pose a growing threat to effective treatment and disease control, fueled by factors including inadequate sanitation management and antibiotic residues in wastewater. The ODIN Consortium aims to address these challenges.

The ODIN project is implemented in Tanzania by the National Institute for Medical Research (NIMR) and the National Public Health Laboratory (NPHL-Tanzania), in collaboration with global partners from Europe and Africa.

The project aims to strengthen national genomic surveillance capacity by building local expertise through targeted training in Next-Generation sequencing (NGS) and bioinformatics. This empowers Tanzanian scientists to enhance early detection, monitoring, and response to waterborne disease outbreaks and AMR threats, while addressing climate change impacts on pathogen emergence and transmission in the context of One Health.

This initiative directly supports the achievement of Sustainable Development Goal 6 (Clean Water and Sanitation), and promotes resilient health systems, thereby advancing interconnected SDGs related to health (SDG 3), climate action (SDG 13), and poverty reduction (SDG 1) in Tanzania.

The ODIN Consortium is funded by the European Union through the Global Health Partnership (EDCTP3) under Grant Agreement ID: 101103253 (DOI: 10.3030/101103253).

## General Objective

To strengthen Tanzania's national capacity for epidemic preparedness and response by empowering local scientists with hands-on training in Next-Generation sequencing (NGS) technologies and bioinformatics analysis for wastewater genomic surveillance of waterborne pathogens.

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## Specific Objectives

i. Train laboratory scientists on theoretical and hands-on sequencing workflows across available platforms.

ii. Strengthen knowledge in molecular techniques such as sample processing, DNA/RNA extraction, and library preparation.

iii. Build technical capacity in basic genome assembly, variant analysis, antimicrobial resistance (AMR) gene identification, and phylogenetics.

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## Training Modules

### Wet-Lab Genomics Training

**Dates:** 21–24 July 2025 | **Venue:** NPHL Mabibo

**Topics Covered:**

I. Overview of complete NGS workflows, advances in technologies, and experimental design considerations
II. DNA extraction from wastewater isolates, cDNA synthesis for RNA pathogens
III. Library preparation (Tagmentation, amplification, cleanup)
IV. DNA quantification using Qubit and NanoDrop
V. Sample pooling, normalization, and denaturation
VI. Flow cell loading and sequencer operation (MiSeq)
VII. Real-time troubleshooting and maintenance

**Bioinformatics Training**

**Topics Covered:**

VIII. Introduction to Linux and command-line interfaces
IX. Data formats (FASTQ, FASTA, SAM/BAM, VCF)
X. Quality control (FastQC, MultiQC), trimming (FastP, Trimmomatic), and alignment (BWA, Bowtie2)
XI. Bacterial genome assembly ~~pipelines~~ (spades)
XII. Functional annotation (SnpEff, Prokka)
XIII. Detection of AMR and virulence genes, Multilocus Sequence Typing (MLST) (abricate tool, ResFinder, CARD)
XIV. Introduction to Automated pipelines for analysis (bactopia)

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**Achievements of the Training**

a) Improved the capacity of local laboratories to perform Next-Generation genomic surveillance of waterborne pathogens and emerging threats.
b) Enhanced ability to detect, analyze, and report emerging pathogens and AMR from wastewater samples.
c) Strengthened regional preparation for waterborne disease outbreaks and emerging threats through early detection tools.
d) Participants gained skills in using the Linux operating system and performing bioinformatics tasks through the command line.
e) Gained proficiency in bioinformatics tools for analyzing genomic sequencing data generated from bacteria isolates.
f) Processed, analysed, and interpreted bacterial sequence data.

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**Target Participants**

The training included laboratory scientists, genomics and molecular biologists, biomedical professionals, microbiologists, and bioinformaticians from:

**National Public Health Laboratory (NPHL)**

**National Institute for Medical Research (NIMR)**

## Co-ordination and Facilitators

1. Ambele Eliah Mwafulango (Director, NPHL)
2. Athuman Masesa (NPHL)
3. Vito Baraka (NIMR Tanga)
4. Eric Lyimo (NIMR Tanga)
5. Jackson Peter Claver (NPHL)
6. Dennis Mrosso Kado (NPHL)
7. Edna Ereneus Mgimba (NPHL)
8. Lawrence Amon Mapunda (NPHL)
9. Monica Fredrick Francis (NPHL)
10. Zulfa Nzali (ScieX)

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## Trainees

11. Felician Paschal Mgassa (NPHL)
12. Ramadhani Libenanga (NPHL)
13. Hamisi Swalehe (NPHL)
14. Modest Chuwa (NPHL)
15. Steven Mnyawonga (NIMR)
16. Edward Msoma
17. Dick Msuha (NIMR)
18. Renatha Akili (NIMR)
19. Omega Machange (NPHL)

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## Challenges

**Lack of dedicated training laptops:** Low-performance computers hindered smooth execution of bioinformatics pipelines, delaying hands-on sessions.

**Limited training duration:** The 10-day period was not sufficient to comprehensively cover all wet laboratory (NGS) and bioinformatics topics to provide adequate hands-on practice for the trainees.

**Small participant group:** The number of trained personnel remains limited relative to the growing national demand for NGS and bioinformatics expertise.

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## Recommendations / Way Forward

**High-Performance Training Laptops:** To enhance future training efficiency, dedicated laptops with sufficient computing capacity should be provided.

**Extension of Training Duration:** Future workshops should be extended to at least two weeks to allow comprehensive coverage of content and practical engagement.

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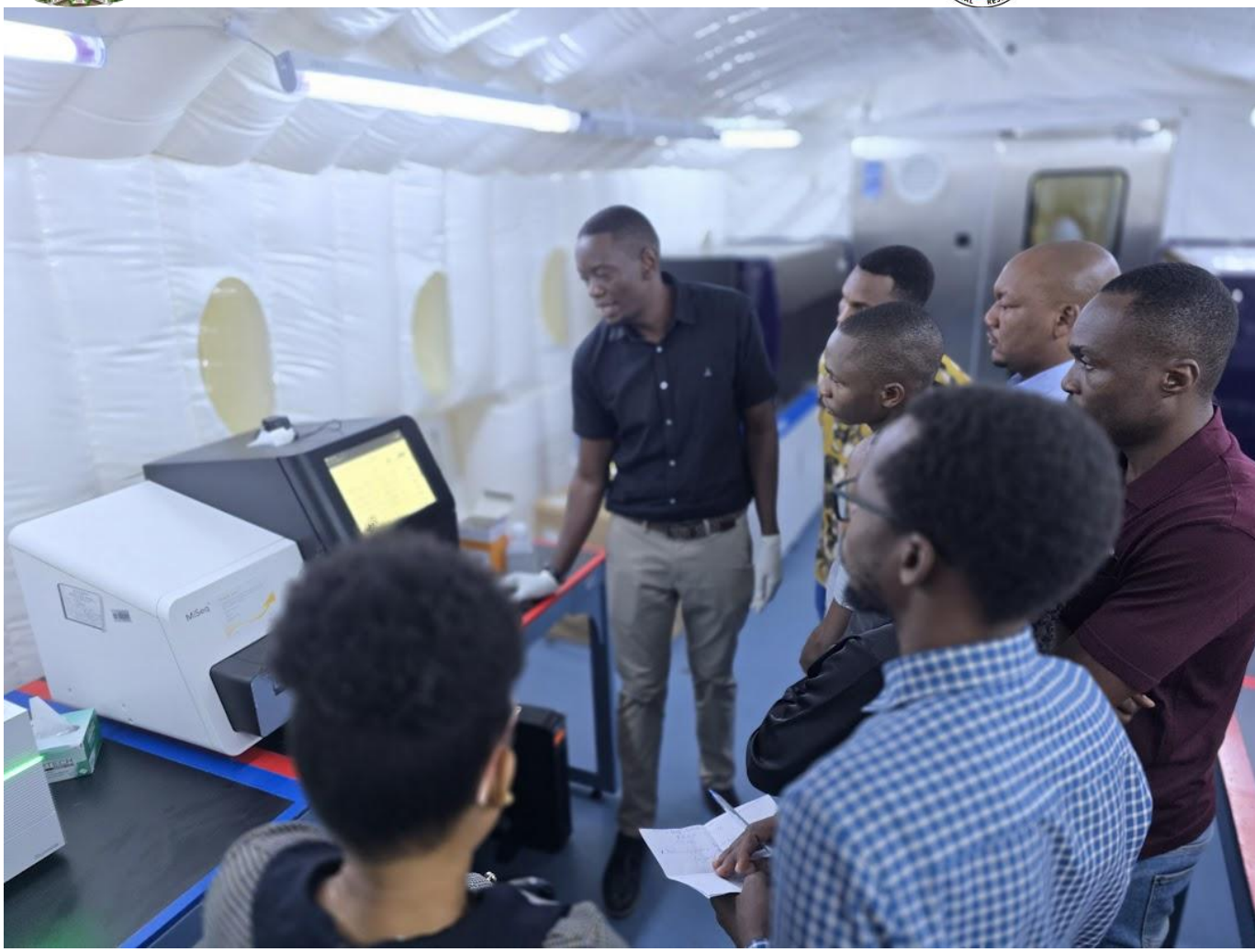
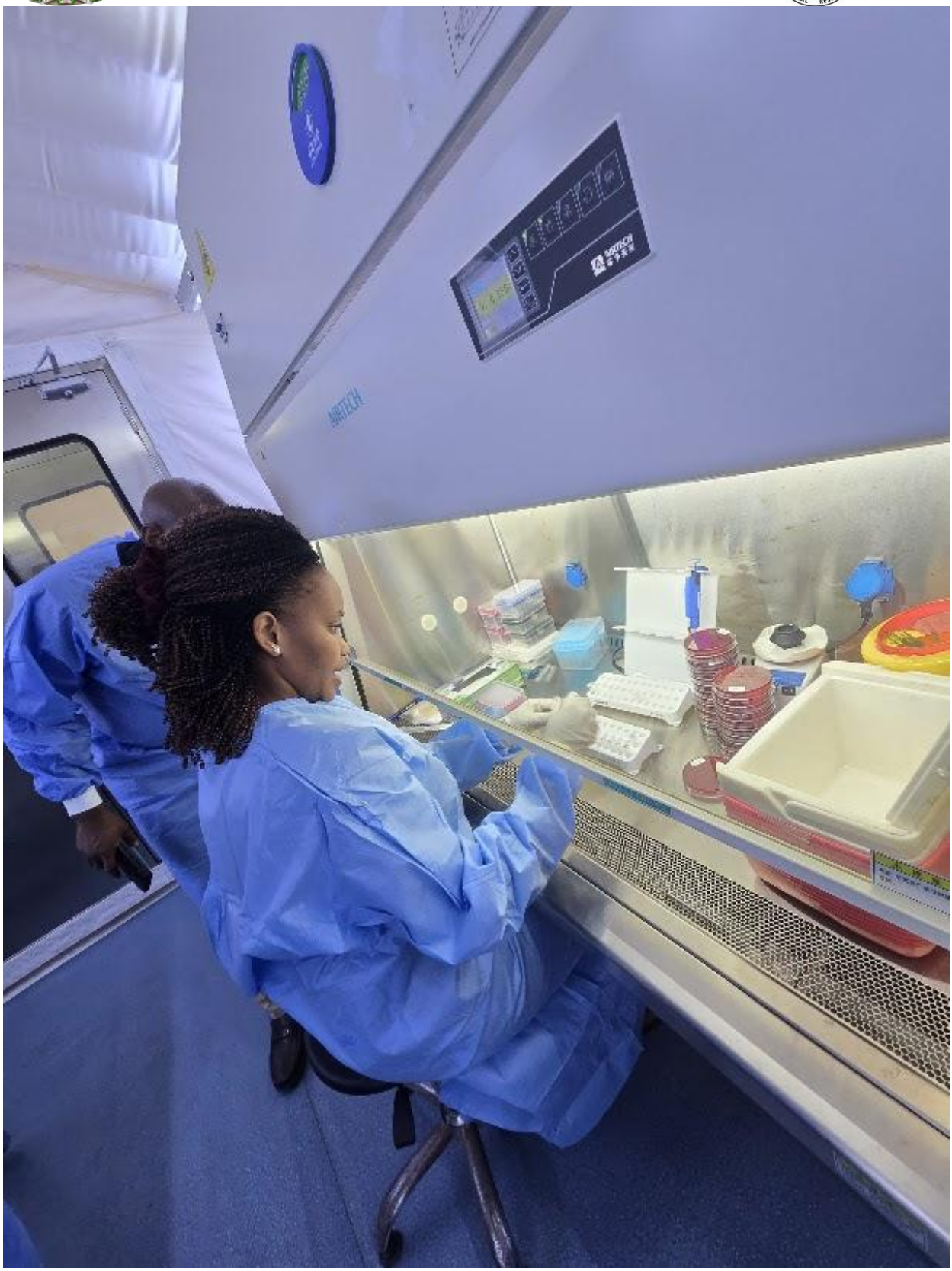
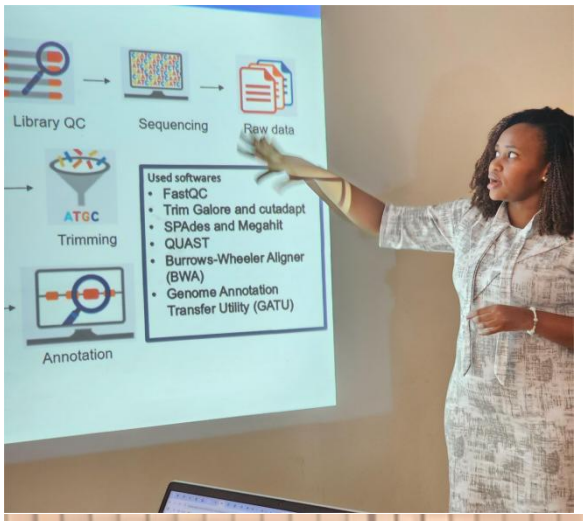
## Pictures

**Group photos of trainees and facilitators**





**Wet-lab activities (Theory training, DNA extraction from bacteria isolates, Quantification, library preparation, and Sequencing)**





Introduction to Bioinformatics & Next-Generation Sequencing (NGS)
for GENOMICS INCOUNTRY TRAINING FOR WET LAB SEQUENCING AND BIONFORMATICS
21st April – 03rd May 2025
National Public Health Laboratory, Dar-es-Salaam, Tanzania
Monica Fredrick Francis (MSc.)
ToT – Bioinformatics


Bioinformatics sessions (Basic command-line operations in a Linux environment, Quality control, genome assembly, Alignment/Mapping, Variant calling, Annotation, and antimicrobial resistance (AMR) gene detection using ResFinder, virulence factor identification, and Multilocus Sequence Typing (MLST))

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**Conclusion**

The workshop was critical in advancing the country public health landscape, significantly enhancing its capacity for early warning system, preparedness and response focusing on waterborne disease outbreaks and emerging health threats such as antimicrobial resistance (AMR). This workshop, fully anchored and supported by ODIN project, demonstrates the ability to effectively implement the ODIN laboratory handbook, across the WES epidemiology from sample collection, laboratory analysis, NGS sequencing and basic bioinformatics analysis.

By building local technical staff in comprehensive skills from NGS laboratory techniques to bioinformatics, the workshop has fostered sustainable improvements in national surveillance and public health systems. The

capacity building is pivotal for robust early warning systems(EWS) responsive to outbreaks, detecting of pathogens, antimicrobial resistance (AMR) and emerging pathogens in WES, enabling timely public health interventions and response. The workshop has impact in strengthening competencies of Tanzanian scientists, to be fully equipped to conduct wastewater based surveillance targeting priority infectious diseases (Vibrio, Salmonella, E. coli and AMR targets), a critical factor in the local , regional and global fight against outbreaks and resistant pathogens.

In the next steps, the ODIN project envisions a sustainable, long-erm national wastewater genomic epidemiology program integrating multipathogen and One health Approach in Tanzania. The program can be institutionalized at NPHI and strategic lab networks capable of wastewater surveillance within the country health system, ensuring continuous monitoring and rapid response capability to infectious disease threats and emerging threats.
Moreover, local experts and scientists trained through this workshop are expected to lead the creation of a national Knowledge Hub and local community of practice. This platform will centralize wastewater genomic data, enable real-time data analytics and support evidence-based decision making to enhance early warning systems (EWS), epidemic preparedness and response. The integration of WES into routine surveillance, together with clinical data, not only strengthens resilience against known and emerging threats but also positions the country as a regional Centre of excellence in environmental surveillance, One Health and innovation within the region.

To further build on gains, the next step is a focused follow up on enhancing data analytics and bioinformatics pipelines specifically for whole genome sequencing (WGS) data, and metagenomics. Focusing on advanced bioinformatics pipelines for WGS and metagenomics within a One Health context will ensure effective data utilization, strong surveillance system, proactive, coordinated public health responses that safeguard both local and broader regional health security.