Whole Genome Sequencing Curriculum

Course Details:

Course Name:	Whole Genome Sequencing Curriculum
Delivery format:	Mostly asynchronous with eventual synchronous activities being added, recorded and becoming asynchronous later.
Workload:	Approximately 11 hours of instructional time total for all modules.

Contact Information:

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Course Description:

Whole genome sequencing (WGS) has become in the last decade the gold standard subtyping method for foodborne pathogens. *Salmonella*, *Listeria*, *E. coli*, *Campylobacter* are among some of the foodborne pathogens for which isolates are routinely sequenced. Sequence data are submitted to a centralized database and available back to Departments of Health through different tools (e.g., SEDRIC), which can be used for comparison of isolates as part of cluster investigations or outbreak responses. This curriculum aims to provide (i) foundational knowledge needed to understand the genetics and genomics of microbial organisms, as well as the WGS data, how it is acquired and processed; (ii) intermediary knowledge regarding how WGS data is used to generate outputs, such as allele codes, phylogenetic trees and single nucleotide polymorphism (SNP) distance matrices, data visualization using SEDRIC, epi-lab communication; and (iii) advanced knowledge on specific topics (e.g., REP strains) that may present additional challenges to surveillance and outbreak investigation.

Prerequisites:

None

Teaching Format:

Recorded webinars, recorded live-learning series (LLS), readings, and eventual synchronous webinars and LLS.

Objectives:

Provide public health professionals working on enterics resources to (i) interpret WGS-based results with confidence, and (ii) carry out investigations more efficiently and accurately. The 3-level modules are designed to help professionals with different backgrounds and training on WGS. The asynchronous, self-paced, format provides flexibility to public health professionals.

By the end of this course, you will be able to:

Learning Outcome	Summary of resources
Understand the differences between viral, bacterial and fungal genomes and how these differences can affect interpretation of WGS results (Module 1)	• Pre-recorded module
Understand how WGS works, from how DNA is sequenced to how SNPs and alleles are identified from the WGS data (Module 1)	• Pre-recorded webinar
Explain how WGS data is used for enterics, including for isolate characterization (e.g., identification of antimicrobial resistance genes, in silico serotyping), and for inferring relatedness (e.g., allele differences, phylogenetic trees) (Module 2)	• Pre-recorded module and webinar
Understand allele codes and how X codes are created and how to handle clusters with X codes (Module 2).	• Pre-recorded Live-Learning Series
Use SEDRIC and NCBI Pathogen Detection for data visualization. Communicate with laboratorians on needs for investigations or surveillance (Module 2)	• Pre-recorded webinars and Live-Learning Series
Identify possible WGS workflows to use, their advantages and disadvantages	• Pre-recorded Live-Learning Series
Identify REP strains, understand their particularities, and develop a strategy to investigate clusters involving REP strains (Module 3)	• Pre-recorded webinar and modules
Identify and use other resources for challenging investigations (Module 3)	• Pre-recorded Live-Learning Series

Overview of Learning Activities:

Module 1 – Basics on microbiology, genetics and WGS
Learning Activities + Assessments
This module will focus on understanding: (1) the differences between various enteric pathogens; (2) genetics and genomics of microorganisms; (3) how sequencing works; and (4) how assemblies are

generated from the raw data.

Through 4 recorded resources (1 module and 3 webinars), you will be introduced to the basics of what makes viruses, bacteria, fungi, and parasites different from each other in terms of their genetics and genomes. You will also see how WGS data is generated and used to assemble genomes that can then be used for identification of genes, alleles, and SNPs.

This module is indicated to those with no Biology background or that would benefit from a refresher before diving deeper on how WGS data is used for enterics.

Module 2 – WGS applied to enterics

This module will focus on understanding how WGS is applied to enterics. These include: (1) what allele type and how they are used in cluster investigation; (2) what in silico characterization can be achieved using WGS data; (3) what are phylogenetic trees and how to use them in surveillance and investigations; (4) how to use SEDRIC, and Pathogen Detection to visualize data; (5) how to interpret allele codes and X codes; and (6) how to efficiently communicate with laboratorians regarding WGS data.

Through a series of pre-recorded webinars and modules, you will learn how WGS subtyping works, how in silico serotyping and identification of AMR genes of certain pathogens (e.g., Salmonella, E. coli) can be helpful for surveillance and investigations, how to navigate several tools for data visualization, and how laboratorians can help you (and how they can´t) in terms of WGS data analyses.

This module is indicated for those who are new to enterics, or those who need a refresher in some intermediate-level aspects of WGS before diving deeper into advanced topics, such as REP strains and additional visualization tools for outbreak investigation.

Module 3 – Advanced topics involving WGS

This module will focus on understanding REP strains and applying visualization tools for outbreak investigation and communication. This will include: (1) learning how REP strains are defined and what differentiates these strains from others; (2) identifying specific strategies for investigating REP strains; (3) identifying tools for WGS data visualization; and (4) learning how to summarize and communicate WGS results.

Pre-recorded webinars and suggested readings will walk you through these advanced topics and provide you with the resources needed to confidently deal with REP strains and X codes in your tasks.

This module is indicated to all epidemiologists working with enterics that have not had previous training on REP strains or visualization tools, and for those looking to refresh their knowledge on these topics.