Introduction to exercises
2nd Multidisciplinary training workshop
October 2023

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Exercises

Learning objectives

- The microbiologist and epidemiologist will throughout the exercise apply steps of an epidemiological outbreak investigation, conduct whole genome sequencing (WGS) analyses and interpret the results

- Each specialist will acquaint themselves with the terminology from the other field of expertise

- The primary focus will be to improve the communication and the information flow between the microbiologist and the epidemiologist

Exercises

Structure requirements

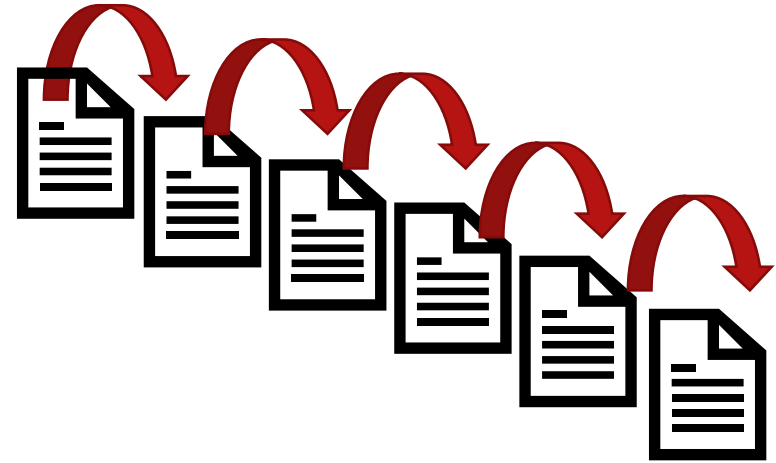- Tabletop outbreak investigation exercise combined with WGS cluster and AMR profile analysis on provided data

The focus is on
- WGS analysis of *Salmonella* / Campylobacter

- cross-sector collaboration

- communications flow

Exercises

Two scenarios

- *Salmonella*
- *Campylobacter*

- Different starting points

- The scenarios develops over time

- **Please DO NOT READ AHEAD**
  - **Some of the answers to the questions will be revealed on the next pages**

General info

IN BLACK:
- Scenario text
- Development of the outbreak, detailed information etc.

IN BLUE:
- *Questions*

Exercises

- Outbreak investigation (some of the 10 steps)
  - Case definition and descriptive epidemiology
  - Patient interviews and hypothesis generation
  - Analytical study
  - WGS analysis and interpretation
  - Traceback and microbiological testing
  - Communication of results

- Open questions to encourage discussion between you (Epi/Micro) or Country
  "How many cases would you inform the epidemiologist about? and how would the information be delivered in your country"?

- **Epidemiologist please include your microbiologist in the interpretation of the epi-data**

- **Microbiologist please include your epidemiologist in the interpretation of the WGS-data**

Exercises

WGS analysis and interpretation

- *Salmonella*:
  - Species identification, subspecies, 7-MLST, serotype, AMR profile, cluster analysis

- *Campylobacter*:
  - Species identification, 7-MLST, AMR profile, cluster analysis

Experience with WGS analyses and interpretation

None   Some   A lot

WGS analysis

Either using your own pipeline setup for cluster analysis and antimicrobial resistance (AMR) profile. Download fastq files **here**, code: FWD_AMR_download

or

Try CGE tools on two fasta files and interpret pre-analysed results
Download fasta files and pre-analysed results **here**, code: FWD_AMR_download

Fastq files

FWD_AMR_download

12 isolates = 24 sequences

Name	Size	Modified	File Download Link
ERR1540398_R1.fastq.gz	251.7 MB	2023-10-16 10:19:55	Download
ERR1540398_R2.fastq.gz	280.8 MB	2023-10-16 10:21:11	Download
ERR1540399_R1.fastq.gz	388.1 MB	2023-10-16 10:22:43	Download

Fasta files

FWD_AMR_download

WING FTP Server

Please input the password for downloading:

[ ] Submit

Wing FTP Server ©2003

2 isolates = 2 fasta files
DATA –HINTS
Outputs CSIPhylogeny (SNPmatrix, newick)

WING FTP Server

Name	Size	Modified	File Download Link
ERR4879885.fa	1.6 MB	2023-10-16 00:39:24	Download
ERR4879914.fa	1.6 MB	2023-10-16 00:39:34	Download
Exercise-Campylobacter_DATA-HINTS.pdf	638.4 KB	2023-10-21 20:47:22	Download
main.snp_matrix_campy.txt	1019 Bytes	2023-10-20 23:39:21	Download
snp_tree.main_tree_campy.newick	400 Bytes	2023-10-20 23:39:25	Download

FWD AMR·
RefLabCap

Data Hints

Links to CGE tools

- *Species identification and contamination evaluation*
- *7 -loci MLST*
- *Serotype*
- *ResFinder*

} *We provide results for 10/12 isolates*

Cluster analysis outputs:

- *CSIPhylogeny (link to the analysis and SNP matrix and newick file)*
- *Enterobase (Allele based) HC levels (Salmonella)*
- *BioNumerics (Enterobase scheme, cgMLST allele differences matrix)*

Breakout session today (from 12:00)

- 5-6 countries/laboratories - one project member

  - Group 1: Egle
  - Group 2: Susanne
  - Group 3: Jette
  - Group 4: Ana Rita
  - Group 5: Jeppe
  - Group 6: Mia

- The breakout session is the final session for today (no plenary afterwards)

FWD AMR·
RefLabCap

Breakout session today (from 12:00)

- Get familiar with the group
- How outbreak investigation in general is organized in the country?
- Criteria for starting investigation (signal detection by lab or epi, number of isolates)?
- How do epi and lab contribute?
- How communication (between epi/micro, to PH authorities, to population)?
- Involvement of other authorities (national and EU level?)
- Point of view on submitting sequences to EpiPulse (real-time, Event, fasta, ENA/NCBI)
- Compare sequences with food/animals?

- How are you planning to conduct the exercise tomorrow (Day 2)
 - together or remotely – teams/zoom?

- Is there a plan for the sequence analysis?
  - Who? Microbiologists and /or Bioinformaticians?
  - How? Own workflows, pipelines or online tools etc.

Exercise release

Today at 13:00 an email with the two exercises will be sent to all participants

- Contact fwdamr@ssi.dk – in case of downloading issues etc.

- Day 2: work with the exercises, the data and interpretation (approx. 3 hours)

Experience with WGS analyses and interpretation

None   Some   A lot
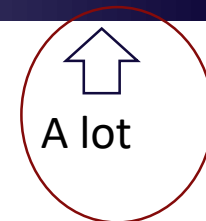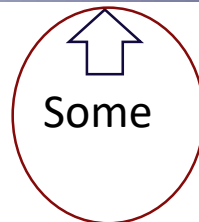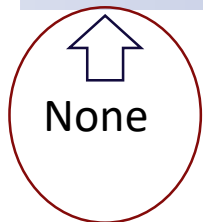
Discuss the exercise in the small groups

Day 3: 9:00 (Group1 -4) or 10:30 (Group 5-6)

- We will talk about the results of the *Salmonella* **exercise**
  - Specific difficulties issues, interpretations, differences between countries etc.
  - lessons learned
  - *only Salmonella labs are invited*

Day 4: 9:00 (Group1 -4) or 10:30 (Group 5-6)
- We will talk about the results of the *Campylobacter* **exercise**
  - Specific difficulties issues, interpretations differences between countries etc.
  - lessons learned
  - *only Campylobacter labs are invited*

Group 5: Egle, Group 6: Susanne

**2ⁿᵈ Multidisciplinary training workshop
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LUNCH BREAK BACK AT 12:00