

Outbreaks, typing and AMR/Day 7

Introduction to the module

Section of Foodborne infections

Dep. of bacteria, parasites and fungi, Statens Serum Institute

March 2024

Overall aim of the module

To provide participants with the **basic theoretical knowledge** and **practical experience** of WGS-based analysis of foodborne pathogens for routine surveillance and outbreak investigations

Program



9-9.25 **Intro to WGS-based FWD surveillance** (*lecture*)

9.25-12 ***Listeria* outbreak detection** (*lecture+practical*)

Lunch

13-14.30 **Serotyping and virulence typing** (*lecture+practical*)

14.30-16 **AMR and point mutations detection in *Salmonella***
(*lecture+practical*)

Teaching team



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Outbreaks, typing & AMR/Day 7

Introduction to WGS-based FWD surveillance workflow

Section of Foodborne infections

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Objectives

Specific objectives of this session:

1. Familiarise with an example of FWD surveillance workflow
patient → result reporting
2. Familiarise with an example of WGS setup for surveillance and outbreak detection of FWD pathogens
sequence → typing results

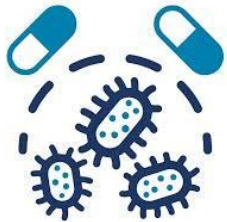
FWD surveillance workflow

Laboratory-based surveillance of FWD infections in Denmark

Real-time typing/characterisation of isolates from patients



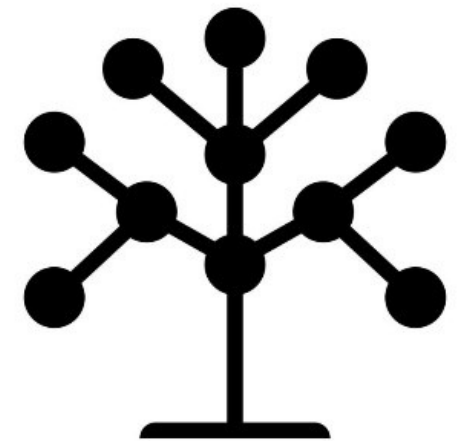
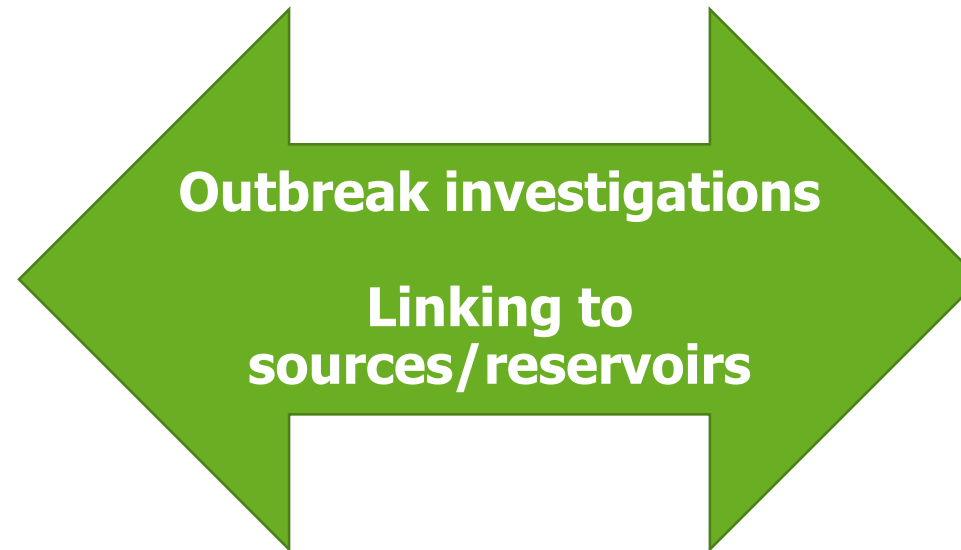
**Species,
serovars**



**Antimicrobial
resistance**



**Virulence
potential**



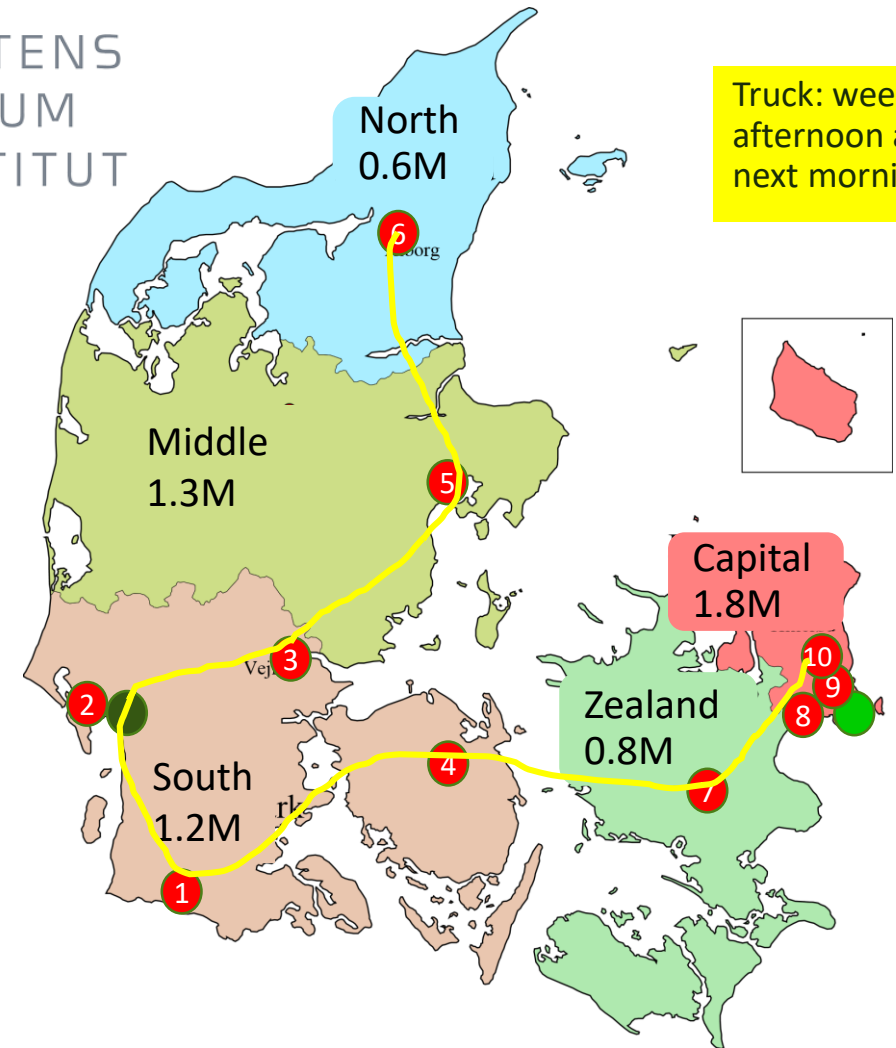
**Cluster
detection**

Clinical isolates for surveillance 1/2



Denmark 5.6M, 5 healthcare regions

- 10 Dept. Clinc. Microbiol. (DCM)
- Copenhagen, SSI=National Ref. Center



Clinical isolates for surveillance 2/2

Listeria

- WGS since 2013, approx. 50 isolates/year
- nearly 100% of the cases

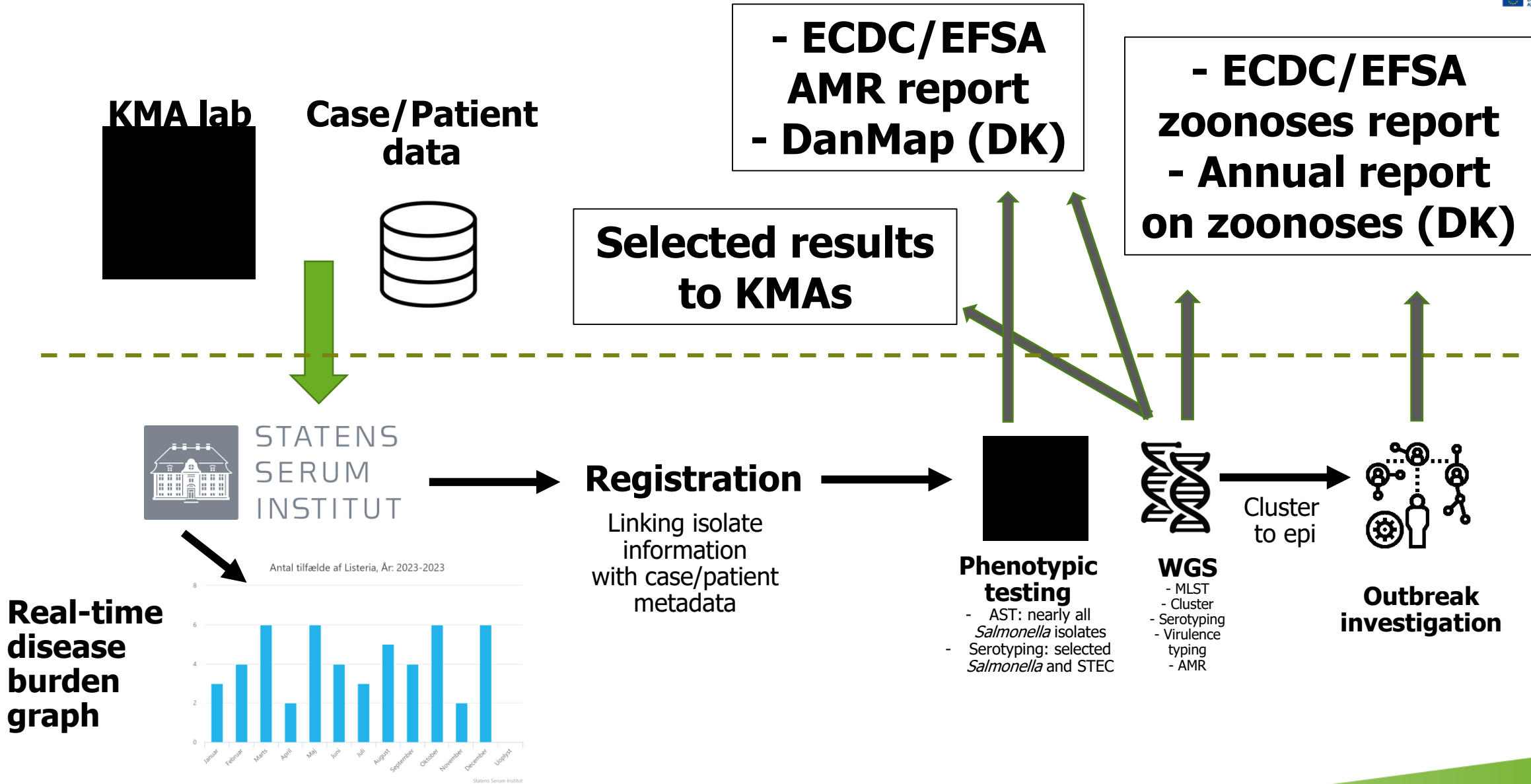
STEC

- WGS since 2015, approx. 450 isolates/year
- only *stx2* or *stx2a* and *stx2d* – positive isolates (30% of cases)

Salmonella

- WGS since 2017, approx. 1000 isolates/year
- >95% of the cases

Surveillance data flow



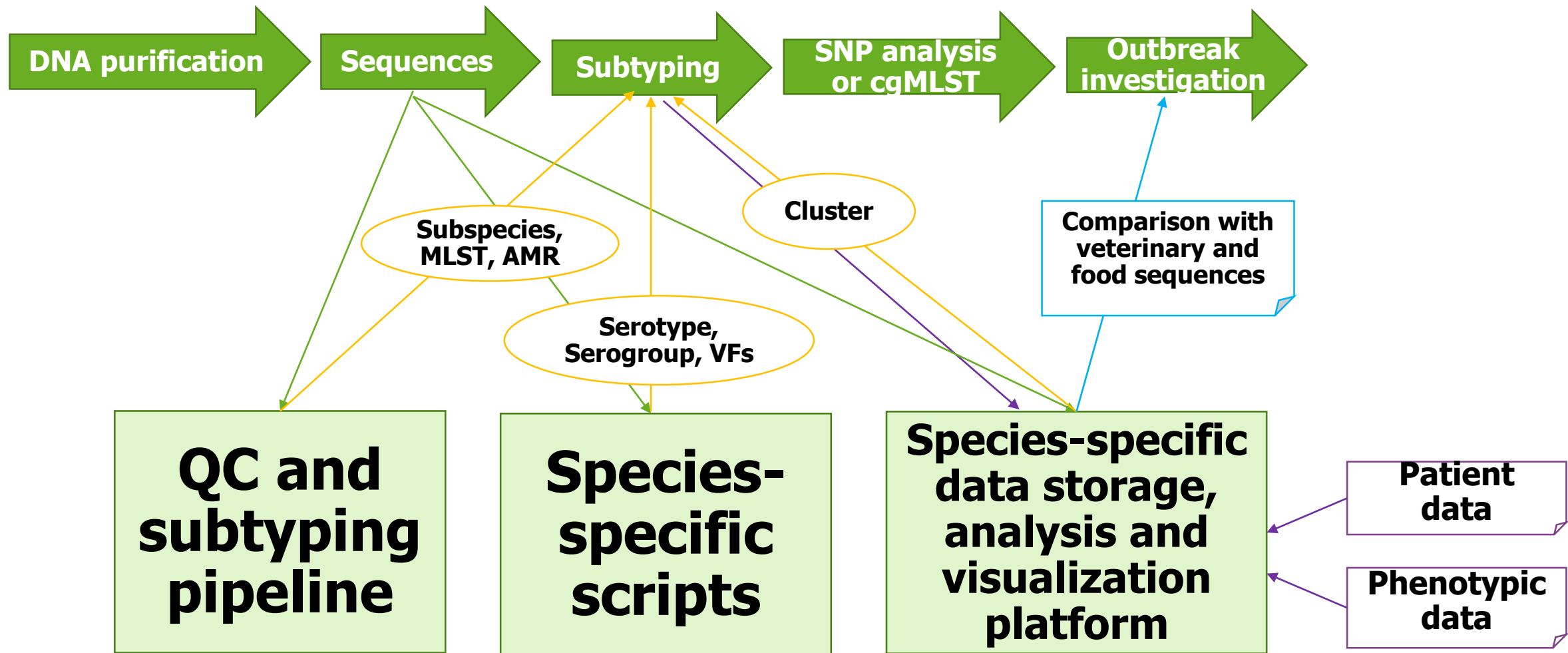
Question for discussion

How FWD surveillance is organized in your country?

- Do you see any similarities and differences?

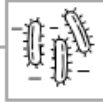
WGS setup for surveillance and outbreak detection

WGS workflow



QC and typing pipeline

Output visible as a web-based dashboard or as *.txt* file.

TRING3S-3


Sample Sheet

Supplied name	TRING3S-3
User Comments	
Supplying lab	FBI
Submitter emails	
Provided species	<i>Salmonella</i>
Read file	TRING3S-3_S3_L555_R1_001.fastq.gz

Detected Organisms

<i>Salmonella enterica</i> + Unclassified	93.98%
<i>Salmonella enterica</i>	88.83%
<i>Escherichia coli</i>	5.09%
Unclassified	7.13%

QC stamps

ssi_stamper	fail:supplying lab
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► MLST/ResFinder/PlasmidFinder/AMRFinderPlus/VirulenceFinder (click to show)

Supplying Lab Feedback: Accept Resequence Other No action

Assemblatron Results

Number of filtered reads	2,999,640
Number of contigs (1x cov.)	260
Number of contigs (10x cov.)	259
N50	38,546
Average coverage (1x)	84.30
Genome size at 1x depth	4,895,661
Genome size at 10x depth	4,895,305
Genome size 1x - 10x diff	356
Genome size at 25x depth	4,889,368
Ambiguous sites	7,421

MLST type: 198

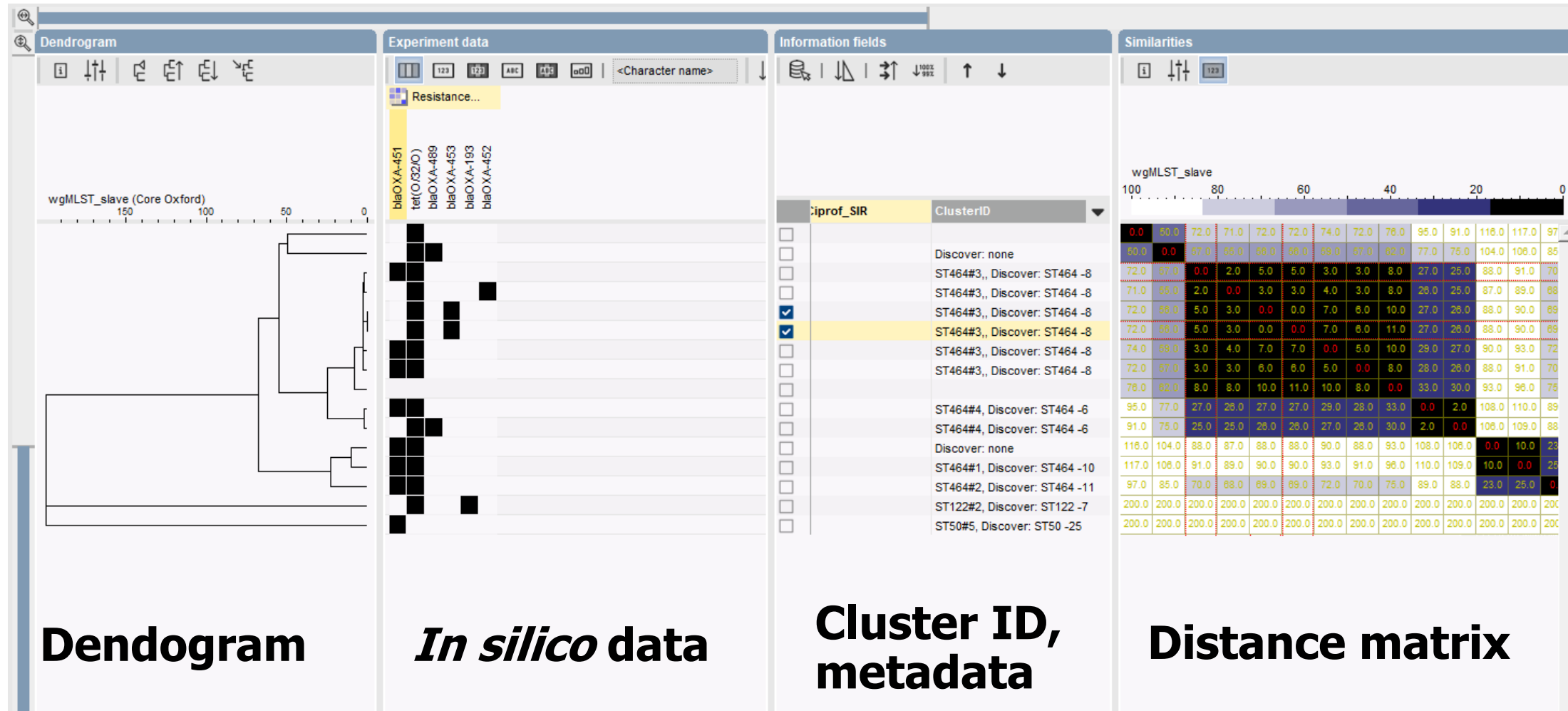
Failed QC tests

Minspecies	Value (0.94) is below threshold (0.95)
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Contains thresholds and provides warnings for actions:

- Unexpected species
- Unexpected genome size
- High number of contigs
- Low average coverage

Platform for data storage, analysis, visualization and reporting



Question for discussion

Do you have a developed bioinformatics infrastructure at your institution?

- Are there plans for it's development?

Take home

FWD surveillance workflow is complex, and may include:

- different institutions
- different departments and units

WGS analysis setup:

- Routinely, WGS data is often analysed using automated pipelines consisting of thoroughly chosen tools, thresholds, nomenclature, etc.

Further reading

[ECDC strategic framework for the integration of molecular and genomic typing into European surveillance and multi-country outbreak investigations 2019-2021. ECDC, 2019.](#)

[Whole genome sequencing and metagenomics for outbreak investigation, source attribution and risk assessment of food-borne microorganisms. EFSA, 2019.](#)

Acknowledgements

The creation of this training material was commissioned by ECDC to Statens Serum Institut (SSI) Danish Technical University (DTU) with the direct involvement of Egle Kudirkiene (SSI), Susanne Schjørring (SSI), Pernille Gymoese (SSI) and Mia Torpdahl (SSI)