Preview of the on-line Result form Cluster Analysis
EURL-*Salmonella* Proficiency Test Typing 2021

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Result form Cluster Analysis

LABORATORY INFORMATION

Laboratory code PT 2021	
Name contact person (Cluster Analysis part)	
E-mail address contact person (Cluster Analysis part)	
Name laboratory or institute (Cluster Analysis part)	
Country	Country:

GENERAL

Did you serotype the strains?
- ○ No
- ○ Yes

Serotyping was done by:
- ☐ Classical serology
- ☐ Molecular method(s), please specify the tool(s) used:

Strain SCA01 serovar name:

Strain SCA02 serovar name:

Strain SCA03 serovar name:

Strain SCA04 serovar name:

Strain SCA05 serovar name:

Strain SCA06 serovar name:

Strain SCA07 serovar name:

Strain SCA08 serovar name:

Strain SCA09 serovar name:

Strain SCA10 serovar name:

REPORTING MLVA RESULTS

Do you want to submit MLVA results?   ○ Yes
                                      ○ No

Please list the allele profile per strain, using the format SENTR7-SENTR5-SENTR6-SENTR4-SE-3
Peferably expressed as e.g.: 3-10-4-4-1

Strain 21SCA01   [   ]

Strain 21SCA02   [   ]

Strain 21SCA03   [   ]

Strain 21SCA04   [   ]

Strain 21SCA05   [   ]

Strain 21SCA06   [   ]

Strain 21SCA07   [   ]

Strain 21SCA08   [   ]

Strain 21SCA09   [   ]

Strain 21SCA10   [   ]

Please report per strain if [yes or no] a clustering match was found with the Reference outbreak strain
in the EURL-*Salmonella* PT Typing 2021:
Salmonella Enteritidis ST11, MLVA type 3-10-4-4-1.
In the PT Typing 2021 setting, the cluster definition for MLVA is set at no loci with a different number of
repeats.

Strain 21SCA01   ○ Yes ○ No

Strain 21SCA02   ○ Yes ○ No

Strain 21SCA03   ○ Yes ○ No

Strain 21SCA04   ○ Yes ○ No

Strain 21SCA05   ○ Yes ○ No

Strain 21SCA06   ○ Yes ○ No

Strain 21SCA07   ○ Yes ○ No

Strain 21SCA08   ○ Yes ○ No

Strain 21SCA09   ○ Yes ○ No

Strain 21SCA10   ○ Yes ○ No

Any comments on the MLVA part: [   ]

REPORTING WGS RESULTS

Do you want to submit WGS results?
○ Yes
○ No

-> Transfer the raw reads (fastq-files), either by using wetransfer.com (multiple sessions may be required) or by uploading the files to the secure RIVM ftp server.
Please contact wilma.jacobs@rivm.nl by email if you need further instructions on the use of the ftp server (also given by email in week 45).

Be sure to name your files including your laboratory code and strain code in the name, preferably like: 21SCA01Lab01_R1.fastq, 21SCA01Lab01_R2.fastq, etc.

Date of sending the WGS fastq files: `dd/mm/yyyy` 📅 dd/mm/yyyy

Do you agree that your raw data files (fastq) from the PT Typing 2021, anonymously re-coded, may also be used for additional research purposes or training?
○ Yes
○ No
○ Other:

-> Email the distance matrix (preferably as an .xls or .csv file) to wilma.jacobs@rivm.nl
Be sure to name the file including your laboratory code, preferably like: Lab01_Distance_Matrix.xls

Date of emailing the distance matrix: `dd/mm/yyyy` 📅 dd/mm/yyyy

If applicable, please enter the md5sum value for the compressed fastq files of the REFerence strain that you downloaded from the secure RIVM ftp server.

md5sum value 21SCA-REF_R1.fq.gz:

md5sum value 21SCA-REF_R2.fq.gz:

DNA extraction was performed:
○ In-house
○ Outsourced

Library preparation was performed:
○ In-house
○ Outsourced

Sequencing was performed:
○ In-house
○ Outsourced

WGS platform used:
○ Illumina HiSeq
○ Illumina MiSeq
○ Illumina NextSeq
○ Illumina NovaSeq
○ Ion Torrent PGM
○ Ion Proton
○ Ion Torrent S5
○ PacBio
○ 454
○ MinION
○ Other:

Please list (up to a maximum of 10) your main criteria that were used to evaluate the quality of the sequence data. If applicable, also include the tool(s) used and the threshold per criterium.
(e.g. contamination, serotype, coverage, N50, number of contigs, etc.)

Criterium 1:

Tool(s) used for criterium 1:

Threshold used for criterium 1:

Criterium 10: [   ]

Tool(s) used for criterium 10: [   ]

Threshold used for criterium 10: [   ]

Please select the analysis used for the WGS data
- ○ SNP-based - reference-based
- ○ SNP-based - assembly-based
- ○ cg-MLST-based
- ○ wg-MLST-based
- ○ Other: [   ]

If you would like to add results performed with a second or even third analysis on the WGS data, please contact wilma.jacobs@rivm.nl by email to receive a second (and third) Lab code for separate results submissions.

Please select the tool(s) used for analysis:
- ☐ BioNumerics
- ☐ Enterobase
- ☐ Ridom SeqSphere
- ☐ Other: [   ]

Which method did you use for cluster analysis?
- ○ Maximum likelihood (ML)
- ○ Minimum Spanning Tree (MST)
- ○ Neighbor joining (NJ)
- ○ Bayesian
- ○ Other: [   ]

Please report per strain if [yes or no] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2021:
21SCA-REF_R1.fq.gz
21SCA-REF_R2.fq.gz
(*Salmonella* Enteritidis ST11, MLVA type 3-10-4-4-1)
In the PT Typing 2021 setting, the cluster definition for WGS is set at maximum 7 allelic differences from the reference sequence.

Strain 21SCA01   ○ Yes ○ No

Strain 21SCA02   ○ Yes ○ No

Strain 21SCA03   ○ Yes ○ No

Strain 21SCA04   ○ Yes ○ No

Strain 21SCA05   ○ Yes ○ No

Strain 21SCA06   ○ Yes ○ No

Strain 21SCA07   ○ Yes ○ No

Strain 21SCA08   ○ Yes ○ No

Strain 21SCA09   ○ Yes ○ No

Strain 21SCA10   ○ Yes ○ No

Any comments on the WGS part: [   ]

FINALLY

Any general comments: [   ]