Proficiency Tests on the identification and typing of pathogenic *E. coli* strains

The use of Whole Genome Sequencing





Proficiency Tests on WGS

PT WGS1 (2017): voluntary inter-laboratory study; only raw data collected

PT23 (2018): characterization by classical methods or WGS; cluster analysis through PFGE

PT26 (2019): characterization by classical methods or WGS; cluster analysis through PFGE or WGS







PT WGS 1 2017-2018

Voluntary inter-laboratories study

The objectives of the study were:

- to evaluate the quality of the sequences produced and the effect on the WGSbased characterisation of STEC
- to evaluate the inter laboratory and platform variability

Methods:

- Wet-lab: Shipment of 6 STEC strains belonging to the same serogroup
- Collection of results: collection of raw reads through IRIDA platform
- **Results analysis**: Analysis of data at EURL VTEC through ARIES Galaxy platform: serotyping, virulotyping, MLST, reference-free wgSNPs, cgMLST, wgMLST





Results PT WGS 1 (2017-2018)

Assembly Coverage

N50 Depth

21 participants (including 3 Italian Official Laboratories) No performance assessment

Results used to evaluate the overall quality of the sequences



Ltbs

1,350

1323

1,700

1.522

1825

1827

1659

1728

LEDT

1302



Strain 5

1800

1843

1185

1792

322

1564

1783

1712

1723

0712

1.305







PTs on NGS E. coli 2018 and 2019 (PT23 and PT26)

The objectives of the studies were:

- The detection of the main virulence genes (for STEC, EAEC and ETEC)
- The detection of a range of relevant serogroups
- stx subtyping
- cluster analysis <u>only through PFGE</u> in PT23 (2018) and <u>through PFGE or WGS</u> (wgSNPs or cgMLST) in PT26 (2019)

The participating Laboratories could submit either the results obtained by applying the laboratory procedures available at the EURL *E. coli* website, based on **conventional and Real Time PCR, or the WGS-based characterization** results.

Methods:

- Wet-lab and dry-lab: Shipment of 6-7 strains, typing results collected
- Collection of results: through a <u>Restricted Area</u> on EURL VTEC website. <u>Manual</u> <u>extraction and analysis</u> of results
- Performance assessment: Same penalty points applied for errors either obtained through conventional methods or through WGS





PTs on NGS E. coli 2020-2022 (PT28, PT31 and PT35)

The objectives of the studies were:

- The detection of the main virulence genes (for STEC, EAEC and ETEC)
- The detection of a range of relevant serogroups
- stx subtyping
- cluster analysis only through WGS (wgSNPs or cgMLST)

The participating Laboratories could submit either the results obtained by applying the laboratory procedures available at the EURL *E. coli* website, based on **conventional and Real Time PCR**, or the WGS-based characterization results.

Methods:

- Wet-lab and dry-lab: Shipment of 8 strains, typing results collected
- **Collection of results**: through <u>Microsoft Forms</u>. <u>Automatic extraction of</u> <u>results, automatic analysis</u> (and individual reports generation from 2021)
- **Performance assessment:** Same penalty points applied for errors either obtained through conventional methods or through WGS





WGS cluster analysis results reporting

- In PT26 (2019): Distance from each of the strains to one of the test strains reported
- From PT28 (2020): only information on the interpretation of results requested:

| | Dic | d you perform cluster analysis? Y/N | |
|-----|------|--|--|
| 47. | Clus | Cluster analysis * | |
| | | ate the method used for the cluster analysis | |
| | | SNP | |
| | | | |
| | | | |

48. Indicate the blind codes of the strains that belong to a cluster, separated by commas *

E.g. 6654, 5278 etc...

Inserisci la risposta

49. Cluster analysis: Indicate distances *

Indicate the range of differences identified among the samples composing the cluster (e.g. 0-5 allelic differences or 0-15 SNPs)

Inserisci la risposta

Participation trend 2018-2022

Increase in the use of WGS vs classical methods



Increase in the use of cgMLST





Lessons learnt

- <u>Collection of raw data</u> requires automatic methods for collection and analysis
- The collection of <u>characterization results</u> allows to avoid intense data treatment and allows to evaluate the interpretation of results in the laboratories
- The use of <u>web forms</u> for results collection allows automatic data analysis, reducing the time needed for reporting
- The collection or results obtained through <u>classical and/or WGS</u> <u>methods</u> allows to compare the performance of the two approaches, with better results for WGS



