

# The use of molecular typing for characterization of a *Salmonella* Enteritidis cluster

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## INTRODUCTION

Although the number of *Salmonella* Enteritidis has been declining in Europe in recent years, due to successful control measures implemented in poultry industry, it remains the most commonly detected serovar of human non-typhoidal salmonellosis. Moreover *S. Enteritidis* accounted for 575 outbreaks in the EU in 2015. Here, we report the first *Salmonella* Enteritidis outbreak (2016) investigated by the Portuguese Reference Laboratory for Gastrointestinal Infections, where traditional typing data was reinforced by Whole Genome Sequencing (WGS) data.

## MATERIAL and METHODS

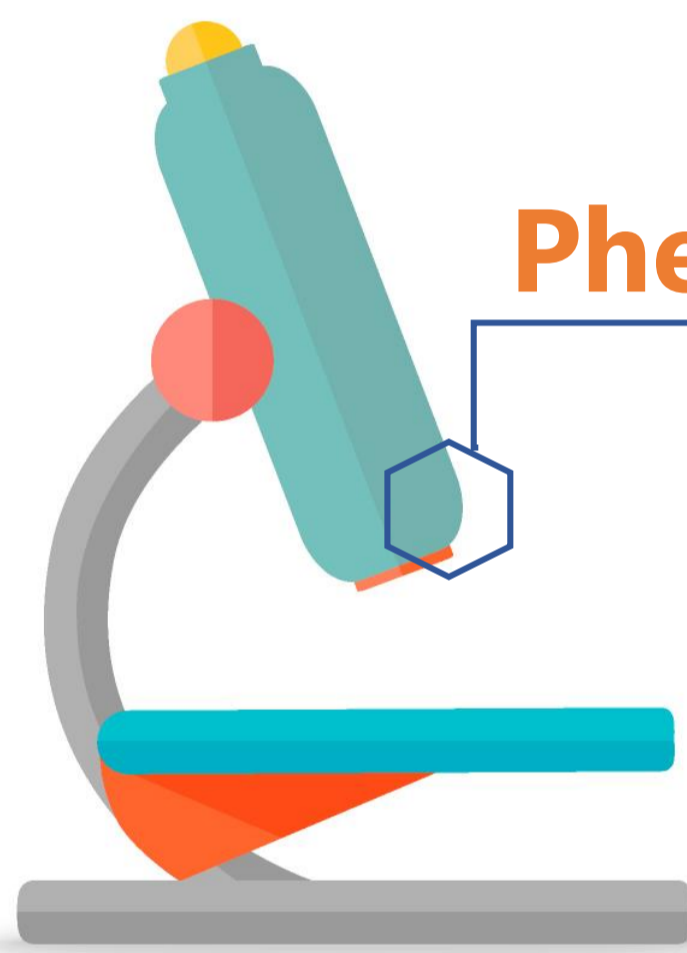
### Phenotypic testing

- 10 strains related to a suspected outbreak in 2016
- Kauffmann-White-de Minor serotyping
- Multilocus Variable Tandem Repeat Analysis (MLVA)
- Multilocus Sequence Typing (MLST)
- Antimicrobial Susceptibility testing (AST)

### WGS

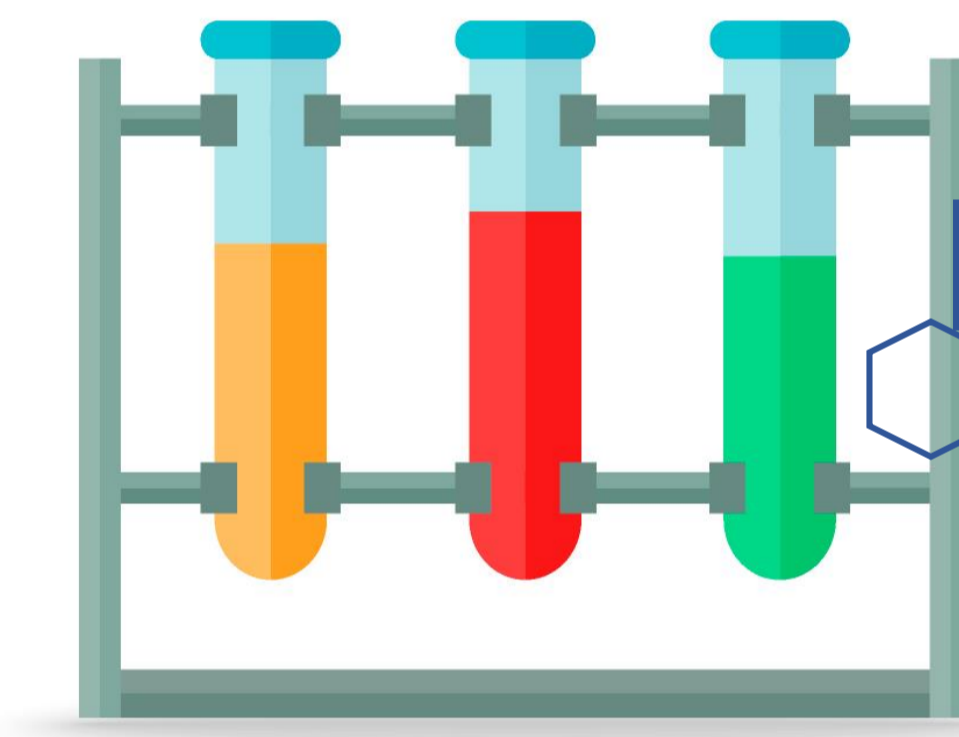
- SeqSero
- CGE MLST profile
- rMLST
- CARD
- PlasmidFinder

## RESULTS



### Phenotypic testing

- All strains were identified as *S. Enteritidis*.
- 9 of the strains were only resistant to nalidixic acid.
- While one was only resistant to sulphamethoxazole.



### Molecular typing

- All strains were identified as ST11.
- Nine of them had the MLVA profile 3-11-5-4-1.
- Another had a rather different MLVA profile, 2-10-9-2-2, hence was not related with the outbreak.



### WGS analysis

- WGS analysis confirmed that the 9 related strains share the serotype *S. Enteritidis*, ST11 and rST 1425.
- D87Y mutation in *gyrA* that confers resistance to Na.
- All the strains have IncF(II)S/IncFIB(S) plasmids, no antimicrobial genes identified.
- Genetic relatedness at whole-genome level (>99% core genome).

## CONCLUSION

MLVA is traditionally used for *Salmonella* Enteritidis surveillance in Europe, since it is a rapid and reproducible high-resolution typing technique that allows detection of national and multinational outbreaks. However, WGS is progressively replacing the traditional genotyping and phenotyping techniques for routine surveillance and outbreak investigation. This study is a good example that not only WGS provides an optimal discriminatory power for outbreak resolution, but also allows performing several subtyping tests (ST determination, in silico serotyping, ribotyping, plasmid identification, resistance genes/mutations identification, etc.) from a single assay. This strategy allowed the confirmation of the results obtained by classical serotyping, MLST, and AST, and also the identification of the mutation responsible for the resistance to nalidixic acid in these strains. Moreover, WGS allowed the identification of the presence of the plasmids IncF(II)S/IncFIB(S) in the 9 related strains. These plasmids have been reported as *Salmonella* virulence plasmids, not necessarily associated with antimicrobial resistance. Unfortunately, no strains from any potential food sources were obtained.

## REFERENCES