Advantage of whole genome sequencing in characterisation of Staphylococcal Food Poisoning Outbreak

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Investigate, evaluate, protect

Scientific context

Staphyloccocus aureus in food :

Produce staphylococcal enteroxins (SE)

Investigation of Staphyloccocal food Poisoning outbreak (SFPO):

27 SEs are described

responsible for foodborne outbreak

> 380 cases in Europe in 2017 (EFSA, 2018)

5 SEs are detected by immunoenzymatic tests
11 SE coding genes are detected by PCR

Objective:

Use of whole genome sequencing to identify strain origin and detect all SE coding genes

Material and Methods

143 strains isolated from SFPO in Europe Genome Illumina sequencing NextSeq technology

Genetic structuration

R package : adegenet and dbscan

SE gene detection

Tool based on Blast approach : NAuRA





Genetic structuration

- Strains isolated the same year belong to different genetic groups
- Strains isolated from the same country belong to different genetic groups

SE gene detection

Some strains have numerous SE genes

Fig. 1: phylogeny on maximum likelihood based on core genome. From the outside to the inside, the 1st circle represents de genetic structuration results and the 24 other circle represent the presence or absence of SE coding genes

- Some strains have few SE genes

sex coding gene was found in 90% of strains

Conclusion and Perspectives

6 genetic groups were defined in *S. aureus* No structuration according : Date of isolation Geographical origin Isolation context

Study the accessory genome to determine specific markers of isolation context

SE gene detection by WGS allows :

To access to the whole toxinic repertoire

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To access to the all sequence diversity

Sequence analysis will be used for the development of methods of SE toxins detection in food