

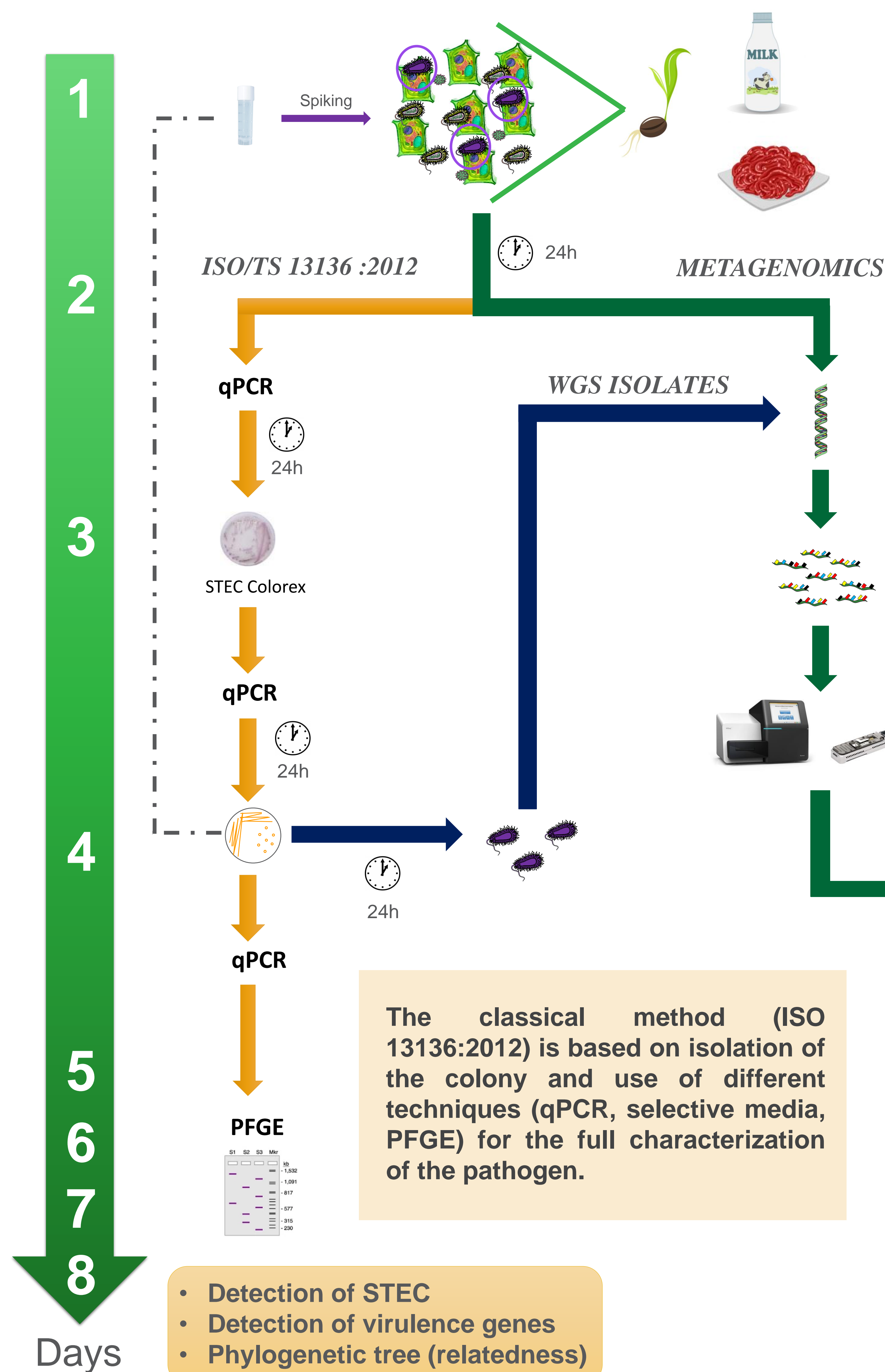
Comparing metagenomics, WGS on isolates and routine classical microbiology methods for foodborne outbreak investigations with STEC as a case study

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“All the information to investigate an outbreak in a single test, in a minimal time frame”

2 Methods



1 Aim

Shotgun metagenomics is a next-generation whole genome sequencing method without prior isolation of the pathogen. In this study, we are developing an integral metagenomics workflow and we compare it in parallel with a workflow based on WGS on isolate and the routine classical microbiology methods (ISO 13136:2012), in order to demonstrate the added value of the metagenomics workflow for the management of outbreaks. This approach is being tested and validated by spiking contaminants in specific food matrices using the Shiga toxin-producing *Escherichia coli* (STEC) as a case study. Subsequently, real-life samples will be investigated.

3 Discussion

The sample is artificially contaminated with a low contamination level (<10 CFU) of STEC isolates chosen from the strain collection of the Belgian NRL and NRC.

Different food matrices are investigated in this project.

Extraction of the DNA containing information of all cells from the sample

2 extraction kits are studied in order to compare their performance on different matrices and with a different background microflora.

Library preparation

2 sequencing platforms are tested :

- Illumina Miseq : short reads, low error rate
- Nanopore MinION : real-time, long reads

Sequencing

Data analysis & Report

- Identification of the strains present in the sample and their proportions.
- Detection of virulence and antimicrobial genes
- Phylogenetic tree (relatedness)

4 Conclusion

Eventually, we will be able to draw conclusions on the possibility to replace classical outbreak investigation techniques with a metagenomics approach and to evaluate if the necessary information can be extracted with appropriate bioinformatics tools in a shorter time-frame.



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