Nestlé's state-of-the-art technologies to keep Food Safe and improve global Public Health

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Introduction

In factories, pathogens such as *Salmonella* or *Listeria monocytogenes* can be introduced in ≠ ways into the production areas:

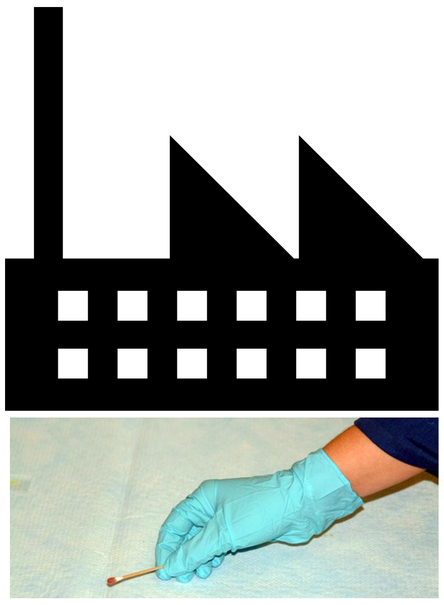
- raw materials,
- dust coming from the outside,
- water infiltration,
- material coming from a lower hygiene level zone,
- and operators.

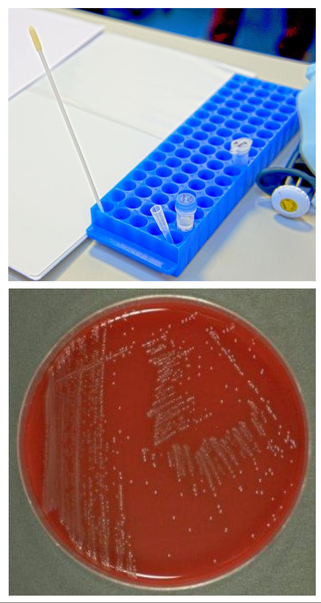
Presence of water residues ➔ risk of pathogen contamination

Pathogen close to the line ➔ high risk of line contamination

Line contaminated ➔ risk of finished product contamination

Routine + investigative sampling to verify that pathogens are kept away is crucial.





At Nestlé, to prevent microbiological contaminants from entering the food stream, systematic screening by swabbing many locations within the factories.

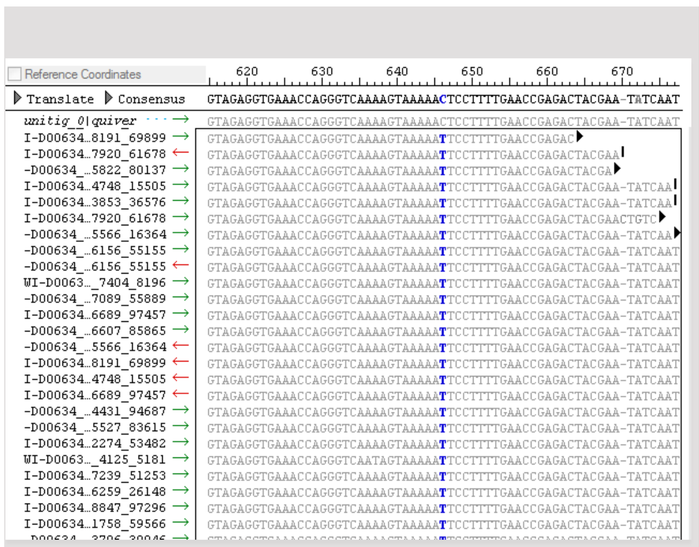
If positive found, root-causes investigation, analysis and corrective actions are taken:

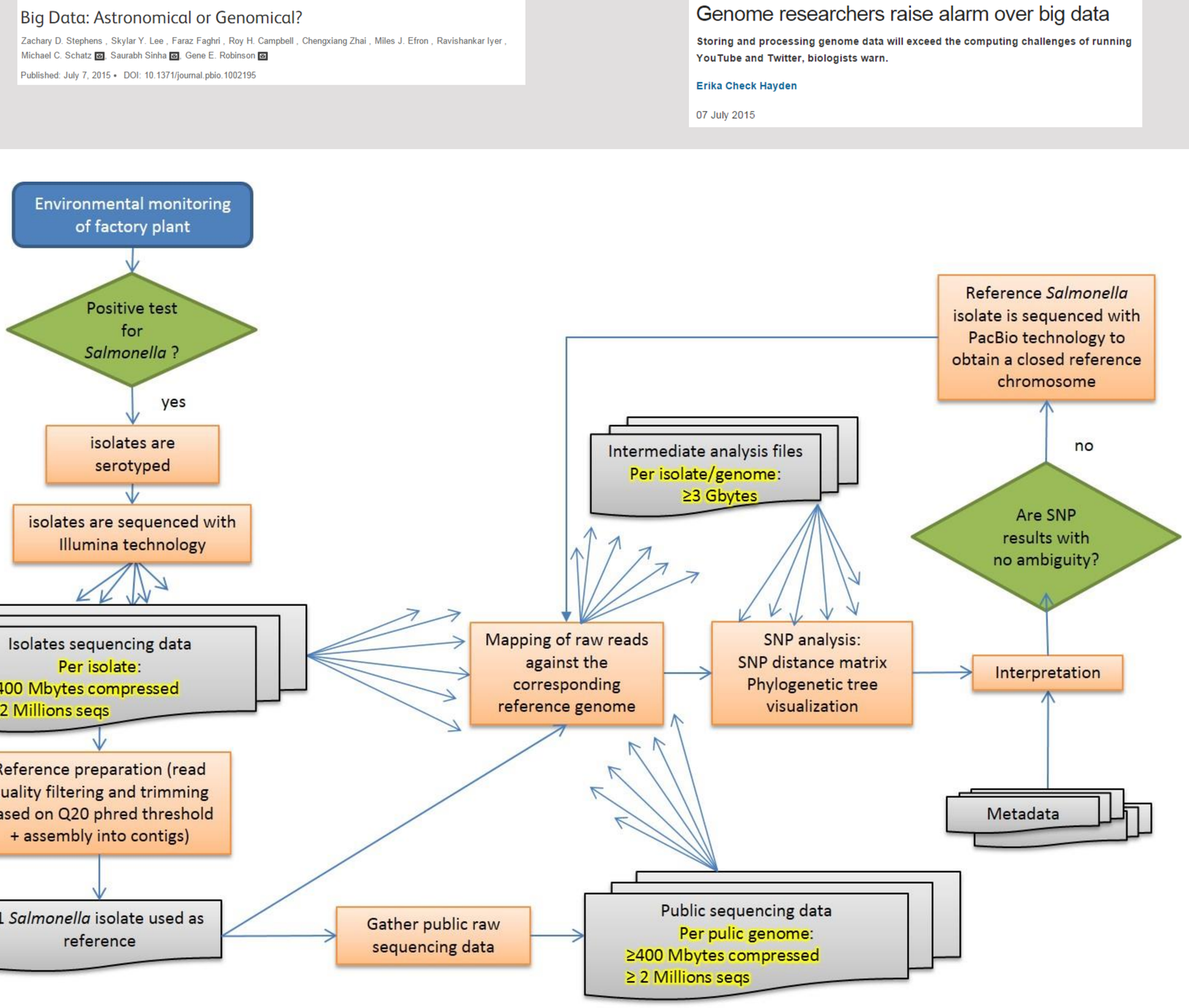
Isolates are collected with associated metadata, purified, cultured and stored in a repository.

Isolates are sent for whole genome sequencing (WGS):

- PacBio technology ➔ close to completion genomes,
- Illumina ➔ large amount of high quality short sequences.

Whole Genome Sequencing analysis generates big data



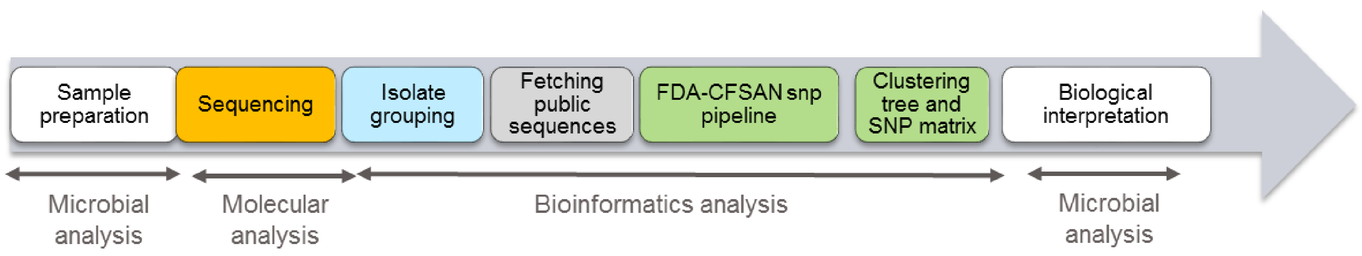


Single Nucleotide Polymorphism (SNP) detection

Compare one or several genomes to a common reference genome, and identify each nucleotide position along the reference sequence where one or several of the compared genomes differ.

SNP detection accuracy is highly dependent on the similarity of the reference compared to the samples, and the sequencing quality of both the reference and the samples to be compared. The reference genome should preferably be a finished genome but can also be in an unfinished version with several contigs.

WGS for pathogen monitoring: from prototype to a commonly used technology



WGS analysis consists of four main stages:

- Microbial analysis: DNA extraction from pure cultures of bacteria,
- Molecular analysis: WGS of the complete genome,
- Bioinformatics analyses: Identification of SNP,
- Microbial analysis: Interpretation of the results.

Why pathogen monitoring in industry needs to deal with big data management?

Because:

- each isolate,
- each analysis,
- public data + internal data

generates several large intermediate files and needs to be accessed and stored in a repository

Powerful IT infrastructure and Bioinformatics expertise are required