

INTRODUCTION AND OBJECTIVES

Metagenomics is the study of genetic material from environmental samples. This field has allowed the study of non-culturable microorganisms and has a wide range of applications. One of them, the detection of foodborne pathogens.

OBJECTIVES: to know the main techniques of next generation sequencing that are used nowadays and to analyse different articles in which the different strategies have been used for the study and control of pathogens derived from food, distinguishing between bacteria, viruses and fungi.

METHODOLOGY

Mainly use of search engines such as PubMed (NCBI) and Mendeley for bibliographic literature.

Reading and synthesizing the collected literature in order to elaborate the written project.

NEXT GENERATION SEQUENCING

There are 4 common steps in almost every next generation sequencing technology:

- **Library preparation:** DNA is fragmented and then ligated to an adaptor.
- **Clonal amplification:** creation of copies of the DNA fragments.
- **Sequencing:** determination of the order of nucleotides in the DNA molecule.
- **Data analysis:** interpretation of the results using specific and complex softwares.

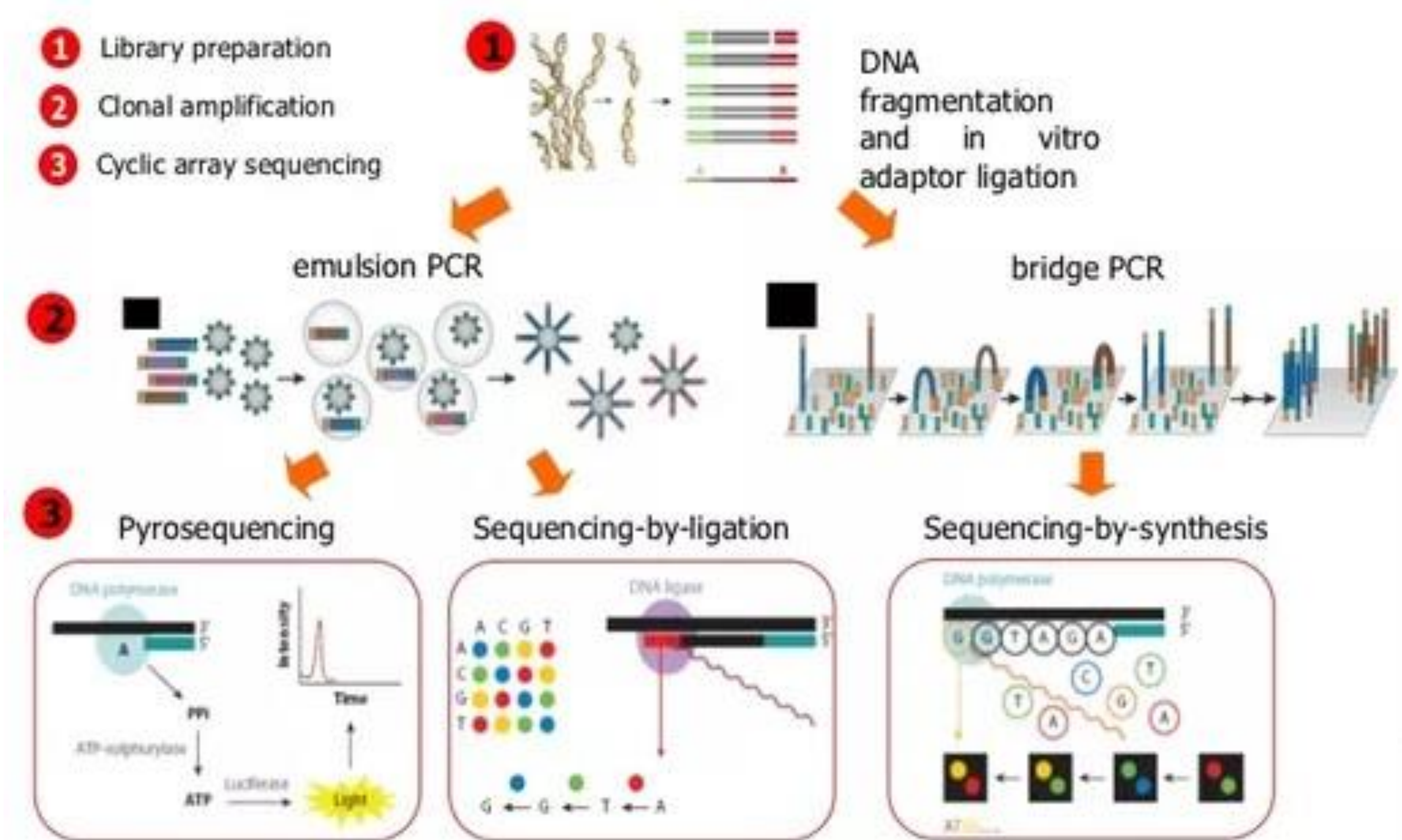


Fig. 1. Steps for next generation sequencing process

DETECTION OF FOODBORNE PATHOGENS

Microorganisms play an important role on the security and stability of food. Detection of those who are pathogenic can be crucial for food safety and public health.

- **Bacterial food pathogens:** some of the most important are *Salmonella*, *Listeria monocytogenes* and Shiga toxin-producing *E. coli* (STEC) causing many outbreaks and sporadic cases with severe or fatal outcome.
- **Viral food pathogens:** the most notable FBP viruses are norovirus (NoV), hepatitis A virus (HAV) and hepatitis E virus (HEV) and RNA rotavirus (RV).
- **Fungal food pathogens:** some of the typical ones are *Fusarium spp.*, *Penicillium spp.* and *Aspergillus spp.*

CONCLUSIONS

- The most used technologies for whole genome sequencing are the ones from ThermoFisher and Illumina.
- Next generation sequencing technologies are beginning to be used for control and outbreak investigations.
- Still not fully implemented in the routine detection of foodborne pathogens due to the data analysis and results interpretation costs, as well as the complexity of bioinformatics tools.
- Potential use in the future as a routine approach when costs decrease over time.

REFERENCES:

[1] Bioinformàtica per a la Recerca Biomèdica | UEB-UAT-VHIR Knowledge Base. <http://ueb.vhir.org/2015-10+Bioinformàtica+per+a+la+Recerca+Biomèdica>.

[2] Forbes JD, Knox NC, Ronholm J, Pagotto F, Reimer A. 2017. Metagenomics: The Next Culture-Independent Game Changer. *Front. Microbiol.* 8:1069. doi:10.3389/fmicb.2017.01069. <http://www.ncbi.nlm.nih.gov/pubmed/28725217>.

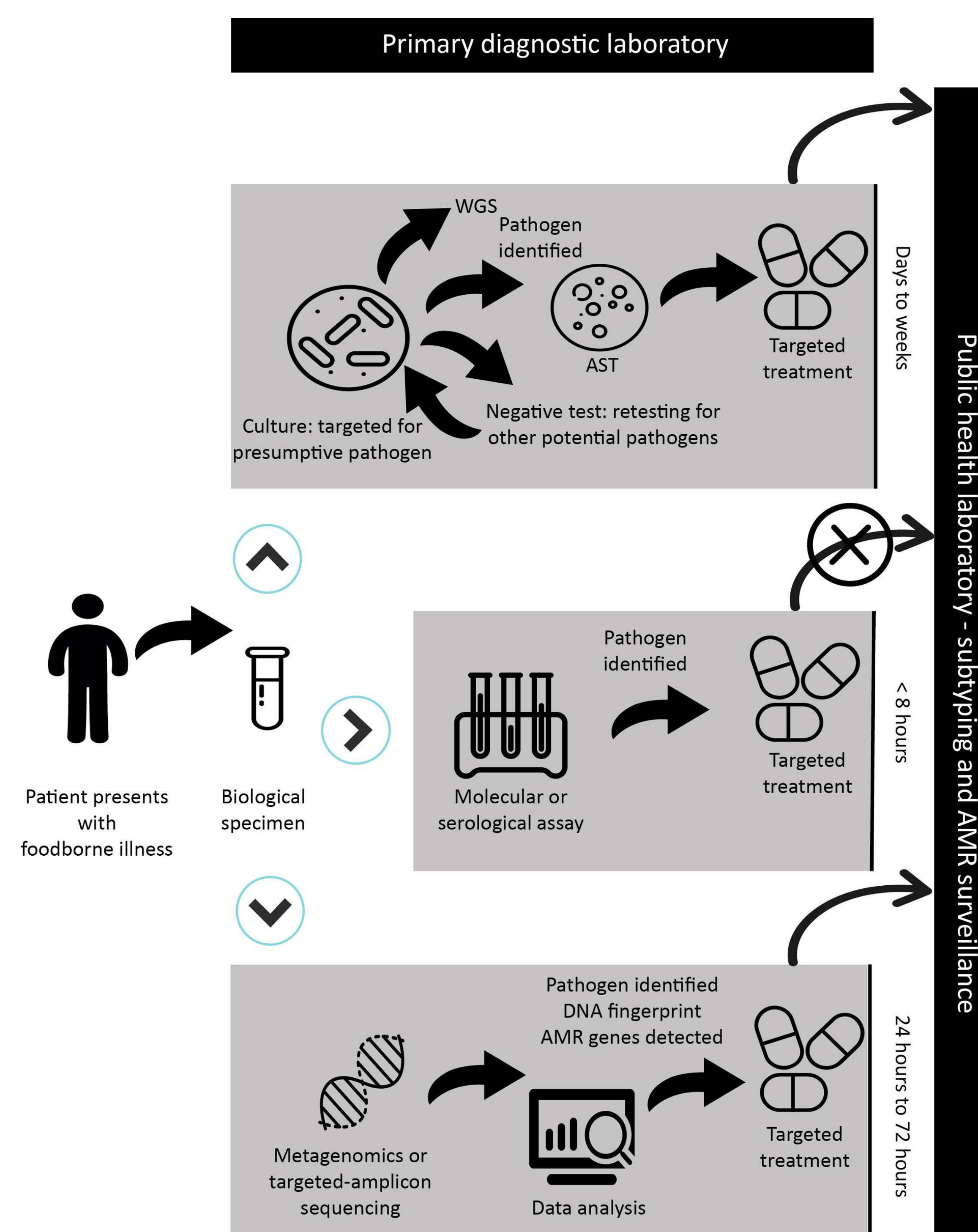


Fig. 2. Schematic representation of a sample workflow with timelines from patient presentation at a primary health care facility through the diagnostic process and public health surveillance in the case of a reportable disease.