



SURVEY SUMMARY





AIM AND BACKGROUND

• Background:

ECDC produced a survey in the spring 2020 for the national public health laboratories in order to explore preparedness for surveillance and outbreak detection using whole genome sequencing (WGS).

• Aim:

To collect information about the handling of Campylobacter strains at the NRLs' for food or primary production samples and to compare the results to that of public health laboratories to further explore preparedness for surveillance and outbreak detection using whole genome sequencing (WGS).





QUESTION: FROM WHAT SOURCES ARE SAMPLES/ISOLATES SENT TO YOUR NRL FOR ANALYSIS OF CAMPYLOBACTER? TICK ALL OPTIONS THAT APPLY.





QUESTION: WHAT IS THE ESTIMATED PROPORTION (%) OF POSITIVE SAMPLES WHERE A CAMPYLOBACTER ISOLATE IS BEING STORED?

N=32 30 25 20 20 No of replies 15 10 5 5 2 2 0 < 1% 1-50% 51-75% > 75% Do not know

QUESTION: FOR HOW LONG TIME ARE CAMPYLOBACTER ISOLATES GENERALLY STORED?





QUESTION: HOW DOES YOUR NRL CHARACTERISE CAMPYLOBACTER ISOLATES FROM ROUTINE SAMPLES? TICK ALL OPTIONS THAT APPLY.



QUESTION:HOW DOES/WOULD YOUR NRL CHARACTERISE CAMPYLOBACTER ISOLATES IN AN OUTBREAK INVESTIGATION? TICK ALL OPTIONS THAT APPLY.



COMMENTS MLST and WGS implemented but not run routinely



QUESTION: DO YOU HAVE A CAPACITY FOR WGS OF CAMPYLOBACTER ISOLATES AT NATIONAL LEVEL?

QUESTION: WHAT IS THE ESTIMATED PROPORTION (%) OF THE CAMPYLOBACTER ISOLATES RETRIEVED/RECEIVED AT YOUR NRL THAT ARE SUBJECTED TO WGS?





- Isolates part of research projects, with interesting AMR profiles, epidemiologically linked to outbreaks
- All strains are sequenced



QUESTION: WHAT PIECES OF INFORMATION TRIGGER AN INVESTIGATION OF A SUSPECTED CAMPYLOBACTER OUTBREAK AT THE NATIONAL LEVEL? TICK ALL OPTIONS THAT APPLY.





GENERAL CONCLUSIONS – BOTH NETWORKS

ISOLATES

- Non-culture based detection of Campylobacter = no isolates
- It is not always isolates are retrieved in the method of analysis (both public health laboratories and NRLs food/animal samples)
- Cultivation-based detection is more common for NRLs food/animal samples than public health laboratories
- But if food or animal isolates are retrieved, they are usually stored for a long time

SEQUENCING

- Most NRLs do not sequence routinely, but for research projects or in outbreak investigations
- Few countries (3-4) sequence >75% of Campylobacter isolates (public health/animal and food)
- Many (>50%) of the food/animal NRLs have the capacity for sequencing – probably similar among public health NRLs



GENERAL CONCLUSIONS – BOTH NETWORKS

OUTBREAK INVESTIGATIONS

- More commonly triggered by unexpected number of human cases than of positive food or animal samples in a certain time period (accounts for both networks)
- Usually triggered by public health laboratories
- It can also be triggered by clustering result (both networks) – but only among those sequencing a large proportion of the isolates





Questions or comments?



GENERAL DISCUSSION

- The more we sequence, the more clusters we discover
- The more we compare data between the sectors, the more outbreaks will be discovered
- Soon the infrastructure is here that makes it possible to extend the comparisons cross-boarder
- If this means we can target sources to reduce burden in Europe it is great, BUT...
- With information comes responsibility and the expectations to act
- Limitations:
- Lack of legal support for food recalls or trade restrictions on EU level
- The sources of food and animal samples may be protected by the secrecy act if not sampled in official control programmes
- Uncertainty how to act on outbreaks on a national level (no actions at all at present in some countries)
- Cross-country level?
- Stable genotypes have been reported from different countries cannot rely only on clustering

