# ECDC/WHO Europe Joint virology working group

## First meeting: 26 January 2021, 13:00-16:00 CET

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**Introduction**

1) Welcome note by 5.1.2e (ECDC) and 5.1.2e (WHO Euro)
2) Introduction to the objectives of the meeting (see slide 3) by 5.1.2e (ECDC).
3) Declaration of Interest (DoI)
   Question to the audience if any new DoI have emerged?
   None declared.
4) Brief ‚tour de table'.
5) Brief presentation of Terms of Reference (see slide 5) by 5.1.2e (ECDC).
6) Information to the audience:
   - Increased number of invited experts (as compared to original plans) due to a non-exclusive approach.
   - Presentation of a timeline: regular meetings on a monthly basis on the last Tuesday of the month (pm). More frequent meetings can be held if necessary.
7) Presentation of proposed outcomes (see slide 7).

**First session**

Objectives of SARS-CoV-2 virological surveillance at European level and how these will translate for surveillance, risk assessment, early warning, outbreak response and pandemic preparedness

1) Virus assessment framework 5.1.2e )
   5.1.2e (ECDC)

- Multiple trigger criteria suggested including virological characteristics (...) to follow up with an investigation
- Components of assessment and sources, based on TIPRA tool for pandemic influenza assessment
- Scientific expert panel including scientists from EU and EEA and observers from other institutions
- ECDC will provide logistics and secretary function

2) Sampling strategy and triggers for virus characterisation
5.1.2e (PHE, UK)

- Broadly based sampling strategy needed to identify size of the problem
- all ages and symptomatic and asymptomatic to be sampled to define relationship between transmission and infection
- Different strains to define relationship between phenotypes and genotype
- Genomic surveillance essential to identify mutations and define their features such as immune escape, increased transmission rate etc.
- A probability indicator ("probability yard stick") should be included when expressing likelihood or confidence to increase clarity
- Identified sequence of concern due to rapid spread, structural predictions, re-infections
- Experimental virological characterisation from a PCR positive test, sequence confirmation and isolation, neutralisation tests, vaccine response analyses and eventually in vivo-studies
- "Proxy indicators" to track the emergence of variants as genomic surveillance might be too slow, e.g. weekly trends of S-gene failure
- Overview over opportunities and pitfalls in virological surveillance

**Discussion**

Question on how to use purely genetic characteristics as criteria.

Usually it is an epidemiological signal of concern that identifies a variant of concern. Not worthwhile relying on point mutation only, the consequences are difficult to foresee.

Using other methods such as pre-screening for the timely detection of variants, followed by sequencing?

Specific PCR (S-gene drop-out) is not sufficient to identify specific variants. Other mutations are also of concern, just looking at S-gene drop-out will lead to missing out other variants.

TESSy reporting

Adapting TESSy to collect data on COVID-19 while keeping the workload for labs to a minimum; Collect case-based and aggregated data;

Can an agreement beeing made with GISAID?

Not much epidemiological data available in GISEAD and legal problems to collect metadata in GISAID.

**Action points**

Draft variables to be shared with the group for discussion and input (ECDC).
Protocols can be shared on platform EXCollab.

**Second session**

Methodological approaches to detect genetic variant viruses

1) Country perspective to screening and sequencing of SARS-CoV-2 variant viruses
5.1.2e (Portugal)

- Portugal has a strong laboratory network and previous networks involved in Acute Respiratory Infections Surveillance, enabling inter-laboratory assays, EQA scheme, national registry
- Sequencing and genetic characterisation on national level
- Coordinated laboratory surveillance identified B.1.1.7 variant in December and B.1.351 in January
- Laboratory surveillance under coordination of INSA (National reference laboratory)

**Discussion**

- Issues with variants being brought into a country by travellers, also indirectly though other countries. Challenge to screen ALL travellers in a short time frame to identify incoming variants.
- Question to the audience about country experiences with pre-screening to identify new variants. Sequencing is necessary for the community containment, for screening of travellers, RADT and RT-PCR is sufficient, triggering isolation. For surveillance purposes, focus on travellers will bias statistics.

Methodological approaches to detect antigenic variant viruses

2) Sampling frame, assays and reference material for phenotypic characterisation
5.1.2e (Switzerland)

- Variants of concern present plenty of challenges as they emerge constantly everywhere
- Isolation, stock production and shipment to other labs is time consuming
- Issue with further mutations in cell culture
- Various experimental systems required to study all different aspects of phenotypes
- Synthetic genetic platforms used to clone RNA virus genomes incl. clinical samples
- SARS-CoV-2 reconstruction and rescue, example of early introduced mutation D614G
- Rapid assessment of variants by reverse genetics (no isolates required)
- Shipment of these isolates complicated

**Discussion**

Question on how many labs in Europe can perform such research and on which labs can perform further neutralisation assays and antigenic characterisation.

Not more than 3-4 labs in Europe can work with the described system. Shipment of isolates is very time-consuming, even production of material is feasible in a small group, but larger groups of interested lab will create problems.

A few pseudovirus studies are already done and often a good indicator. But the virus will be necessary in the long run for further characterisation. Upon reception of the virus, things can happen swiftly.

**Action points**

Virus evolution group and this joint virus characterisation working group have considerable overlap. Important to align frameworks by WHO and ECDC, better coordination required. Sharing of viruses is always a challenge. Question if MTA are really needed? WHO can always support shipping procedures.

**Third session**

1) Current metadata and a proposal for laboratory-based reporting
   5.1.2e (ECDC)

- Objectives of variant detection
- SARS-CoV-2 metadata for surveillance reporting include case-based and aggregated Reporting is technical and presents challenges due to lack of epidemiological info and technical nature
- Issue with growing list of variants which is needed for the case-based reporting
- 7 countries reported case-based, 12 countries report aggregated data and 8 countries reported both; 8 of 21 countries reported variants to TESSy
- Several challenges with case-based reporting for collection of laboratory data
- Presentation of a separate virus-based record type for an additional data base.
- Presentation of laboratory-related variables

**Discussion**

Concerns about the upcoming workload in connection to this new reporting.

Issues with GDPR prohibits, for instance, sharing national data in some countries. Genetic characterisation is difficult to connect to metadata, i.e. connecting the sequencing data with the metadata poses issues.

**Action points**

Asking for comments by countries on the variables.

Coded list should be extended to include variants under investigation.

Also, ECDC would like to get feedback on feasibility to report characterised viruses (variants of concern).

Specific questions:

Is it feasible to report laboratory data?

Do laboratory OCPs have access for reporting in the MS?

Will you be able to link epi and lab data?

Issues with GDPR reason for very few sequence ID reported?

Which variables do you consider should be the minimum starting point?

Which variables should be mandatory?