World Health Organization
REGIONAL OFFICE FOR Africa

VARIANT SURVEILLANCE GUIDANCE : EXECUTIVE SUMMARY

As of 29th June 2021, WHO has designated 7 Variants of Interest (VOIs) and 4 Variants of Concern(VOCs)

This document aims to **describe a minimum set of surveillance activities** recommended at the national level to detect and monitor SARS-CoV-2 variants and **outline a set of activities for the characterization and assessment of risk posed by SARS-CoV-2 variants.** A set of indicators is also provided in order to standardize monitoring and public reporting of variants circulation.

1. Surveillance of SARS-Cov2 Variants

Alert triggers : data sources

- Routine surveillance (cases, deaths, Health workers, hospitalizations etc)
- EBS

Sensitive triggers can be used to launch investigations:

- Increasing trend for 2 consecutive weeks
- Doubling of cases from one week to another

Examples of disease surveillance indicators, alert and trigger thresholds from routine surveillance

Indicators	Alert for further monitoring	Triggers	Special focus on vaccinated groups
Cases	Increase for 1 week	Increase for 2 consecutive weeks Doubling of cases from one week to another	
Age-disaggregated cases	Increase of cases in specific age groups (under 18, under 65, to be determined locally)	Idem	Targeted age groups
Cases among Health workers	Idem	Idem	Targeted group for vaccination
Case Fatality Rate	Idem	Idem	
Age disaggregated deaths	Increase of cases in groups aged <65		
Hospitalizations/ICU admissions or bed occupancy rate	Increase of cases in groups aged <65	Idem	
Test Positivity rate	Idem	Idem	

These triggers and thresholds should be adapted to local situations, investigation capacity and expected sensitivity.

2. Sampling strategies

Sampling is advised to be conducted on a weekly basis, for sensitive analysis of trends, and simultaneous analysis with routine surveillance.

	Pros	Cons
1- Representative sampling	High sensitivity	Large sample size: capacity challenge
2 Fixed proportion of confirmed cases	Medium sensitivity	Operationally difficult to weekly adjust sample size and operational logistics to number of cases
3- Fixed sample size	Operationally practical If stable, can allow to follow trend of circulating variants	Low sensitivity Low representativity (geographical, population based)

- Sampling strategy assessment for monitoring of changes in variant prevalence

Representative sample

Weekly number of SARS-CoV-2 detections	Sample size based on the difference in the proportion of a certain variant, from one week to another	
	From 2.5% to 5%	**From 2.5% to 10%**
>100 000	725	129
<500	296	103

Fixed sample size : must be representative, depends on sequencing capacity

  - Sentinel sites for ILI/ SARI (GISRS) : 15-150 samples per week per county

- Sampling strategy assessment for detection of low circulating variant
  - Representative sampling

Weekly number of SARS-CoV-2 detections	Sample size based on the minimum prevalence to be detected (randomized, representative sample)		
	1%	**2.5%**	**5%**
>100 000	1522	600	292
<500	377	273	185

  - Targeted Sampling:
    - PCR Screening
    - Vaccinated cases
    - Suspected reinfections
    - Unusual clinical presentation or poor response to therapeutics
    - Immunocompromised patients with chronic infection
    - Point of Entry testing on cases with travel history from locations with high transmission of variants
  - Outbreak and cluster investigations : see alert triggers

Total sequencing samples=

Samples for prevalence monitoring

\+ Targeted sampling

\+ Outbreak/cluster investigations

3. Characterization of variants

Public health risk domain	Characteristics	Epidemiologic investigations		
		Surveillance evidence	Epidemiological studies	In vitro
Transmissibility	Risk of infection	Increased Rt, Contact tracing data (secondary infection rate)	Household transmission studies, Expanded contact definitions	Binding affinity (ACE-2)
	Animal reservoir		First Few X (FFX) cases, animal reservoir investigations	
	Disease course (incubation, onset, viral shedding, recovery, symptomatic vs asymptomatic)	Contact tracing (time from exposure to symptom onset/ transmission)	First Few X (FFX) cases: clinical follow up, Cohort studies	Recurrent RT-PCR testing throughout disease course, Viral culture
Clinical course	Signs and symptoms (relation to case definition)		FFX cases: signs and symptoms, Sensitivity and specificity of symptom clusters	Compare detection in URT vs LRT samples
	Severity	Age-disaggregated case fatality ratios, Hospitalization ratios	First few cases follow up: hospitalization, CFR	
Laboratory diagnostics	Diagnostics detection		RT-PCR target failures	RT-PCR target failure or failure of other diagnostics
Neutralization	Neutralization by treatments			Monoclonal antibody and antibody cocktail neutralization
	Neutralization by sera		Vaccine effectiveness studies	Convalescent sera, Vaccinee sera
	Length of immunity		FFX cases follow up Serological studies	

4. Reporting

Overall, for all sequences, Member States are requested to:

- Share genomic sequences on public databases (e.g., GISAID, etc)
- Regularly publish findings, incl. contextual information around cases
- Report to WHO of first cases/clusters identified associated with a VOC through IHR mechanism
- Inform WHO of potential new VOI/VOCs through established WCO and RO channels/networks:
- Include as much detail as possible to support assessments e.g., person, place, time, clinical, evidence of phenotypic impacts

The following recommended indicators are recommended for national reporting and international sharing for each VOI or VOC, and variants of national interest:

Label	Description	Method
Date reported to WHO	Date the variant strain was reported to WHO either through official channels like IHR notification, EWRS, official announcements or unofficial EBS signal	Varies VOI versus VOC, see above
Date of first case in the country	Date the first case of the variant strain was reported in the country (date of onset if possible, or date of sequencing confirmation for VOC)	
Quantification method for variant	subset sampling of whole genome sequencing, or screening with target PCR	
Number of variants in sequenced samples (numerator)	Proportion of variant strain identified from the total sample sequenced.	This can also be done through target PCR: num-ber of samples positive for target PCR
Number of sequenced samples (denominator)	Number of samples sequenced	If done through target PCR, this should be the number of cases screened