

Case study #4: Arboviruses

Activity 1: “Using genomics for arboviral to understand arboviral outbreaks”

Room logistics

Easel with butchers’ paper for note taking.

Slide deck will show a QR code, which links to a google drive containing the different scenarios. Four slides already prepared if participants would prefer to prepare answers electronically.

Activity brief

All scenarios will have the same core **five** questions.

1. What are the likely uses of genomics in your scenario ?
2. Outline potential sectors and surveillance partners to address the main aim of the scenario?
3. What would be the most feasible and cost-effective sampling strategy?
4. Does the scenario setting have sufficient capacity to address the main aim of genomics surveillance? If insufficient, what actions can be taken to strengthen in an outbreak scenario?
5. Who are the target reporting stakeholders and how often should reports be generated?
6. What are the key barriers to implementing genomic surveillance within existing surveillance systems for your pathogen?

Setting the scene: Group 1

High capacity

Pathogen	Dengue
Aim	A new vaccine is about to be rolled out in a country with multiple circulating serotypes of Dengue. MOH is keen to use genomics along with other complimentary methods to assess the impact of vaccination on circulating dengue viruses in the country.
Case numbers	Hyper-endemic with high seasonal case numbers
Current genomics activities	<ul style="list-style-type: none"> • Convenience sampling of Dengue cases for E gene Sanger sequencing • Routine SARS-CoV-2 genomic surveillance • Other traditional surveillance methods such as PCR, serology assays for Dengue are available.
Sequencing platforms (status)	<ul style="list-style-type: none"> • Illumina Nextseq 500 (workhorse) • Oxford Nanopore GridION (have access if required)

Guidance notes

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Setting the scene: Group 2

Moderate capacity

Pathogen	Zika virus
Aim	<p>There has been a recent increase of microencephaly in newborns. In a private hospital, a case has come up PCR positive for Zika virus.</p> <p>Zika is not new to this Asian country, although not previously linked with microencephaly. MOH is keen to sequence the circulating strains to inform treatment and control response.</p>
Case numbers	5 cases of microencephaly within two months
Current genomics activities	<ul style="list-style-type: none"> • Dengue sequencing capacity, but no routinely conducted • SARS-CoV-2 genomic surveillance • Other traditional surveillance methods such as PCR, serology assays for Zika are available.
Sequencing platforms (status)	<ul style="list-style-type: none"> • Illumina <u>Nextseq</u> 500 (workhorse) • Oxford Nanopore <u>GridION</u> (have access if required)

Guidance notes for discussion

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Setting the scene: Scenario 3

Moderate capacity

Pathogen	Japanese encephalitis virus (JEV)
Aim	In a <u>non-endemic</u> country, there has been a case of encephalitis that is PCR confirmed to be JEV. The case has no history of travel. The MOH is keen to investigate with genomics the possible exposure event.
Case numbers	>50 RT-PCR confirmed cases
Current genomics activities	Genomic surveillance of Dengue virus only Samples of convenience used for dengue surveillance
Sequencing platforms	<ul style="list-style-type: none"> • Illumina <u>iSeq</u> • Oxford Nanopore <u>GridION</u>

“Secret-expansion-styled” question

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Setting the scene: Scenario 4

High capacity

Pathogen	Arbovirus X
Aim	An outbreak of severe febrile illness with neurological symptoms is occurring. Coincidental deaths of birds at the zoo have also been reported. Serum antibodies give weak signal to dengue, hence it is suspected the outbreak maybe caused by a flavivirus.
Case numbers	>100 cases
Current genomics activities	<ul style="list-style-type: none">• Whole genome sequence of Dengue cases only• Other traditional surveillance methods such as PCR, serology assays are only available for dengue.
Sequencing platforms (status)	<ul style="list-style-type: none">• Illumina <u>Nextseq</u> 500 (workhorse)

Guidance notes

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Activity2: “Closer to home”

Room logistics

Slide deck will show a QR code, which links to a google drive containing the different scenarios.

No need for easel with this one.

Activity brief

- Fill up the pathogen priority toolkit for *Dengue*.
- Reflect on your current country’s current capacity and Dengue burden.
- Consider the possible implementation steps for the integration of genomic sequencing into your country’s arbovirus control program.

Prompts for activity

Before start

- Ensure at least one person per country download the WHO TB app

During activity:

- For R0 to be filled, refer to the slide with the multiple R0 values.
- Let participants consider their local TB epi scenario and choose the most appropriate to what they think is true for their case.
- Prompts for capacity (infrastructure) are as follows:
 - Industry partners
 - Sequencing capacity: in-house or outsourced?
 - Supply chains
 - Computational power
 - People power