

## Global burden of dengue virus (DENV)



Half of the world's population is at risk of infection

~ 100 million symptomatic cases annually Economic burden on low-income countries



Defined by *Aedes aegypti* and *Aedes albopictus* mosquitoes

Increasing trends in dengue cases

Surveillance is patchy

# Transmission cycle of dengue virus

### **Urban cycle**

- 1. Mosquito takes a blood meal (~2 µL) from a person acutely infected with dengue virus
- 2. Virus replicates in the mosquito and disseminates to the salivary gland (8-10 days)
- 3. Mosquito takes secondary blood meal and sheds virus in saliva upon biting
- 4. Replication in exposed human and symptom onset (4-7 days after exposure)

## Sylvatic cycle

Transmission between NHPs and arboreal mosquito species

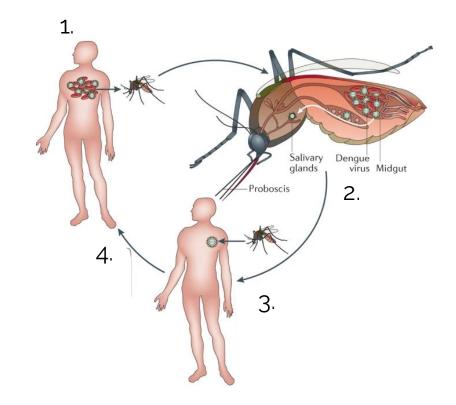
## Other methods of spread

#### **Humans**

- Perinatal transmission from mother to baby
- Sexual contact

### Mosquitoes

Transovarial transmission and survival



## Clinical features

Self-limiting febrile disease in the majority of cases

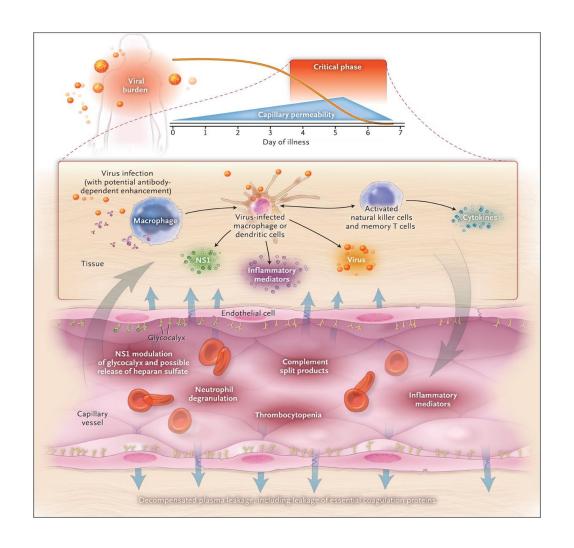
• Headache, vomiting, myalgia, joint pain and rash

Severe dengue develops in a minority of patients (< 1 %)

- Plasma leakage, dengue shock, severe bleeding and organ failure
- Increased risk of developing severe dengue on secondary infection

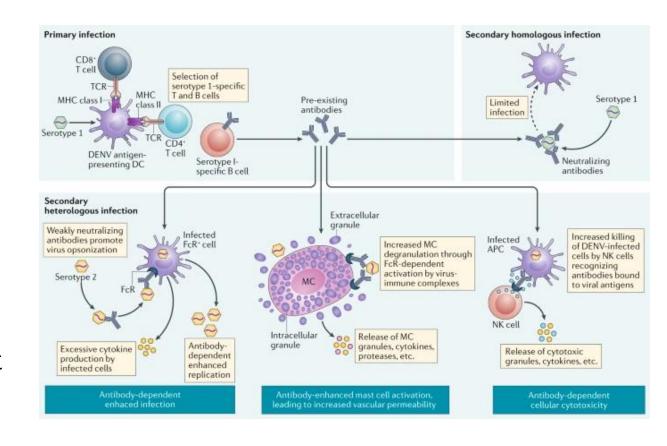
Treatment involves careful management of patients with signs of severe dengue in hospital

- by restoring plasma volume with fluid therapy
- costly for health-care systems



# Heterosubtypic infection and increased disease risk

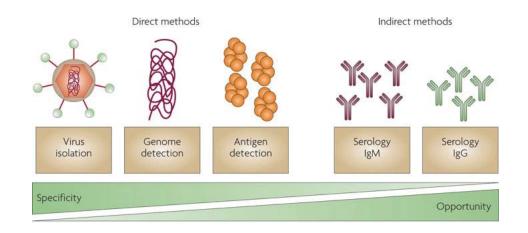
- There are four antigenically distinct types (serotypes) of dengue virus (DENV-1-4)
- Primary infection can induce lifelong immunity to the same dengue type
  - Antibodies (IgM and IgG) and T cells
- Primary infection or vaccination (if naïve Dengvaxia) can induce cross-reactive
  antibodies that enhance disease upon
  sequential dengue infection with a different
  type
- Highlights the significance of serotype replacement



## Laboratory diagnosis

Serum, plasma or whole blood samples collected for laboratory diagnosis via:

- Direct methods virus
  - Limited to viremic phase (within 10 days post symptom onset)
  - o Genome detection typing assays
- Indirect methods serology
  - Cannot determine type too much cross-reactivity
  - Paired sera ideal for diagnosis as IgM/IgG might indicate prior infection



**Genomics relevance:** PCR assay used can have implications for the sequencing pipeline used.

- Typing assay, then a type-specific amplicon panel and reference mapping is possible
- Non-typing assay, then a pan-serotype method can be used for all sequences and reads mapped to several references (DengueSeq)

## Dengue virus particle

### **Size**

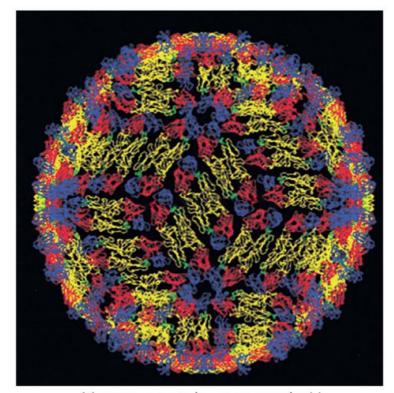
40-60nm

## **Structural proteins**

- Envelope (E)
   Attachment and uncoating
- Membrane (M)
   Virion maturation
- Capsid (C)
   Associated with viral RNA in the core

#### Gen epi relevance:

E is the most commonly sequenced part of the genome and has been widely used to map the global footprint of dengue genotypes



Mature particle at neutral pH

## **Genome organisation**

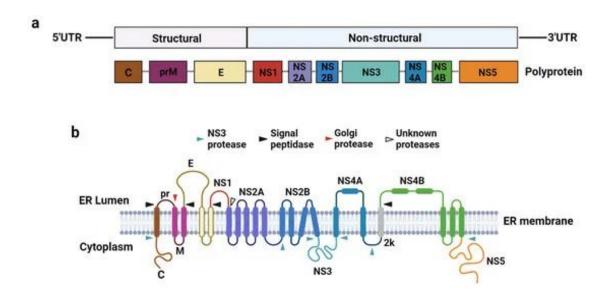
### Flaviviridae, orthoflavivirus

### +ssRNA genome (~11kb)

- m7GpppN (5') cap
- UTR most diagnostic PCRs target the 3'UTR

#### Genome encodes:

- 3 structural proteins (C, M, E)
- 7 non-structural proteins (NS1, NS2A+B, NS3, NS4A+B, NS5)
- Genome consists of a single ORF from which a long polyprotein is produced
- Polyprotein is cleaved after translation in the ER by viral and host proteases



**Gen epi relevance:** for communication purposes these are not technically genes i.e. not the E gene but sequence encoding the E protein.

# Genome classification and diversity

#### Lineage classification system

Based on the PANGO nomenclature system for SARS-CoV-2

Serotypes (1-4)

Serotype-specific differences in clinical manifestation

**Genotypes (I - VII)** 

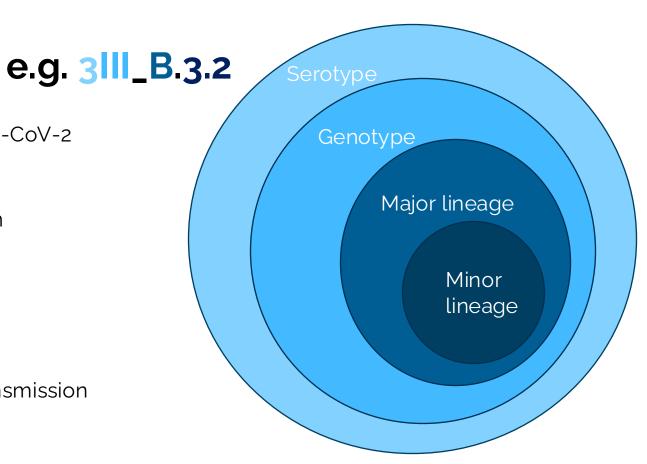
Regional distribution

#### **Major lineages**

Characterise regional and country-level trends in transmission dynamics

#### Minor lineages

Characterise fine-scale trends in transmission dynamics



**Gen epi relevance:** Having a structured classification system to describe genomic diversity enables characterization at different levels, for different epidemiological purposes and is an invaluable tool to interpret epidemiological signals using equitable terms

## Overview of steps in genome classification

DengueSeq Reads Alignment Consensus .bam .fasta .fastq Reads mapped Contiguous to references sequence extracted Nextstrain Tabulated file with Multiple sequence Phylogenetic tree metadata and alignment .newick assigned lineages fasta .CSV Sequence Lineage evolution classified inferred by according to algorithms and position in

models

phylogeny