9TH ASIA DENGUE SUMMIT 2026

SCIENCE FOR SOLUTIONS

15-17 June 2026

Orchard Hotel Singapore

PROGRAMME BOOK

International Co-convenors:

ADVA
Asia Dengue Voice & Action Group

gdac
GLOBAL DENGUE + AEDES-TRANSMITTED DISEASES CONSORTIUM

SEAMEO TROPMED

The International Society for Neglected Tropical Diseases
www.isntd.org

Local Host:

DukeNUS Medical School

NANYANG TECHNOLOGICAL UNIVERSITY SINGAPORE

LEE KONG CHIAN SCHOOL OF MEDICINE

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WELCOME MESSAGE

Dear Colleagues,

We are delighted to be able to welcome you to Singapore for the 9th Asia Dengue Summit (ADS).

As you will be aware, research on all fronts, from clinical epidemiology to virology and entomology, have made important breakthroughs in our understanding of dengue in recent years. Some of which are ripe for translation into interventions to alleviate the illness that billions live at risk of in Asia each year. However, the volume of published literature is large – in just the last 5 years, more than 10,000 papers have been published in peer reviewed journals. Sieving through this evidence to identify findings that are ready for translation is increasingly challenging.

The annual ADS has served as a platform for the community of clinicians, public health officials and scientists to meet, exchange the latest knowledge and establish new collaborative networks. We will gather thought leaders in the dengue field to synthesize the evidence and distil it into actionable nuggets. We will also hear the latest findings from those in the forefront of research, from field studies to molecular virology and immunology. Finally, it is our hope that the ADS will serve to catalyse translation of science into action to reduce the dengue burden and even eliminate dengue deaths.

We welcoming you to Singapore.

With best wishes,

Eng Eong Ooi and Lee Ching Ng (Co-organisers)
Shirin Kalimuddin (Chair of Scientific Committee)

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ABOUT US

The Asia Dengue Voice & Action Group (ADVA) was officially set up in 2013 with a mission to identify opportunities to make practical recommendations in dengue-related areas such as improving surveillance and laboratory capacity for dengue disease confirmation with other relevant dengue initiatives, including V2V (vaccine to vaccination) and the Dengue Vaccine Initiative.

ADVA advocates for a collaborative approach to sharing surveillance data and relevant information to ensure the success of dengue prevention through vaccination across regions. ADVA also reinforces the importance of a united front against dengue, and presents a collaborative model for joint effort in the region to prevent the disease through the introduction and implementation of dengue vaccination.

The group has formulated recommendations with an ultimate aim of translating the science of dengue vaccination into messages for policy makers, general public and health care workers.

The Global Dengue & *Aedes*-Transmitted Diseases Consortium (GDAC) is a consortium composed of the Partnership for Dengue Control (PDC), the International Vaccine Institute (IVI), the International Vaccine Access Center (IVAC) at the Johns Hopkins Bloomberg School of Public Health and the Sabin Vaccine Institute. The World Health Organization advises and collaborates with GDAC.

The Southeast Asian Ministers of Education Organization (SEAMEO) is a regional intergovernmental organization established in 1965 among governments of Southeast Asian countries to promote regional cooperation in education, science and culture in the region.

The ISNTD is an independent organisation providing a multidisciplinary global platform to an international network of individuals working in the fields of Neglected Tropical Diseases, diseases of poverty and global development. The aim of the ISNTD is to focus on and highlight the research and programmes of colleagues and organisations worldwide, to ultimately have an impact on the health and prosperity of the world's poorest and most vulnerable, while sharing the goal of reaching sustainable healthcare provision & poverty reduction in the developing world.

The ISNTD believes that this goal cannot be achieved without strengthening the ties between all the parties already involved in NTD alleviation and addressing the socio-ecological and socio-political context of NTDs, in order to achieve not only the cure but also the prevention of NTDs with true and sustainable local leadership.

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COMMITTEE

Local Organising Committee:

Ooi Eng Eong

Jarir At Thobari

Sim Shuzhen

Lim Jue Tao

Sylvie Alonso

Shirin Kalimudidin

Ng Lee Ching

Asia Dengue Voice & Action Group (ADVA) Steering Committee:

Zulkifli Ismail

Usa Thisyakorn

Sri Rezeki Hadinegoro

Daniel YT Goh

Maria Rosario Capeding

Terapong Tantawichien

Sutee Yoksan

Asia Dengue Voice & Action Group (ADVA) International Advisors:

Duane Gubler

Tikki Pangestu

Ooi Eng Eong

Lulu Bravo

Pratap Singhasivanon

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CHIKUNGUNYA VIRUS
HOW FAR WOULD YOU GO
TO PROTECT YOUR TRAVELS?

AGENDA

14 June 2026, Sunday – Pre-Summit Workshop
Venue: Grand Ballroom 1 + 2

Dengue Prevention – 7 Years of TAK-003 Clinical Experience, Real World Evidence Advancement and Beyond

TIME	PROGRAMME	MODERATOR / SPEAKERS
1200 – 1300	**Lunch available for participants**	
1300 – 1315	**Welcome and Global Context Setting**	Shirin Kalimuddin
1315 – 1355	**Long Term Clinical Evidence for TAK-003**	Eduardo Lopez Medina
	Q&A Panel	Eduardo Gomensoro, Shibadas Biswal, Eng Eong Ooi, Eduardo Lopez Medina
1355 – 1445	**Real-World Evidence: Safety and Effectiveness Across Diverse Settings**	**Speaker:** Julio Croda Pablo Bonvehi Vianney Tricou
1445 – 1500	**Tea Break**	
1500 – 1555	**DEN-Talk (immunology chapter)**	
	Correlates of Protection: Why Dengue Is Different	Eng Eong Ooi
	Dengue infection elicits skin tissue-resident T cells	Laura Rivino
	Innate Immune Reprogramming and Emerging Concepts	Eng Eong Ooi
	Dichotomy between nAb and T cells	Shirin Kalimuddin
	TAK-003 immunogenicity – in the context of emerging evidence on protective immunity	Mayuri Sharma (chair)
	Q&A Panel	Mayuri Sharma (chair **Panelists:** Eng Eong Ooi, Laura Rivino, Shirin Kalimuddin
1555 – 1650	**Expert Panel Discussion:** • Dengue Surveillance and Epidemiology; Integrated Dengue Prevention Framework; Country experiences, NIP, Public programmes; What's the best way to deliver TAK-003 in public programmes. • Questions from participants via Slido	Eduardo Lopez Medina (chair) **Panelists:** Wanatpreeya Phongsamart, Jarir At Thobari
1650 – 1700	**Key Takeaways and Close**	Shirin Kalimuddin

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AGENDA

Day 1 - 15 June 2026, Monday

TIME	PROGRAMME	MODERATOR / SPEAKERS
0800 – 0845	**Registration**	
0845 – 0900	**Welcome Address**	Eng Eong Ooi, *Co-organiser, 9th ADS*
0900 – 0930	**Keynote Lecture: Back to the future – Lessons for dengue research from the HIV field**	Nelson Michael, *WRAIR, USA*
0930 – 1040	**Symposium 1: Setting the stage**	**Moderator:** Jarir At Thobari
	Why is dengue surging globally?	Henrik Salje, *Cambridge University*
	Dengue vaccines – Lessons learned from the pursuit of perfection	Stephen Thomas, *SUNY Upstate*
	Will Wolbachia be a public health success: Evidence from Brazil	Albert Ko, *Yale University*
	Short talk: Integrating global dengue surveillance to give insights into climactic drivers, growth trends, outbreak forecasting	Oliver Brady, *LSHTM, UK*
1040 – 1100	**Tea Break**	
1100 – 1230	**Symposium 2: Lessons from the field**	**Moderator:** Eng Eong Ooi
	Arbovirus surveillance and molecular epidemiology	Nuno Faria, *Imperial College, London*
	Dengue, climate change, and mitigation approaches	Borame Dickens, *SSHSPH, Singapore*
	Community dengue spread: implications for interventions	Martin Hibberd, *LSHTM, UK*
	Updates on V181 phase 3 clinical trial	Soumya Chatterjee, *MSD*
	Short talk: Stepwise approach for dengue vaccine introduction to National Immunization Programme in Thailand	Anyarat Thamjaroen, *National Vaccine Institute, Thailand*
1230 – 1330	**Lunch**	

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AGENDA

Day 1 - 15 June 2026, Monday *(Continued)*

TIME	PROGRAMME	MODERATOR / SPEAKERS
1330 – 1445	**Industry Symposium A (Takeda):** **From Vaccine To Vaccine-nations – Solutions For Dengue Prevention**	
	Welcome	Tikki Pangestu
	TAK-003 The Comprehensive Clinical Development & Global Vaccine Experience	Derek Wallace
	Country perspectives in vaccine implementation in public and private settings	**Moderator:** Choo Beng Goh **Speakers:** Julio Croda Thanyawee Puthanakit
	Turning Insights into Action: Panel Discussion on Dengue Prevention	**Moderator:** Choo Beng Goh **Panelists:** Derek Wallace Julio Croda Thanyawee Puthanakit Tikki Pangestu
	Key Takeaways and Close	Tikki Pangestu
1445 – 1540	**Symposium 3: A dengue drug – why we need one and how we get there (I)**	**Moderator:** Jenny Low
	Current state of play of dengue therapeutic development	Andre Siqueira, *DNDi*
	Adaptive platform trials for dengue therapeutics	Sophie Yacoub, *Oxford University*
	Short talk: Anakinra for dengue patients with hyperinflammation: a phase II double-blind randomized controlled trial	Huyen Bang Tran, *OUCRU, Vietnam*
1540 – 1600	**Tea Break**	
1600 – 1720	**Symposium 4: New Challenges- from Virus evolution to climate change**	**Moderator:** Kevin Tetteh
	Collective Action on Dengue	Kevin Tetteh, *CAD*
	Dengue virus genetics and Wolbachia	Chantal Vogels, *Yale University*
	Single amino acid change on E protein prevents IgM-mediated neutralization during DENV2 infection	Sylvie Alonso, *NUS, Singapore*
	Host-virus interactions in dengue	Laura Martin-Sancho, *Imperial College, London*
	Flavivaccine: Targeting mosquito saliva factors blocks flavivirus transmission and disease	Julien Pompon, *IRD, France*
1720 – 1745	**Break**	

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Day 1 - 15 June 2026, Monday *(Continued)*

TIME	PROGRAMME	MODERATOR / SPEAKERS
1745 – 1845	**World Dengue Day Session**	
	Welcome Remarks	Marianne Comparet, *ISNTD*
	Opening Remarks	Janil Puthucheary, *Senior Minister of State for Sustainability and the Environment, Singapore*
	Online Statements from Around the Globe:	Messages of support and perspectives from International partners and representatives
	Panel Discussion	Janil Puthucheary, *Senior Minister of State for Sustainability and the Environment, Singapore* Diana Rojas Alvarez *Head (a.i.) Emerging Zoonosis and High Impact Epidemics Unit, WHO* Julio Croda *Federal University of Mato Grosso do Sul, Yale School of Public Health, and Oswaldo Cruz Foundation*
	Group Photo for the Panelists	
	MOU Announcement: • Asia Dengue Voice & Action Group (ADVA) • Dengue Prevention Advocacy Malaysia (DPAM) • Empowering Networks to Defeat Dengue (E.N.D. Dengue Coalition) • Koalisi Bersama Lawan Dengue (Joint Coalition Against Dengue – KOBAR)	
	Group Photo for MOU Partners	
	Reception (Held in Partnership with Temasek Foundation)	
Close of Day 1		

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AGENDA

Day 2 - 16 June 2026, Tuesday

TIME	PROGRAMME	MODERATOR / SPEAKERS
0820 – 0830	**Welcome Back**	Lee Ching Ng
0830 – 0945	**Symposium 5: Dengue immunity (I) – what protects and what makes us sick?**	**Moderator:** Sylvie Alonso
	Pathogenesis of severe dengue beyond ADE	Adam Waickman, *SUNY Upstate*
	Contributions of circulating & skin-resident T cells to protective immunity in dengue	Laura Rivino, *Liverpool School of Tropical Medicine*
	De-risking ADE, Revealing Mechanism: Fusion Loop-Mutated prM/E Zika Vaccines Protect via CD8 T Cells, but Not Durably	Sujan Shresta, *La Jolla Institute of Immunology, USA*
	Immune response in asymptomatic dengue	Ponpan Matangkasombut Choopong, *Mahidol University*
0945 – 1005	**Tea Break**	
1005 – 1120	**Symposium 6: Dengue immunity (II) – what protects and what makes us sick?**	**Moderator:** Shirin Kalimuddin
	Correlates of protection and risk in dengue: lessons from cohort studies	Leah Katzelnick, *NIH, USA*
	Short talk: Prior Zika virus imprints subsequent dengue virus neutralizing antibodies by skewing the repertoire of antibody-secreting cells	Tulika Singh, *UC Berkeley, USA*
	Short talk: Is homotypic reinfection a key feature of dengue endemic settings?	Jair Andrade, *University of Cambridge, UK*
	Short talk: Mechanistic insights into dengue virus-induced reprogramming of innate immune response	Usama Ashraf, *Duke-NUS*
1120 – 1235	**Symposium 7: Emerging challenges in dengue management**	**Moderator:** Rose Capeding
	Dengue and obesity	Neelika Malavige, *Sri Jayewardenepura University, Sri Lanka*
	Novel biomarkers for severe dengue prediction	Nguyen Lam Vuong, *OUCRU, Vietnam*
	Post-acute burden of dengue	Wee Liang En Ian, *SGH, Singapore*
	Real-time continuous clinical monitoring for dengue	Ho Quang Chanh, *OUCRU, Vietnam*
1235 – 1335	**Lunch**	

Day 2 - 16 June 2026, Tuesday *(Continued)*

TIME	PROGRAMME	MODERATOR / SPEAKERS
1335 – 1440	**ADVA Educational Symposium 1: Innovations for Aedes-borne disease control** *(Supported by: Bavarian-Nordic & World Mosquito Program)*	**Moderator:** Lulu Bravo
	Global evidence base for vector control	Jue Tao Lim, *NTU, Singapore*
	Updates from World Mosquito Program	Bekti Andari, *World Mosquito Program*
	Updates on Chikungunya	Tsin Wen Yeo, *NTU, Singapore*
1440 – 1630	**Poster Session (and tea break served at 1600)**	
1630 – 1740	**Symposium 8: A dengue drug – why we need one and how we get there (II)**	**Moderator:** Zulkifli Ismail
	Clinical management for zero dengue deaths: How can we do better?	Giri Shan Rajahram, *QEII Hospital, Malaysia*
	Update on ISLA-101 development	David Foster, *Island Pharma*
	Short talk: A role for sphingosine-1-phopshate analogues in dengue shock?	Angela McBride, *Oxford University*
	WHO Dengue TPP	Xin Hui Chan *UK Health Security Agency*
	Panel Discussion / Q&A	Andre Siqueira, Giri Shan Rajahram, David Foster, Xin Hui Chan, Angela McBride
1740	**Close of Day 2**	

AGENDA

Day 3 - 17 June 2026, Wednesday

TIME	PROGRAMME	MODERATOR / SPEAKERS
0730	**Registration starts**	
0815 – 0820	**Welcome Back**	Eng Eong Ooi
0820 – 0950	**ADVA-JA Dengue Slayers Challenge**	
0950 – 1010	**Tea Break**	
1010 – 1115	**Symposium 9: New developments in dengue vaccines**	**Moderator:** Ignacio Esteban
	GAVI and dengue vaccines	Ignacio Esteban, *GAVI*
	Updates from TAK-003 Booster Trial data	Shibadas Biswal, *Takeda*
	Development of a live-attenuated tetravalent dengue vaccine (KD-382)	Motoharu Abe, *KM Biologics*
	Acceptability and barriers to dengue vaccination	Hannah Clapham, *SSHSPH, Singapore*
1115 – 1215	**ADVA Educational Symposium II: New tools to combat dengue** **Supported by: Roche, Sysmex, ProImmune**	
	Advancing Dengue Diagonstics: Leveraging Antigen and IgM Immunoassays with Automation to Overcome Diagnostic Challenges	Carolin Bier, *Roche*
	Beyond the count: What the full blood count reveals in dengue	Yap Eng Soo, *Ng Teng Fong General Hospital*
	Antigen-specific T cell characterisation and immune monitoring tools & Ankyrons® – Next generation target binding and detection	Chua WenZhe, *ProImmune*
1215 – 1315	**Lunch**	
1315 – 1410	**Symposium 10: Interrupting dengue transmission**	**Moderator:** Shuzhen Sim
	Long terms outcomes of Wolbachia Aedes Replacement	Eggi Arguni, *Universitas Gadjah Mada, Indonesia*
	Wolbachia Aedes suppression for dengue control	Milly Choy, *NEA, Singapore*
	Short talk: Strategic deployment of wMEL-SG for suppression of wALB-SG populations established in the field	Li Yun Tan, *NEA, Singapore*

AGENDA

Day 3 - 17 June 2026, Wednesday *(Continued)*

TIME	PROGRAMME	MODERATOR / SPEAKERS
1410 – 1525	**Symposium 11: Real-world evidence in dengue control**	**Moderator:** *Jue Tao Lim*
	Gaps in Real-world Evidence generation	Derek Cummings, *Johns Hopkins University*
	Real world evidence of dengue vaccination in Brazil	Julio Croda, *Universidade Federal de Mato Grosso do Sul, Brazil*
	Effectiveness of integrated dengue control measures	Nurulhusna Ab Hamid, *MOH, Malaysia*
	Public Health impact and cost-effectiveness of dengue vaccination	Jing Shen, *Takeda*
1525 – 1545	**Tea Break**	
1545 – 1700	**Symposium 12: Innovative Solutions for Dengue** • Urban Planning • Community-based care • Innovative Financing	
	Panel Discussion	Tikki Pangestu *YLL School of Medicine, NUS* Graham Alabaster *Former Director, UN-Habitat* Michelle Tan *SGH, Singapore* Patsian Low *Asia Venture Philanthropy Association (AVPN)* A. Vigneswari *For APEC Dengue Roadmap (Crowell Global Advisors)*
1700 – 1720	**Award Ceremony and Closing**	Lee Ching Ng

AGENDA

18 June 2026, Thursday – Post-Summit Workshop
Venue: Grand Ballroom 1 + 2

ASIA WOLBACHIA DIALOGUE 2026

Organized by Asian Development Bank (ADB), in collaboration with, Singapore National Environment Agency (NEA), and Indonesia Ministry of Health (Kemenkes), and Asia Dengue Voice & Action (ADVA)

TIME	PROGRAMME	MODERATOR / SPEAKERS
0800 – 0815	**Registration**	
0815 – 0845	**Welcome and Overview** – NEA – ADB – Indonesia MoH – ADVA	Lee Ching Ng, *NEA Singapore* Eduardo Banzon, *Director, Health, ADB* Andi Saguni, *Acting DG, Communicable Disease Control, Indonesia MOH* Zulkifli Ismail, *ADVA*
0845 – 0855	**Keynote Speech 1**	Hon. Budi Sadikin, *Minister of Health, Republic of Indonesia*
0855 – 0905	**Keynote Speech 2**	Md. Quamruzzaman Chowdhury, *Secretary, Health Services, Ministry of Health & Family Welfare, Bangladesh*
0905 – 0925	**Wolbachia: WHO Policy and Guidance**	Lauren Carrington, *Technical Officer, WHO*
0925 – 0950	**Epidemiological evidence supporting Wolbachia as an intervention and its benefits**	Lim Jue Tao & Jo Yi Chow, *Nanyang Technological University, Singapore*
0950 – 1015	**Tea Break**	
1015 – 1100	**Brief Overview: Wolbachia Approaches** **Panel Discussion: Practical considerations for selecting Replacement v Suppression approaches**	**Moderator:** Lee Ching Ng, *Group Director, NEA Singapore* **Panelists:** Peter Ryan, *Director, Technical Engagement, World Mosquito Program* Zhiyong Xi, *Michigan State University / Wolbaki* Florence Fouque, *Ex-WHO TDR, Affiliated Scientist, Institute of Microbiology, SUPSI Switzerland* Katie Anders, *Associate Professor (Research) and NHMRC Emerging Leadership Fellow, Monash University*
1100 – 1130	**Wolbachia Operational Delivery Models**	Jenny Zhang, *Regional Senior Associate, Dengue, Clinton Health Access Initiative*

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18 June 2026, Thursday – Post-Summit Workshop *(Continued)*
Venue: Grand Ballroom 1 + 2

ASIA WOLBACHIA DIALOGUE 2026

Organized by Asian Development Bank (ADB), in collaboration with, Singapore National Environment Agency (NEA), and Indonesia Ministry of Health (Kemenkes), and Asia Dengue Voice & Action (ADVA)

TIME	PROGRAMME	MODERATOR / SPEAKERS
1130 – 1200	**Investment Case for Wolbachia**	Aman Singh, *Senior Social Sector Specialist, Health, ADB* Oliver Brady, *Professor of Spatial Epidemiology and Lead of Centre for Mathematical Modelling of Infectious Diseases, LSHTM UK*
1200 – 1320	**Lunch**	
1320 – 1500	**Wolbachia Implementation Overview – Asia and Pacific** **Country Journeys and Plans:** • Brazil • Singapore • Indonesia • Malaysia • Lao PDR **Q&A**	James F. Kelley, *Technical Officer, WPRO* *Country/Government Representatives*
1500 – 1515	**Tea Break**	
1515 – 1510	**Wolbachia Implementers' Session** **Q&A**	Wolbachia Implementers' Session Q&A
1610 – 1655	**Donor Panel Discussion** **Q&A**	**Moderator:** Martin Edlund, *CEO Billion Scale Health* **Panelists:** Eduardo Banzon, *Director, Health, ADB* Sasha Lee, *Assistant Director, Pacific Health Section, DFAT* Fook Kay Lee, *Director, Pandemic Preparedness, Temasek Foundation* Rahul Chandran, *Chief Strategy and Partnerships Officer, Grand Challenges Canada (TBC)* Kapila Kannangara, *Acting Director, National Dengue Control Unit, Sri Lanka*
1655 – 1700	**Closing Remarks**	ADB and ADVA

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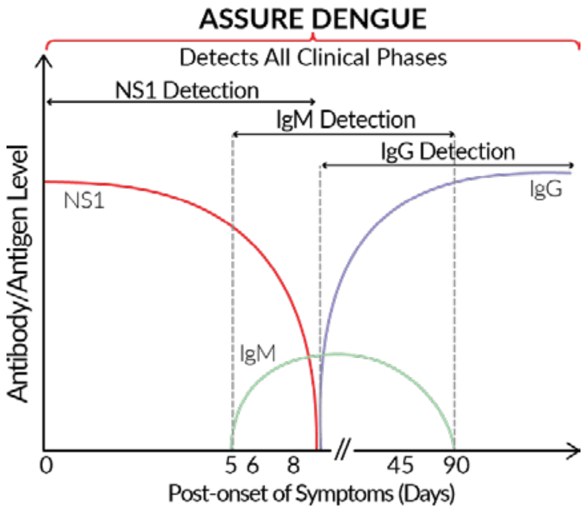
MP Biomedicals is a global life science and diagnostics company with headquarters in California and regional offices across the globe. The company offers a diverse portfolio of life science products, fine chemicals, and diagnostics used in industries ranging from basic research to clinical diagnostics and pharmaceuticals.

The MP Diagnostics **ASSURE Dengue Ab/Ag Rapid Test** is a qualitative *in vitro* immunochromatographic test that is intended to detect and differentiate IgG/IgM antibodies against Dengue virus and NS1 Dengue antigen in human plasma or serum or finger pricked whole blood or whole blood with anti-coagulants.



- ✓ The only test capable of detecting and differentiating dengue antigen (NS1) and antibodies (IgM and IgG) in a SINGLE cassette.
- ✓ Designed to detect ALL 4 Dengue serotypes (DEN-1, 2, 3 and 4) in a single test.
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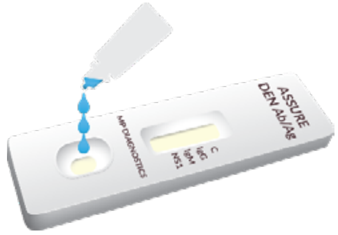
- ✓ Specimen: Finger-pricked blood, whole blood, human serum and plasma.
- ✓ Results ready to read in 15 minutes.

Assay Procedure

Step 1	Step 2	Step 3
Add 30 µL of sample into the sample well 	Add 3 drops of chase buffer into the same sample well 	Start the timer • Read results at 15 minutes • Do not read results after 20 minutes

Diagnostic Performance

Diagnostic Parameter	Performance of ASSURE Dengue Ab/Ag Rapid Test	95% Confidence Interval
Sensitivity (n=341)	100%	97.42% - 100%
Specificity (n=289)	100%	98.73% - 100%
Positive Predictive Value (PPV)	100%	97.42% - 100%
Negative Predictive Value (NPV)	100%	98.73% - 100%

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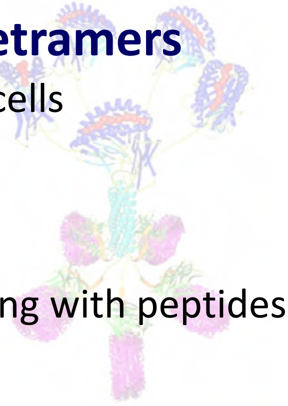

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ProVE® *SL* Self-loading MHC Class I Monomers

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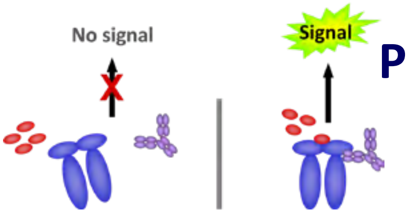
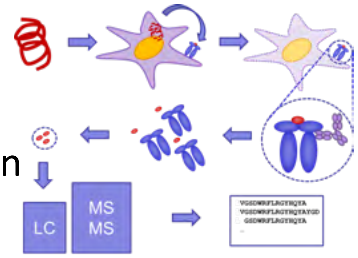


ProImmune REVEAL® MHC-Peptide Binding Assays

Confirm physical binding characteristics of actual peptides and validate *in silico* predictions



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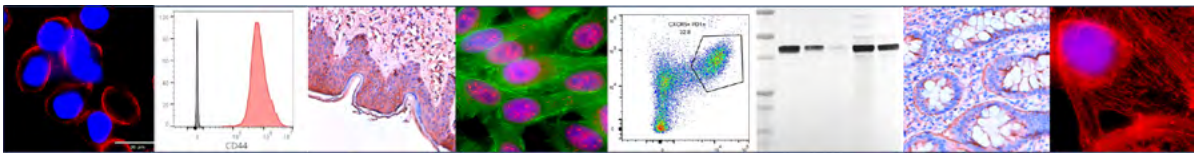
Identifies naturally processed and presented peptides from antigen

Ankyrons®

Overcome the challenges of research antibodies with next-generation reagents for target binding and detection



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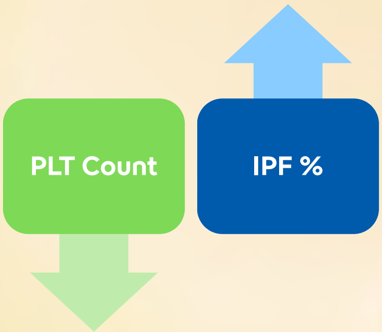
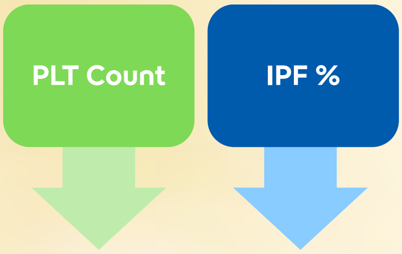
IPF (Immature Platelet Fraction)

Measures platelet production status.



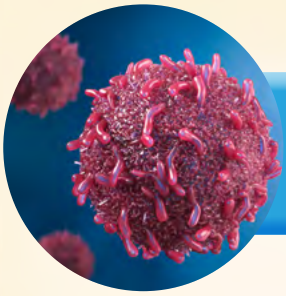
Platelet recovery is expected within 24-48 hours.



Platelet recovery absent.

An Early Indicator

Monitoring during critical Dengue haemorrhagic phase



Monitoring of bone marrow engraftment

Scan here to learn more.

IPF	Predicting Recovery	Cutoff*
	93.75%	>10%

**Dadu T et al. (2013) Int J Lab Hem 36(5):499-504*

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OOI ENG EONG

BMBS, PhD, FRCPath
Duke-NUS Medical School

Eng Eong is a Professor in the Programme in Emerging Infectious Diseases and serves as the Associate Dean for Early Research Career Development at Duke-NUS Medical School. He trained in medicine at the University of Nottingham and completed his PhD studies on molecular epidemiology at the National University of Singapore. He has, for more than 25 years, been conducting research on dengue, starting with epidemiology of dengue in Singapore before focusing on dengue virology and human immune response to infection. He is a three-time recipient of the Clinician-Scientist (Senior Investigator) Award and currently holds the Singapore Translational Research Award, all from the National Medical Research Council of Singapore. He has served in advisory capacities to the pharmaceutical and vaccine industry. He is a member of the Scientific Advisory Board of *Science Translational Medicine* and an Editorial Board member of *PLoS Biology*.

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ORGANISING COMMITTEE

JARIR AT THOBARI

Faculty of Medicine, Public Health and Nursing
Universitas Gadjah Mada (UGM)

Professor Jarir At Thobari is a clinical pharmacologist, vaccinologist, and epidemiologist at the Faculty of Medicine, Public Health and Nursing Universitas Gadjah Mada (UGM), Indonesia, with over two decades of experience in infectious disease research, vaccine evaluation, and health technology assessment. His work focuses on rotavirus, typhoid, dengue and other infectious diseases, integrating clinical trials, disease surveillance, and health economic modelling to inform vaccine policy and implementation.

He has led multiple vaccine clinical trials in Indonesia and spearheaded national studies, including on dengue surveillance and the cost-effectiveness of dengue vaccination programs. His research provides critical evidence for the introduction of vaccines into Indonesia's national immunisation strategy.

He also serves as a member of Indonesia's Technical Advisory Group on Immunisation (ITAGI) and the Health Technology Assessment (HTA) Committee, contributing to evidence-based decision-making for vaccine introduction. He is an active member of the Asia Pacific Vaccine Research Network (APVRN) and a WHO-TDR Regional Training Centre (RTC) trainer for Good Clinical Practice and Clinical Research Leadership.

SIM SHUZHEN

Director,
Microbiology and Molecular Epidemiology Division,
Environmental Health Institute,
National Environment Agency, Singapore

Dr Sim Shuzhen is Director of the Microbiology and Molecular Epidemiology Division at the Environmental Health Institute, National Environment Agency, Singapore. She oversees multidisciplinary efforts on risk assessment and surveillance of infectious diseases in the environment, including vector-borne diseases, wastewater surveillance, and environmental monitoring of antimicrobial resistance. She has research and applied experience in dengue-mosquito interactions, evaluation of vector control interventions, and risk prediction. During the COVID-19 pandemic, she also led field and epidemiological investigations of airborne transmission risk in the built environment, and contributed to guidelines, standards and mitigation measures for ventilation and indoor air quality.

LIM JUE TAO

Lee Kong Chian School of Medicine
Nanyang Technological University

Assistant Professor Lim Jue Tao is an Assistant Professor in the Lee Kong Chian School of Medicine at Nanyang Technological University. He holds a BSc (Hons) in Economics, as well as a Masters in Statistics. He obtained his PhD in Public Health from the Saw Swee Hock School of Public Health in 2021, where his work was focused on modelling the transmission dynamics of vector-borne diseases.

He is a biostatistician and infectious disease modeller with a long-standing and deep interest in developing new models for infectious disease forecasting, transmission and control. His laboratory is focused on developing novel frameworks to (1) assess interventions in complex, large-scale field trials to stave vector-borne diseases and (2) forecast and project disease burdens over short and long temporal scales. He uses these tools to provide forward guidance on the future epidemiology of diseases and to advise and design disease control implementation and policy. He is primarily focused on studying the transmission dynamics of climate and behaviour-sensitive pathogens, such as Chikungunya, dengue, gonorrhoea, SARS-CoV-2 and syphilis. He has published over 120 articles in leading medical and scientific journals, including the New England Journal of Medicine, Lancet Planetary Health, Lancet Microbe, Lancet Infectious Diseases and JAMA Neurology.

SYLVIE ALONSO

Department of Microbiology and Immunology,
Yong Loo Lin School of Medicine,
National University of Singapore

Dr Alonso obtained her PhD degree in Microbiology and Molecular Biology from Universite Claude Bernard Lyon I (France). She then continued her post-doctoral training at Pasteur Institut de Lille (France) where she developed bacterial vaccine delivery systems, followed by another two years at Cornell University (NY, USA) where she studied the molecular pathogenesis of tuberculosis. In 2004, she was awarded the Lee Kuan Yew post-doctoral Fellowship and joined the Department of Microbiology at the National University of Singapore (Singapore). She was recruited as an Assistant Professor in 2007 and promoted to Associate Professor with tenure in 2013. For the past 15 years, Dr Alonso's research team has studied the host-pathogen interactions during viral infections, including Hand, Foot and Mouth Disease (HFMD) and Dengue. She has also pursued her long-time interest in vaccine development against viral diseases. In 2022, she was appointed Lead of the Vaccines&Therapeutics Co-Operative under the national Programme for Research in Epidemic Preparedness and Response (PREPARE). Her role is to develop and support the local pandemic preclinical research in Singapore.

SHIRIN KALIMUDDIN

Senior Consultant
Department of Infectious Diseases
Singapore General Hospital

Shirin Kalimuddin is a clinician-scientist and practicing infectious disease physician. She is a Senior Consultant in the Department of Infectious Diseases at Singapore General Hospital, and an Assistant Professor with the Program in Emerging Infectious Diseases at Duke-NUS Medical School. Shirin received her medical degree from King's College London in 2005, following which she returned to Singapore to complete her specialist training in adult infectious diseases. She later earned a Master of Public Health from the Johns Hopkins Bloomberg School of Public Health and then completed her PhD training at Duke-NUS Medical School. Her research combines experimental medicine and immunology to understand the human host-response to orthoflaviviral infections such a dengue, with a particular focus on the role of cell-mediated immunity in disease protection and pathogenesis. As part of her current research portfolio, Shirin co-leads Translational Research and Clinical Trials for the SingHealth Duke-NUS Medicine Academic Clinical Programme and serves on the Executive Council of the Singapore Infectious Diseases Clinical Research Network. She is a recipient of the National Medical Research Council of Singapore (NMRC) Transition Award (2019), NMRC Research Training Fellowship (2021) and NMRC Clinician-Scientist Award (2025).

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NG LEE CHING

Group Director,
Environmental Health Institute (EHI),
National Environment Agency, Singapore

Assoc Prof Ng Lee Ching is the Group Director of Environmental Health Institute (EHI) at the National Environment Agency in Singapore. She has spent more than 20 years building scientific capabilities for Singapore's environmental public health, conducting research to understand disease risk and transmission, and developing tools and strategies for mitigation of risks.

She has co-authored more than 200 scientific papers and book chapters, in the area of vector borne diseases, COVID-19, food borne diseases, anti-microbial resistance, indoor air quality etc.

She serves as an Adjunct Associate Professor at the Saw Swee Hock School of Public Health at National University Singapore, Adjunct Associate Professor at Nanyang Technological University of Singapore and as the Director of the WHO Collaborating Centre for Reference and Research of Arbovirus and their Associated Vectors.

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SPEAKERS' BIOGRAPHIES

NELSON L. MICHAEL

Director, Center for Infectious Disease Research
Walter Reed Army Institute of Research

Nelson L. Michael, M.D., Ph.D. is the Director, Center for Infectious Diseases Research. Dr. Michael graduated summa cum laude from University of California, Los Angeles in 1979 with a degree in biology and from Stanford University with M.D. and Ph.D. (cancer biology) degrees in 1986. He trained in internal medicine at Harvard Medical School, Massachusetts General Hospital from 1986-1989.

Prior to his current position, Dr. Michael served for 29 years in the U.S. Army at WRAIR including 12 years as the Director of the U.S. Military HIV Research Program (MHRP) at WRAIR and 8 months as the WRAIR Deputy Commander. He was deployed in 2013 with the 1st Armored Division to the Kingdom of Jordan. Dr. Michael retired from the U.S. Army on 30 September 2018 at the rank of Colonel.

MHRP is an international HIV vaccine and remission research program that successfully integrates HIV/AIDS prevention and treatment. Dr. Michael guided MHRP through the completion of the RV144 HIV prime-boost vaccine clinical trial, an international collaboration that involved more than 16,000 Thai volunteers and provided the world's first demonstration that a preventive HIV vaccine was possible. Dr. Michael entered his Army service in 1989 in WRAIR's Department of Vaccine Research, Division of Retrovirology, and later served as the Chief of the Department of Molecular Diagnostics and Pathogenesis.

Dr. Michael served on President Obama's Presidential Commission for the Study of Bioethical Issues (2009-2016) and the Operation Warp Speed Vaccine Development Team (2020-2022). He currently serves on the Vaccine Research Center Scientific Advisory Working Group (NIAID, NIH).

Dr. Michael's research interests include SARS-CoV-2, HIV molecular pathogenesis and host genetics, HIV clinical research and HIV/Ebola/MERS Co-V and ZIKV vaccine development. He is a Professor of Medicine at the Uniformed Services University and is a Diplomate of the American Board of Internal Medicine. He serves as a peer reviewer of many scientific journals and is the author or coauthor of more than 480 scientific publications and eight textbooks. Honors include Army Commendation Medal (1992, 1996), Joint Service Commendation Medal (2013), Army Achievement Medal (1996, 2018), Army Meritorious Service Medal (2004, 2010, 2018), the Defense Meritorious Service Medal (2013), Legion of Merit (2018), the Hero of Military Medicine (Army) Award (2013) the Army Civ Svc Medal (2020) and Army Superior Civ Svc Medal (2022)

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HENRIK SALJE

Department of Genetics
University of Cambridge

Henrik is a Professor in the Department of Genetics at the University of Cambridge where he heads the Pathogen Dynamics Unit. He works on the spread of infectious diseases. He uses mathematical, computational and field research to help our understanding of how pathogens spread in populations, to assess control efforts and support policy making. This includes working with a diverse range of datasets including epidemiological, genomic, serological and behavioural data. He works closely with an established network of collaborators across laboratories, field-based epidemiologists, hospitals and public health agencies. He has a particular interest in the dynamics of arboviruses such as dengue, Zika and chikungunya viruses.

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STEPHEN THOMAS

Distinguished Professor of Microbiology and Immunology
Professor of Public Health and Preventive Medicine
SUNY Upstate Medical University

Professor Stephen Thomas is an Infectious Diseases physician-scientist from SUNY Upstate Medical University in Syracuse, NY, USA. He is a Professor of Medicine and Professor of Microbiology & Immunology. Dr. Thomas currently directs the Upstate Global Health Institute and is the Frank E. Young, MD '56 and Leanne Young Endowed Chair of Microbiology & Immunology. Dr. Thomas earned his Bachelor of Arts with Honors in Biomedical Ethics from Brown University, his Medical Degree from Albany Medical College, and completed his Internal Medicine residency and Infectious Diseases fellowship at the Walter Reed Army Medical Center and the National Capital Consortium. Prior to joining Upstate, Dr. Thomas served in the U.S. Army at the Walter Reed Army Institute of Research and completed his career as the institute's Deputy Commander for Operations. He also served as the Infectious Diseases Consultant to the U.S. Army Surgeon General. Dr. Thomas specializes in the study of infectious diseases with a focus on diseases caused by viruses. He spent more than five years of his early military career living and working in Thailand and Southeast Asia. Dr. Thomas played key leadership roles in the U.S. government response to the West Africa Ebola outbreak (2014-2016) and advised senior government leaders during the planning and execution of the Obama Administration's Operation United Assistance. He represented the Department of Defense in the U.S. government response to the MERS-CoV and Zika epidemics. Dr. Thomas served as the global coordinating principal investigator for the Pfizer / BioNTech COVID vaccine efficacy trial. Dr. Thomas serves on numerous advisory boards for the US government, non-governmental organizations such as the WHO and CEPI, and industry. He is a contributor to Forbes magazine and entrepreneur, co-founding start-ups in life sciences consulting, biotech, and digital marketplaces.

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ALBERT ICKSANG KO

Yale School of Public Health
Yale University

Dr. Albert Icksang Ko is the Raj and Indra Nooyi Professor of Public Health at the Yale School of Public Health and Collaborating Researcher at the Oswaldo Cruz Foundation, Brazilian Ministry of Health. He served as Chair of the Department of Epidemiology of Microbial Diseases at Yale (2010-2021) after being stationed with the Brazilian Ministry of Health in Brazil for 15 years. His research centers on the health problems that have emerged due to rapid urbanization and social inequity. Dr. Ko coordinates an urban health program, which focuses on delineating the role of marginalization, urban ecology, and climate on infectious diseases in urban informal settlements and implementing community-driven interventions. He and his team have mobilized public health and research responses to multiple epidemics, which include meningitis, leptospirosis, dengue and Zika virus infection and associated birth defects. He is a member of the WHO R&D Blueprint Working Group and Taskforce for Zika Virus and the NASEM Forum of Microbial Threats. During the pandemic, he was the co-chair of Reopen Connecticut Advisory Group which developed the states COVID-19 response plan and served as advisor to Governor Lamont, in addition to providing support to the Oswaldo Cruz Foundation for its pandemic response in Brazil.

NUNO FARIA

Department of Infectious Disease Epidemiology
Imperial College London

Nuno Faria is a Professor in Virus Genomic Epidemiology at the MRC Centre for Global Infectious Disease Analysis, Imperial College London, where he co-leads the Pathogen Genomic Epidemiology theme. He also holds a Visiting Professor appointment at the Institute of Tropical Medicine from the University of São Paulo in Brazil.

He has worked on the evolution and epidemiology of a range of rapidly evolving viruses, including Zika, dengue, chikungunya, yellow fever, HIV, Ebola, and influenza. He currently serves on various boards and technical advisory groups (TAGs), including the WHO Global Arbovirus Initiative and the WHO Virus Evolution TAGs. He has worked with the WHO Eliminating Yellow Fever (EYE) strategy and contributed to the first WHO guide to the implementation of genomic sequencing of SARS-CoV-2 for maximum impact on public health.

He obtained his PhD from the Rega Institute, KULeuven in Belgium, and was a Lecturer in Infectious Disease Control, a Wellcome Trust Sir Henry Dale Fellow, a Balliol Fellow in Sciences, and an Associate Professor at the University of Oxford, where he was also a member of the Pandemic Genomics programme at the Oxford Martin School.

Currently, he leads the DeZi Network (Dengue and Zika Immunology and Genomics Multi-Country Network) funded by Wellcome Trust, and co-leads the FEEVIR project (Metagenomic surveillance for epidemic prevention in the DRC-Angola cross-border) funded by the WHO Berlin Hub Catalytic grants. He has recently co-led the UK-Brazil Centre for Arbovirus Discovery, Diagnostic, Genomics and Epidemiology (CADDE), the ArboSPREAD project with the National Institute of Research at the Ministry of Health, Angola, and the Zika in Brazil real-time analysis (ZiBRA) project. His work has received funding from the MRC, FAPESP, British Council, Wellcome Trust, WHO, GCRF, and Bill and Melinda Gates Foundation.

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BORAME SUE LEE DICKENS

Saw Swee Hock School of Public Health
National University of Singapore

Borame L Dickens is an Assistant Professor at the Saw Swee Hock School of Public Health, National University of Singapore.

She is a geospatial modeler with an interest in examining the efficacy of interventions for through the use of individual based models (IBMs). Her work has been published in top public health journals including Lancet Infectious Diseases, Lancet, Lancet Western Pacific, Clinical Infectious Diseases, Journal of infectious Diseases, Journal of Travel Medicine, BMJ Open Diabetes Research & Care, Nutrients and Environment International. Along the infectious disease branch, she examines border control, disease spread and the impact of interventions through IBMs. Within chronic diseases, she has been actively working on estimating the burden of hypertension, obesity and hyperlipidemia in Singapore, as well as the impacts of screening on cancers. Her work often involves Bayesian statistical methods, mathematical modelling and the exploration of the influence of the environment on disease prevalence.

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MARTIN HIBBERD

Professor of Emerging Infectious Disease and Head of DIB
London School of Hygiene & Tropical Medicine

Martin L. Hibberd is Professor of Emerging Infectious Diseases (since 2012) and Head of the Department of Infection Biology (since 2022) at the London School of Hygiene and Tropical Medicine (LSHTM). He has adjunct positions at University of the Philippines, Manila, in Human Genetics (at NIH) and the Genome Institute of Singapore (where he was previously associate director from 2003 to 2016).

Martin graduated in Applied Biology from Brunel University, London in 1985 and worked in the (then) Public Health Laboratory Service, both at Porton Down, at the Centre for Applied Microbiology & Research, (Legionella Reference Laboratory) and Central Public Health Laboratory Colindale (Enteric Pathogens). He later received his Doctorate on the immune-genetics of the human T-cell antigen receptor at King's College, London in 1994 and obtained a lectureship in Paediatric Infectious Disease at Imperial College, London, in 1996.

In 2003 Martin moved to the Genome Institute in Singapore (GIS) where he developed Human Genetic and Infectious Disease work to become associate director and senior group leader for Infectious Disease. He then joined LSHTM in 2012 and is now Head of the Department of Infection Biology.

Some of Martin's previous achievements include: the first comprehensive Genome Wide Association Studies of infectious diseases, the initiation of transcriptomic host response diagnostics for infectious diseases and pathophysiology descriptions of both host and pathogen in diseases such as dengue and TB, particularly in relation to clinical trials.

He has over 250 journal publications, and 25,000 citations, reflecting a broad interest in both infectious agents, and the human host responses that they initiate. A very active lecturer on LSHTM MSc programmes, Martin is also an expert contributor to The Lancet, The Guardian, The Times and the BBC.

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SOUMYA CHATTERJEE

Senior Principal Scientist and Clinical Director, Merck

Dr. Soumya Chatterjee is a physician-scientist and vaccine development leader with more than 17 years of experience spanning clinical research, translational medicine, regulatory science, and global vaccine development. He currently serves as Senior Principal Scientist and Clinical Director at Merck & Co., where he leads the clinical development of innovative vaccines targeting infectious diseases. His expertise encompasses vaccine immunology, immune mechanisms of disease, immune correlates of protection, and the strategic development and deployment of vaccines worldwide.

Prior to joining Merck, Dr. Chatterjee served as a Medical Officer at the U.S. Food and Drug Administration (FDA) – Center for Biologics Evaluation and Research (CBER), where he reviewed and evaluated clinical data and regulatory submissions for both investigational and licensed vaccines. His work provided critical insights into regulatory requirements, vaccine safety, and evidence-based product evaluation.

Throughout his career, Dr. Chatterjee has received numerous honors, awards, and research grants, including the prestigious ASTMH/Burroughs Wellcome Career Development Award and an NIH Merit Award. He has authored 15 peer-reviewed scientific publications and is recognized for his leadership in multidisciplinary collaboration, scientific mentorship, and global health innovation.

Driven by a commitment to improving health outcomes worldwide, Dr. Chatterjee is dedicated to advancing vaccine science and expanding access to life-saving interventions, particularly for underserved and vulnerable populations.

TIKKI PANGESTU

Visiting Professor
Yong Loo Lin School of Medicine
National University of Singapore

Professor Tikki PANG is an Indonesian citizen and is presently Visiting Professor, Yong Loo Lin School of Medicine, National University of Singapore. He was previously Visiting Professor, Lee Kuan Yew School of Public Policy, National University of Singapore (2012-2020) and Director, Research Policy & Cooperation, World Health Organization (WHO), Geneva, Switzerland (1999-2012). Prior to joining WHO, he was Professor of Biomedical Sciences, Institute of Postgraduate Studies & Research, University of Malaya, Kuala Lumpur, Malaysia (1989-1999) and Lecturer/Associate Professor, Dept of Microbiology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia (1977-1989). He was Co-Director of the WHO Collaborating Centre for Dengue & Dengue Haemorrhagic Fever at the University of Malaya, Kuala Lumpur, Malaysia (1982-1995). He holds a PhD in Immunology-Microbiology from the Australian National University, Canberra, Australia and is a Fellow of the Royal College of Pathologists (UK), Institute of Biology (UK), American Academy of Microbiology (USA), Academy of Medicine of Malaysia, and Academy of Sciences for the Developing World (TWAS). He is currently Chair of the Board of Directors, Asia Pacific Leaders Malaria Alliance (APLMA) and Co-Chair of the Asia Pacific Immunization Coalition (APIC). He has published >250 scientific articles and 12 books and was lead author on several major WHO reports including the World Health Report 2013: Research for Universal Health Coverage (2013), Knowledge for Better Health (2004) and Genomics and World Health (2002). Professor Pang has a recognisable profile as a public health expert both nationally and internationally. His research interests are in the epidemiology, pathogenesis, laboratory diagnosis and prevention of infectious diseases, biosecurity and dual-use research, genomics & health, and in health research policy, health research systems, global health governance, development of research capabilities in developing countries, linkages between research and policy, vaccine confidence and harm reduction approaches to mitigate health problems. He has >30 years of teaching experience at undergraduate & postgraduate levels in the fields of medical microbiology, immunology, global health policy & issues, and in evidence-informed policy development. He has supervised 20 Master's degree and 10 PhD candidates.

SPEAKERS' BIOGRAPHIES

DEREK WALLACE

President
Global Vaccine Business Unit
Takeda Pharmaceuticals

With over 17 years of experience in vaccine research, Derek currently serves as the Head of Dengue Strategy, leading teams on the development and global delivery of Takeda's Tetravalent Dengue Vaccine – Qdenga. Derek joined Takeda in September of 2013 and has held various leadership roles across the dengue and vaccine programs.

Derek obtained his Bachelor of Medicine and Bachelor of Surgery (MBBS) from The University of Queensland, his Diploma of Pharmaceutical Medicine from the Royal College of Physicians in the UK and his Diploma of Vaccinology from Institute Pasteur in Paris. Before joining Takeda, Derek worked in a clinical setting as well as at Merck, Novartis and Sanofi.

Based in Massachusetts, he enjoys gardening and woodworking in his free time.

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JULIO CRODA

Oswaldo Cruz Foundation
Federal University of Mato Grosso do Sul
Yale School of Public Health

Julio Croda is a physician-scientist and public health leader with extensive experience in infectious diseases, vaccine research, and global health policy. He is a Senior Researcher at the Oswaldo Cruz Foundation (Fiocruz), Mato Grosso do Sul, and an Associate Professor at the Federal University of Mato Grosso do Sul (UFMS). He also holds an academic appointment at the Yale School of Public Health.

Dr. Croda has played a central role in the design, implementation, and evaluation of large-scale clinical trials and real-world evidence studies, particularly in dengue, tuberculosis, and other infectious diseases of public health importance. He has served as principal investigator or co-investigator in multiple vaccine studies, including COVID-19, dengue, tuberculosis, and chikungunya, with a strong focus on effectiveness, safety, and implementation in low- and middle-income settings.

In dengue research, his work spans vaccine effectiveness using test-negative designs, pharmacovigilance, outbreak response, and the integration of vaccination strategies with surveillance systems. He has collaborated closely with national immunization programs, state health authorities, and international partners to support evidence-based decision-making during dengue epidemics in Brazil.

Dr. Croda has held several leadership roles at the national and international levels, including President of the Brazilian Society of Tropical Medicine, President of Rede-TB, and Director of the Department of Immunizations and Communicable Diseases at the Brazilian Ministry of Health. During the COVID-19 pandemic, he contributed to national response strategies and modeling efforts to inform public health actions.

He is widely published in high-impact journals and currently serves on editorial boards of leading infectious disease journals. His work bridges science and policy, with a strong commitment to improving access to vaccines, strengthening health systems, and advancing global equity in infectious disease prevention and control.

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THANYAWEE PUTHANAKIT

Faculty of Medicine,
Chulalongkorn University

Professor Thanyawee Puthanakit is a pediatric infectious disease specialist at Department of Pediatrics, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand. She is a former trainee of the Johns Hopkins University Fogarty AIDS International Training and Research Program. She is a leader in pediatric HIV treatment and care in Asia. She leads several multicenter research projects in Thailand, Cambodia, Indonesia and also collaborates with TREAT Asia research program and PENTA-ID network. She has served on the writing committee for the WHO's pediatric HIV treatment guideline and Thai National Guideline. Her current research interest includes clinical trials on new antiretroviral drug for HIV treatment and prevention focusing on adolescent and young adult.

JENNY LOW

Senior Consultant
Singapore General Hospital

Prof Jenny Low is a board-certified senior consultant with the Department of Infectious Diseases in the Singapore General Hospital and a Professor in the Programme in Emerging Infectious Diseases at Duke-NUS Medical School. Concurrently, she is the Deputy Medical and Scientific Director of the SingHealth Investigation Medicine Unit. Her research interest is to develop pathways for rapid bench-to-bedside translation of vaccines and therapeutics against acute viral diseases. Her approach is to combine novel trial design with state-of-the-art molecular investigations to generate deep data that enrich first-in-human and early phase clinical trials. Towards this goal, she co-founded and co-directs the Viral Research and Experimental Medicine Centre, SingHealth Duke-NUS Academic Medical Centre (ViREMiCS) to develop relevant molecular assays into ISO-accredited tests to support the translation of new vaccines and therapeutics into licensed products. This approach has been used to evaluate both small molecules as well as therapeutic antibodies against flaviviral diseases, such as dengue, Zika and yellow fever. More recently, she has expanded on this experimental medicine approach to rapidly develop a deeper understanding Covid-19 and the host response to SARS-CoV-2 infection, the knowledge of which was used to evaluate investigator-initiated and industry-sponsored therapeutic strategies and vaccine candidates against Covid-19. These efforts, apart from contributing to knowledge, have also increased Singapore's profile as a preferred site for early phase, proof-of-concept clinical trials for acute viral diseases. She has authored and co-authored more than 130 publications in peer-reviewed journals and has more than 14,000 citations with H-index of 51 and i10-index of 111. She has been awarded the Singapore National Medical Research Council Clinician-Scientist Award in 2016 and 2019. For her contribution, she has also received a series of research awards from SingHealth/Duke-NUS since 2014. She has also being recognised as Clarivate's Highly Cited Researchers in 2022, 2023, 2024.

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ANDRE SIQUEIRA

DNDi
Fiocruz

Andre Siqueira, MD, MSc, PhD is a infectious diseases physician-scientist and global health researcher currently serving as Head of the Dengue Global Programme at the Drugs for Neglected Diseases initiative (DNDi). He has over 20 years of experience across clinical care, research, and public health policy, with a strong focus on tropical and emerging infectious diseases, including being a PI in pivotal dengue vaccine and therapeutics clinical trials.

At DNDi, Dr. Siqueira leads the development of safe, effective, and affordable dengue treatments, overseeing portfolios that include host-directed therapies, antivirals, monoclonal antibodies, and innovative clinical trial designs. He is closely involved in regulatory strategy, evidence generation, and global stakeholder engagement to accelerate access to therapies in endemic countries.

He plays a key role in the Dengue Alliance, a South-South collaboration aimed at reducing dengue-related morbidity and mortality, and actively contributes to international discussions, promoting integrated, equity-driven approaches to dengue control.

SOPHIE YACOUB

Pandemic Sciences Institute
University of Oxford

Sophie is an associate professor of infectious diseases at the Pandemic Sciences Institute, University of Oxford. She is a Wellcome Trust Clinical Career Development Fellow and Physician in Infectious Diseases and General Medicine. She holds an honorary consultant appointment at London North West University Healthcare NHS Trust in the UK. She has a PhD from Imperial College London and an MSc from the London School of Hygiene and Tropical Medicine. She is a member of the Royal College of Physicians in London. Sophie led the dengue research group at the Oxford University Clinical Research Unit (OUCRU-Vietnam) from 2017-2025 where she set up a large translational programme of dengue research, focusing on clinical trials, pathogenesis studies and innovative technology centered on wearable devices, physiological monitoring and utilizing AI for medical imaging and clinical decision support systems. She is now leading a phase 2 platform trial for novel and repurposed antivirals in early disease (ADAPT trial) as well as a large phase 3 global platform trial to investigate multiple host-directed therapeutics for patients hospitalised with moderate-severe dengue (DEN-HOST).

KEVIN TETTEH

Collective Action on Dengue (CAD)

KEVIN TETTEH joined FIND in January 2023 as Director of the Malaria & Fever Programme and also leads the organisations Climate and Health strategy. He previously served as Associate Professor of Infectious Diseases, and on the Board (Council) at the London School of Hygiene and Tropical Medicine (LSHTM). Kevin brings over 20 years of experience across academia, the biotherapeutics industry, and industrial partnerships. He also led the vaccine innovation theme and served on the steering committee of the LSHTM Vaccine Centre. Passionate about health equity and applying innovative and interdisciplinary approaches to global health challenges, Kevin leads efforts to build strategic public and private partnerships to advance equitable diagnostic solutions for malaria and other febrile illnesses, including dengue. Throughout his career, he has spearheaded initiatives to strengthen research capacity across Africa and Southeast Asia, and now LATAM, supporting technology transfer and advancing work in infection biology, disease surveillance, diagnostic innovation, and zoonotic diseases.

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CHANTAL B.F. VOGELS

Yale School of Public Health
Yale University

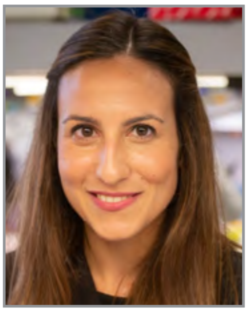
Assistant Professor at the Department of Epidemiology of Microbial Diseases, Yale School of Public Health, Dr. Vogels has a multidisciplinary background spanning ecology, medical entomology, virology, and genomics.

During her PhD at Wageningen University & Research, she investigated the role of Culex pipiens mosquitoes in the transmission of West Nile virus in Europe. Her interdisciplinary research integrated field-based mosquito surveillance, laboratory vector competence studies, and computational modeling. This work generated important insights into the role of climate as a limiting factor in the transmission of West Nile virus across Europe.

As a postdoctoral researcher at Yale School of Public Health, Dr. Vogels shifted her focus to genomics, examining how viral evolution contributed to the unexpected scale and severity of the Zika virus epidemic in the Americas. Using a reverse genetics platform, she engineered Zika virus mutations and evaluated their effects on transmission by Aedes aegypti mosquitoes under laboratory conditions.

With the onset of the COVID-19 pandemic, Dr. Vogels temporarily redirected her research efforts to support the global public health response, applying her expertise in molecular virology and genomics. Building on this work, her team recently developed amplicon sequencing approaches for emerging viruses, including dengue virus, to better understand their patterns of emergence and spread.

In the Vogels Lab, Dr. Vogels and her team employ experimental approaches to investigate the ecology, evolution, and epidemiology of arthropod-borne (arbo)viruses. By integrating field, laboratory, and computational methods, they study the complex interactions among arboviruses, their vectors, and environmental factors that shape transmission dynamics. Their research aims to advance understanding of the drivers and barriers of arbovirus transmission and to inform more effective prevention and control strategies.



LAURA MARTIN-SANCHO

Department of Infectious Disease
Faculty of Medicine
Imperial College London

Laura Martin-Sancho is an Assistant Professor at Imperial College London. As part of her training, she received a PhD in Molecular virology from the Max Planck Institute for Infection Biology in Germany and pursued a postdoctoral training in Systems Biology at the Scripps Research Institute in the USA. Her primary research interests are understanding virus-host interactions that underlie pathogenesis of emergent viruses, with a major focus on dengue and other mosquito-transmitted viruses.

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JULIEN POMPON

Institut de Recherche pour le Développement
(the French National Research Institute for Sustainable Development) IRD

Dr. Julien Pompon studies the molecular mechanisms underlying flavivirus transmission by mosquitoes, focusing on the triangular interactions between viruses, mosquito vectors, and human hosts. Using molecular biology, transgenics, mouse models, high-throughput sequencing, and metabolomics, his research revealed that all mosquito-vectored flaviviruses secrete non-coding viral RNA in salivary extracellular vesicles to enhance transmission. Building on his expertise in lipidomics and a mosquito-to-mouse transmission model, his team further discovered that vesicle-associated lipids also increase viral transmission. Dr. Pompon is now leveraging these fundamental insights to develop novel strategies for arbovirus control. His work has been published in high-impact journals including Cell Metabolism, PNAS, Nature Communications, PLoS Pathogens, and PLoS Biology. He currently coordinates a multinational Horizon Europe grant aimed at designing and characterizing a pan-flavivirus vaccine candidate.

MARIANNE COMPARET

Co-Founder & Director
The International Society for Neglected Tropical Diseases

Marianne Comparet is currently Director at the International Society for Neglected Tropical Diseases, based in London. She has an academic background in Development Economics, and has previously worked at the World Trade Institute in Bern, the emerging markets division of Citibank and at JP Morgan before joining The Economist Newspaper as an Economist/Statistician. She has lived in Jakarta, Paris and London.

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DIANA PATRICIA ROJAS ALVAREZ

Head (a.i.) Emerging Zoonosis and High Impact Epidemics Unit
World Health Organisation (WHO)

Dr. Diana Patricia Rojas Alvarez is a Colombian physician, epidemiologist, and global health leader specializing in arboviral and emerging infectious diseases. She currently serves in senior leadership roles within the World Health Organization (WHO), where she has led global initiatives on dengue, chikungunya, Zika, yellow fever, and other vector-borne diseases. Her work focuses on strengthening surveillance systems, outbreak preparedness, evidence-based policy development, and international coordination for emerging health threats Dr. Rojas Alvarez is also instrumental in developing WHO's integrated clinical management guidelines for arboviral diseases, promoting a unified approach to diseases that often present with similar clinical symptoms and circulate simultaneously in many regions. She has also championed multidisciplinary and One Health approaches that integrate human, animal, and environmental health perspectives in disease prevention and control.

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ADAM WAICKMAN

Department of Microbiology and Immunology
SUNY Upstate Medical University

Adam T. Waickman, PhD, is Associate Professor in the Department of Microbiology and Immunology and Chief Scientific Officer of the Global Health Institute at SUNY Upstate Medical University in Syracuse, New York. His research focuses on adaptive and innate immune responses to dengue virus infection and vaccination, with particular emphasis on how pre-existing flavivirus immunity shapes vaccine immunogenicity and efficacy. Dr. Waickman received his PhD in Immunology from Johns Hopkins University School of Medicine and completed postdoctoral training at the National Cancer Institute and the Walter Reed Army Institute of Research.

LAURA RIVINO

Reader of Immunology, Tropical Disease Biology
Liverpool School of Tropical Medicine

Dr Laura Rivino is an Associate Professor/Reader in Immunology at the Department of Tropical Disease Biology of the Liverpool School of Tropical Medicine, Liverpool (UK). Her team studies anti-viral immunity in human infection and vaccination. Dr Rivino's team has a strong interest in T and NK cells and in defining broad correlates of protection and immunopathology for dengue.

Dr Rivino completed a PhD in Immunology at the Institute for Research in Biomedicine, Switzerland, studying the mechanisms driving the generation and maintenance of human memory T cells. During her post-doctoral training in Singapore at NUS and Duke-NUS Medical School she became interested in the role of T cells in virus infections of clinical importance including dengue, Hepatitis B and human cytomegalovirus infections. Dr Rivino was Assistant Professor at Duke-NUS from 2016 to 2019; she subsequently joined the School of Cellular and Molecular Medicine at the University of Bristol as Senior Lecturer in 2019 and was promoted to Associate Professor in 2023. In April 2026 Dr Rivino joined LSTM to develop a research programme in human immunology of tropical diseases, including dengue and zika.

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SUJAN SHRESTA

La Jolla Institute for Immunology
University of California, San Diego

Professor Sujan Shresta's laboratory is focused on elucidating the mechanisms of viral pathogenesis and immunity and leveraging this knowledge to enable the rational design of antiviral therapies and vaccines against globally significant human pathogens. Following graduate training at Washington University in St. Louis, where she studied cytotoxic T cell effector mechanisms, Dr. Shresta sought to apply her expertise in basic immunology to infectious diseases with broad global impact, particularly in resource-limited settings such as Nepal. She subsequently pursued postdoctoral training in orthoflavivirus virology at the University of California, Berkeley. Her laboratory has since advanced the study of orthoflavivirus pathogenesis and immune responses through the development of mouse models and human cell culture systems. More recently, her group has established collaborative research partnerships linking investigators in high-income and low- and middle-income countries to support dengue virus cohort studies in Nepal, Vietnam, and Thailand. Insights gained from these experimental and clinical studies are being translated into the development and evaluation of vaccine and therapeutic candidates, in collaboration with academic and industry partners.

PONPAN MATANGKASOMBUT

Single-cell Omics and Systems Biology of Diseases Research Unit
Department of Microbiology, Faculty of Science
Mahidol University

Ponpan Matangkasombut is a physician-scientist, Allergist-Immunologist. After finished medical school at Chulalongkorn University in Thailand, she continued her clinical training and certified American Board of Internal medicine and American Board of Allergy and Immunology. She then obtained Doctor of Science degree in Immunology and Infectious Disease from Harvard School of Public Health. She is now an Associate Professor and a deputy head of the Department of Microbiology and led Single-cell omics and Systems Biology of Diseases Research Unit, Faculty of Science, Mahidol University, Thailand. Her research focuses on the mechanism of human immune response to infectious diseases particularly in dengue viral infection using cohorts of natural dengue infection of varying severity and household surveillance. Currently, she uses single-cell immune profiling to dissect the protective and pathogenic immune response in human diseases ranging from infectious disease, particularly dengue, to allergy and cancer as well as study regional diversity in the Asian Immune Diversity Atlas project. She also serves as Human Cell Atlas (HCA) diversity task force, HCA Asia steering committee, Toward Human Exposome Atlas committee and a councillor of the Federation of Immunological Societies of Asia-Oceania (FIMSA).

LEAH C. KATZELNICK

Chief, Viral Epidemiology and Immunity Unit
National Institutes of Health (NIH)

Dr. Leah Katzelnick pursued a Ph.D. studying antigenic variation among dengue viruses at the University of Cambridge and the National Institutes of Health as an NIH OxCam Scholar and Gates Cambridge Scholar. After receiving her Ph.D. in 2016, she conducted her postdoctoral work at the University of California, Berkeley and University of Florida on determinants of dengue and Zika disease, spending a year in Ecuador and Nicaragua to work closely with research teams conducting longitudinal cohort studies. In September of 2020, Leah became an Earl Stadtman tenure-track investigator and NIH Distinguished Scholar in the Laboratory of Infectious Diseases in NIAID. She is Chief of the Viral Epidemiology and Immunity Unit.

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ROSE CAPEDING

Pediatric Infectious Disease Specialist, Clinician, Researcher Scientist

Head, Medical Research Unit,
Tropical Disease Foundation, Inc

Consultant, Infectious Diseases
Asian Hospital and Medical Center
Philippines

Dr. Capeding is a pediatrician, an infectious disease specialist, and a clinical microbiologist of the Research Institute for Tropical Medicine, Philippines. She is the Head of the Department of Microbiology, Consultant of the Medical Department, and Head of the Dengue Study Group of the said institute. She is the Section Head of Infectious Diseases of the Department of Pediatrics, Asian Hospital and Medical Center, Philippines.

She has engaged in significant researches on the safety, immunogenicity and efficacy of childhood vaccines: Haemophilus influenzae type b, Pneumococcal and Meningococcal Conjugate; Influenza; Hepatitis A; Hepatitis B; DtaP-Hib-IPV-HepB combination vaccine; Typhoid Conjugate; Cholera; Japanese Encephalitis, and Dengue.

She is an accomplished medical researcher though her contributions: 54 original articles and reviews in peer reviewed international and local journals; presented scientific papers in 77 international medical conferences; acted as an expert or member of advisory board to 31 international consultative meetings; and 47 completed and current researches and clinical trials. She is an active member of national and international professional medical societies and global, regional scientific fora. She is also a frequent lecturer to numerous conventions of medical societies, postgraduate courses and local chapter meetings.

Dr. Capeding is an awardee of the 23rd Dr. Jose P. Rizal Memorial Award for Research by the Philippine Medical Association (PMA). She was given the distinction as one of the world’s Top Women in Biotech Industry 2014. The paper, Clinical Efficacy and Safety of a Novel Tetravalent Vaccine in Healthy Children in Asia: Phase 3, Randomized, Observer-Masked, Placebo-Controlled Trial, Maria Rosario Capeding, Ngoc Huu Tran, Sri Rezeki, et. al. (The Lancet, 2014. 384:1358-1365 was adjudged Paper of the Year 2014 by the International Society for Vaccines (ISV). She is a recipient of the 2015 Outstanding Professional of the Year Award in the Field of Medicine and Eric Nubla Excellence Award given by the Philippine Professional Regulation Commission.

NEELIKA MALAVIGE

Institute of Allergology and Immunology
University of Sri Jayewardenepura

Neelika Malavige is a Professor in the Department of Immunology and Molecular Medicine at the University of Sri Jayewardenepura and an Academic Visitor at the Weatherall Institute of Molecular Medicine, University of Oxford. She is also the President-Elect of the International Society for Infectious Diseases. Her research focuses on the immunopathogenesis of dengue, with particular emphasis on identifying biomarkers and immune correlates of protection and translating these insights into clinical trials. She is also particularly interested in how metabolic disease, including obesity, influences dengue disease severity and antiviral immune responses. She previously led the global dengue programme at the Drugs for Neglected Diseases Initiative (DNDi) and continues to contribute her expertise through numerous national and international scientific advisory boards, funding panels, and editorial boards, serving as a member or chair. Beyond her research and leadership roles, she is deeply committed to mentoring and public engagement and has received multiple national and international awards in recognition of her contributions, including the Outstanding Role Model Award and the Most Inspiring Woman Award.

NGUYEN LAM VUONG

Oxford University Clinical Research Unit, Vietnam

Dr. Nguyen Lam Vuong is a medical doctor and researcher with a passion for applying biostatistics to medical research, particularly regarding dengue disease.

Dr. Vuong began his medical career at the University of Medicine and Pharmacy at Ho Chi Minh City (UMP HCMC), graduating with his Doctor of Medicine degree in 2010. He further specialized in the field, completing his residency in Cardiovascular and Thoracic Surgery in 2014 at the same university.

In 2014, Dr. Vuong transitioned to a research career, leveraging his medical expertise in the Department of Medical Statistics and Informatics at the Faculty of Public Health, UMP HCMC. Since 2017, he has focused his research efforts on dengue at the Oxford University Clinical Research Unit, Ho Chi Minh City (OUCRU HCMC).

Dr. Vuong's research journey at OUCRU HCMC began as a Research Assistant (2017-2020). He then pursued a PhD in the Biostatistics group, successfully defending his dissertation titled "Biomarkers, Plasma Viremia, and Clinical Outcomes in Dengue" in February 2024.

Currently, Dr. Vuong holds a dual appointment as a lecturer at the Department of Medical Statistics and Informatics (UMP HCMC) and a postdoctoral researcher in the Biostatistics group at the OUCRU HCMC.

WEE LIANG EN IAN

Department of Infectious Diseases, Singapore General Hospital
Department of Infection Prevention and Epidemiology, Singapore General Hospital
Communicable Diseases Agency, Singapore

Ian is a Consultant with the Department of Infectious Diseases and Department of Infection Prevention and Epidemiology at the Singapore General Hospital. He is also Clinical Assistant Professor at the Duke-NUS Medical School, Singapore, and holds concurrent appointments at the Communicable Diseases Agency, Singapore. He has an active research interest in infectious diseases, epidemiology and public health, including long-term sequelae post-viral infection and infections in immunocompromised hosts. He has published over 100 papers in peer-reviewed journals, including Clinical Infectious Diseases; Clinical Microbiology and Infection; JAMA Pediatrics; JAMA Neurology; JAMA Network Open, Lancet Respiratory Medicine. His current work is mainly focused on viral epidemiology, including acute and long-term sequelae following dengue infection.

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HO QUANG CHANH

Oxford University Clinical Research Unit
Centre for Tropical Medicine and Global Health, University of Oxford

Dr Chanhs research focuses on translational dengue research and healthcare quality improvement for critically ill paediatric patients. His work aims to improve the management and monitoring of patients during episodes of critical illness in low- and middle-income countries through rigorously conducted, clinically relevant research. He has a particular interest in personalised treatment approaches using intelligent technologies and linked large-scale clinical data.

LULU BRAVO

Professor Emeritus at the College of Medicine,
University of the Philippines

Lulu Bravo is a Professor Emeritus at the College of Medicine, University of the Philippines Manila. She is the former Vice Chancellor for Research and Executive Director of the National Institutes of Health, University of the Philippines Manila (2005 – 2011) and current head of the Vaccine Study Group of the NIH – UPM.

She is the President of the Immunization Partners in Asia Pacific (IPAP), current Executive Director and past President of the International Society of Tropical Pediatrics (ISTP) 2008 – 2011, past Chair and Founder of the Asian Strategic Alliance for Pneumococcal Disease Prevention (ASAP) 2007 – 2011, and Executive Director, Sec-General (1998 – 2006) & past President of the Asian Society for Pediatric Infectious Disease (ASPID) 2006 – 2008. She has served in various capacities in many other Asian medical and professional societies and as WHO Technical Advisor. She has served as well in national medical organizations such as PMA, PPS, PIDPS, PSMID and the Philippine Foundation for Vaccination (PFV) of which she is the founding President and current Executive Director. In the international scene, she is a member of the Rota Council, Pneumococcal Awareness Council of Experts (PACE) and member of the Dengue Vaccine Initiative (DVI). Her work has earned for her various national and international honors and awards in the professional, academic and research fields, including the Outstanding Physician (2009) and the prestigious Dr Jose P. Rizal Memorial Award for Academe (2011) given by Philippine Medical Association, the 2012 Asian Outstanding Pediatrician Award given by the Asia Pacific Pediatric Association and 2018 Outstanding Professional in Medicine given by the Professional Regulation Commission of the Philippines. In 2008, she presented both written and oral evidence to the UK's House of Commons to justify the $ 2.5 Billion vaccination advance market commitment to provide needed vaccines for the developing world. She was named Pneumonia Fighter in 2018 by the JustActions Organization, a US-based advocacy movement and corporation associated with People Empowerment.

Dr Lulu Bravo completed her MD, pediatric residency and subspecialty training in infectious disease at Philippine General Hospital-College of Medicine of the University of the Philippines Manila. She supplemented her fellowship in pediatric infectious disease at the University of Texas Southwestern Health Science Center in Dallas, USA in 1986. She has published more than 100 scientific articles, books and book chapters in both local and international circles.

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BEKTI ANDARI

World Mosquito Program

Bekti Andari is a project management professional with more than eight years' experience at the World Mosquito Program (WMP), leading stakeholder engagement, community partnerships, and program implementation across the Asia-Pacific region. She currently serves as Senior Project Manager, overseeing complex, multi-country initiatives and ensuring effective coordination among governments, donors, health authorities, research institutions, and community stakeholders. Bekti has played a key role in supporting the implementation of WMP's Wolbachia-based dengue prevention programs in Indonesia, Vietnam, Laos, Timor-Leste, Sri Lanka, and Kiribati, including project planning, budgeting, risk management, regulatory compliance, and partnership development. She is particularly experienced in designing and delivering stakeholder and community engagement strategies that build trust, foster participation, and enable sustainable public health interventions. With a background in Psychology and Development Studies, Bekti also serves as WMP's GEDSI (Gender Equality, Disability, and Social Inclusion) focal point, promoting inclusive practices across programs.

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YEO TSIN WEN

Lee Kong Chian School of Medicine,
Nanyang Technological University

Associate Professor Yeo Tsin Wen is an Associate Professor at the Lee Kong Chian School of Medicine, Nanyang Technological University. A/Prof Yeo graduated from the National University of Singapore, and went on to complete an internal medicine residency at the University of Hawaii as well as an infectious disease fellowship at the University of Utah. He did his PhD at the Menzies School of Health Research and University of Queensland on the treatment and pathogenesis of severe malaria based in Indonesia Papua. Upon completion of his PhD, he worked as a research fellow at the Menzies School of Health Research and as an infectious physician at Royal Darwin Hospital in Australia. In 2016, Professor Yeo Tsin Wen was awarded the Clinician-Scientist Award (CSA) in the Investigator (INV) category from Singapore’s National Medical Research Council (NMRC).

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ZULKIFLI ISMAIL

Chairperson, Asia Dengue Voice and Action Group
Secretary General, Asia Pacific Pediatric Association & Chairman, Immunise4Life
Technical Committee, Malaysia

Prof. Zulkifli Ismail is a consultant paediatrician and paediatric cardiologist at a private hospital and Clinical Professor at the KPJ Healthcare University College. He was formerly a professor of paediatrics and paediatric cardiology in the Universiti Kebangsaan Malaysia (UKM). Dr Ismail has served as the head of the paediatric department and the director of Hospital Universiti Kebangsaan Malaysia (HUKM) as well as the medical director of its private wing, UKM Specialist Centre.

Prof. Zulkifli also served as a past president of the Malaysian Paediatric Association (MPA) and is currently the editor of Berita MPA, a quarterly newsletter publication distributed to fellow members of the Association. He chairs the Positive Parenting Management Committee (www.mypositiveparenting.org) and serves as the chief editor of the Positive Parenting Guide, a quarterly publication aimed to equip Malaysian parents with reliable and practical local information on maternal, child and family care since 2002. He is the Technical Chairman of Immunise4Life (www.ifl.my), a vaccination advocacy programme of the Ministry of Health Malaysia.

Prof. Zulkifli is currently the president of the Asia Pacific Paediatric Association (APPA) and current chairman of the Asian Strategic Alliance for Pneumococcal disease prevention (ASAP). He also serves as a board member of the National Population and Family Development Board (LPPKN), a member of the Ministry of Health Unrelated Transplant Approval Committee (UTAC) and in the editorial board of the Malaysian Journal of Paediatrics & Child Health (MJPCH). He has also served as a reviewer for the Medical Journal of Malaysia and the Philippines Paediatric Infectious Disease Journal.

Prof. Zulkifli has more than 35 publications in peer-reviewed international and local journals in addition to numerous abstracts and articles for the lay-public on various issues involving child health, paediatrics and vaccinology. He has authored or co-authored two books for parents, one for medical students and one for nurses. In 2008, he was conferred the Darjah Panglima Mahkota Wilayah by the Malaysian King that carries the honorific title of 'Datuk'.

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GIRI RAJAHRAM

Head, Department of Medicine,
Queen Elizabeth Hospital II

Dr Giri is an Infectious Diseases and Global Health Consultant in Sabah, Borneo. His clinical work involves providing care to the state's indigenous and marginalised communities. He is responsible for guiding policy and providing technical advice on infectious diseases and clinical medicine for Sabah and Malaysia. Aside from that, he is also a transdisciplinary global health practitioner leading a multinational research team that addresses epidemiological trends and clinical research on regional infectious diseases of interest in Southeast Asia. He was awarded the Endeavour Leadership Award for his research on Plasmodium knowlesi malaria. His team's research findings have been communicated to various stakeholders, enabling the implementation of evidence-based health policies in Malaysia and the World Health Organisation's malaria treatment guidelines.

DAVID FOSTER

Managing Director
Island Pharmaceuticals Ltd.

Dr Foster has 20+ years experience in life sciences representing pharmaceutical, biotherapeutic and diagnostic companies, while in private legal practice. He served as intellectual property counsel at Medarex, a mid-sized biotherapeutics company, acquired by Bristol-Myers Squibb. Dr Foster co-founded Roberts Foster LLP - a technology focused law firm, bionorthTx- a regional life science trade association, and multiple private biotechnology companies.

He is a board member of bionorthTx and private biotechnology companies, and is a Member of Australian Institute of Company Directors. He holds a Ph.D. from The University of Texas Southwestern Medical Center and J.D. from Golden Gate University School of Law.

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CHAN XIN HUI

Medical Consultant in Clinical Countermeasures &
Consultant Infectious Diseases Physician
UK Health Security Agency

Dr Xin Hui Chan is Medical Consultant in Clinical Countermeasures at the UK Health Security Agency and an Honorary Consultant in Infectious Diseases and General Internal Medicine at Oxford University Hospitals NHS Foundation Trust. She was previously a Consultant in Infectious Diseases and Anti-infective Pharmacology at the Department of Malaria and Neglected Tropical Diseases at the World Health Organization (WHO) where she coordinated with Dr Raman Velayudhan the development of the WHO Target Product Profiles for Treatments for Dengue.

IGNACIO ESTEBAN

Senior Policy Manager
Gavi, the Vaccine Alliance

Dr. Ignacio Esteban is an accomplished global health and vaccine development leader with extensive experience spanning vaccine research, clinical development, global immunization strategy, and public-private partnerships. Throughout his career, he has played pivotal roles in advancing equitable access to vaccines and strengthening global preparedness against infectious disease threats.

Dr. Esteban worked closely with governments, manufacturers, international organizations, and funding partners to strengthen vaccine delivery systems, accelerate the introduction of new vaccines, and improve access to life-saving immunization programs.

His work contributed to the broader goal of ensuring that scientific innovation translates into meaningful public health impact, particularly in regions facing the greatest disease burden.

Dr Esteban is currently serving as Senior Policy Manager at Gavi, the Vaccine Alliance.

SHIBADAS BISWAL

Clinical Lead of Dengue and Senior Medical Director
Takeda

Shibadas Biswal leads the Clinical Science group at Takeda Vaccines based in Boston, USA. His work mainly involves clinical development, registration, and life cycle management of Takedas dengue vaccine. He has nearly 20 years of experience in pharmaceutical industry after obtaining medical degree and clinical pharmacology training in India.

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MOTOHARU ABE

Specialist, Production Technical Development Department, KM Biologics Co., Ltd.
Professor, DEJIMA Infectious Disease Research Alliance (DIDA), Vaccine Research and Development Center (VRDC), Nagasaki University

Dr. Motoharu Abe is a Specialist of Production Technical Development Department, at KM Biologics Co., Ltd. (KM Biologics). KM Biologics is a leading vaccine manufacturer in Japan, taking its roots back to 1945. Dr. Abe has been working for KM Biologics and its predecessor, The Chemo-Sero-Therapeutic Research Institute (Kaketsuken) for around 30 years. During his career he has been continuously involved in numerous human vaccine research and development projects. Notably, Dr. Abe has contributed significantly to the development of a Japanese encephalitis vaccine and DTaP-Sabin IPV, and research into an influenza vaccine. He is now pursuing the development of several vaccines especially a live attenuated Dengue vaccine as the specialist, and containment of polio virus as the general director of the internal committee of GAPIV, which is WHO Global Action Plan to minimize poliovirus facility-associated risk after type-specific eradication of wild polioviruses and sequential cessation of oral polio vaccine use. Furthermore, Dr. Abe is also dedicating his time and effort as a professor of DEJIMA Infectious Disease Research Alliance (DIDA), Vaccine Research and Development Center (VRDC) at Nagasaki University.

HANNAH CLAPHAM

Director of the Centre for Epidemic Research and Modelling (CERM); Programme Leader (Infectious Diseases)
Saw Swee Hock School of Public Health
National University of Singapore

Associate Professor Hannah is an infectious disease epidemiologist whose work applies mathematical modelling and data analytics to understand disease transmission and control of infectious diseases. Her research spans arboviruses, vaccines, sero-epidemiology, and preparedness modelling. Prior to joining the School in 2020, she conducted postdoctoral research in the United States and led the mathematical modelling group at the Oxford University Clinical Research Unit in Ho Chi Minh City, Vietnam. Since 2022, she has served with distinction as Leader of the School's Infectious Diseases Programme. She has a particular interest in arboviruses and sero-epidemiology.

CAROLIN BIER

Global Medical Affairs Manager
Roche

Dr. Carolin Bier is a Global Medical Affairs Manager at Roche Diagnostics in Switzerland, specializing in vector-borne diseases with a particular focus on dengue fever. With a PhD in Biochemistry from the University of Frankfurt a.M., Germany, she brings over a decade of experience in infectious disease diagnostics, having joined Roche Diagnostics in 2012.

In her current role, she leads global medical affairs initiatives for vector-borne diseases, with deep expertise in the diagnostic challenges unique to dengue fever. Her work centers on advancing the accuracy and reliability of diagnostic testing through innovative approaches and automation technologies that enhance clinical decision-making and improve patient outcomes across endemic, as well as non-endemic regions.

Her presentation at the Asia Dengue Summit will address critical diagnostic challenges in dengue and demonstrate how precision testing combined with automation can provide robust, scalable solutions to strengthen disease surveillance and control efforts in Asia.

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YAP ENG SOO

Head & Senior Consultant,
Department of Laboratory Medicine,
Ng Teng Fong General Hospital

Dr Yap completed his medical degree at the National University of Singapore. He then underwent further clinical training in Internal Medicine and Haematology at the National University Hospital. He obtained his fellowship from the Royal College of Pathologists (Haematology) while spending a year doing epidemiology and statistics as a researcher at the Department of Epidemiology, Leiden University Medical Centre, Netherlands. His clinical interest is in the treatment of benign haematological conditions with a special focus on thrombosis and haemostasis. His research interests include the epidemiological link between arterial and venous thrombosis, bleeding disorders and medical education. Dr Yap was the past President of the Singapore Society of Haematology. He is passionate about medical education and is actively involved in undergraduate and post-graduate medical education. He was previously the Haematology residency programme director and core faculty member of the Medicine residency programme at the National University Hospital. He is also an adjunct Associate Professor with the Yong Loo Lin School of Medicine, National University of Singapore, as well as clinical teacher for Lee Kong Chian School of Medicine, National Technological Unversity, Singapore.

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CHUA WEN ZHE

ProImmune

Wen Zhe is an immunology sales specialist based in Singapore, responsible for the APAC region. He graduated from National University of Singapore with a major in Chemistry. He joined ProImmune in early 2023 and supported many academic and research institutes alike by facilitating in-depth discussions, sharing relevant case studies, and engaging in thought experiments to help ensure their projects are well-conceived.

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EGGI ARGUNI

Pediatric Infectious Disease Consultant
Sardjito General Hospital

Dr. Eggi is a pediatrician, lecturer, and researcher in the Department of Child Health and the Center for Tropical Medicine at the Faculty of Medicine, Public Health, and Nursing, Universitas Gadjah Mada. She also serves as a pediatrician in the Division of Infectious and Tropical Diseases at Dr. Sardjito General Hospital.

She earned her Doctor of Philosophy (PhD) in Molecular Biology and Immunology from the Graduate School of Medicine at Chiba University. Her research focuses primarily on infectious and tropical diseases in pediatric patients, with particular interests in dengue, sepsis, infection control, HIV, and COVID-19.

One of her current research collaborations is with World Mosquito Program Yogyakarta, an affiliate of World Mosquito Program. Through this collaboration, she is involved in developing complementary technologies for dengue vector control using an innovative approach based on Wolbachia, a non-pathogenic bacterium. This research aims to advance sustainable and effective strategies for reducing dengue transmission and improving public health outcomes.

MILLY CHOY

Deputy Director (Applied Entomology)
National Environment Agency, Singapore

Dr Milly Choy is a Senior Scientist at Singapore's National Environment Agency (NEA), Environmental Health Institute, where she contributes to research and applied science supporting vector-borne disease surveillance and control. Her work focuses on dengue and mosquito-borne diseases, including the biology of Aedes mosquitoes, dengue virus transmission, and evidence-based strategies to reduce disease risk in urban settings.

At NEA, Dr Choy's expertise supports Singapore's integrated dengue control efforts, including scientific work linked to Project Wolbachia and mosquito surveillance. By combining laboratory research, entomology and translational public health applications, she helps bridge basic science with operational disease-control programmes. Her work contributes to Singapore's broader efforts to strengthen preparedness against dengue and other emerging mosquito-borne threats.

DEREK CUMMINGS

Johns Hopkins Bloomberg School of Public Health
John Hopkins University

Derek A. Cummings, PhD, is Bloomberg Distinguished Professor of Infectious Disease Dynamics in the Departments of Epidemiology and Biomedical Engineering at Johns Hopkins University. His work centers on strengthening global pandemic preparedness through the integration of field epidemiology, immunology, and quantitative modeling to understand how pathogens emerge, spread, and evolve in human populations. Cummings leads research programs on arboviruses including dengue, Zika, and chikungunya as well as work on influenza and other respiratory pathogens. His work focuses on developing generalizable frameworks for early detection and surveillance, estimation of population dynamics of immunity, and estimation of intervention effects. Cummings employs advanced serological platforms, antigenic cartography, viral kinetic modeling, and life-course immunology to characterize population immunity and identify gaps where future epidemics are most likely to ignite. Cummings has worked on large-scale intervention trials including trials of Wolbachia introgression to prevent arboviral transmission and fractional doses of Yellow Fever vaccine for outbreak response. He has directed and collaborated on large-scale cohort studies and multinational surveillance networks across the Americas and Asia. Cummings works closely with public health agencies and international academic collaborators to translate analytic innovations into operational tools for outbreak forecasting, response, vaccine policy, and global health security.

NURULHUSNA BINTI AB HAMID

Head Of Medical Entomology Unit, Infectitous Diseases Research Centre,
Institute For Medical Research, National Institute Of Health, Ministry Of Health Malaysia

Dr. Nurulhusna Ab Hamid is a Research Officer and the current Head of the Medical Entomology Unit at the Infectious Diseases Research Centre, Institute for Medical Research (IMR), under the Ministry of Health Malaysia. With nearly two decades of dedicated service, she has established herself as a leading expert in vector control and medical entomology. She holds a PhD from Universiti Malaysia Pahang, Malaysia, where her research focused on the behavioural responses of the Aedes aegypti mosquito. Her professional portfolio is extensive, ranging from managing a major randomized controlled trial for dengue management (iDEM) to serving as the Quality Assurance Officer for the OECD-accredited Med-Entomo GLP Lab. Beyond her primary research, Dr. Nurulhusna plays a vital role in institutional governance and academic leadership. She acts as the Secretariat for the IMR Biosafety and Biosecurity Committee (IMR-IBBC) and serves as the Deputy Dean for the Post Graduate Diploma in Applied Parasitology and Entomology (PGDAPE). An avid mentor, she has supervised numerous international scholars and graduate students while contributing to national policy as an advisor to the National Special Task Force Dengue Committee. Her contributions to public health have been widely recognized, resulting in frequent invitations to speak at local and international forums.

JING SHEN

Director Health Economics, Vaccines at Takeda

Dr. Jing Shen is an accomplished health economist and outcomes research leader with more than two decades of experience spanning academia, pharmaceutical research, and global healthcare strategy. She currently serves in a senior leadership role at Takeda, where she contributes to the development of evidence-based strategies that support patient access to innovative therapies and inform healthcare decision-making worldwide.

GRAHAM ALABASTER

Former Director, UN-Habitat

Dr. Graham Alabaster is currently on loan to WHOs Department for Public Health and Environment from UNHABITAT, where he is developing joint programmes on urban development, health and environment. He is currently the co-chair of the UN-Watre taskeforce on wastewater and water quality. In UNHABITAT he was Section Chief responsible for Africa and Latin America in Human Settlements Financing Division of UNHABITAT. He is an Engineer by profession, with first degree in Chemical Engineering and a PhD in Civil Engineering. Starting his professional life as a Research Fellow, he travelled extensively in Africa, Asia and Latin America, providing technical assistance on sustainable wastewater management and sanitation, thereafter as an International consultant. He joined UNHABITAT in 1992 and has played a key role in building the Water, Sanitation and Infrastructure Branch. He is a Charted Engineer and Fellow of the Royal Society of Health. He represents UNHABITAT on many inter agency bodies. He was the agency representative on the WHO Panel of Experts for the Environmental Control of Vector-borne Diseases (PEEM), with a special interest in urban vector-borne diseases. He has over 25 years experience in the water sanitation and solid waste management working in over 30 countries. In addition to designing and implementing projects in Africa and Latin America, he has global responsibility for policy issues relating to sanitation, pro-poor water and sanitation governance, solid and hazardous waste management, and monitoring water and sanitation MDGs.

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MICHELLE TAN WOEI JEN

Senior Consultant
Head, Department of Family Medicine and Continuing Care (FMCC)

Dr Tan is a Senior Consultant and Head of the Department of Family Medicine and Continuing Care (FMCC), and the Clinical Director for Integrated Continuing Care Services within the Population Health & Integrated Care Office (PHICO) at Singapore General Hospital (SGH). She plays a key role in driving strategic institutional transitional care initiatives that strengthen continuity of care and enhance patient experience across the care continuum. She is also the Clinical Lead for SGH@Home, SGH's Mobile Inpatient Care @ Home (MIC@Home) programme, and has been instrumental in its design, implementation, and operations since inception.

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PATSIAN LOW

Asia Venture Philanthropy Association (AVPN)

Patsian is AVPN’s Chief of Markets and Deputy CEO. She will lead AVPNs market-focused activities, including driving growth in membership, enhancing the value proposition for capital providers, cultivating new partnership opportunities, and supporting AVPNs overall strategic direction. As a part of the management team, Patsian will help to guide AVPN’s growth in the future, drawing from her diverse experience in impact and sustainable finance, purpose-driven businesses, philanthropy, CSR, sustainability, non-profit leadership, and commercial finance across the US and Asia. Patsian has spent 30 years across the continuum of capital, holding leadership positions in philanthropy, social impact, CSR and sustainability in organisations from public and private sectors. These include roles in Visa, DBS and DBS Foundation, Singapore’s National Volunteer & Philanthropy Center, State Street Bank, Deutsche Bank and her own impact enterprise. She also advises organisations like Tri-Sector Associates, Center for Sustainable Finance and Private Wealth, and other early-stage impact startups. She is also on several non-profit boards and committees. Patsian holds an MBA from New York University’s Stern School of Business, and is presently pursuing her 2nd Masters from University of Cambridge Institute of Sustainability Leadership. As a mother of two, Patsian feels strongly about the empowerment of working women and their growth as holistic, well-rounded individuals. She spends her spare time working hard at Flamenco dance, fitness, travelling and foreign languages.

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VIGNESWARI A

Crowell Global Advisors

Vigneswari brings passion to her work on health policy matters. As a Senior Consultant at Crowell Global Advisors (CGA), her expertise spans cervical cancer elimination, pandemic preparedness, cancer control, and sustainable health financing. She develops strategies for clients across a spectrum of industries, including major life sciences companies, insurance companies, and governments, and regularly represents CGA at high-level industry events across the Asia-Pacific region.

At CGA, Vigneswari has led landmark public health initiatives across the region. She spearheaded the development of Indonesia's first Cervical Cancer Elimination Plan in collaboration with the Indonesia Ministry of Health, an evidence-based plan shaped by extensive multisectoral stakeholder consultation across government, industry, and civil society. She also led the development of two pivotal APEC roadmaps: the APEC Cervical Cancer Roadmap 2026 to 2030, designed to accelerate cervical cancer elimination in alignment with WHO goals on vaccination, screening, and treatment, and the inaugural APEC Dengue Prevention and Control Roadmap 2026 to 2030. To advance these and broader public health goals such as cancer control and pandemic preparedness, she has organized and led in-person roundtable country engagements across Japan, Korea, Indonesia, Malaysia, Philippines, Vietnam, and Taiwan, bringing together multisectoral partners from government, industry, and civil society. She has also represented CGA at prominent forums, including the AmCham Malaysia Healthcare Conference and the Selangor International Health Conference.

In her previous work at ACCESS Health, Vigneswari co-authored and led a whitepaper on insurance innovations in Asia. She traveled throughout Southeast Asia to speak on the role of private health insurance in achieving universal health coverage, rallying stakeholders across government, health, and technology sectors to strengthen health systems. She has spoken on prominent platforms including the Asia Insurance Review Conference in 2022 and the Singapore Week of Innovation and Technology (SWITCH) 2022.

Prior to ACCESS Health, Vigneswari worked as a civil servant at the Ministry of Health, Singapore, formulating policies and programs to promote successful aging among the nation's senior citizens. Her strong network within the government healthcare sector complements her consulting skill set and her expertise with health policymaking in Singapore.

She holds a bachelor of science (and received honors with distinction), with a double major in life sciences and political science, from the National University of Singapore.

A-116 Inferring The Global Risk of Dengue Outbreaks

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Background: Dengue is an escalating global health challenge, with transmission expanding beyond traditionally endemic tropical and subtropical regions. Most research targets mean disease burden, yet such approaches fail to capture extreme outbreaks that disproportionately strain healthcare systems. We quantified the magnitude and frequency of extreme dengue outbreaks using extreme value theory (EVT).

Methods: We analysed 42,193 monthly dengue incidence records (2010-2023) obtained from the OpenDengue platform across 693 geographic units defined by the Global Administrative Areas database. We applied EVT to characterise the tail risk of dengue outbreaks and develop a framework for selecting models and thresholds. Block maxima and peaks-over-threshold approaches estimated return levels, quantifying incidence expected to be exceeded within specified return periods. Spatial and temporal patterns of extremes were evaluated across multiple recurrence intervals.

Results: Regions in South America and Southeast Asia, including Nicaragua, Brazil, Argentina, Colombia, the Philippines, and Laos, are estimated to experience outbreaks surpassing reference levels approximately once every 5-30 years, illustrating the recurrent nature of dengue epidemics. Additionally, 101 geographic units are projected to exceed their historical maxima within the next century; Argentina, Nepal, and the Philippines emerge as most at-risk. Central Visayas (Philippines) is expected to surpass its historical maximum within 25 years, with return levels exceeding 4,100 cases per 100,000 persons per month.

Conclusion: Our findings underscore substantial spatial heterogeneity in dengue tail risk, suggesting that true outbreak risk is likely underestimated due to detection limitations. These results can inform public health preparedness, resource allocation, and future surveillance strategies.

A-122 Beneath the Epidemic: The Persistent Whisper of Sylvatic Dengue in Senegal

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Background: Dengue virus (DENV) is an increasing public health concern in Africa, where surveillance data on circulating variants remain limited. Senegal has experienced annual dengue outbreaks since 2017 in a hyperendemic context, yet the diversity, origin, and persistence of DENV lineages particularly sylvatic strains are poorly understood. This study aimed to characterize circulating DENV serotypes and genotypes in Senegal and investigate unexplained serotyping failures.

Methods: Between 2019 and 2023, remnant sera from 8,746 individuals enrolled in the national 4S sentinel syndromic surveillance network were analyzed. Viral RNA was detected using real-time RT-PCR, followed by molecular serotyping with the CDC Dengue Typing Kit. Whole-genome sequencing was performed using a serotype-specific multiplex PCR tiling approach and Oxford Nanopore MinION sequencing. Phylogenetic and phylogeographic analyses were conducted to infer viral diversity, origin, and dispersal. In silico analyses assessed primer and probe mismatches.

Results: A total of 434 samples (4.96%) tested positive for DENV RNA, revealing co-circulation of DENV-1, DENV-2, and DENV-3. Among serotyped samples, DENV-3 predominated (72.82%), followed by DENV-1 (17.41%) and DENV-2 (1.05%). Several samples from southern Senegal failed molecular serotyping and were identified through sequencing as sylvatic DENV-2 genotype VI (DENV-2/GVI). In silico analysis revealed critical mismatches in CDC serotyping probe binding sites. Sequencing generated 39 near-complete genomes, identifying multiple clades within DENV-3 genotype III and DENV-1 genotype V. Phylogeographic reconstruction dated the introduction of DENV-2/GVI to approximately 2009, indicating sustained cryptic circulation.

Conclusion: The detection of persistent sylvatic DENV-2 circulation within a hyperendemic setting highlights significant gaps in dengue diagnostics and surveillance. These findings underscore the need for genomic-informed surveillance, One Health approaches integrating non-human primates and arboreal vectors, and reassessment of diagnostic and vaccine strategies in Senegal and across Africa.

A-130 Measuring spatially adjusted temperature-dependent transmissibility for vector-borne diseases

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1 Nanyang Technological University

Background: Accurate real-time estimation of the effective reproduction number is critical for infectious disease surveillance and response. In vector-borne diseases like dengue, transmission is strongly shaped by temperature and spatial constraints, yet most estimation methods assume fixed generation times and homogeneous mixing, leading to biased estimates in environmentally heterogeneous settings.

Methods: We developed and evaluated two novel frameworks for estimating a temperature-dependent reproduction number that dynamically updates the generation time using observed temperature data and incorporates spatial transmission via a distance-based likelihood formulation, including an individual-level reproduction number approach. Using simulated epidemics with varying characteristics, we compared temperature-dependent, temperature-independent, and angular reproduction numbers, the latter of which does not require generation time specification. Performance was evaluated using classification accuracy for epidemic growth detection and percent error relative to a temperature-dependent ground truth.

Results: Temperature-dependent reproduction numbers consistently outperformed alternative approaches, achieving the highest classification accuracy in 54/72 simulation scenarios, particularly under high temperature variability. Models combining temperature-dependent generation times with a Gaussian spatial decay kernel yielded the lowest percent errors (16–38%). Application to Singapore’s 2019 dengue outbreak showed that the individual-level reproduction number was more responsive to fluctuations in daily case counts than other methods.

Conclusion: These results demonstrate that incorporating temperature and spatial transmission constraints improves real-time reproduction number estimation for vector-borne diseases and enhances detection of changes in transmissibility. The proposed framework is broadly applicable to climate-sensitive pathogens and extensible to additional covariates.

A-135 Unraveling Dengue's Spatiotemporal and Serotype Dynamics in Singapore (2019–2023)

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Background: The COVID-19 pandemic disrupted global dengue transmission patterns. Singapore experienced a marked dengue resurgence during and after lockdowns, contrasting with declines in some neighboring countries, pointing to unique local transmission drivers.

Methods: We integrated fine-scale spatiotemporal dengue case data and *Aedes* mosquito surveillance data across Singapore's planning areas from 2019–2023. An agent-based model (ABM) incorporating serotype-specific cross-protection was developed to simulate transmission dynamics. Model performance was validated against a simplified SIR framework to assess operational utility for surveillance.

Results: Fine-scale analysis revealed pronounced spatiotemporal clustering of wild-type female *Aedes* mosquitoes, closely aligned with local case surges. Predictive models closely matched observed cases in key planning areas, validating the integration of localized surveillance data. ABM simulations reproduced cyclical epidemic–endemic patterns only when serotype cross-protection was included, supporting serotype replacement as a central mechanism behind resurgence in the pandemic period.

Conclusion: The interplay of localized *Aedes* density and serotype dynamics underpinned Singapore's dengue surges from 2019–2023. Integrating high-resolution surveillance data with mechanistic modelling improves outbreak forecasting and enables targeted vector control, offering a robust framework for dengue monitoring in urban environments.

A-139 Serological and Seasonal Patterns of Dengue among Febrile Patients in Kathmandu, Nepal (2023–2025)

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1 Nepal Medical College

Background: Dengue is an emerging public health threat in Nepal, with recurrent outbreaks and expanding transmission into high-altitude urban areas, including the Kathmandu Valley. Major epidemics in 2023 and sustained transmission during 2024–2025 indicate a shifting dengue epidemiology. Laboratory confirmation using dengue NS1 antigen and IgM/IgG serology remains essential for diagnosis and surveillance.

Methods: A hospital-based retrospective observational study was conducted at a tertiary care center in Kathmandu from 2023 to 2025. Febrile patients were tested using rapid diagnostic tests detecting dengue NS1 antigen, IgM, and IgG antibodies. Serological profiles, hematological and liver function parameters, seasonal trends, and circulating serogroups were analyzed.

Results: Among 5,584 febrile patients evaluated, 1,015 were serologically positive for dengue. Acute dengue infection (NS1 and/or IgM positive) was identified in 904 (16.2%) cases, while IgG seropositivity was observed in 12.9%. Hematological parameters were normal in 40.8% of dengue-positive patients. Thrombocytopenia occurred in 29.6%, leukopenia in 36.0%, and monocytosis in 4.4%. Elevated liver enzymes were detected in 8.8% of cases, and severe dengue was documented in 3.5%. Dengue incidence peaked during the post-monsoon period, with year-to-year variation in circulating serogroups.

Conclusions: Sustained dengue transmission with distinct seasonal and serological patterns was observed in Kathmandu. Integrated laboratory and temporal surveillance are critical for early outbreak detection and targeted public health responses in Nepal.

A-148 National dengue control and resurgence following programme termination in Vietnam: a segmented interrupted time series analysis

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Background: Dengue incidence has increased substantially over recent decades, particularly in endemic settings. National dengue control programmes have been implemented in several countries to reduce disease burden. However, evidence on the impact of such programmes remains limited. We evaluated the impact of the national programme on dengue incidence and assessed the consequences of programme termination.

Methods: A segmented interrupted time series analysis of monthly dengue incidence from 1994 to 2025 was conducted using negative binomial regression with seasonal Fourier terms and a population offset. Two interruption points were specified in 1999 (programme initiation) and 2020 (termination). Counterfactual projections assuming continuation of the programme after 2020 were generated from the fitted model. Incidence rate ratios (IRRs) and 95% confidence intervals (CIs) were estimated.

Results: Before programme initiation, dengue incidence increased by 35% annually (IRR 1.35; 95% CI: 1.29-1.41). During the programme implementation, the annual growth rate was attenuated to 3% per year (IRR: 1.03; 95% CI: 1.02-1.04). Programme termination was associated with an immediate increase in incidence (IRR: 2; 95% CI: 1.09-3.65), followed by a continued upward trend. Observed post-termination incidence exceeded the projected continuation scenario (IRR: 1.77; 95% CI: 1.54-2.47).

Conclusion: Implementation of the national programme was associated with a substantial reduction in the annual growth rate of dengue incidence, whereas its termination coincided with renewed increases and subsequent outbreaks. These findings highlight the critical importance of sustained National dengue prevention and control strategies.

A-150 Modelling climate change impact on the risk of dengue fever outbreak in in South and Southeast Asian settings

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Background: Compared to temperate regions, tropical and subtropical places like South and Southeast Asia are expected to maintain a more favourable condition for dengue fever vectors in the future along with climate change. This investigation used a disease transmission model parametrized with changes of temperature and rainfall to simulate dengue fever epidemics under different greenhouse gas emission scenarios.

Methods: Weekly dengue fever incidence rate, daily mean temperature and rainfall from 2012 to 2020 in four South and Southeast Asian settings (Singapore, Colombo, Selangor, and Chiang Mai) were collected. We developed a compartmental model incorporating vector-human transmissions, and projected the dengue fever epidemics until 2090s under SSP126, SSP245, and SSP585 scenarios.

Results: Compared with 2030s, the peak incidence would be increased by 1.3 times in Singapore, 2.3 times in Colombo, 1.4 times in Selangor, and >10 times in Chiang Mai in the 2090s under SSP585; even in a milder SSP126 scenario, the annual epidemic size was projected to be increased by 6.0%, 10.8%, 13.0%, and 70.0% from the 2030s-2090s in these locations. Additionally, the peak epidemic times and outbreak durations were projected to be earlier in general.

Conclusion: The findings support that climate change is likely to reshape dengue fever outbreaks, especially under high emission scenarios and after the middle of this century. Limiting greenhouse gas emissions could be crucial in lowering the risk of dengue fever outbreaks in the future.

A-156 Clinical and Epidemiological Characteristics of the 2025 Dengue Outbreak in Bangladesh

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Background: Bangladesh experiences recurrent dengue outbreaks with substantial morbidity and case fatality. During recent epidemics, shifts in disease severity and clinical presentation have posed significant challenges to the health system. This study aimed to describe the clinical and epidemiological characteristics of adult patients with dengue fever during the 2025 outbreak in Bangladesh.

Methods: This observational study was conducted across four tertiary care hospitals in Bangladesh from June to October 2025. It included 590 laboratory-confirmed (NS1-or IgM-positive) adult dengue patients. Demographic data, clinical presentations, and laboratory findings were collected via face-to-face interviews, physical examinations, and medical record reviews. A pretested semi-structured case record form was used for data collection. Disease severity was classified using the revised WHO 2009 dengue criteria.

Results: The mean age of participants was 34·3 years (SD 12·6), with a marked male predominance (73·7%). Fever (92·7%), headache (82·7%), myalgia (76·9%), arthralgia (68·0%), nausea (59·8%), anorexia (44·7%), vomiting (42·5%), and diarrhoea (18·3%) were the most frequently reported symptoms. Warning signs were observed in 31·5% of patients, most commonly abdominal pain (41·2%), lethargy (18·1%), restlessness (17·3%), fluid accumulation (ascites 16·9%, pleural effusion 9·0%), and respiratory distress (14·6%). Severe dengue was identified in 32·7% of cases, manifesting as plasma leakage (16·4%), bleeding complications (melena 8·5%, haemoptysis 5·3%), neurological involvement (confusion 5·3%, convulsions 1·2%), and shock (6·8%). Two deaths were recorded during the study period.

Conclusion: This study found a predominance of young adult males, with nearly one-third developing severe dengue during the 2025 outbreak in Bangladesh.

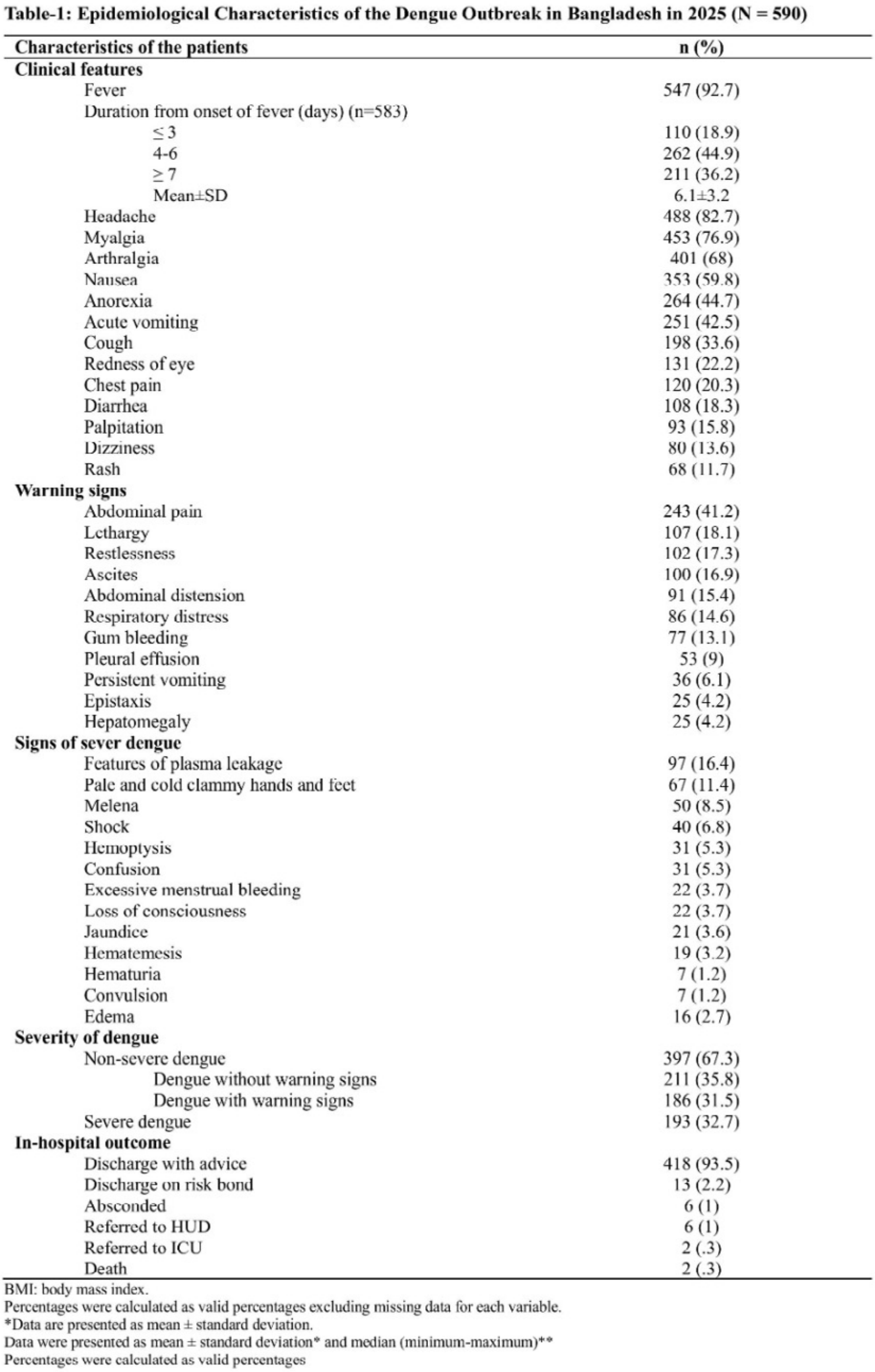

Table-1: Epidemiological Characteristics of the Dengue Outbreak in Bangladesh in 2025 (N = 590)

Characteristics of the patients	n (%)
Clinical features	
Fever	547 (92.7)
Duration from onset of fever (days) (n=583)	
≤ 3	110 (18.9)
4-6	262 (44.9)
≥ 7	211 (36.2)
Mean±SD	6.1±3.2
Headache	488 (82.7)
Myalgia	453 (76.9)
Arthralgia	401 (68)
Nausea	353 (59.8)
Anorexia	264 (44.7)
Acute vomiting	251 (42.5)
Cough	198 (33.6)
Redness of eye	131 (22.2)
Chest pain	120 (20.3)
Diarrhea	108 (18.3)
Palpitation	93 (15.8)
Dizziness	80 (13.6)
Rash	68 (11.7)
Warning signs	
Abdominal pain	243 (41.2)
Lethargy	107 (18.1)
Restlessness	102 (17.3)
Ascites	100 (16.9)
Abdominal distension	91 (15.4)
Respiratory distress	86 (14.6)
Gum bleeding	77 (13.1)
Pleural effusion	53 (9)
Persistent vomiting	36 (6.1)
Epistaxis	25 (4.2)
Hepatomegaly	25 (4.2)
Signs of sever dengue	
Features of plasma leakage	97 (16.4)
Pale and cold clammy hands and feet	67 (11.4)
Melena	50 (8.5)
Shock	40 (6.8)
Hemoptysis	31 (5.3)
Confusion	31 (5.3)
Excessive menstrual bleeding	22 (3.7)
Loss of consciousness	22 (3.7)
Jaundice	21 (3.6)
Hematemesis	19 (3.2)
Hematuria	7 (1.2)
Convulsion	7 (1.2)
Edema	16 (2.7)
Severity of dengue	
Non-severe dengue	397 (67.3)
Dengue without warning signs	211 (35.8)
Dengue with warning signs	186 (31.5)
Severe dengue	193 (32.7)
In-hospital outcome	
Discharge with advice	418 (93.5)
Discharge on risk bond	13 (2.2)
Absconded	6 (1)
Referred to HUD	6 (1)
Referred to ICU	2 (.3)
Death	2 (.3)

BMI: body mass index.
Percentages were calculated as valid percentages excluding missing data for each variable.
*Data are presented as mean ± standard deviation.
Data were presented as mean ± standard deviation* and median (minimum-maximum)**
Percentages were calculated as valid percentages

A-163 Rainfall-Driven Mosquito Dynamics in Vientiane Villages: Evidence for Climate-Informed Dengue Surveillance

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Background: Climate variability, particularly rainfall, influences *Aedes aegypti* breeding and dengue transmission. With limited treatment options and low vaccine coverage, dengue control depends on vector surveillance and climate-informed predictive tools. This study assessed rainfall–mosquito dynamics to inform integration into public health monitoring and preparedness.

Methods: Monthly rainfall data (2016–2017) were obtained from TerraClimate. Mosquito collections were conducted in four villages of Vientiane Capital. Scatter plots and Spearman correlation analyses, including 1- and 2-month lags, were used to evaluate associations between rainfall and mosquito abundance.

Results: Mosquito populations peaked one month after rainfall, consistent with the mosquito life cycle. Rainfall showed a positive correlation with mosquito counts (r=0.68, p=0.004), with stronger association at 1-month lag (r=0.84, p=0.0002). Excessive rainfall reduced larvae through flushing, indicating a non-linear relationship.

Conclusion: Rainfall is a key climate driver of mosquito dynamics, with direct implications for dengue surveillance and early warning systems. Findings support the integration of climate-based predictive tools into monitoring and evaluation frameworks, enabling timely resource allocation and community-level interventions. Future work will expand to nonlinear modelling, spatial mapping, and develop predictive model on climate and dengue vector and the inclusion of this model into the climate and dengue case prediction to strengthen policy relevance and implementation strategies.

A-190 Age- and Serotype-Dependent Differences in Dengue Virus Transmission and Clinical Outcomes: Evidence from Cluster Investigations in Kamphaeng Phet, Thailand

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Background: All four dengue virus serotypes can cause infection, yet routine clinical surveillance primarily captures symptomatic illness and incompletely reflects subclinical infection and community transmission. Consequently, transmission risk and clinical outcomes are often characterized separately, limiting comparisons across stages of the infection pyramid within the same populations.

Methods: Using combined cluster-cohort studies (2004-2007, 2009-2012, and 2015-2023), we characterized age- and serotype-specific patterns of infection and clinical illness among 2,373 household members and neighbors associated with 403 identified dengue illness cases across exposure clusters.

Results: Across serotypes, the probability of infection among household members or neighbors ranged from 18.8% to 26.2%, corresponding to an average of one to two additional infections per cluster per clinically apparent case. DENV-2 was associated with higher odds of infection across all ages, while DENV-4 was associated with the highest secondary attack rate among participants aged >45 years. Among infected individuals, 69.1% reported febrile illness, and 22.1% of these were hospitalized, of whom 53.9% were diagnosed with dengue hemorrhagic fever. Although DENV-4 was associated with a lower proportion of symptomatic infection, the proportion of dengue hemorrhagic fever among hospitalized cases was comparable across serotypes.

Conclusion: Together, these findings demonstrate that all dengue serotypes contribute meaningfully to transmission and clinical burden in endemic settings, with evidence of age-dependent heterogeneity in serotype-specific transmission risk, consistent with incomplete or non-sterilizing immunity in older adults. Serotype-specific estimates across stages of the infection pyramid help distinguish apparent clinical prominence from underlying transmission burden, improving interpretation of dengue surveillance data.

A-202 Temporal Associations among Dengue Incidence, Vector Mosquito Density, and Meteorological Factors in Dhaka, Bangladesh

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Dengue is a major public health concern in Bangladesh and other tropical and subtropical regions, with meteorological factors strongly influencing vector density and outbreak timing. Understanding the delayed (lag) effects of climate on mosquito populations and disease transmission is critical for developing early warning systems (EWS) and effective prevention strategies. Surveillance of immature and adult mosquitoes was conducted at five purposively selected sentinel sites in the Dhaka North City Corporation (DCCC) from May 2024 to November 2025 using standard sampling methods. Dengue case data and meteorological records were obtained from the DGHS and BMD, respectively. Data analysis, including visualization, Spearman rank correlation, and negative binomial regression, was performed in R (version 4.5.2) to assess lagged effects up to 12 weeks. In 2025, 102,861 dengue hospitalizations were reported in Bangladesh, with males accounting for 62.5% and females 37.5%. Vector densities increased from May, peaking in July, and remained high until October, closely correlating with dengue cases ($p < 0.001$). Precipitation, temperature, and relative humidity showed significant lagged associations with mosquito abundance. *Aedes* abundance had the strongest correlation with dengue incidence at a 6-week lag ($\rho = 0.827$, $p < 0.001$), confirmed by regression modeling (IRR = 1.01, $p < 0.001$). These findings emphasize the strong link between climate variability, vector dynamics, and dengue transmission. Integrating entomological and meteorological data can support EWS and targeted interventions. Implementing similar studies in other cities with dengue risk can improve national planning for outbreak prediction, prevention, and control.

A-205 Dengue Serotype Distribution and Dynamic Routine Laboratory Profiles Across Clinical Severity: A Multicenter Study in Indonesia

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Background: Dengue remains a leading cause of acute febrile illness in Indonesia, and shifts in circulating serotypes may affect outbreak patterns and clinical burden. Although serotyping enhances molecular surveillance, routine laboratory tests are still the most accessible tools for bedside evaluation. We aimed to describe the distribution of dengue serotypes and assess dynamic changes in routine laboratory parameters across different clinical phases and severity in a hospital-based cohort.

Methods: We conducted a multicenter observational study across five hospitals in Indonesia from November 2024 to October 2025. Dengue was confirmed by NS1 and/or RT-PCR. Routine laboratory parameters were extracted from medical records and analyzed by clinical phase using the WHO 1997 classification. Laboratory trajectories were compared by serotype and clinical severity. **Results:** Among 141 suspected cases, 96 (68.1%) were NS1-positive, and 45 (31.9%) were NS1-negative. RT-PCR detected DENV in 94/96 (97.9%) NS1-positive samples and 21/45 (46.7%) NS1-negative samples. Overall, 110 cases were RT-PCR-confirmed, with DENV-3 predominating (46.4%), followed by DENV-2 (20.9%). Platelet counts diverged markedly between dengue fever (DF) and dengue hemorrhagic fever (DHF), with significantly lower values in DHF from day 3 onward, persisting through days 4–8 and reaching a nadir during the critical phase. Hemoglobin, hematocrit, and leukocyte trajectories showed limited or inconsistent differences.

Conclusion: RT-PCR serotyping complemented NS1 testing and enhanced case confirmation, particularly among NS1-negative suspected cases. Among routine laboratory markers, platelet trajectories most clearly distinguished DF from DHF, supporting thrombocytopenia as a practical bedside indicator of dengue severity.

A-213 Molecular epidemiology of Dengue virus in Singapore from 2015 to 2025

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Background: In dengue hyperendemic settings, dengue virus (DENV) population dynamics are constantly shaped by virus introductions and transmission patterns that are attributed to recurrent outbreaks. This study describes the molecular epidemiology of DENV, comparing temporal dynamics of DENV lineages and their outbreak behaviour over a decade in Singapore.

Methods: Envelope gene sequences of four DENV serotypes (n=4,157) generated from 2015 to 2025 were analysed to determine the diversity, temporal dynamics and likely origins of strains/lineages and their contribution to autochthonous transmission.

Results: High strain diversity, turnover and diverse origins reflected the hyperendemic transmission of DENV shaped by repeated virus introductions in Singapore. The overall strain diversity declined gradually after 2016 (slope=-7.164, R 2 =0.69), coincidentally with the expansion of Project *Wolbachia*. Of 289 strains detected, only 41 (14%) established sustained local transmission. These "established" lineages accounted for marginally higher proportion of genotyped cases during outbreaks (mean=95.7%; range=93.9-100%) than non-outbreak periods (mean=91.4%; 81.6-95.5%). The number of "established" lineages showed weak positive correlation with the annual case burden (Pearson correlation coefficient=0.21). This weak correlation was due to the superior dominance of two "established" lineages that sustained significantly longer transmission (10-11 yrs; p=0.02-0.04) than other "established" lineages (mean=3.6 yrs) and were primary drivers of outbreaks in 2016, 2019-2020 and 2022.

Conclusions: Genomic surveillance is the key to identify major viral contributors to dengue epidemiology in endemic areas. Besides providing deep insights into outbreak risk assessment, the spatio-temporal dynamics of DENV lineages are important to monitor the effectiveness of disease control measures, including novel vector control approaches such as *Wolbachia-Aedes* strategies as well as vaccine design, evaluation and post-implementation efficacy studies.

A-222 Lessons Learned from Applying SARIMAX Models to Dengue Forecasting: Insights from a Short Time Series in Vientiane Capital, Laos

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Background: Forecasting dengue outbreaks requires models that integrate climatic and entomological drivers. Seasonal AutoRegressive Integrated Moving Average with eXogenous regressors (SARIMAX) offers a promising approach, but its performance depends heavily on data length and quality. This study reports lessons learned from applying SARIMAX to a short dengue surveillance dataset.

Methods: Monthly dengue case data (May 2016–December 2017) were analysed alongside precipitation, and larval index. Stationarity was assessed using the Augmented Dickey-Fuller test. SARIMAX models were fitted in R using auto.arima, with model selection guided by AIC/BIC. Forecast accuracy was evaluated using RMSE, MAE, and MAPE.

Results: The optimal model was a regression with ARIMA(0,0,0) errors, indicating that external regressors explained most of the variation. Precipitation ($\beta = 0.006$, $p < 0.05$) and ovitrap index ($\beta =-0.029$, $p < 0.05$) were significant predictors, while mosquito index was not statistically significant. Model performance yielded RMSE = 8.96 and MAE = 6.43, but MAPE was high (123%), reflecting the limitations of short time series forecasting.

Conclusion: This proof-of-concept highlights both the potential and constraints of SARIMAX for dengue forecasting. Significant associations with precipitation and larva indices underscore the importance of integrating climate and entomological surveillance into routine monitoring. However, the high MAPE demonstrates that short datasets limit predictive accuracy. For SARIMA/SARIMAX models to capture seasonal dynamics and provide reliable forecasts, dengue surveillance systems should maintain datasets longer than 20 months, ideally spanning multiple years. Strengthening surveillance length and quality will enhance the utility of predictive models and support the development of robust early warning systems for dengue control1111.

Keywords: Dengue, SARIMAX, precipitation, ovitrap, forecasting, surveillance, lessons learned

A-227 A Utility-Based Evaluation Framework for Dengue Outbreak Forecasting Models

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Background: Dengue early warning systems support vector control and public health response, yet most forecasting studies rely on accuracy metrics (e.g., RMSE, MAE, AUC) that ignore the timing of outbreak alerts. Predictions made at different lead times may receive similar scores despite differing operational value. This study develops a unified utility-based evaluation framework that explicitly accounts for timeliness and actionability of outbreak predictions.

Methods: We evaluated dengue forecasting models from publicly available GitHub repositories, including statistical (ARIMA), machine learning (Random Forest), and deep learning (LSTM) approaches. Models were executed using their original datasets and pipelines. Outputs were standardized into a unified format (model, region, time step, observed incidence, predicted incidence). Outbreak onset was defined as the first time incidence exceeded a seasonal baseline ($\mu + k\sigma$) computed from historical data. A decision-centric utility scoring function quantified forecast value based on lead time relative to outbreak onset, rewarding alerts within actionable windows (1–6 weeks) and penalizing late alerts, false positives, and missed events.

Results: The framework differentiates models based on alert timing rather than accuracy alone. Models generating earlier alerts within intervention windows achieved higher utility scores despite comparable RMSE/MAE values. Model rankings changed under utility-based evaluation, indicating that accuracy metrics may overlook operationally valuable models.

Conclusion: This framework shifts evaluation from accuracy-centric to decision-centric assessment by incorporating lead time and intervention constraints. It enables consistent comparison across heterogeneous models and supports development of outbreak forecasting systems aligned with real-world public health decision-making.

A-229 Disentangling cross-reactive and multitypic Dengue infection dynamics using multiplex serology

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Background: There is a growing interest in the use of high throughput multiplex serology to understand historic exposure patterns in parallel. In theory, with a single drop of blood, we can understand whether an individual has been exposed to different infectious diseases. However, it remains unclear how to interpret the readouts from multiplex assays. In particular, there is frequently substantial cross-reactivity between antigenically similar pathogens which can result in false positive signals. Specifically in regions with co-endemically circulating pathogens, cross reactive responses against pathogens can increase antibody titre signal for another pathogen. In addition, in co-circulation settings, individuals are often infected more than once, making the number of infections important in shaping serological immune profiles. Dengue (DENV) makes an excellent case to study this. DENV comprises of four co-circulating serotypes, resulting in complex immune dynamics. In particular, primary infection induces serotype-specific antibodies with only short-lived cross-protection against heterologous serotypes, followed by a window of immune enhancement during which secondary infection carries a significantly elevated risk of Dengue haemorrhagic fever (DHF) relative to DENV-naïve individuals. Standard seropositivity classifications fail to distinguish between monotypic and multitypic individuals.

Methods: Using longitudinal serological data, we develop a suite of mechanistic models, defining parameters that differentially characterise monotypic and multitypic infections and associated cross-reactive titre shifts.

Results: We evaluate model performance to infer both pathogen-specific and monotypic/multitypic infection burden.

Conclusion: By accounting for cross-reactivity and explicitly distinguishing monotypic and multitypic infection histories, these models help to maximise epidemiologic inference from multiplex serology data, offering a framework for characterising Dengue immune dynamics in endemic settings.

A-233 Combining new interventions with urban development as a path to effective, consistent, and durable control of dengue

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Background: A growing range of control tools for dengue have now demonstrated effectiveness in randomised controlled trials. Policymakers now need to decide which interventions to invest in and how to integrate them with existing vector control programmes to meet their short-and long-term control goals. The experience of countries such as Singapore, where dengue resurgence occurred after decades of suppression, underscores the need to understand how interventions interact with population immunity, local ecology, and programme costs over the long term.

Methods: We applied a compartmental mathematical model to 1,634 cities at risk of dengue worldwide and performed independent validation against reported case count data. For each city, we projected cumulative hospitalisations averted and financial costs of different combinations of enhanced vector control, vaccination, *Wolbachia* replacement, and urban environmental improvements ("building out *Aedes* ") over a 25-year time horizon.

Findings: *Wolbachia* was predicted to deliver substantial long-term reductions in dengue burden in many locations; however, its performance varied widely across cities. Pairing *Wolbachia* with enhanced vector control improved and reduced the variance of long-term predicted impact, but required sustained investment and rising operational costs as population susceptibility increased over time. The most effective and sustainable strategy combined novel and conventional approaches with gradual, structural reductions in mosquito habitat suitability through "building out *Aedes* ."

Interpretation: Sustainable dengue control will require long-term, integrated strategies that acknowledge changing population immunity and the changing role of routine vector control once novel tools are introduced. Single interventions are unlikely to achieve durable burden reductions in many settings where dengue currently circulates. Cities should consider integrated strategies that use conventional and novel interventions to suppress dengue transmission in the short term while more permanent changes can be made to remove mosquito habitat in the urban environment to ensure that control remains sustainable.

A-237 Quantifying post-primary DENV infection cross-protection using a nationwide cohort emulation in Singapore

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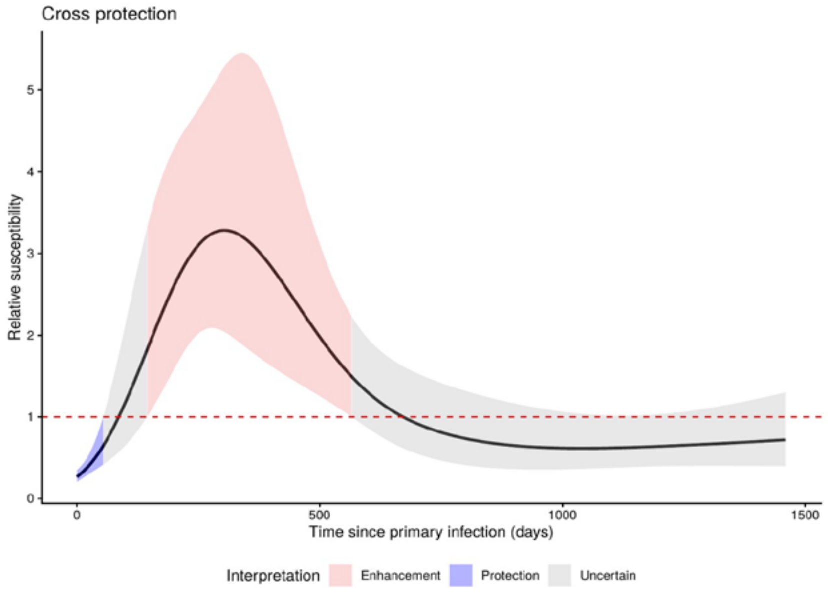
Background: After primary dengue infection, individuals may experience transient cross-protection against heterologous serotypes, followed by a return to baseline or elevated susceptibility. Existing evidence relies on categorical risk windows or fixed immune states in transmission models; direct, continuous estimation of time-varying relative susceptibility remains limited. We aimed to estimate continuous relative susceptibility to notified non-primary dengue as a function of time since primary infection.

Methods: We emulated nationwide cohorts using Singapore’s population registry, dengue notifications, and seroprevalence surveys (2012–2024). In the birth cohort (born ≥2012), primary infection was defined by the first notified episode. In the adult cohort (born <2012), primary infection timing will be imputed from age-stratified seroprevalence via multiple imputation with Rubin’s rules (n = 500). Relative susceptibility $r(\tau)$, the risk of notified non-primary dengue at time τ post-primary relative to the background force of infection, was estimated via Cox regression on the calendar-time scale using a natural cubic spline parameterisation. Robustness was assessed through variation of spline specifications, negative control outcomes, and negative exposure tests.

Results: The birth cohort comprised 575,487 individuals (3,922,455 person-years; 3,021 primary, 46 non-primary notified episodes). $r(\tau)$ was below 1 during the first 100 days, consistent with transient cross-protection, before rising to a peak of 3.28 (95% CI: 2.05–5.27) at 10 months, suggesting elevated susceptibility, then declining below 1 by two years. Confidence intervals were wide throughout. Sensitivity analyses and placebo tests supported the main findings.

Conclusions: Nationwide birth-cohort emulation provides direct, continuous evidence of transient post-primary cross-protection followed by elevated susceptibility to notified dengue in Singaporean children. Interpretation requires caution given the low event count and restriction to notified infections, which may differentially capture primary versus non-primary episodes. Adult cohort analyses and formal notification ascertainment bias correction are underway.



A-240 Estimating outbreak characteristics of dengue using an individual-based model incorporating pre-existing immunity

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Background: Dengue epidemics in endemic settings exhibit multiannual cyclical patterns, with large outbreaks often associated with serotype switches. While population immunity is an established driver of serotype dynamics, the presence of four serotypes and their immunological interactions result in difficulty in characterising immunity from data, rendering serotype dynamics challenging to predict.

Methods: We developed a simple individual-based model of dengue transmission, simulating across a range of transmission intensities and immunity settings, to study the impact of local immunity and transmission on outbreak outcomes: serotype-specific probabilities of outbreak establishment and predominance. We further examined how uncertainties in immunity affect modelled outbreak outcomes, specifically model structure with the allowing of post-secondary infection and different interpretations of serological data to inform baseline population immunity.

Results: Population immunity was a key determinant of outbreak outcomes in higher transmission settings, with transmission amplifying the competitive advantage conferred by lower serotype-specific immunity. Although serotypes facing pre-existing population immunity had reduced outbreak establishment probabilities, these were non-zero, indicating that no serotype is entirely precluded from causing outbreak. Allowing post-secondary infection produced deviations in estimated outbreak outcomes in high immunity settings, with no such observation made in low immunity settings. Lastly, different interpretations of serological data yielded markedly different population susceptibilities, significantly altering modelled outbreak characteristics.

Conclusion: Population immunity is a key determinant of dengue outbreak characteristics, particularly through its interaction with local transmission. Predictive modelling frameworks should prioritise careful interpretation of serological surveys and explicit incorporation of immunity, as these methodological choices influence outbreak projections.

A-242 Comparative analysis of XGBoost and Bayesian Ridge Regression for dengue forecasting in the District of Gampaha, Sri Lanka

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Background: In modern vector control programmes, incorporation of advanced statistical modeling is essential for reliable dengue forecasting. The prediction requires robust approaches to capture nonlinear climate-driven dynamics in Gampaha District, Sri Lanka. This study addresses developing and evaluating XGBoost and Bayesian Ridge models using previous surveillance data for enhanced dengue prediction.

Methods: XGBoost (gradient boosting) and Bayesian Ridge Regression were developed using monthly dengue cases (2012-2021) with 74 engineered features including, lags (1-3 months), rolling means (3-6-months), polynomial transformation, seasonality encoding, Principal Component Analysis (PCA) (coverage 76% variance-5 variables) from climate data (Temperature, rainfall, humidity and windspeed). Chronological train, validation and test split was performed along with hyperparameter tuning via Python 3.10 followed by analysis of performance using R^2, RMSE, MAE, MAPE, ACF1 residuals.

Results: Bayesian Ridge performed better overall with R^2=0.80, RMSE =360.15, MAE =264.59, ACF1=0.17 capturing 80% variance, with stable residuals. XGBoost is the best on minimizing errors but struggled with peaks; RMSE=287.44, MAE=234.78, R^2=-1.30 (after post-tuning) model indicated overfitting. Hence, Bayesian Ridge outperformed in variance explanation while XGBoost model minimized prediction error.

Conclusion: Bayesian Ridge provided significant interpretability and high variance forecast in resource limited setting. However, XGBoost presented the lowest errors despite overfitting. Therefore, hybrid model arrangement could be recommended to optimize dengue surveillance in study setting, incorporating Bayesian for planning and XGBoost for real-time dengue alerts. Acknowledgment: National Science Foundation, Sri Lanka (RPHS/2016/D 03) and International Atomic Energy Agency (SRL 5047) for funding and technical-cooperation respectively.

Keywords: Baysien Ridge, XGBOOST, Dengue, Forecasting, Gampaha

A-244 Genomic epidemiology of dengue in the Philippines 2022-2024

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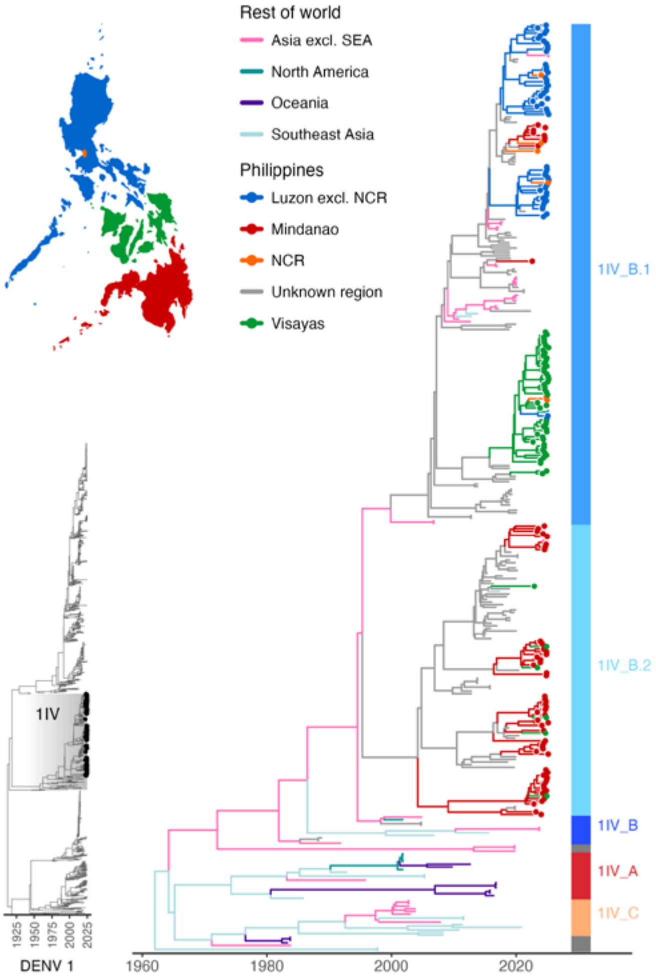
Background: Understanding viral population structure and dynamics is essential to inform dengue control strategies. Dengue surveillance at the resolution of serotypes is valuable but cannot provide additional context, particularly in hyperendemic regions where all serotypes co-circulate. Whole genome sequencing can distinguish endemic circulation from novel introductions and infer the likely age and geographical expansion of endemic strains.

Methods: In partnership with the National Reference Laboratory for Dengue and other Arboviruses and the Medical Entomology Department at the Research Institute for Tropical Medicine (RITM), Philippines, we applied the Comprehensive Sequencing of MOSquito-borne pathogens (COSMOS) bait-capture sequencing approach to 646 serum specimens collected from clinically suspected dengue cases between 2022–2024. Routine dengue RT-PCR serotyping identified 353 dengue-positive, and 293 dengue-negative specimens. Samples were selected to represent all regions of the Philippines and dengue serotypes.

Results: COSMOS sequencing recovered complete dengue genomes from 56% (192/353) of RT-PCR positive cases with 95% concordance to serotyping. All four dengue serotypes circulated, with dengue 1 predominating (n=92, genotype 1IV_B.1; n=47, genotype 1IV_B.2). Phylogenetic analysis demonstrated clustering within lineages previously reported in the Philippines (Figure 1). Phylogeographic analysis showed sub-clades specific to local regions in the Philippines, with evidence of inter-region introductions. Adequate representative sampling and the availability of contextual global sequences remains a challenge.

Conclusion: COSMOS sequencing proved highly effective for arbovirus surveillance, enabling high-resolution dengue genomic recovery and accurate serotyping. Phylogenetic findings indicate sustained local dengue transmission with geographic expansion of genotypes, emphasizing the importance of continuous genomic monitoring.



A-246 Methods for Spatial Risk Mapping of Dengue: A Scoping Review of Current Approaches and Their Public Health Utility

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Background: Dengue virus remains a critical global health threat, with shifting spatial distributions driven by climate change and rapid urbanisation. High-resolution risk maps optimise intervention programs and resource allocation. However, the diversity of modelling approaches often complicates stakeholder decision-making. This review aims to synthesise contemporary modelling methods, evaluating their operational utility and limitations for different surveillance objectives.

Methods: A literature review was conducted using PubMed, OVID Medline, and Embase to identify spatial risk mapping methodologies. Following structured inclusion criteria, studies were selected if they employed spatial mapping or extrapolation to predict dengue risk. Temporal-only and non-spatial predictor analyses were excluded. Selected papers were categorised by their primary estimation method and spatial extrapolation frameworks.

Results: Key findings revealed that Bayesian inference and machine learning ensembles have become preferred for high-resolution (1-5km) spatial extrapolation. While mechanistic models provide biologically grounded transmission thresholds, they remain constrained by high data requirements. Alongside methodological trends, modelling efforts are shifting from predicting crude incidence towards metrics such as the force of infection and climate-driven suitability indices. Although temperature and precipitation remain the dominant predictors, socioeconomic and human mobility data are increasingly integrated to capture risk heterogeneity.

Conclusion: The optimal spatial risk modelling approach depends on data availability, resolution, and policy objectives. This paper offers a comprehensive overview to guide modellers and a framework for policymakers to translate diverse outputs into actionable strategies. Future efforts should focus on establishing standardised, comparable metrics that health authorities can readily implement for dengue virus control.

A-250 Measuring Surveillance System Performance for Dengue Control in Kendal Regency, 2024

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Background: Dengue hemorrhagic fever (DHF) in Kendal Regency has emerged as the most frequently reported case in Central Java, with a notable increase in incidence over the past two years and a Case Fatality Rate reaching 7.7. Consequently, an evaluation of the DHF surveillance system's implementation in Kendal Regency is warranted.

Methods: A descriptive quantitative approach was utilized in this study. The sample comprised 20 DHF officers from puskesmas in Kendal Regency. Interviews were conducted based on the structure, function, and attributes of the surveillance system.

Results: The study revealed that the implementation of DHF surveillance has been generally effective. However, several issues were identified: all puskesmas lacked a Memorandum of Understanding with surveillance networks; 40% of puskesmas employed manual recording methods; 95% of puskesmas had DHF records that did not match those of Kendal District Health Office; only 60% of puskesmas conducted data analysis based on person, time, and place; and none of the puskesmas conducted risk factor analysis. Several aspects require improvement to ensure the system operates effectively. **Conclusions:** Recommended to implement data synchronization and digitalization, alongside enhancing the epidemiological analysis capacity of health personnel

Keywords: *Evaluation, Surveillance System, DHF*

A-252 A one health regional framework for predictive dengue surveillance and early warning in Southeast Asia

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Background: Dengue continues to pose a significant public health challenge across Southeast Asia, necessitating improved surveillance and predictive approaches. The SEA-ROADS initiative (South East Asia – Regional One Health Approach for Dengue Surveillance), launched in 2025 across Phnom Penh, Bangkok, Vientiane, Hanoi, and Ho Chi Minh City, aims to strengthen dengue forecasting through integrated, multi-country surveillance.

Methods: Standardized dengue and mosquito monitoring were implemented using a unified methodological framework. Urban areas were delineated into spatial clusters based on building-level Voronoi polygons and five-dimensional feature vectors capturing structural and landscape characteristics, followed by refinement using minimum spanning trees, principal component analysis, and hierarchical clustering to derive representative urban classes.

Result: Mosquito surveillance was conducted using 72 larvitraps per city, sampled weekly to quantify *Aedes aegypti* and *Ae. albopictus* abundance, while monthly dengue case data were collected in collaboration with local health authorities. Human mobility patterns were incorporated using point-of-interest data from Meta, aggregated into 200-m grid cells and summarized through principal component analysis, with the first axis representing urban centrality. Across cities, four to six urban classes were identified, ranging from vegetated open areas to highly dense micro-building and high-rise zones.

Conclusion: Preliminary analyses indicated a moderate positive association between *Ae. aegypti* abundance and dengue incidence with a short lag of 0–4 weeks, whereas *Ae. albopictus* populations remained relatively stable. By integrating entomological, epidemiological, and mobility data, SEA-ROADS enhances dengue risk prediction, supports identification of transmission dynamics, and enables the development of near real-time surveillance dashboards, strengthening regional capacity for proactive dengue control.

DELEGATES' ABSTRACTS

A-259 The Economic Burden of Dengue among ASEAN countries: A Systemic Literature Review

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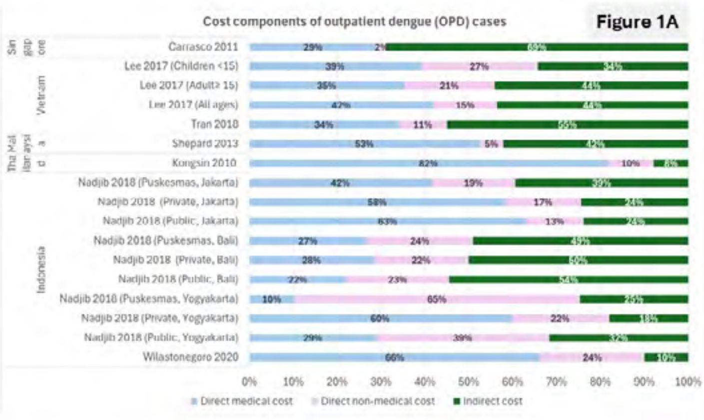
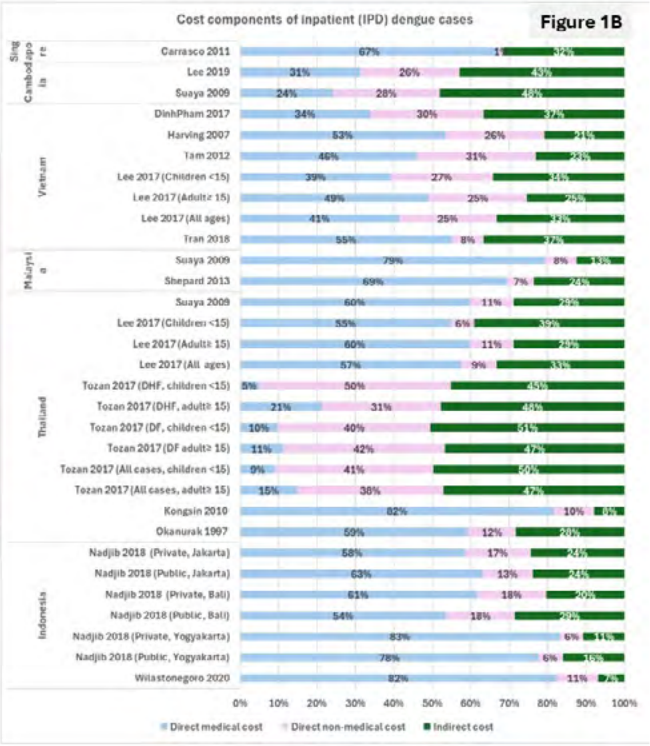
Background: Dengue remains a major public health challenge in ASEAN countries, contributing not only to substantial disease burden but also significant economic losses. This study aimed to synthesize current evidence on the cost of illness associated with dengue across ASEAN populations.

Method: We conducted a systematic review of PubMed, Embase, and Scopus, including published and grey literature from 2010 to 2025. Study selection performed independently using predefined criteria. Observational and economic studies reporting dengue-related costs were included. Data were analyzed descriptively and stratified by outpatient (OPD) and inpatient (IPD) settings.

Result: Seventeen studies were included. In OPD settings, indirect costs (primarily productivity loss) predominated, accounting for up to 69% in Singapore (high-income) and 34–55% in Vietnam and Malaysia. Direct non-medical costs varied substantially by location and facility type (13–65%), particularly in Indonesia (upper-middle-income) (Figure 1). In contrast, direct medical costs were the main driver of total dengue expenditure in IPD settings, accounting for 55–82% in Thailand and 69–79% Malaysia (upper-middle-income). Direct non-medical costs remained substantial, ranging from 20–30% in lower-middle-income countries such as Cambodia and Vietnam (Figure 2).

Conclusion: Distinct patterns were observed across income settings, with productivity loss predominated in high-income settings, health system costs in upper-middle-income countries and household financial burden in lower-middle-income countries. These findings support targeted, policy-driven strategies to reduce both health system and household burden in each country.





A-263 Advances in Phylodynamic Models of co-circulating dengue strains in Thailand 1960-2020

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Background: Nearly half of the world's population is at risk of dengue virus (DENV) infection. As dengue expands, understanding how viral genetic diversity shapes fitness and epidemiology could improve outbreak prediction and prevention. However, quantifying DENV strain fitness and identifying mutations associated with increased fitness remain challenging. We adapted a phylogenetic fitness model previously applied to other pathogens like SARS-CoV-2, to reconstruct DENV dynamics in Thailand across 60 years for all four co-circulating serotypes, identify novel lineage groupings, and link their emergence to amino acid changes

Methods: The model uses time-resolved phylogenies and assumes that fitter strains expand more rapidly under coalescent theory. Because it is lineage-agnostic, it defines groups based on inferred fitness rather than existing genotype labels. We analyzed clinical isolate sequences collected in Thailand from 1960–2020 to infer lineage structure within each serotype.

Results: By updating our previous model novel biological constraints and 10 additional years of sequences the model regrouped DENV1–4 into a greater number of lineages than current lineage definitions. In DENV3, inferred lineages closely matched previously proposed envelope protein mutations associated with antigenic variation. Logistic growth models showed that predicted lineage fitness closely tracked observed dynamics for all serotypes except DENV4, which diverged in the early 2000s and was associated with a major outbreak. We also identified several candidate lineage-defining mutations across serotypes.

Conclusion: Phylogenetic fitness models can capture important features of DENV evolution and may help identify emerging, fitter lineages during outbreaks.

A-266 How to prevent a country or area from becoming dengue-endemic

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Background: Incidence rates of dengue have dramatically increased in many countries and areas worldwide.

Methods: Global epidemiology of dengue involves four stages: (1) "a small outbreak" with sporadic cases in local areas, (2) "a large epidemic" with cases spreading from one area to others, (3) "dengue-endemic" with occurrence of dengue cases all-year-round as dengue viruses (DENVs) residing there, and (4) "hyper-endemic" as children are infected with more than one DENV serotype. Taiwan has successfully maintained as "a dengue non-endemic area".

Results: Taiwan's success results from a combination of six elements. First, local health authorities employ an intelligent surveillance system that includes important risk factors for dengue (such as patients' demographical variables, mosquitoindices from *Aedes* mosquito breeding areas, environmental factors, high population-density districts, reporting-delay days, levels of medical seeking units, clinical symptoms/signs etc.). Second, laboratory supports help identify the serotypes and genotypes of DENVs. Third, contact-tracing is essential to find out common exposure sites. Fourth, the dynamics in spatio-temporal trends of dengue cases/clusters, and their correlations with mosquito indices should be monitored. Fifth, immediate intervention strategies must be implemented. Sixth, the success and failure in prevention and control measures need to be cautiously evaluated.

Conclusion: Integrated surveillance systems and immediate prevention/control can minimize epidemic severity. Global increase in dengue severity can be supported by Taiwan's findings on dynamic changes of DENV-2 variants and selecting DENV-variants with higher epidemic potential. **Interrupting transmission and spotting mosquito breeding sites can reduce epidemic severity and prevent becoming dengue-endemic, and thus promoting global health.**

A-270 Dengue transmission heterogeneity across Indonesia's archipelago: Climate-driven spatiotemporal patterns and policy implications

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Background: Indonesia has the highest dengue burden in Southeast Asia, yet spatiotemporal transmission patterns across its 34 provinces remain poorly characterised. Understanding province-level heterogeneity in outbreak timing and climate associations is essential for optimising early warning systems.

Methods: We analysed province-level dengue surveillance data (2010–2024) from Indonesia's Ministry of Health alongside local climate variables (precipitation, temperature) and regional climate indices (ONI, DMI). Using wavelet phase analysis, dynamic time warping clustering, and distributed lag non-linear models, we characterised heterogeneity in outbreak timing and identified provinces where climate-dengue relationships were sufficiently consistent for early warning applications.

Results: We identified a systematic west-to-east gradient in outbreak timing across western Indonesia, with Sumatran provinces peaking up to four months earlier than Java-Bali (Spearman $\rho = 0.7$), following monsoon progression. This gradient weakened in eastern Indonesia. Strong El Niño events were associated with major outbreak years, with incidence 96% higher during strong El Niño periods ($\rho = 0.83$). Phase coherence analysis identified 18 provinces with consistent rainfall-dengue timing; DLNM confirmed significant dose-response associations in 11 of these.

Conclusion: Indonesia's dengue-climate relationships exhibit structured heterogeneity that precludes uniform national prediction approaches but enables province-specific early warning in high-coherence areas. A two-tier system combining ENSO monitoring for strategic preparedness with local rainfall monitoring for tactical intervention could improve outbreak response.

A-273 Analyzing lag period from the recent years dengue surge in Dhaka city: Correlation with weather factors and implications for public health response

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Background: Variation in weather has intensified dengue infections in Dhaka in recent years, placing a substantial burden on public health infrastructure. This study investigated the dengue surge from 2022 to 2025 and its association with meteorological factors, with particular emphasis on lag effects to improve the prediction of dengue incidence for 2026.

Methods: A retrospective ecological time series analysis was conducted using dengue case data from Dhaka city (2022–2025), obtained from the Dengue Daily Bulletin of the Directorate General of Health Services, Ministry of Health and Family Welfare, Bangladesh. Meteorological variables (temperature, humidity, rainfall) were sourced from the Bangladesh Meteorological Department. Monthly aggregated data were analyzed using Pearson correlation to assess overall associations, while daily data were examined to explore lagged relationships across multiple time intervals.

Results: Dengue incidence and mortality consistently rose in July, peaked between August and October, and declined thereafter. In 2023, the year recorded the highest burden of cases and deaths. Monthly correlation analysis revealed significant associations between dengue incidence and rainfall ($r=0.420$, $p=0.003$) and humidity ($r=0.365$, $p=0.011$), while temperature showed no significant monthly effect ($r=0.227$, $p=0.121$). Lag analysis using daily data demonstrated that correlations with humidity and rainfall peaked at approximately 30–35 days, whereas temperature exhibited the strongest association at a lag of 40 days.

Conclusion: Rainfall and humidity are major drivers of dengue transmission in Dhaka, with lag effects evident after 30–40 days. Incorporating these climate indicators into predictive models can enhance early warning systems and strengthen public health responses.

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A-279 Molecular characterization of dengue virus strains circulating in 2025, Taiwan

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Background: Dengue is not endemic in Taiwan, but outbreaks happened by accident continue to be a threat in Taiwan. In 2025, 29 indigenous dengue cases were detected. We performed molecular analyses of these cases to gain valuable epidemiological information.

Methods: Suspected dengue cases were confirmed by NS1 antigen, RT-PCR, and serological methods. The envelope gene of DENV was sequenced using the Sanger method. Phylogenetic analyses were conducted using MEGA version 6.

Results: The results showed that eight different DENV strains co-circulated in Taiwan in 2025. There were three DENV-1 strains, each caused one case in Yilan County, Kaohsiung City, and New Taipei City; the first one's serotype was determined by NS1 serotyping; the other two belongs to genotype I and II were closely related to viruses from Vietnam and the Philippines, respectively. There were four DENV-2 strains belonging to the cosmopolitan genotype, two strains closely related to viruses from Vietnam, one caused 12 cases in Kaohsiung City, and the other caused one case in Taipei City. The other two DENV-2 strains were closely related to viruses from Malaysia, one caused 7 cases in Taoyuan City, and the other caused 3 cases in Kaohsiung City and Pingtung County. Also, a DENV-3 genotype I strain closely related to viruses from the Philippines caused 3 cases at the workplace in Tainan City.

Conclusion: The results provided strong evidence that dengue is not endemic in Taiwan. Constant importation of dengue viruses from neighboring countries was responsible for local outbreaks each year.

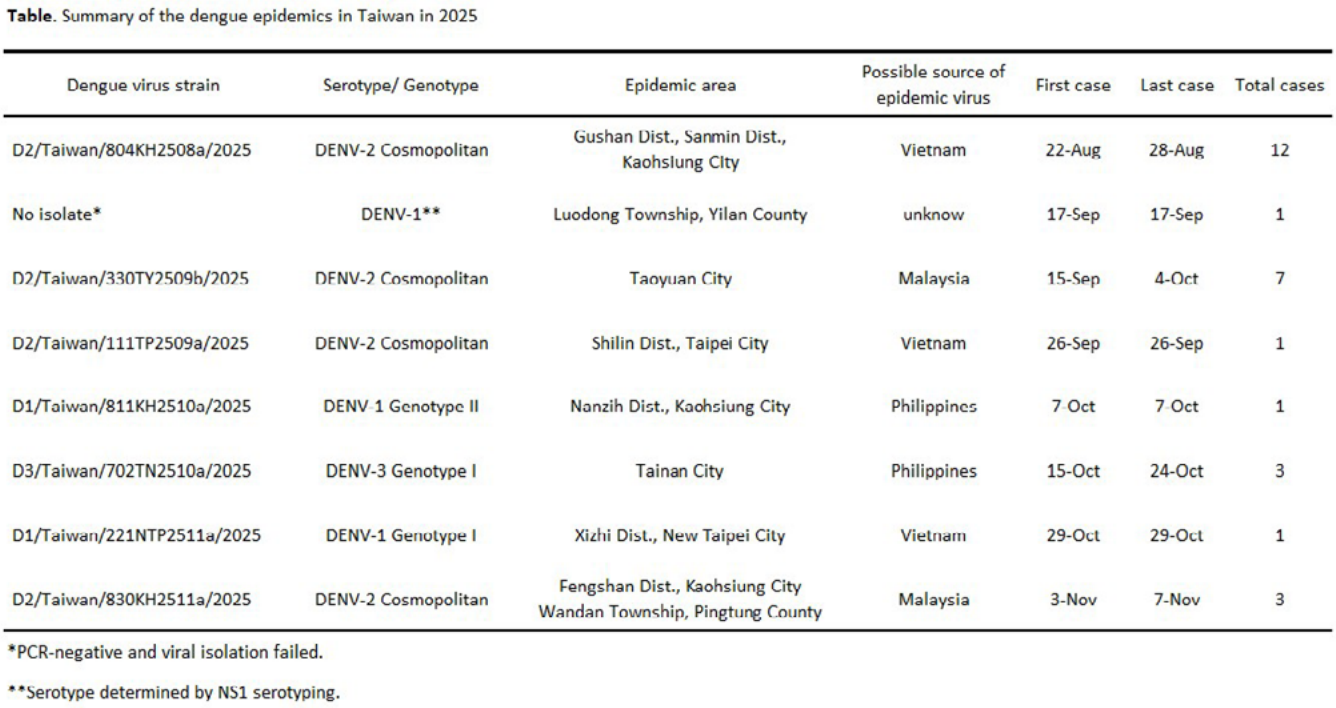

Table. Summary of the dengue epidemics in Taiwan in 2025

Dengue virus strain	Serotype/ Genotype	Epidemic area	Possible source of epidemic virus	First case	Last case	Total cases
D2/Taiwan/804KH2508a/2025	DENV-2 Cosmopolitan	Gushan Dist., Sanmin Dist., Kaohsiung City	Vietnam	22-Aug	28-Aug	12
No isolate*	DENV-1**	Luodong Township, Yilan County	unknow	17-Sep	17-Sep	1
D2/Taiwan/330TY2509b/2025	DENV-2 Cosmopolitan	Taoyuan City	Malaysia	15-Sep	4-Oct	7
D2/Taiwan/111TP2509a/2025	DENV-2 Cosmopolitan	Shilin Dist., Taipei City	Vietnam	26-Sep	26-Sep	1
D1/Taiwan/811KH2510a/2025	DENV-1 Genotype II	Nanzih Dist., Kaohsiung City	Philippines	7-Oct	7-Oct	1
D3/Taiwan/702TN2510a/2025	DENV-3 Genotype I	Tainan City	Philippines	15-Oct	24-Oct	3
D1/Taiwan/221NTP2511a/2025	DENV-1 Genotype I	Xizhi Dist., New Taipei City	Vietnam	29-Oct	29-Oct	1
D2/Taiwan/830KH2511a/2025	DENV-2 Cosmopolitan	Fengshan Dist., Kaohsiung City Wandan Township, Pingtung County	Malaysia	3-Nov	7-Nov	3

*PCR-negative and viral isolation failed.

**Serotype determined by NS1 serotyping.

A-281 DENV3 lineage replacement in Nicaragua is associated with reduced disease severity

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Background: The 4 dengue virus serotypes (DENV1-4) are a major global public health concern. DENV3 (lineage III.C.2.1, historical, 2007-2014) has been associated with clinical severity in Nicaragua. After no circulation since 2015, DENV3 re-emerged in 2022 with a new lineage (III.B.3.2, emergent, > 2022).

Methods: We compared the clinical characteristics of these two DENV3 lineages confirmed by molecular and serological methods in two pediatric dengue studies in Managua. Sequencing was performed using Oxford Nanopore and Illumina. DENV3 lineages were stratified per Nexstrain, and no co-circulation detected. Immune status (primary [1°] vs secondary [2°] response) was determined by Inhibition ELISA. Outcomes included Severe Dengue [SD] (WHO 2009), DHF/DSS (WHO 1997), shock, plasma leakage (PL), and gallbladder wall thickening (GBWT)—an ultrasound marker of capillary leak not affected by fluid management.

Results: We performed a multivariable logistic regression controlling for immune status, age, and sex. Of 1,317 DENV3 cases, the III.B.3.2 lineage had higher prevalence in 2° infections (71.3% vs. 47.6%; OR 2.73, 95% confidence interval (CI) 2.18-3.43, $p<0.001$). The emergent lineage was independently associated with reduction of GBWT (aOR 0.42, 0.26–0.66, $p<0.001$), PL (aOR 0.20, 0.15–0.26, $p<0.001$), SD (aOR 0.06, 0.04–0.10, $p<0.001$), shock (aOR 0.06, 0.03–0.09, $p<0.001$), and DHF/DSS (aOR 0.08, 0.05–0.14, $p<0.001$). Notably, the III.B.3.2 lineage showed a reduction in all severe outcomes in both 1° and 2° infections. III.B.3.2 exhibited marked phenotypic attenuation compared to III.C.2.1, suggesting that lineage-specific viral factors contribute to modulating clinical outcomes.

Conclusions: These findings underscore the importance of integrated continuous genomic and clinical surveillance.

A-283 First Identification of Dengue and Chikungunya Viruses in Mosquitoes and Concurrent Detection of Dengue Viruses in Human Serum from Nepal, 2023

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Background: Dengue has posed an escalating public health threat in Nepal since its first detection in 2004, followed by chikungunya in 2013. The country has experienced periodic dengue outbreaks and is expanding into climate-sensitive high-altitude regions. A major epidemic occurred in 2023 in central Nepal and spread all over the country. Dengue virus (DENV) and chikungunya virus (CHIKV) share overlapping clinical symptoms and are transmitted by *Aedes* mosquitoes. Until now, no detections of DENV or CHIKV in mosquitoes had been reported in Nepal.

Materials and Methods: This study investigated the presence of arboviruses in mosquito larvae collected from Kathmandu, Bhaktapur, Lalitpur, and Dhading districts during the 2023 dengue outbreak. A total of 105 mosquito pools (20 mosquitoes per pool), comprising *Aedes aegypti* and *Aedes albopictus*, were tested using quantitative real-time RT-PCR. Concurrently, 396 serum samples from febrile patients suspected of dengue were tested by RT-PCR.

Results: Of the 105 mosquito pools, 16 (15.2%) tested positive for DENV and six (5.7%) for CHIKV. DENV-2 was the predominant serotype (11.4%), followed by DENV-3 and DENV-4 (1.9% each), mirroring the pattern observed during the 2023 outbreak. Among 396 dengue suspected cases, 70.2% were confirmed DENV infections. Multiple serotypes (DENV-1, DENV-2, and DENV-3) were identified. DENV-2 (97.5%) re-emerged in Dhading after six years, and DENV-3 was detected for the first time.

Conclusion: This study provides the first evidence of DENV and CHIKV in *Aedes* mosquitoes in Nepal, including high-altitude areas. These findings highlight the importance of integrating mosquito surveillance with human dengue surveillance to strengthen early warning systems and mitigate future arboviral outbreaks.

Keywords: Nepal, Dengue, Chikungunya, Mosquito virus detection.

A-288 Modelling the impact of DENV-ZIKV cross-reactivity in Thailand

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Background: Zika virus (ZIKV) transmission in Asia remains poorly understood. In Thailand, where Dengue virus (DENV) is hyperendemic and ZIKV appears to persist, it remains unclear whether and how cross-reactivity between DENV and ZIKV affects their transmission in the population.

Methods: We developed a deterministic age-structured compartmental model including four DENV serotypes and one ZIKV serotype under a changing demographic background informed by Thailand. We simulated two transmission scenarios: ZIKV introduction into a DENV-endemic population and sustained DENV–ZIKV co-circulation. We considered a range of cross-reactivity assumptions combining varying strengths of temporary cross-protection, which reduced susceptibility, and alternative configurations of antibody-dependent enhancement (ADE), which increased susceptibility and symptomatic risk after protection waned.

Results: In the ZIKV introduction scenario, DENV showed transient suppression followed by resurgence after ZIKV introduction. Suppression duration varied from 0.94 to 11.56 years across cross-reactivity assumptions, and resurgence peaks reached up to 1280 cases per 100,000 population per month. Stronger cross-protection prolonged suppression and generally increased resurgence magnitude, while broader enhancement shortened suppression duration and intensified resurgence. Under co-circulation, DENV remained comparatively stable, whereas ZIKV was much more sensitive to cross-reactivity assumptions. ADE increased mean annual ZIKV burden by about 2.4-fold and shortened recurrence intervals between extreme surges. Cross-protection tended to produce more unstable transmission dynamics over time.

Conclusion: DENV-ZIKV cross-reactivity changes the timing and variability of their transmission, which may complicate the interpretation of surveillance patterns. These findings support joint consideration of age-stratified surveillance and population immunity monitoring in Thailand and similar endemic settings.

A-293 Genomic surveillance of dengue virus during major outbreaks in Nepal

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Background: Gobal rise in dengue virus (DENV) infections calls for a continued vigilance since the Asian region remains more vulnerable to outbreaks and Nepal is no exception to this. However, the molecular characteristics of the circulating DENV remain poorly understood in Nepal.

Methods: We performed DENV serotyping, genotyping, whole genome sequence analysis of the major outbreaks in Nepal during 2022 to 2024.

Results: All four DENV serotypes were detected in Nepal for first the time after 2010. The majority were DENV-1 and-3 in 2022, and DENV-2 in 2023 and DENV-2 and 3 in 2024. Re-emergence of DENV-2 and new introduction of DENV-3 was identified as serotype switching phenomenon during big outbreak in Nepal. Circulating DENV strains belonged to Genotype V of DENV-1, Cosmopolitan Genotype of DENV-2 and Genotype III DENV-3. All of these strains showed a close similarity with DENV strains circulating in neighboring India. DENV-3 had nonsynonymous mutations in NS proteins only, while DENV-1 and-2 had these mutations in all genes. E, NS3, NS4A and NS5 proteins showed higher frequencies of nonsynonymous mutations. Furthermore, there were several critical amino-acid mutations in the E protein region of Nepal-DENV strains compared to current DENV-vaccine strains which may impact the future vaccination strategies.

Conclusion: These findings call for an urgent scaling up of DENV genomic surveillance for dengue control and prevention in Nepal. DENV genotypes with a close relationship with Indian strains suggests for a regional and cross-border coordination and collaboration to fight against growing incidence of dengue.

A-308 Global Climate-Driven Dengue Risk Mapping Using Deep Learning Transformers Under Present and Future Warming Scenarios

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Background: With new vaccines being developed for dengue, understanding when and where they may be most needed is essential for global public health. Accurately identifying the regions at risk for vector-borne, climate-related diseases such as dengue can aid in guiding future prevention and vaccine deployment strategies.

Methodology: In this study, we develop a deep learning framework based on transformer architectures to learn the magnitudes at which climate variables-including but not limited to temperature, rainfall, and humidity-are associated with the highest disease risk. Weekly dengue case data from Vietnam (2000–2018) and multiyear records from Paraguay (for Dengue) form the core epidemiological training sets. These are supplemented with publicly available WHO surveillance data to expand geographic representation and improve model knowledge. A Temporal Fusion Transformer (TFT)–based model is trained to capture nonlinear climate–disease relationships, identify key climate thresholds for each disease, and estimate how far in advance environmental signals predict risk.

Results: These learned climate–risk relationships are then projected onto global gridded climate datasets to generate high-resolution maps of present-day dengue suitability. Using future climate pathways (CMIP6 warming scenarios), we produce forward-looking risk projections that highlight regions where environmental changes may increase transmission suitability. The resulting global risk maps provide an evidence-based tool for identifying emerging hotspots, prioritising surveillance, and informing long-term vaccine strategy and resource allocation.

Conclusion: This work demonstrates the utility of spatio-temporal deep learning models systems for uncovering climate–disease dynamics and supporting proactive public health planning under climate change.

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Revealing Climate-Dependent Drivers of Dengue Transmission: Temperature, Rainfall, and Dry Season Regularity

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Background: Dengue fever continues to pose a significant global health challenge and has increasingly spread into previously non-endemic regions, a trend largely driven by climate change. Despite extensive research, the mechanisms through which climatic factors shape dengue transmission remain insufficiently characterized.

Methods: To address this, we employed a general ODE-based inference (GOBI) framework to examine the effects of temperature and rainfall on dengue incidence across 16 regions in the Philippines. This approach allows for the detection of nonlinear relationships and interactions between climate variables.

Results: We found that higher temperatures consistently increased dengue incidence across all regions. In contrast, the impact of rainfall depends on the regularity of the dry season, an often overlooked climatic variable. In regions with regular dry seasons, rainfall is linked to reduced dengue incidence, possibly due to the disruption of mosquito breeding sites. On the other hand, in regions with irregular dry seasons, rainfall increased incidence, likely by facilitating the formation of additional breeding habitats. Similar patterns were observed when the same analysis was applied to a different geographic setting, further supporting these findings.

Conclusion: These results emphasize that intervention strategies should be guided by region-specific patterns in climatic variables, particularly the differing roles of rainfall under varying dry season regularity, rather than relying on uniform dengue control approaches.

A-317 PRISM-H: A Government-Integrated AI Early Warning System for Dengue Forecasting in Karnataka, India

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Background: Dengue surveillance in India is largely reactive. IDSP and NVBDCP detect outbreaks only after patients present at facilities, closing the window for early intervention. India officially reports around 230,000 dengue cases annually, but true burden is estimated at nearly 300 times that figure due to chronic underreporting. High-burden states lack district-level forecasting to pre-position vector control resources before outbreaks occur. This paper describes development, validation, and deployment of PRISM-H(Platform for Research-Integrated Surveillance and Management of Health), a climate-driven AI early warning system for dengue in Karnataka.

Methods: PRISM-H integrates four data streams: IMD weather &ERA5 reanalysis (temperature, rainfall, humidity); IDSP&NVBDCP case records from 2015 to present; ISRO satellite-derived land-use and NDVI layers; and entomological indices (House Index,Breteau Index) from over 1.2million households. An ensemble of LSTM networks, Negative Binomial Regression, XGBoost, and ARIMA generates probabilistic district,sub-district forecasts with up to four weeks’ lead time, retrained fortnightly. Outputs were validated against 2023–2025 case records and benchmarked against WHO risk thresholds, with independent review by ICMR-NIE and NVBDCP.

Results: The Negative Binomial Regression model scored 0.60 on a cost-sensitive ordinal classification score, penalising missed warnings more heavily than false alarms. The LSTM ensemble achieved 0.72 accuracy on binary outbreak classification using the WHO operational dengue definition. Field teams mapped over 50,000 active breeding sites statewide. Since launch by Karnataka’s Health Minister, the system runs in daily workflows at BBMP and state NVBDCP, covering approximately 67million residents. Expansion pilots are underway in Odisha (8 districts, with PATH) and Andhra Pradesh(RTGS).

Conclusion: A four-week lead time enables proactive larvicide pre-positioning, targeted fogging, and fever clinic activation—shifting dengue response from reactive to anticipatory. PRISM-H shows that government-integrated AI surveillance is achievable in resource-constrained settings. Released as open source and cited in the UN World Cities Report 2024, it provides a replicable model for dengue surveillance across South Asia.

A-318 The Economic Burden of Dengue in Indonesia: Evidence on Disease Severity and Socioeconomic Inequality

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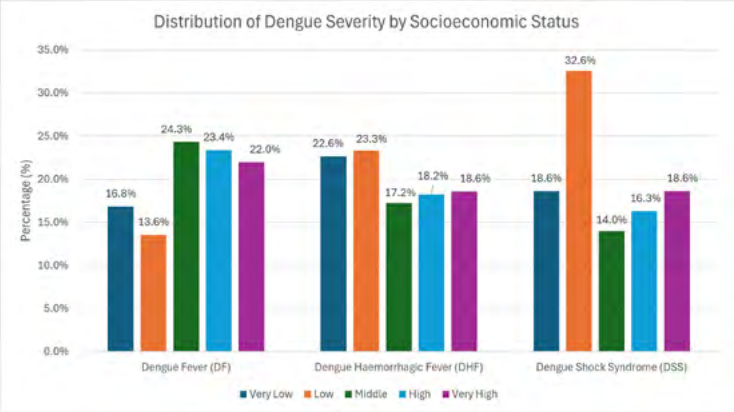
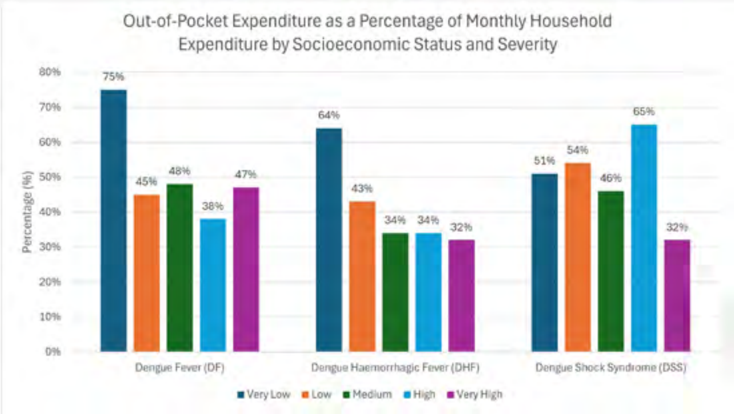
Background: Dengue imposes a substantial economic burden in Indonesia, yet limited evidence exists on how this burden varies across disease severity and socioeconomic groups. This study aimed to estimate the societal economic burden of dengue and examine its variation by disease severity and socioeconomic status.

Methods: A mixed-methods economic burden study was conducted from a societal perspective. Direct medical costs were estimated using administrative and health facility data, while direct non-medical costs and productivity losses were derived from patient survey data (n = 553). All cost components were extrapolated to the national level. The survey data were also used to assess variation in disease severity (DF, DHF, DSS) and out-of-pocket (OOP) burden across socioeconomic quintiles.

Results: The national total annual economic burden of dengue was estimated at USD 549,329,164. Although costs per episode increased with disease severity, DF accounted for the largest share of total burden (53%) due to its high incidence. In the study sample, severe dengue was disproportionately concentrated among lower socioeconomic groups, with the two lowest quintiles accounting for nearly half of DHF cases and more than half of DSS cases. Among surveyed patients, OOP reached up to 75% of monthly household expenditure in the lowest socioeconomic groups.

Conclusions: Dengue imposes a large economic burden in Indonesia. Patient-level findings suggest disproportionate impacts on lower socioeconomic groups through higher severity and financial strain, despite health insurance coverage. Strengthening prevention and financial protection for vulnerable populations is essential.





A-319 A weather-and serotype-informed dengue forecast model in Singapore: an ensemble approach

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Abstract: Dengue poses an increasing threat to global health due to climate change and rapid urbanisation. While numerous models forecast dengue cases, few effectively integrate multiple surveillance data streams. This study evaluates individual and ensemble models combining weather, dengue serotype, and vector breeding data to forecast dengue cases in Singapore across outbreak (2022) and non-outbreak (2023) years, focusing on 2-to 8-week forecast horizons. We developed four individual models (SARIMA, LASSO, random forest, and INLA) incorporating different combinations of climate variables (temperature, rainfall, humidity), serotype switching patterns, and vector breeding index, alongside two ensemble approaches. Individual models performed variably; SARIMA excelled at short horizons (2–4 weeks) but with large uncertainty, while LASSO showed superior 8-week performance but consistently underpredicted cases. Random forest and INLA models effectively utilised serotype dynamics to explain the 2022 outbreak, generating predictions with smallest uncertainty but highest false alarm rates. Ensemble models, combining predictions from all four individual models, consistently ranked high in performance across all horizons and years, with the inverse WIS-weighted ensemble performing best, demonstrating superior case prediction accuracy, reduced bias, and excellent outbreak detection. These results highlight the value of integrating diverse surveillance data sources through ensemble approaches to improve dengue forecast accuracy and reliability for public health decision-making.

A-326 Maternal Acceptability of Longitudinal Saliva-Based Surveillance in Mother-Child Dyads: A Mixed-Methods Study in Kamphaeng Phet, Thailand

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Background: Longitudinal surveillance of dengue and other flaviviruses is often hindered by the invasiveness of repeated blood sampling, particularly in pediatric populations. Saliva-based specimen collection offers a non-invasive alternative, but its success depends on participant acceptability and operational feasibility in long-term monitoring.

Methods: We conducted a mixed-methods study evaluating perceptions of saliva collection among 39 mother-child dyads in a household of dengue cohort in Kamphaeng Phet. The cohort included newborn dyads (monthly collection) and older children (quarterly collection). Assessment involved structured Likert-scale questionnaires and open-ended interviews regarding experience and preferences.

Results: High acceptability was reported across all participants, with 100% stating that saliva collection was easy and painless. While mothers and older children performed self-collection, staff performed infant collection with no reported discomfort. Crucially, for longitudinal monitoring of their children, 46% of mothers explicitly preferred saliva over blood, citing convenience and lack of distress. Although some expressed higher trust in blood-based diagnostics, all participants supported continued saliva-based surveillance.

Conclusion: Saliva-based sampling is a highly acceptable, non-invasive tool for sustainable mother-child healthcare monitoring. Its successful implementation in this longitudinal dengue cohort demonstrates its potential to expand for the routine detection of congenital infectious diseases, such as Zika syndrome. By reducing the physical and emotional burden on dyads, saliva-based surveillance can improve the longitudinal tracking of infectious threats in maternal and neonatal populations

A-328 The dengue epidemic in Brazil is associated with amino acid substitutions in the polymerase of dengue virus type-1

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Background: Among the four dengue viruses (DENV-1 to DENV-4), DENV-1 has been most prevalent cause of dengue over the past 20 years in Brazil. Nonetheless, Brazil experienced a large dengue outbreak in 2024 from DENV-1 transmission. This unexpected surge cannot suggests that genetic changes in DENV-1 rather than low population immunity drove the 2024 epidemic.

Methods: To identify the genetic changes, a time-scaled phylogenetic analysis was conducted using full-length viral genome sequences. Comparative sequence analysis identified nonsynonymous mutations. Infectious clone constructed followed by site-directed mutagenesis were used to reconstruct the epidemic (2024) and endemic (pre-2024) DENV-1, along with single mutants on viral genes of interest. Replication of the endemic and epidemic strains, along with the mutants, were assessed using plaque forming units, plaque diameter and viral replication rates in primary human monocytes.

Results: Epidemic DENV-1 clustered closely on a time scaled-phylogenetic tree with DENV-1 isolated from the 2009 dengue outbreak in Argentina, within lineage E.1; the endemic strains were in lineages A and D.1. Comparative analysis identified 22 nonsynonymous mutations, with 5 amino acid substitutions in the polymerase domain of NS5. Substitution of these 5 amino acid residues individually on the epidemic strain genome significantly reduced plaque size, slowed viral replication kinetics and induced higher levels of interferon-beta expression, replicating the endemic strain phenotype.

Conclusion: These findings suggest that genetic differences in the NS5 protein, at least in part, enhanced epidemiological fitness of DENV-1 and contributed to the magnitude and severity of the 2024 dengue outbreak in Brazil. Mechanistic studies to identify the underpinnings of the phenotypic differences through these substitutions in NS5 are in progress.

A-336 Mapping dengue risk in Singapore: an update on risk-based stratification

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Abstract: Dengue is the most prevalent mosquito-borne viral disease primarily transmitted to humans by *Ae. aegypti* and *Ae. albopictus*. Previously, Singapore's annual dengue risk map utilized random forest based on dengue cases within 1 km 2 grids and quartile risk stratification. This study improved the map to better support government operations by predicting risk groups directly at designated sector while incorporating Gravitrap *aegypti* index (GAI) to better reflect vector abundance. Using a generalized additive model (GAM), we predicted dengue risk in 2025 using sector-level data from 2020-2024, including historical and neighboring dengue burden, cluster burden, annual average GAI and its lag terms, dengue risk threshold based on GAI, total dwelling units, NDVI and housing-related characteristics. Results showed that higher predicted risk groups generally corresponded to higher observed dengue cases counts across 2025. In terms of importance, historical dengue burden and vector-related variables were the strongest predictors, with annual dengue cases lagged by two years, total dwelling units, annual average GAI, and GAI-based cluster-risk indicators ranking highest. These results highlight that the updated map captures broad sector-level gradients in dengue risk and highlights the continued importance of historical dengue burden and vector-related indicators in shaping transmission patterns.

A-337 Ecological Receptivity Outweighs Importation Volume in Determining Potential Secondary Dengue Outbreak Risk in China: A Data-driven Modeling Study

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Background: Dengue fever has become an expanding public health concern globally. Xishuangbanna, Yunnan Province, serves as a critical epicenter for both cross-border and domestic spread. However, quantitative evidence linking human mobility and ecological receptivity with nationwide dengue diffusion remains limited.

Methods: We developed a data-driven, three-stage modeling framework integrating local dengue surveillance data from Xishuangbanna, intercity mobility flows derived from Baidu migration indices, and climate-driven vector-host transmission models. The framework quantified the number, timing, and spatial pattern of dengue importations across 339 Chinese cities in 2023, and evaluated secondary outbreak potential under varying ecological conditions. Model performance was validated by comparing simulated and observed case counts across all cities.

Results: Xishuangbanna reported 7,136 dengue cases in 2023. Simulations estimated 1,180 imported infections nationwide, with two-thirds of cases occurring between July and August. High-risk destinations included Kunming, Shanghai, and provincial capitals of neighboring provinces. Geographic proximity and city income levels were key determinants of importation risk. More importantly, secondary outbreak potential displayed a pronounced non-linear threshold determined by ecological receptivity: in high-transmission regions, a single imported case could trigger epidemics exceeding 1,000 infections, whereas low-transmission areas remained largely unaffected.

Conclusions: Population mobility substantially expands the reach of Dengue beyond its ecological core. Ecological receptivity, rather than importation volume alone, is the dominant factor determining secondary outbreak potential. Focused surveillance and vector control during the July–August high-risk window, particularly in receptive southern hubs, could substantially enhance national preparedness. Grounded in 2023 Xishuangbanna outbreak, this framework offers quantitative, transferable insights for *Aedes*-borne diseases.

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A-347 Spatial structure of dengue transmission in Kamphaeng Phet Thailand

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Background: The endemic circulation of the four serotypes of dengue virus (DENV) results in many discrete and overlapping transmission chains across time and space. As a result, our understanding of the underlying patterns of transmission and drivers of transmission is limited.

Methods: We utilised statistical methods to analyse data over a 25 year period. The data included geolocated case data (N=7,487) that was serotyped alongside a subset of the sequences of the viruses (N=302) that made them sick. The data was obtained from individuals from the largest hospital in Kamphaeng Phet Province, Thailand.

Results: We found that transmission of DENV is localised at distances of up to 5 km, thereby resulting in localised serotype-specific patterns of immunity in the following years. Furthermore, within a 78.5 km 2 area there were 9.6 distinct transmission chains at any time and each 1,000 increase in population size was associated with another 11.2 chains. We also investigated local diversity as a correlate of epidemic size. Although local viral diversity was correlated with epidemic size, its predictive power on epidemic diversity was found to be moderate.

Conclusion: In conclusion, we have used the geolocated case information to shed light on how the ecology of the virus is spatially variable and intricate in endemic settings of considerable immunity. This study emphasises the utility of combining different data sources to understand disease ecology. Notably, the geolocated case information and their corresponding serotype were vital in identifying localised differences in the behaviour of the virus.

A-348 No Sustained Chikungunya Transmission in Singapore 2025 despite multiple importations

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Background: Chikungunya virus (CHIKV) re-emerged in 2025 as a major arboviral threat with >500,000 cases and ~200 deaths globally. As a global hub, Singapore saw increased cases (2025-33 cases; 2024-14 cases). No disease clusters or sustained transmission were reported.

Methods: We analysed cases and CHIKV envelope 1 (E1) gene sequences reported globally (n=3,208) and in Singapore (n=13) to understand case trends, global distribution of CHIKV lineages, likely routes of introductions and transmissibility potential, based on vector-adaptive mutation profiles, spatial distribution of *Aedes* species and historical association with previous local outbreaks.

Results: CHIKV East, Central and South African (ECSA) genotype dominated in 2025, but lineage distribution differed worldwide. ECSA-Indian Ocean Islands lineage (ECSA-IOL; *Ae. albopictus*-adapted E1-A226V mutation) was associated with outbreaks in Indian Ocean Islands and China, while ECSA-Indian sub-continent lineage (ECSA-ISC; *Ae. aegypti*-adapted E1-A226+K211E mutations) mainly circulated in South/Southeast Asia. All Singapore E1 gene sequences in 2025, except one, belonged to ECSA-ISC, suggesting CHIKV lineage introductions from regional countries which are potentially better transmitted by *Ae. aegypti* than *Ae. albopictus* . Integrated vector control, including *Wolbachia*-mediated incompatible insect technique, manages *Ae. aegypti* to a low level across Singapore. However, *Ae. albopictus* abundance is expanding islandwide.

Conclusion: Comprehensive vector control measures with *Wolbachia*-*Aedes* population suppression concomitantly mitigated sustained CHIKV transmission in Singapore in 2025. Continued vigilance remains necessary to prevent future outbreaks, given the persistent risk of virus introductions adapted to both vectors, low population exposure and presence of competent vectors.

A-357 UNITEDengue and DeZi: An integrated genomic surveillance partnership for global arbovirus preparedness

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Background: Dengue epidemics have escalated globally, with 2024 reaching a record 14 million cases. Climate change, including rising temperatures and more frequent intense storms, is expanding transmission geographically, while increased international travel accelerates cross-border spread of mosquito-borne viruses. Despite these pressures, critical gaps persist in arbovirus surveillance and risk assessment. Epidemic potential of viral lineages is often identified retrospectively, regional knowledge gaps in strain evolution and transmission hinder variant risk assessment, and dengue–Zika co-circulation remains poorly understood. To address these gaps, UNited in Tackling Epidemic Dengue (UNITEDengue) was launched in 2012 as a regional arbovirus surveillance research network promoting data sharing and capacity building to strengthen dengue surveillance. Since 2025, with additional support from the Temasek Foundation and Singapore's National Environment Agency, UNITEDengue has expanded to incorporate Zika virus monitoring, enhanced genomic surveillance, and advanced real-time data analysis tools. This effort is further strengthened through partnership with the Wellcome Trust-funded Dengue and Zika Immunology and Genomics Network (DeZi), which connects partners across Asia, Africa, and the Americas.

Methods: UNITEDengue and DeZi programmes aim to strengthen dengue surveillance and risk assessment across participating countries through: (1) harmonised protocols and monitoring; (2) disease burden and serological surveys; (3) innovative diagnostic and predictive tools; and (4) scientific capacity strengthening and knowledge sharing. Together, these activities establish a coordinated, multi-regional framework for arbovirus surveillance and response.

Expected outcomes: Participating countries will implement integrated work packages spanning clinical, serological and genomic surveillance, alongside vector competence studies. These activities will enhance understanding of transmission dynamics, evolution patterns, and disease burden, while strengthening capacity for timely risk assessment. Joint training activities will further build regional technical and analytical capability among partners.

Conclusion: By combining UNITEDengue's established regional network with DeZi's global reach, this partnership creates a collaborative platform for shared tools, data, and expertise, strengthening coordinated arbovirus surveillance and improving global preparedness for future epidemics.

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A-359 Combining vaccination with wMel for dengue control in Brazil

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Background: Dengue is a growing threat to global health, causing severe disease burden across tropical regions. Brazil reports the highest burden of dengue globally, with unprecedented outbreaks in recent years. After decades of few effective tools, novel vaccine and *Wolbachia* technologies offer a potential path to dengue control; however, both technologies have limitations and how best to employ them remains poorly understood.

Methods: We combined subnational estimates of the dengue transmission intensity, demographic projections and intervention efficacy estimates within a stochastic metapopulation model framework to simulate future dengue burden in Brazil. We then evaluated the potential public health impact of different intervention scenarios considering cases, hospitalisations, deaths and DALYs averted.

Results: We estimate that a *Wolbachia* release campaign targeting 300 municipalities could avert 15-26% of cases over the next 10 years, while a vaccination campaign primarily targeting 10 year olds could avert 7-9% of cases in the total population and 60% of cases within the vaccinated cohort. We then considered potential longer-term impacts of *Wolbachia* releases on dengue dynamics finding that, over the next 75 years, scenarios with *Wolbachia* releases could increase population susceptibility and drive up the mean age of dengue cases beyond increases due to ageing populations. Finally, we found preemptive vaccination and *Wolbachia* releases could help to mitigate the future burden in southern Brazil, where climate change is rapidly increasing dengue risk.

Conclusions: These findings highlight the need for public health strategies to consider the two technologies in parallel to optimise combating future dengue burden.

A-360 Lessons from a Large-scale Dengue epidemic in a Non-endemic City of Taiwan: Implications of Differing Spatio-temporal Patterns Between DENV-1 and DENV-2 for the Global Reduction of Severe Dengue

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Background: Temporal heterogeneity from different circulating serotypes of dengue viruses (DENVs) remains underexplored—particularly the role of these differences in driving severe cases in non-endemic areas.

Methods: We analyzed all laboratory-confirmed dengue cases from 2023 in Kaohsiung, Taiwan, where DENV-1 and DENV-2 had been co-circulating. The five districts with the top numbers of DENV-1 and DENV-2 cases were analyzed for their three temporal indices—occurrence, duration, and intensity—to characterize serotype-specific viral transmission patterns.

Results: Elderly patients made up a significantly higher proportion of severe cases than of non-severe cases (87.5% vs. 27.9%; $p<0.0001$). DENV-1 showed uniform and diffuse spread patterns across districts, whereas DENV-2 displayed wide spatial heterogeneity in different districts, consistent with cluster-driven transmission. In districts with larger elderly (> 65 years) populations, both DENV-1 and DENV-2 had lower likelihoods of occurrence and mean duration/wave, but only DENV-1 had increased transmission intensity. This indicated that DENV-1 can have more intensive local transmission in the elderly, even within more limited timeframes. Notably, in districts with severe cases, DENV-1 cases occurred more often and had longer mean duration, whereas DENV-2 cases showed no clear pattern—highlighting prolonged transmission as a potential driver of DENV-1's clinical severity for this epidemic.

Conclusion: District-specific temporal indices provide a sensitive framework for disentangling DENV serotype-specific transmission patterns and high-risk conditions. Adding these temporal metrics into integrated digital surveillance systems can enable earlier and more efficient targeted interventions—limiting prolonged transmission and effectively reducing severe dengue from low-immunity, non-endemic settings like Taiwan to dengue-endemic areas in Asia.

A-367 Managing dengue risk along the China-Laos Railway: An HEDRM approach

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Background: Human mobility drives dengue transmission dynamics, whereas transport network contributes to disease introduction and epidemics in connected populations. Laos experiences recurrent dengue outbreaks, and transport corridors like the China-Laos Railway (CLR) amplifies transmission. Health Emergency and Disaster Risk Management (HEDRM) offers an all-hazards systematic framework to reduce morbidity, mortality, and service disruption.

Methodology: This study used a corridor-based risk-reduction model by integrating targeted vector control with community protection and education along the CLR. From May to July 2024, 871 mosquito lamps were installed along all 29 railway stations, together with widespread display of educational printed media in the form as posters and advertisement in all stations. Multiple surprise on-site visits, cross-sectional interviews, and online surveys were conducted 1-year post-intervention to evaluate intervention effectiveness and dengue education uptake.

Results: On-site observations showed pervasive and continuous use of lamps, with visible insect reduction. 60 interviews were done, and 1243 survey responses from staff and passengers were collected. 69.76% of respondents reported lamps were effective and 73.84% reported fewer mosquito bites 6 months from implementation. Over 90% found the education materials useful. More than half expressed increased knowledge and intention to adopt preventive measures.

Conclusions: The HEDRM approach combining physical dengue prevention and risk communication at this major transport infrastructure was shown to be feasible, acceptable and valuable for reducing mosquito populations and dengue transmission. Results demonstrated positive user outcomes like self-perceived mosquito reduction, which is important to meet community needs for a comfortable living and working environment. The model generated broader system-level benefits. It is a practical and replicable approach to build dengue resilience at high-mobility cross-border corridors, with actionable implications for transport-health policies and practices.

A-376 Dengue Control Strategies in ASEAN: A Systematic Review of Effectiveness Evidence and Evidence-to-Policy Translation

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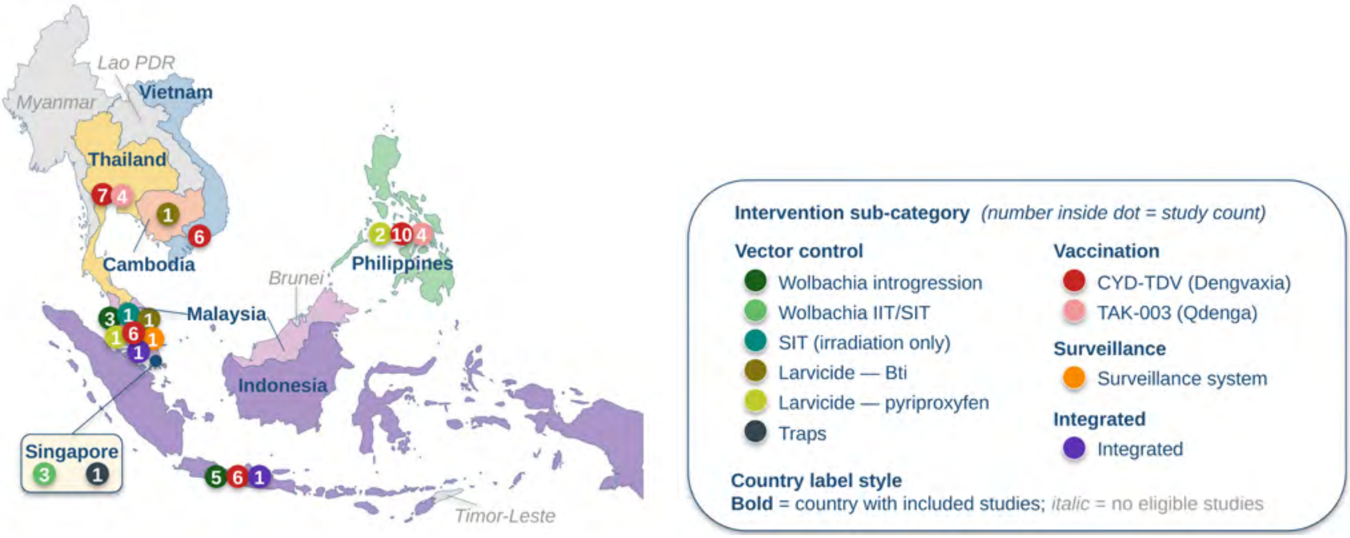
Background: Dengue is among the fastest-growing mosquito-borne viral infections, and ASEAN bears one of the highest regional burdens globally. Multiple interventions have been deployed, yet no prior systematic review has synthesised effectiveness across intervention categories in ASEAN or examined evidence-to-policy translation. This review aimed to (i) map ASEAN's landscape of evaluated dengue interventions, (ii) synthesise effectiveness evidence across intervention categories, and (iii) track research-to-policy pathways across ASEAN.

Methods: This review was registered on PROSPERO and reported using PRISMA 2020. Five databases were searched for evaluations of dengue interventions across ASEAN countries, published from 2015 to 2025, supplemented by citation searching. Risk of bias was assessed using RoB 2 (randomised studies) and ROBINS-I (non-randomised studies). Findings were synthesised narratively following SWiM guidance.

Results: This review included 36 studies from 6 ASEAN countries covering vector control (n=18), vaccination (n=15), surveillance (n=1) and integrated approaches (n=2). Across evaluations, Wolbachia introgression exhibited the strongest evidence with two independent national programmes in Indonesia and Malaysia showing converging effectiveness of 40–83%. Vaccination had the most complete research-to-policy pathway, encompassing CYD-TDV age restriction, pre-vaccination serostatus screening, and TAK-003 regulatory approval. Routine vector control measures were assessed at serious risk of bias, with consistent entomological suppression but limited epidemiological evidence.

Conclusion: The most widely deployed dengue intervention in ASEAN demonstrated the weakest evidence while the newer techniques showed the strongest evidence, exhibiting an inverse evidence-deployment gradient. Future research should prioritise epidemiological evaluation of routine vector controls, harmonise outcome indicators, and expand to under-represented high-burden ASEAN countries.



A-378 Disentangling the Climate Drivers of Dengue in Punjab and Sindh: A Skillfull Rainfall-driven Early Warning System for Pakistan

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Background: Pakistan faces an important dengue burden, with transmission dynamics characterized by regular seasonal outbreaks following monsoon rains and marked interannual variability. Identifying specific outbreak precursors is essential for developing robust predictive tools that can help mitigate regional health crises. This work was done under the ESA GDA Health programme and in collaboration with the Asian Development Bank.

Methods: Bayesian hierarchical models were employed to quantify the relationship between dengue incidence and climate, socioeconomic, and urbanization factors at the district level across Punjab and Sindh, the two most populous provinces in the country. Models were implemented in R-INLA using the GHRmodel package to handle complex spatiotemporal dependencies.

Results: The analysis identified that urbanization covariates shaped the spatial structure of dengue outbreaks, while the combined Standardized Precipitation Index (SPI) during July (monsoonal peak) and September (monsoonal end) were strong predictors of annual dengue incidence. This association was consistently high, explaining more than 50% of interannual variation across all districts. Notably, in Sindh and selected Punjabi districts, monsoon SPI explained ~90% of interannual dengue variability, highlighting an exceptionally rainfall-driven transmission cycle. Based on these predictors, a prototype Early Warning System (EWS) was developed to forecast outbreak intensity. Top-performing models were highly covariate-driven; by utilizing only seasonal without standard spatial or yearly random effects, the system achieved superior out-of-sample performance, greater parsimony, and clearer mechanistic interpretation.

Conclusions: The high sensitivity of Pakistan's dengue dynamics to monsoon rainfall anomalies enables the operation of a reliable EWS. In a region home to nearly 200 million people, these findings provide a scalable framework for climate-informed public health interventions and proactive resource allocation.

A-380 ENSO-driven climate variability reconfigures the altitudinal frontier of dengue risk in the Andes

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Background: High-elevation regions like the Andes or the Himalayas have historically been partly protected from dengue epidemics due to unfavourable environmental conditions for the mosquito vectors. However, the shifting altitudinal limits of dengue transmission remain poorly understood. Understanding these drivers is critical for rapidly urbanizing Asian highland regions facing climate-driven shifts under climate change. This study utilizes longitudinal data from the Colombian Andes to model the mechanics of dengue’s altitudinal expansion.

Methods: Municipal monthly dengue and climate data in the Colombian Andes were analyzed using spatiotemporal decomposition techniques including Singular Spectrum Analysis (SSA) and EOF analysis. Mechanistic modeling was employed to isolate and quantify primary drivers of transmission at the elevational fringe.

Results: We identified a mechanistic cascade linking: (1) El Niño–Southern Oscillation (ENSO) to local climate, accounting for ~85% of interannual temperature variability; and (2) local climate to dengue, explaining ~63–76% of incidence and ~42–55% of its altitudinal range. This effect was dominated by temperature. While ENSO-driven temperature anomalies lack a clear elevational signature, steep non-linear effects in high-altitude fringe cities cause a strong increase in vectorial capacity, which results in an upward shift of the median transmission elevation.

Conclusions: Dengue incidence and transmission altitude expand exponentially in the Andes during warm ENSO phases, producing an upward stretch of the transmission distribution that exposes immunologically naïve populations in highland areas previously considered unsuitable. This suggests that interannual climate variability, rather than gradual warming trends, is the primary driver of altitudinal expansion. This result challenges the prevailing model of incremental altitudinal migration, proving that dengue does not simply extend upward with mean temperatures, but rather surges into high-elevation zones during climate extremes. This study provides a generalizable approach applicable to Asian highland regions facing similar threats from ENSO or the Indian Ocean Dipole.

A-388 Genomic Evidence Linking Dengue Virus from Sabang, Indonesia to a Travel-associated Outbreak in Italy

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Background: Dengue viruses (DENV) continue to spread beyond endemic regions, often facilitated by human mobility. However, genomic data from source locations remain limited, restricting confirmation of transmission. This study aimed to characterize DENV isolates from Sabang, Indonesia and to assess their genetic relationship to global strains.

Methods: A subset of archived febrile patient samples collected from Sabang in 2020 (n=74) was tested for DENV by qRT-PCR. Positive DENV-1 samples underwent whole-genome sequencing. Genomic similarity analysis was performed, and phylogenetic analysis of the Envelope gene was conducted using the obtained sequences alongside available genomic data.

Results: Among tested samples, 19% were DENV-positive. The predominant serotype was DENV-1 (57%), followed by DENV-4 (29%) and DENV-2 (14%), with no detection of DENV-3. Five DENV-1 isolates (Genotype I) were sequenced. Genomic characterization linked the Sabang strains to viruses isolated during outbreak in Italy in 2020. Notably, Sabang DENV-1 isolates exhibited very high genomic similarity (99.9%) to the Italy outbreak strain and formed a tight cluster in the phylogenetic tree, indicating minimal genetic divergence. These viruses belonged to a lineage previously reported in China (2014-2016) and Malaysia (2015-2018) and were closely related to Indonesian isolates from Lampung and Yogyakarta (2019), suggesting persistence and regional circulation prior to its detection in Europe.

Conclusion: These findings demonstrate a strong genomic link between DENV circulating in Sabang and a travel-associated outbreak in Italy, underscoring the role of human mobility in long-distance DENV transmission. Genomic surveillance has proven useful in identifying the origin of pathogens causing outbreaks.

A-389 AI Agent Orchestration as a Novel Platform for Dengue Genomic Epidemiology, Immune Escape Mapping, and Antiviral Target Identification Across 1,000 Asian Genomes

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Background: Despite its importance, comprehensive genomic epidemiology combining phylodynamics, epitope mapping, and drug target analysis is limited in practice by labor-intensive workflows and substantial computational requirements, especially in resource-poor settings. We developed BiomeStat, an AI agent orchestrating bioinformatics tools to autonomously execute this workflow.

Methods: BiomeStat curated 1,000 Asian dengue virus (DENV1–4) genomes (2000–2025) and autonomously executed MAFFT, IQ-TREE, TreeTime, and GPU-accelerated BEAST2 analyses. It further computed Shannon entropy across key viral proteins ((E, NS1, NS3, NS4A, NS4B, NS5), while independently optimizing parameters and correcting software errors.

Results: The effective reproductive number (Re) declined from 1.027 (2000–2005) to 0.979 (2020–2025), indicating stabilized endemic transmission. Of 2,955 amino acid sites, 1,869 (63.2%) were identified as potential immune escape candidates. Among these, 1,355 (72.5%) overlapped with validated IEDB epitopes, with the highest validation rates observed in key proteins: Envelope (79.2%; 317/400), NS1 (73.7%; 151/205), and NS5 (73.7%; 656/890).

In contrast, 176 highly conserved sites (>99.5% identity) were identified as promising pan-dengue antiviral targets. Notably, all 13 binding pocket residues for NS4B inhibitors JNJ-1802 and NITD-688 met this conservation threshold, and no known resistance-associated substitutions were detected across 992 intact NS4B sequences.

Conclusion: Over the past 25 years, dengue transmission has shifted from epidemic expansion to endemic stability, with no detectable pre-existing resistance to NS4B antivirals. AI-driven orchestration overcomes key bioinformatics bottlenecks, enabling comprehensive genomic surveillance at scale and paving the way for routine global implementation.

A-393 Estimating the importation risk of dengue viruses in Hong Kong and its implications for local transmission

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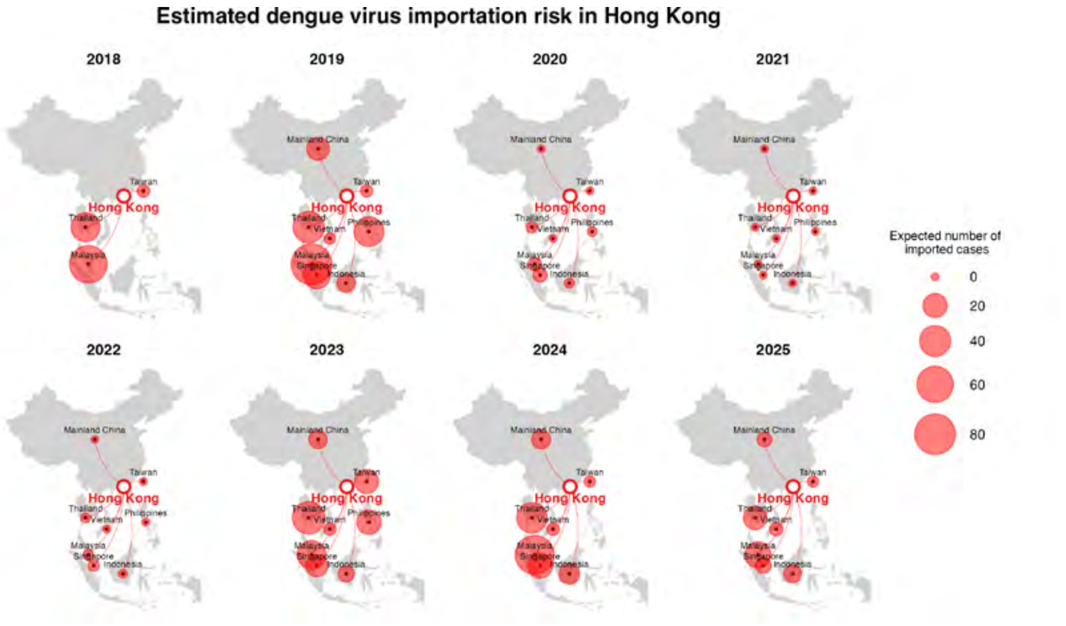
Background: Dengue virus (DENV) remains a significant public health threat in Asia, with international travel facilitating to cross-border spread and potential local transmission. This study estimated the risk of DENV importation into Hong Kong from high-risk countries in South and Southeast Asia across pre-pandemic, pandemic, and post-pandemic periods.

Methods: A probabilistic risk model was developed using country-specific DENV incidence, travel volumes, travel duration, and infection dynamics for eight high-risk countries. Infection probabilities were derived from reported incidence and under-ascertainment by assuming that 18% of infections were symptomatic. A binomial framework was used to estimate infections among travelers, incorporating uncertainty using Bayesian methods with 95% credible intervals (CrI).

Results: Estimated DENV importation varied substantially over time, reflecting changes in travel restrictions and regional dengue activity. During the pandemic (2020–2022), annual imported cases from high-risk countries were low, with an estimate of 3.14 cases (95% CrI: 0.36, 15.2), consistent with remarkedly reduced travel. Following travel resumption, importation risk increased sharply during 2023–2025, with estimates reaching up to 136 cases (95% CrI: 28, 563), driven by restored mobility and concurrent regional outbreaks. Overall, the estimated imported DENV burden in Hong Kong during 2018-2025 was 93.3 cases/year (95% CrI: 23.3, 345).

Conclusion: DENV importation risk in Hong Kong is highly dynamic and shaped by travel patterns and regional epidemiology. Strengthened surveillance, timely risk assessment, and integrated vector control are essential to reduce the risk of local transmission from imported cases.



A-395 Uncovering dengue serotype-specific transmission and cross-reactivity patterns from cross-sectional serosurveys

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Background: Dengue remains a growing global health concern, with four co-circulating serotypes (DENV-1 to DENV-4). Cross-sectional serosurveys are essential for inferring past transmission and population immunity, but serotype-specific interpretation is constrained by broad antibody cross-reactivity.

Methods: We developed a catalytic model explicitly accounting for cross-reactivity to estimate serotype-specific force of infection (FOI) from cross-sectional dengue serosurveys, using serostatus classification alone or combined with titre values.

Results: In simulations, the model effectively recovered FOI and cross-reactivity patterns across varying endemicity levels, sampling designs, and age ranges. Applied to annual cross-sectional serosurveys in Vietnam (2013-2017), the model inferred serotype-specific FOI of similar overall magnitude to previous estimates that required supplementary longitudinal data, while further identifying higher transmission intensity of DENV-3. We also estimated asymmetric cross-reactivity in primary infections, and high probabilities of cross-reactivity to heterotypic serotypes in post-primary infections (96-98%). We reconstructed population immune profiles by age, time, serotype, and infection number, resolving monotypic and multitypic immune components not directly distinguishable from observed seroprevalence. Our estimates showed that susceptibility to secondary dengue infection by each serotype in Vietnam was concentrated in young age groups, peaking at approximately 10 years old. Additionally, the titre-incorporated extension enabled individual-level inference of infection histories, revealing primary-infection titre profiles that varied by infecting serotype despite limited serotype specificity.

Conclusion: These findings show that improved modelling can substantially expand the information recoverable from cross-sectional serology, strengthening the cost-efficiency and public health utility of serosurveys for outbreak preparedness, burden assessment, and vaccination planning.

A-405 18,857 dengue deaths in Brazil: age, comorbidities and deaths in the recovery phase

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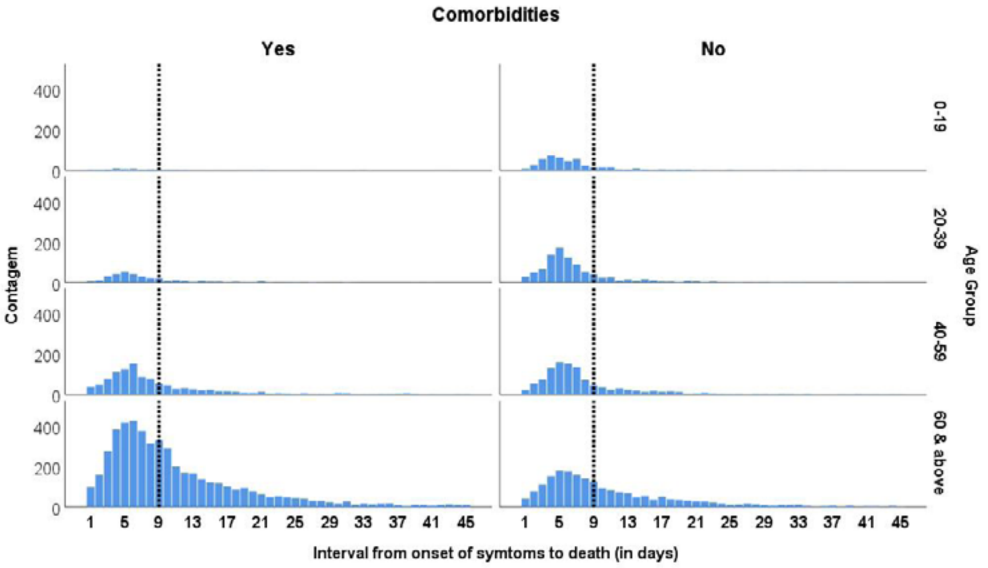
Background: Dengue fever has been endemic/epidemic in Brazil since 1984, and the number of deaths has increased dramatically since 2010. Here, we characterize trends in dengue deaths in Brazil, focusing on age shifts, comorbidities, and the interval to death.

Methods: This is a cross-sectional study using data from the national dengue surveillance system, which includes notification of all suspected cases at public and private health-care facilities. We identified deaths among patients reported and confirmed as dengue cases, according to the WHO 1997 (2000-2013) and 2009 (2014-2025) definitions. Data on demographics, clinical, laboratory, and comorbidity characteristics, and the interval from onset of symptoms to death were analyzed.

Results: 18,857 dengue-related deaths were registered from 2000 to 2025, ranging from 20 in 2001 to 6,395 in 2024. Deaths were initially detected in young adults, but from 2017 to 2025, 59.4% were observed in the elderly, especially in the Central-South regions (median age of 68 years). 64.4% of the deaths occurred during the critical phase. However, among the elderly, 43% of the deaths were observed during the recovery phase. A significantly higher proportion of deaths during the recovery phase was observed when comparing patients with and without comorbidities (40% vs 30%, $p<0.05$).

Conclusion: The increasing number of dengue deaths among the elderly in Brazil highlights the need to understand the determinants and improve case management in these patients, taking comorbidities into account. Deaths were observed during the critical phase, but also during the recovery phase, especially among those with comorbidities.



A-411 From innovation to impact: Surveillance as the discovery engine of a unified framework for dengue control in the WHO South-East Asia Region

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Background: Globally, dengue is escalating rapidly, prompting a multi-region Grade 3 Public Health Emergency in 2024. Cases in the WHO South-East Asia Region have risen 12-fold over a decade. New vaccines, diagnostics, and vector control tools offer unprecedented opportunity. Yet burden continues to escalate despite proven tools and an expanding innovation pipeline, pointing to a critical systemic gap: the absence of epidemiological intelligence to guide when, where, and how any tool is deployed.

Methods: A situational analysis applied the Discovery–Development–Delivery (3D) framework to dengue control in SEAR, repositioning surveillance as the foundational Discovery function, the core system that determines the effectiveness of all tools, proven or novel. Assessment examined how well the surveillance data leads to action, how precisely we target interventions, how we adopt new innovations, and whether the overall system is equipped to deliver real results.

Results: Innovations often face barriers: regulatory gaps, cold-chain complexity, seroprevalence data deficits, and resource constraints. Simultaneously, biologically effective proven methods e.g. larval source management, environmental control etc., fail to achieve expected impact not from biological limitation but from programmatic fragmentation, poor targeting, and absent feedback systems. Both issues stem from the same root problem that surveillance merely counts cases instead of generating actionable insights. In the 3D framework, these ‘Discovery’ gaps undermine development and make it impossible to deliver tools effectively, keeping the outbreak cycle alive.

Conclusion: Maximizing dengue innovation impact while deploying proven tools requires the same foundation: surveillance-anchored epidemiological intelligence. Positioning surveillance as the Discovery engine of the 3D ecosystem - guiding targeted deployment, enabling adaptive programme management, and accelerating innovation integration - is the essential pre-condition for translating scientific advances into measurable public health outcomes.

A-412 Dengue fever in pregnant women in Brazil: 2016-2025

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Background: Dengue fever in pregnant women has been associated with the development of pre-eclampsia, eclampsia, hemorrhage, maternal deaths, fetal deaths, and prematurity. Objective: To characterize probable cases of dengue fever in pregnant women reported in Brazil from 2016 to 2025.

Methods: Descriptive study of sociodemographic, epidemiological, clinical, and laboratory characteristics, using data from the Notifiable Diseases Information System.

Results: Between 2016 and 2025, 123,472 probable cases of dengue fever in pregnant women were reported in Brazil, distributed across the five major regions of the country, with the highest concentration of cases in the Southeast region (48.9%), followed by the South (16.1%), Northeast (15.9%), Midwest (15.6%), and North (3.5%) regions. The annual incidence of dengue fever in pregnant women ranged from 89.5 (2018) to 1969.4 cases per 100,000 live births (2024). Among the probable cases of dengue fever in pregnant women, 83.5% were investigated, 34.9% were laboratory-confirmed, and 1.7% were classified as severe. The predominant serotypes during the period were DENV1 and DENV2. Hospitalization and case fatality rates were 6.9% and 0.6%, respectively. 78.3% of deaths occurred during the critical phase. The risk of death from dengue was higher in the pregnant population than in the non-pregnant women of childbearing age population (risk ratio=1.42; 95% confidence interval (95% CI) =1.20;1.85), being higher in the third trimester of pregnancy (risk ratio=3.16; 95% CI=2.27;4.41).

Conclusion: the results highlight the burden of dengue among pregnant women, their vulnerability to complications and death from the disease.

A-419 DENGUE VIRUS TRANSMISSION CONNECTIVITY IN SALATIGA, A REGION ADJACENT TO WOLBACHIA INTERVENTION SITES IN CENTRAL JAVA, INDONESIA

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Background: Dengue remains a major public health problem in Indonesia with continuous circulation of multiple dengue virus (DENV) serotypes and genotypes. Salatiga in Central Java, Indonesia, is located near Wolbachia implementation areas, including the randomized controlled trial site in Yogyakarta and the pilot Wolbachia project currently in progress in Semarang. However, genomic surveillance data from nearby regions remain limited. This study investigated the genomic epidemiology and phylogenetic relationship of DENV circulating in Salatiga, Central Java, Indonesia.

Methods: A total of 256 dengue patient samples collected in Salatiga during 2023–2025 were screened, and 52 complete DENV genomes representing all four serotypes were successfully sequenced using Nanopore technology. Phylogenetic and genotype analyses were performed and amino acid changes in the envelope region were evaluated to identify unique mutations.

Results: A shift of dominant serotype was observed from DENV-3 during 2023–2024 to DENV-2 in 2025. Multiple genotypes and lineages were identified, including DENV-1 genotypes IV_B, I_K, and I_K.3; DENV-2 genotypes II_F.2, II_F.1.3, and II_C; DENV-3 genotypes I_A and I_A.1; and DENV-4 genotypes I_A.3 and II_A. Phylogenetic analysis showed close relationships between Salatiga isolates and viruses from Yogyakarta, other Indonesian regions, and from surrounding countries. Non-synonymous mutations in the Envelope gene were identified.

Conclusion: DENV circulating in Salatiga showed high genomic diversity and regional transmission connectivity near Wolbachia implementation areas. Continuous whole-genome genomic monitoring is important to understand dengue transmission dynamics and to monitor potential changes in viral genetic diversity in areas with Wolbachia implementation programs in Indonesia.

A-425 Forecasting Dengue in Bangladesh Using Deep Learning Methods

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Abstract: Dengue forecasts can support timely outbreak response and prioritisation of interventions, particularly in resource-constrained settings such as in Bangladesh. The country has experienced increasing dengue transmission in recent years, highlighted by the large nationwide outbreak in 2023 with more than 320,000 reported cases and weekly case counts exceeding 20,000 in September.

In collaboration with the Bangladesh Institute of Epidemiology Disease Control and Research (IEDCR), WHO South-East Asia Regional Office (SEARO), and Imperial College London, we used data on the weekly number of reported dengue cases across 64 districts from 2019 to 2024, district-level population-weighted weekly precipitation data from CHIRPS, and temperature and humidity data from ERA5-Land, to train and tune forecasting models, leaving the 2025 data for model evaluation. We implemented four neural network architectures (TFT, TiDE, NBEATS, and TSMixer), each trained with two sets of hyperparameters obtained by varying the tuning loss function (totalling 8 models). Models were evaluated on the test set across 1- to 8-weeks-ahead forecast horizons using the continuous ranked probability score (CRPS) computed with log transformed case counts.

While there was no single best model across all districts, Time series Dense Encoder (TiDE) had the best average performance across districts and horizons, (mean log CRPS at 4-weeks-ahead of 0.4181 and 0.5177 at 8-weeks-ahead). Mean coverages of the 95% and 50% prediction intervals were 95.37% and 65.30% at 4-weeks-ahead and 90.71% and 60.74% at 8-weeks-ahead.

Forecasts agreed well with the test set. Work is under way to operationalise this forecasting pipeline at the IEDCR.

A-426 Deep learning model ensembles for hierarchical forecasts of dengue in Sri Lanka

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Abstract: Dengue remains a growing concern in Sri Lanka where outbreaks occur annually. Incidence forecasts can help assist intervention and capacity planning, but while well-trained individual models can generate good forecasts, combinations of models (ensembles) can improve performance.

We tuned and trained 12 models, four neural network architectures (TFT, TiDE, NBEATS, TSMixer), three hyperparameter sets each, using the weekly number of dengue cases from 2017-2023 across 26 districts and 34 medical officer of health areas (forming Colombo and Gampaha) provided by the Ministry of Health National Dengue Control Unit (MOH-NDCU). For covariates, we used the Oxford COVID-19 stringency index, temperature, humidity, and precipitation. 52-week forecasts were generated over the 2024 test set (hidden from model training and selection). We combined models by pooling forecast samples, evaluating naïve methods (e.g. pooling all models) and selections based on historical performance.

The best ensemble combined the top five models based on validation set continuous ranked probability score (CRPS), which gave better average performance (test set log CRPS: 0.404) than the best individual model, NBEATS (log CRPS: 0.417). Notably, an ensemble combining all 12 models produced near-best average performance (log CRPS: 0.405), while having the best worst-case performance (max log CRPS in any admin unit: 0.816, versus 0.856 with NBEATS), though prediction intervals (PIs) were conservative (95% PI coverage: 99.3%).

Model ensembles improved both average and worst-case forecast performance. We are developing tools to operationalise ensembles within the MOH-NDCU, allowing regular dengue forecasts which are informing the targeted use of vector control interventions.

A-428 Reconstructing changes in dengue transmission intensity in Bangladesh

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4 Charles Sturt University, Australia, 5WHO SEARO
* joint first author

Background: Dengue has emerged as an increasingly significant public health threat in Bangladesh, with recent years marked by larger and more frequent outbreaks including the largest reported outbreak in 2023. Previous work quantified the intensity of dengue transmission from serological data. This study reconstructs spatiotemporal changes in dengue transmission intensity from case notification data and explores their association with climate.

Methods: We fitted a catalytic model to the age-stratified dengue case data routinely collected by the national surveillance system in Bangladesh from 2022 to 2024 and estimated the time-constant and time-varying FOI (i.e. force of infection, per-capita risk of infection) at district-level.

Results: We find that the total dengue FOI has increased over time across most districts in Bangladesh, with values ranging from 0.004 (95%CrI: 0.004, 0.004) in Chattogram in 2022 to 0.421 (95%CrI: 0.369, 0.478) in Barguna in 2025. The highest seroprevalence at 9 years at the beginning of 2026 was estimated to be 39.8% (95%CrI: 11.8, 67.8) in Jhalokati. Multivariable regression showed no significant correlation between the dengue yearly average FOI and rainfall, maximum temperature and humidity over the study period.

Conclusion: The FOI estimates generated in this study are broadly consistent with the FOI estimates derived from seroprevalence across Bangladesh, which indicates that routinely collected case notification data can be used to reconstruct seroprevalence estimates. The heterogeneity in FOI observed in this study can be used to inform targeted public health interventions, for dengue control planning and outbreak preparedness.

A-433 Integrating Aedes Vector Surveillance into Dengue Early Warning Systems: Evidence from Colombo District, Sri Lanka

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Background: Dengue fever is a rapidly spreading mosquito-borne viral disease in Sri Lanka. Traditional entomological surveillance has limited predictive accuracy, necessitating improved methodologies to predict and mitigate outbreaks.

Methods: This study evaluated temporal associations between adult *Aedes aegypti* vector indices and monthly dengue transmission across CMC-D1, Nugegoda, and Kolonnawa health administrative areas in Colombo District (2019–2022). Adult House Index (AHI), Adult Density (AD), and Resting Ratio (RR) were calculated with data collected using Prokopack aspirators. A Negative Binomial Generalized Linear Mixed Model with log link function analyzed the lagged effects (0–3 months) of a one-unit increase in each index on dengue cases to determine their predictive value for outbreak forecasting.

Results: The analysis showed a consistent temporal pattern, with significant associations occurring at a one-month lag (Lag 1). This suggested increases in vector density one month preceding the occurrence of dengue cases. At Lag 1, AHI showed the strongest temporal association (β: 0.0103; p<0.001), followed by RR (β: 0.006; p<0.001) and AD (β: 0.004; p<0.001). All indices remained statistically significant but weaker at Lag 2 (AHI, β: 0.00660; p=0.012; AD, β: 0.002; p=0.011; RR, β: 0.003; p=0.013) while associations at Lag 0 and Lag 3 were non-significant (p>0.05).

Conclusion: Adult mosquito indices share a robust temporal relationship with dengue transmission, providing the strongest at 1 month, with weaker but significant effects at 2 months. Based on these findings, we recommend incorporating adult entomological surveillance as an early warning tool to enable proactive dengue outbreak management

Key words: Dengue incidence, *Aedes aegypti*, Adult mosquito surveillance, Prokopack aspiration, Vector–disease dynamics

A-436 Primary Dengue Virus Infection in Children from a Hyperendemic Region of Sri Lanka: Incidence, Clinical Outcomes, and Circulating Serotypes

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Background: Although most primary dengue virus (DENV) infections are asymptomatic, a small proportion progress to clinically apparent disease. Understanding factors associated with symptomatic versus asymptomatic primary dengue infection (PDI) is important for identifying determinants of disease susceptibility and transmission dynamics.

Methods: A longitudinal cohort of 4,161 children aged 4–16 years was established in a high dengue transmission area in the Western Province of Sri Lanka. Participants underwent annual follow-up with serological sampling. DENV seroconversion was assessed annually, and infecting serotypes in children experiencing PDI were identified using a Luminex assay incorporating DENV and Zika virus EDIII antigens.

Results: At baseline (2023), 1,051/4,161 (25.3%) children were DENV seronegative. Among these, 243/1,051 (23.1%) seroconverted between 2023 and 2024, while 99/849 (11.7%) seroconverted between 2024 and 2025. Only 10/342 (2.9%) children with PDI developed symptomatic infection. The frequency of PDI did not differ across age groups. DENV-3 was the predominant infecting serotype during both study periods, accounting for 41/192 (21.3%) infections in 2023–2024 and 19/70 (27.1%) infections in 2024–2025, followed by DENV-2. In addition, 26/243 (10.7%) children who seroconverted based on DENV-specific IgG responses showed evidence of Zika virus infection.

Conclusions: Children residing in the Western Province of Sri Lanka experience high rates of asymptomatic primary dengue infection, highlighting intense community transmission. DENV-3 was the predominant circulating serotype, consistent with contemporaneous hospital-based surveillance. The marked reduction in seroconversion rates during 2024–2025 coincided with a large chikungunya outbreak and warrants further investigation.

A-437 Temporal serotype diversification and emergence of DENV-3 driving cyclical dengue dynamics in Angola

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Background: Angola has documented progressive dengue serotype diversification over the past decade: DENV-1 (2013)1, DENV-2 (2017-2018)2, and recently DENV-3 lineage III_B.3.2, in 2024 likely imported from the Americas in late 20223. Each serotype introduction occurred in a population with partial prior immunity, creating successive windows of antibody-dependent enhancement risk. A national surveillance study (Acevedo et al., 2025) described case burden and distribution across 2015-2025.

Methods: We used the retrospective descriptive analysis reported between 2015 and 2025 (Acevedo et. al, 2025), along with previous reports of DENV-1, DENV-2 and DENV-3 emergence and circulation. Temporal trends were assessed using the Mann-Kendall test 4,5. Epidemic phases were delineated descriptively and aligned with published serotype data. Case fatality rate were examined across to assess changes in clinical outcomes over successive serotype eras.

Results: Trend analysis to the surveillance record of 17,063 cases confirms an incidence rise of 193-fold from 0.04/100,000 in 2015 to 7.72/100,000 in 2025 (Acevedo et al.,2025). The Mann-Kendall test showed no monotonic trend ($\tau=0.455$, $p=0.060$), statistically consistent with a rise the cyclical epidemic dynamics1,2,6. Each serotype introduction coincided temporally with a new epidemic peak: 2018 with the surge of DENV-2 (incidence of 8.55/100,000) and 2023-2025 with the introduction and local spread of DENV-3 lineage III_B.3.2 (incidences of 7.95 in 2023 and 7.72/100,000 in 2025) 3. Case fatality rate declined markedly across serotype eras, from a mean of 1.37% during the early DENV-2 period (2017–2018) to 0.09% in the subsequent period (2019–2025).

Conclusion: Angola's dengue epidemiology is shaped by temporal serotype diversification, with each introduction resetting epidemic potential in a partially immune population. The arrival of DENV-3 represents a critical inflection point requiring integrated serological, genomic and epidemiological surveillance to anticipate future serotype-driven resurgences and mitigate the risk of severe dengue at scale in Angola and neighbouring countries.

A-423 Strengthening Infection Prevention and Control (IPC) Systems at Airports with Three-Pillars of Strategic Surveillance in Integrated Multidimensional IPC System

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Background: Airports are point of entries for current re-emerging global health threat, Dengue (Hemorrhagic) Fever. It is strongly influenced by climate change and increased human mobility which poses significant risks for local outbreaks and higher mortality through new strain introduction. The upcoming El-Nino urges a strengthening of Infection-Prevention-and-Control-(IPC)-Systems at Airports to ignite early warning system timely before both erupt.

Methods: Narrative synthesis using 19 studies, 10 Indonesian and international regulations that were published in 2005-2026, were made in 5 major themes; Dengue Epidemiology In Globalisation & Climate Change, Airport IPC-Systems Regulatory Framework, Effectivity of Surveillance Strategy, Integrated IPC-System Architecture, and Emerging Challenges and Future-Preparedness.

Results: The reviewed literature consistently identified globalization and climate change as major drives of dengue epidemiology global expansion. Increased international mobility through commercial aviation has accelerated the spread of vector-borne diseases including dengue fever. Rising climate temperature expands vector habitats, density, and transmission season duration. WHO, ICAO, and IATA internationally regulate implementations of effective IPC system as protection strategies and emergency response coordination. Three-Pillars-of-Strategic-Surveillance: fever screening, rapid NS-1 test, and sentinel-surveillance are more effective than fever screening only in improving outbreak detection. An integrated multidimensional IPC is more effective than multiple isolated interventions. Indonesia faces geographic complexity, unequal healthcare infrastructure, high population mobility, and varying regional emergency response capacity. Global future preparedness strategy should prioritize international collaboration, standardized data-sharing, sustainable IPC-financing, technology-driven surveillance, and adaptive regulatory frameworks.

Conclusion: IPC within international airports remain a critical point of global health security. Existing evidence demonstrates that integrated multidimensional IPC strategies can significantly reduce dengue transmission, new strain spread & mortality risks. Future research is needed to evaluate real-time technological integrated surveillance implementation & long-term efficacy.

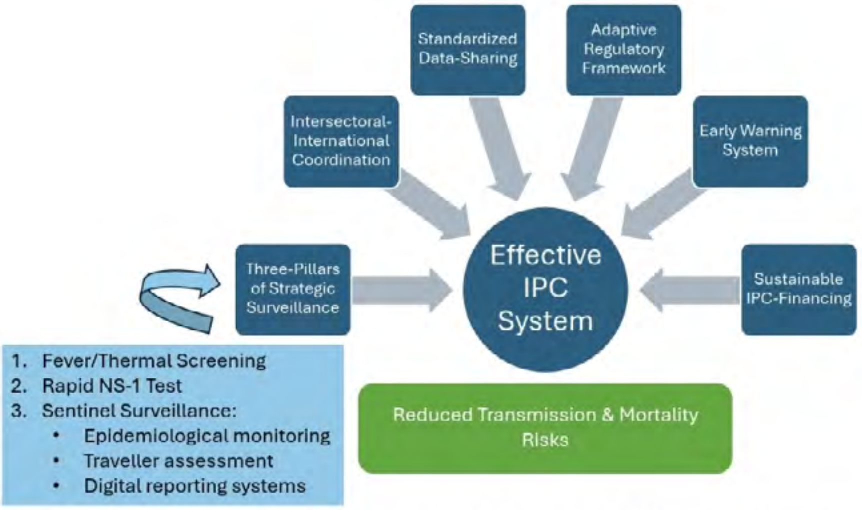

Figure 1. Conceptual Framework of Integrated Multidimensional IPC System as Dengue Surveillance

A-424 Genomic Surveillance of DENV-2 in Kuala Lumpur, Malaysia: Lineage Dynamics of Cosmopolitan Genotype II

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Background: Dengue remains a major public health concern in Malaysia and Southeast Asia. Continuous genomic surveillance is required to monitor lineage dynamics and genotype shifts. This study assessed whole genome sequencing performance and investigated the molecular epidemiology of dengue virus type 2 DENV 2 samples collected from a teaching hospital in Kuala Lumpur in 2024–2025.

Methods: Ninety clinical samples were retrospectively sequenced using Oxford Nanopore technology across two multiplexed runs: 18 samples on a single MinION flow cell over 72 hours, and 72 samples on another over 29 hours. Consensus sequences were aligned with Malaysian and global references, phylogenies inferred with FastTree, and lineages validated using the Genome Detective Typing Tool.

Results: The first run with 18 samples achieved a mean depth of 46,032×, with 231,869 reads per sample (19.5%) passing $Q \geq 20$. The second run with 72 samples reached 3,452×, with 33,752 reads per sample (25.7%) passing $Q \geq 20$, both exceeding the threshold for consensus assembly. Fifty sequences successfully achieved ≥98% coverage. Older Malaysian strains clustered within Genotype VI, while 2014–2015 and 2024–2025 sequences belonged to Cosmopolitan genotype II, forming a homogeneous cluster mainly from lineages F.1.1.3 (n=54) and F.1.1 (n=34). Variant analysis identified a nonsynonymous mutation, V484I, within the transmembrane domain 2 of the envelope gene in the majority of samples (n=72), absent in 2014–2015 strains but observed in those from 2008.

Conclusion: Current DENV 2 populations in Kuala Lumpur are dominated by Cosmopolitan genotype II. Both sequencing runs provided coverage far beyond optimal depth, suggesting that future surveillance workflows could be optimized by increasing multiplexing density and reducing run times.

A-430 Twenty-Six Years of Dengue Surveillance and Viral Change in Cambodia

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Background: Dengue virus (DENV) remains a major public health threat in Cambodia, where recurrent epidemics and sustained transmission continue to burden healthcare systems. Long-term surveillance provides an opportunity to understand shifting epidemiology and strengthen outbreak preparedness. This study characterized demographic, seasonal, and virological trends among hospitalized dengue cases over 26 years.

Methods: Between January 2000 and 17 April 2026, demographic and clinical data from hospitalized patients with suspected dengue were prospectively collected through the Cambodia National Dengue Control Programme across hospitals in all 25 provinces. Serum samples were tested at IPC using RT–qPCR and/or IgM ELISA for laboratory confirmation.

Results: Among 22,955 serum samples tested, 15,200 (66.2%) were laboratory-confirmed dengue cases. Confirmed cases were evenly distributed by sex (50.8% male), while 24.8% presented with hemorrhagic manifestations. Major epidemic peaks occurred in 2007 (1,282 cases), 2012 (1,010), 2019 (858), 2023 (991), and 2025 (1,825), with seasonal amplification consistently observed between July and August. Hospitalized disease remained concentrated among children, although the age profile shifted from predominance in children under 10 years before 2014 toward those aged 10–14 years from 2017 onwards. All four DENV serotypes co-circulated with cyclical replacement, including predominance of DENV-3, DENV-2, and DENV-1 during distinct periods. Early 2026 surveillance suggests renewed DENV-3 predominance.

Conclusion: Dengue in Cambodia is defined by seasonal transmission, shifting pediatric risk, and cyclical serotype replacement. The apparent re-emergence of DENV-3 in 2026 highlights the importance of sustained surveillance for early outbreak detection and timely public health response.

A-431 First dengue outbreak at high altitude in Cochabamba, Bolivia

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Background: Dengue in Bolivia has historically been associated with tropical lowland regions where Aedes aegypti is endemic. However, recent evidence indicates a geographic expansion of the vector into higher-altitude environments. In 2024, Cochabamba (~2,550 m above sea level) experienced its first recorded dengue outbreak.

Methods: Epidemiological and laboratory data from suspected dengue cases were collected between January 2 and July 15, 2024 in Cochabamba, Bolivia. Serum samples were tested for dengue virus using RT-PCR, NS1 antigen detection, or IgM ELISA depending on the day of illness. A subset of positive samples was selected for whole-genome sequencing, and phylogenetic analyses.

Results: A total of 9,576 suspected dengue cases were reported, of which 5,923 were laboratory-confirmed. Cases were detected in municipalities up to 2,719 m above sea level, with the highest burden in Cochabamba city (4,104 cases, 69.3%; 2,558 m) and the highest incidence in Capinota (839 cases per 100,000 population; 2,386 m). Genomic analyses identified DENV-2 genotype II (clade F.1.1.2) as the predominant strain. Phylogenetic reconstruction revealed two distinct clades closely related to strains from southern Brazil, suggesting at least two independent introductions in late 2023. Limited regional genomic surveillance, however, precludes definitive inference of the outbreak's origin.

Conclusion: This study provides the first comprehensive characterization of the 2024 dengue outbreak in Cochabamba, highlighting sustained transmission at unusually high altitudes. These findings support a potential expansion of dengue transmission risk in Bolivia, likely driven by the spread of Aedes aegypti into higher elevations, with environmental and climatic change as potential contributing factors.

A-438 Impact of meteorological factors in dengue incidence during the 2024 outbreak in Chitwan, Nepal

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Background: Meteorological factors likely influence vector breeding and subsequent dengue transmission globally. However, very little is known about the impacts of such factors in Nepal's dengue transmission. Therefore, this study aimed to explore the impact of meteorological factors in dengue incidence in Chitwan, Nepal.

Methods: Dengue cases were defined as those positive by NS1 antigen assay, and 2024 datasets were obtained from Bharatpur hospital. We used daily observations of precipitation, maximum and minimum temperature from Rampur station, Chitwan and analyzed by weekly time-series framework. This harmonized dataset aligned weather exposures and dengue outcomes on a common weekly timescale, facilitating temporal lag analysis and visualization of weather–dengue relationships.

Results: Of the 9914 dengue suspected cases, 1643 (16.6%) were dengue confirmed in Chitwan. Precipitation at maximum lag period of 10 weeks remained as a strong predictor for dengue active cases. Temperature characteristics (TNx, TXn and TNn), had the maximum correlation and minimum p-value observed at lag weeks of 13,16 and 11 weeks, respectively. TNn showed highest dengue cases at 11-week lag period with weekly dengue cases exceeding 180, at temperature range 20.9 – 24.1°C. Similarly, TNx indicated that at lag period 12- and 13-week, maximum weekly dengue cases reached > 120 from 23.4 to 27.1°C.

Conclusion: Precipitation and temperature were found to be the significant drivers for dengue incidence and perhaps the mosquito growth too. Developing early warning systems based on nation-wide weather data is essential for timely prediction and climate-informed policy formulation in Nepal's dengue control.

A-440 Unifying Global Dengue Genomic Surveillance: Actionable Insights through Integrated Tools within the GISAID EpiArbo Platform

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Abstract: We introduce the capabilities of GISAID's EpiArbo platform, designed to overcome the fragmentation of global arbovirus sequence data and provide user-friendly tools for public health teams while protecting the submitters' rights through a transparent auditable record of data usage.

EpiArbo hosts the broadest global coverage of DENV genomic surveillance sequences. Submissions undergo an expert workflow combining automated quality control with expert human curation to standardize metadata and clean sequence inputs. A new key feature of the platform is its capacity to link defined sequence datasets directly to relevant published literature and vice versa enabling easily citable reproducible science.

The platform provides dynamically updated global and regional phylogenetic trees that map viral migration and track the emergence of novel variants and lineages. Users can visualize and track amino acid substitutions mapped directly onto the three-dimensional structures of the Envelope (E) protein, allowing researchers to evaluate potential impacts on vaccine-induced immunity and neutralizing antibody responses.

By combining the world's largest repository of curated arboviral sequences with structural and evolutionary analysis tools, GISAID EpiArbo acts as a critical, open-access bridge between raw genomic sequencing and proactive global outbreak response

B-175 Identification and characterization of global host factors that interact with Dengue virus NS3 protein

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Background: Dengue virus (DENV) NS3 protein, a multi-domain enzyme required for viral genome replication. However, the role in modulating the host cellular landscape remains poorly understood.

Methods: We employed TurboID-based labeling and mass spectrometry approach, to identify protein interactomes associated with DENV NS3 and its catalytic mutant. We performed TRIBE analysis to identify host RNA interactors of DENV NS3.

Results: GFP-DENV NS3 expressed along with GFP nanobody-TurboID to identify the protein interacting partners. GFP control was used to subtract any non-specific background interactions. Proteomics analysis identified only 63 proteins in untransfected cells, while 486 and 530 proteins were captured in GFP-TurboID and GFP-NS3-TurboID confirming a robust labelling of biotinylated peptides. Fold enrichment depicted 30 proteins in GFP-NS3-TurboID which have 5-8 enrichment pathways: retrograde traffic being the most significant pathway. Helicase dead NS3 mutant identified 49 specific proteins. Nine proteins were shared between the WT and mutant NS3 which have 5 enriched hubs, again phosphorylation signaling being the most enriched. TRIBE identified about 800 host target mRNA as targets of DENV-NS3 and showed a strong preference for CDS and CA/CU rich sequences suggesting a potential role in global translation control.

Conclusion: DENV NS3 protein maintains specialized and dynamic interface with the host cell. Wild-type NS3 facilitates viral replication through the modulation of retrograde trafficking pathways, the loss of helicase activity in the catalytic mutant leads to a significant interactome expansion and sequestration within host machinery. We are currently exploring the significance of this interaction with respect to viral infection.

B-198 Dengue virus infection on mitochondrial function and host metabolism

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Background: Dengue is a mosquito-borne acute febrile illness that half the world's population is at risk of, some of potentially fatal severe disease. Dengue pathogenesis involves virus-host interactions, including the balance between metabolism to fuel viral replication and innate immune evasion. Despite this, the role of the mitochondria in dengue pathogenesis remain poorly defined.

Methods: We have started a study using wild-type DENV2/16681 and its attenuated derivative DENV2/PDK53 to dissect metabolic responses responsible for disease. We also used reverse genetics to substitute nucleotide residues in prM and NS1 to create 16681 mutants bearing mechanistically-defined attenuating mutations of PDK53. We over-expressed flag-tagged prM protein to discover host interacting partners of wild-type and mutant prM.

Results: Whole genome microarray analysis showed negative enrichment of genes involved in lipid, carbohydrate metabolism and respiratory electron transport chain in PDK53 compared to 16681 infected cells. These differences were reproduced with the prM but not NS1 mutation on 16681 backbone. Seahorse analysis revealed lowered oxygen consumption in PDK53 infected MRC5 cells and primary monocyte derived dendritic cells. Immunoprecipitation identified CPT1A, a fatty acid oxidation pathway transporter, as an interacting partner of mutant PrM but not wild type prM. Interestingly, PDK53 infected MRC5 cells showed reduced expression of CPT1A, which is also seen in 16681 harbouring PrM and NS1 mutations.

Conclusions: Our findings reveal that altered interactions with host metabolic proteins could underpin dengue pathogenesis. They also suggest the possibility of identifying mutations that alter host metabolism as an approach to discover attenuated DENVs for future vaccine development.

B-211 De novo assembly of DENV infectious clones from reported sequences enables rescue of DENV lethal challenge strains for AG129 mice

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Background: Access to well-characterised dengue virus (DENV) challenge strains for mouse studies is essential for vaccine and pathogenesis research, yet is often constrained by limited access to infectious source material. We sought to determine whether lethal DENV challenge strains could be reconstructed de novo from reported genomic sequences without access to infectious source material.

Methods: cDNA infectious clones were assembled from commercially synthesised DNA fragments derived from reported DENV sequences. Recombinant viruses were rescued in Vero cells and minimally passaged prior to use. Replication kinetics were characterised in vitro, and virulence was evaluated in AG129 mice.

Results: De novo assembly and rescue of infectious DENV were achieved for the candidate strains, DENV4-TVP-376 and DENV2-TW2015. The recovered viruses exhibited robust replication in mammalian and mosquito cell culture. In vivo studies demonstrated that the DENV4-TVP-376 strain reproduced its previously reported lethal phenotype in AG129 mice. The DENV2-TW2015 strain also exhibited a lethal phenotype in AG129 mice, consistent with previous reports of lethality in other interferon signalling-deficient mouse models. Notably, lethal phenotypes were observed using low-passage virus stocks, indicating that lethality is intrinsic to the viral sequences rather than arising from prior adaptation.

Conclusion: De novo assembly of DENV infectious clones from commercially synthesised DNA fragments enables rescue of lethal DENV challenge strains without reliance on infectious source material. This approach enables independent access to well-defined viral strains and provides a flexible platform for downstream investigations into dengue pathogenesis, therapeutic and vaccine evaluation, and reverse genetic analysis.

B-212 Understanding attenuating mutations in the DENV4 PDK48 live-attenuated vaccine candidate

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Background: Tetravalent dengue vaccine development has relied on serendipitous discoveries, some of which have since become licensed vaccines. An example is DENV-2 PDK53, which is now a key component of TAK-003, and was one of the vaccine strain developed by a consortium led by Mahidol University. This consortium also developed DENV-4 PDK48, which phenotypically was similar in attenuation profile as PDK53 in phase 1 clinical trial. Herein, we dissected the attenuating mutations of PDK48, relative to its wild-type parent DENV-4 (1036) strain. **Methods:** We constructed DENV-4 (1036) infectious clone and used site-directed mutagenesis to probe each of the mutation found in PDK48, relative to its 1036 parent in vitro, using both human cell lines as well as primary monocyte-derived dendritic cells. **Results:** We identified a E345K substitution in the envelope (E) protein and G32W substitution in the non-structural 3 (NS3) protein that could each reproduce the small plaque phenotype of PDK48. However, the phenotype of the E E345K mutation alone was not stable in mammalian cells. A second mutation, NS3 G32W substitution also recapitulated the replication kinetics of PDK48 in both Huh7 cells and moDCs. The G32W substitution did not directly impair NS3 protease activity. However, immunoprecipitation studies suggested reduced digestion of host proteins, particularly those involved in translation. **Conclusions:** E345K and A single NS3 G32W are attenuating mutations of PDK48, with the latter impairing interactions between NS3 and host proteins, particularly those involved in metabolism that ultimately altered host response to infection.

B-269 Comparative Analysis of Dengue Virus Serotype 1 Isolates in AG129 Mice: Growth Kinetics, Lethality, and Neurotropism

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Background: Dengue virus serotype 1 (DENV1) periodically drives outbreaks in Singapore when it emerges as the dominant circulating serotype, with distinct genotypes and lineages contributing to each wave. The 2013 outbreak was attributed to genotype III, lineage A, whereas the 2023 outbreak was associated with genotype I, lineages K.1.1 and K.2.

Methods: We compared representative low-passage isolates from these outbreak lineages using in vitro mammalian and mosquito cell culture systems and an in vivo AG129 mouse model.

Results: All isolates exhibited comparable replication kinetics in vitro. However, marked differences in virulence were observed in vivo. Notably, the I_K.2 isolate was uniformly lethal in AG129 mice, causing 100% mortality at inoculation doses ranging from 1×10^6 to 1×10^4 PFU per mouse. In contrast, no lethality was observed for the other isolates. Lethality in I_K.2-infected mice was associated with neuroinvasion. Although the I_K.2 isolate was cleared from systemic circulation by day 4 post-infection, infectious virus was recovered from the brain from day 8 onwards, with higher titres at the humane endpoint. The closely related I_K.2 and I_K.1.1 isolates share 97.63% nucleotide and 98.97% amino acid sequence identity, differing by only 35 amino acid residues. Accordingly, an infectious clone of the I_K.2 isolate was constructed to enable reverse genetic studies to define viral determinants of neuroinvasion in AG129 mice.

Conclusion: These findings demonstrate intrinsic neurotropism of the DENV1 lineages in mice without prior adaptation, raising questions about potential links between these isolates and recent reports of neurological complications in dengue infection.

B-314 An outbreak of secondary dengue infections caused by Dengue virus-4-clade-Id strain results in mild clinical outcomes in the National Capital Region of India

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Background: A new sub-clade of DENV-4 (subclade Id) was reported from other parts of India in recent years with speculations of positive selection driving DENV-4 evolution. But there were no reports to assess whether DENV-4-Id strains have the ability to escape immune responses and have enhanced replication fitness.

Methods: In this cross-sectional study, we tested serum samples from acute febrile illness patients at a tertiary care hospital at the city of Faridabad, National Capital Region, India. Dengue positivity was determined by non-structural protein-1 (NS-1) rapid diagnostic test (RDT). Viral RNA was estimated by qRT-PCR and serotype was determined by nested PCR. Neutralising antibody (N a/b) titers were estimated by microneutralization assay. DENV-4 was isolated from clinical samples by inoculating C6/36 mosquito cell lines and low-passage virus isolates were processed for whole genome sequencing. Growth kinetics of clinical isolates were compared in C6/36 and U937-DC-SIGN monocytic cell line.

Results: 1470 (29·7%) cases out of 4951 tested for Dengue NS-1 were positive and most of the cases were secondary dengue and were classified as mild dengue. 565 out of 874 samples (64·7%) had detectable levels of DENV RNA and majority of the samples were positive for DENV-4. The RNAemia was about three orders of magnitude higher in the case of DENV-4 as compared to our previous studies. DENV-4-Id sequences showed divergence from other DENV-4 clades and 2021 isolates showed slightly better replication efficiency.

Conclusions: DENV-4-Id infections resulted in clinically mild dengue. N a/b levels negatively correlated with RNAemia and high levels of multitypic N a/bs neutralized both circulating and international DENV-4 strains. Cross-reactive cellular and humoral immunity confer protection against severe disease in symptomatic secondary dengue cases. This would be an important parameter to assess vaccine efficacy in the ongoing Phase III trials in India for dengue vaccines.

B-323 Superposition of Cryo-EM and AlphaFold Predictions of Dengue Antigen-Antibody Complexes

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Background: Accurate prediction of antibody–antigen interfaces is essential for structure-based drug design (SBDD) and vaccine development. The dengue virus envelope (E) protein is a major target of neutralizing antibodies and has been extensively characterized structurally. Although deep-learning methods such as AlphaFold have achieved near-experimental accuracy for protein structure prediction with strong multiple sequence alignment (MSA) support, their reliability in predicting antibody–antigen complexes remains insufficiently assessed.

Methods: We selected the dengue virus serotype 2 (DENV-2) envelope (E) protein in complex with the neutralizing antibody 2D22 (PDB: 8Y3H) as a model system. Five independent structure predictions were generated using AlphaFold 3 with minimal constraints, and the resulting models were compared against a high-resolution cryo-electron microscopy (cryo-EM) structure using PyMOL to assess structural discrepancies.

Results: AlphaFold 3 accurately reproduced the global fold of the E protein; however, substantial heterogeneity was observed at the antibody–antigen interface. The predicted complexes clustered into three distinct binding modes, none of which recapitulated the experimentally determined epitope centered on residues A150–154 and A360–364. Moreover, key residue-level interactions observed in the cryo-EM structure were not recovered in the predictions.

Conclusion: These findings demonstrate that while AlphaFold 3 reliably predicts antigen backbone structure, it remains limited in accurately resolving antibody binding sites on flexible viral antigens. This highlights the continued importance of experimental validation and integrative modeling in guiding antiviral antibody and vaccine design.

B-330 Dengue viruses: Four serotypes of one virus or Four different viruses

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Background: The aetiology of dengue is customarily referred to as one dengue virus (DENV) with four serotypes. However, these viruses share only ~60% genetic similarity – making them as different as orthoflaviviral species within the Japanese encephalitis virus complex, such as Japanese encephalitis and West Nile viruses. Thus, these four DENVs may not just be genetically but also phenotypically distinct.

Methods: We explored the phenotype of four DENVs, including the strains within, using infection of a human cell line, A549, as well as primary human monocytes. Bulk RNA sequencing profiled the transcriptomic response to infection with 30 virus strains: nine DENV-1, ten DENV-2, six DENV-3, and five DENV-4 strains. Orthogonal Partial Least Square-Discriminatory Analysis (OPLS-DA), a supervised machine learning algorithm, was used to identify gene expression differences specific to each DENV. The hits were tested again with infection in primary monocytes.

Results: OPLS-DA and pathway enrichment analysis identified unique transcriptomic signatures and pathways, respectively, for each DENV type; cell cycle (DENV-1), antimicrobial response (DENV-2), TNF response (DENV-3), protein folding (DENV-4). Of note is the differential expression of genes involved in antigen presentation, such as IFN-inducible immunoproteasomes (*PSME1, PSMB8*) and HLA molecules (*HLA-A, HLA-B*). Greatest suppression of expression was found in DENV-3 infected cells, potentially explaining the DENV-3 T cell epitope enrichment in structural over non-structural proteins. Similar transcriptional responses were found in DENV-infected primary human CD14+ monocytes.

Conclusion: Infection with each DENV type elicited unique host transcriptomic responses suggesting that the genetic distance between the four DENVs are translated to consistent phenotypic differences.

B-333 N153-linked glycans on the envelope protein of orthoflaviviruses antagonize antibody-mediated host defenses

N153-linked glycans on the envelope protein of orthoflaviviruses antagonize antibody-mediated host defenses

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Abstract: Dengue virus (DENV) poses a significant disease burden globally with an estimated 390 million infections annually. The envelope (E) protein of DENV is glycosylated at two highly conserved asparagine (N) sites (N67 and N153). While the functions of these glycans have been extensively studied in vitro, their biological roles have largely been overlooked in vivo .

A DENV2 mutant lacking N153-linked glycans (N153Q mutant) was engineered and found to be mildly impaired in vitro but drastically attenuated in a symptomatic mouse model of severe dengue, as evidenced by accelerated viral clearance. B cell depletion and knockout (KO) in mouse model restored N153Q parental virulence, suggesting the involvement of B cells in N153Q mutant attenuation. Homologous passive transfer of purified IgM from infected B-cell proficient mice into B cell-KO mice cleared N153Q mutant from blood circulation. *In vitro* neutralization assay using mouse sera showed that WT and N153Q viruses were not significantly neutralized. These data suggest that N153Q mutant attenuation was due to non-neutralizing IgM-mediated viral clearance mechanism. Interestingly, heterologous passive transfer of purified IgM from WT-infected mice into N153Q-infected B cell-KO mice did not clear the mutant, suggesting that infection with WT DENV and N153Q mutant induced distinct antibody repertoires.

These findings represent a novel immune evasion strategy for orthoflaviviruses and have important implications for the development of antibodies, live attenuated vaccine and antiviral.

B-340 Unlocking the Mechanism: A Salivary Gland Transcriptomic Pipeline to Decipher *Wolbachia*-Mediated Pathogen Blocking

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Background: *Wolbachia* is a maternally inherited endosymbiont that can block arbovirus infection in *Aedes aegypti*, though vector competency varies between lines. The transcriptional landscape of salivary glands — the final biological barrier to viral transmission — remains poorly characterised in *Wolbachia*-infected mosquitoes. Utilising two Singapore-outcrossed lines harbouring *Wolbachia* (*w*AlbB-SG and *w*Pip-SG) with distinct vector competencies, we developed a salivary gland transcriptomic pipeline to identify molecular signatures associated with these phenotypic differences.

Methods: Salivary glands were dissected from 7–10-day-old *Aedes aegypti* females from three lines — *w*AlbB-SG, *w*Pip-SG, and *Wolbachia*-free controls. Total RNA was extracted from pooled salivary glands using TRIzol reagent. RNA-sequencing libraries were sequenced on the Illumina NovaSeq platform. Raw PE150 reads were quality-filtered using FastQC/TrimGalore, aligned to the *Aedes aegypti* reference genome (AaegL5) using HISAT2, quantified using featureCounts, and differentially expressed genes identified using DESeq2 (adjusted p-value <0.05). Functional enrichment analysis was performed using GO and KEGG databases (FDR <0.05).

Results: Transcriptomic analysis of *Aedes aegypti* salivary glands revealed significant differential gene expression between *w*AlbB-SG and w Pip-SG. *w*AlbB-SG mosquitoes, which exhibit low vector competence, showed upregulation of innate immune genes — including antimicrobial peptides — and concurrent downregulation of ER chaperones and heat shock proteins. Conversely, *w*Pip-SG mosquitoes, characterised by high vector competence, displayed the inverse gene expression profile. These findings suggest that *Wolbachia*-mediated pathogen blocking involves a dual mechanism whereby immune priming and disrupted ER proteostasis may contribute collectively to the antiviral phenotype.

Conclusion: This salivary gland transcriptomic pipeline successfully identified key molecular differences between pathogen-blocking and non-blocking *Wolbachia*-infected *Aedes aegypti* lines, providing a robust framework for screening *Wolbachia* lines as candidates for vector control applications.

B-353 NS5-565 variation shapes dengue viremia and disease severity through distinct viral mechanisms

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Background: Dengue causes a spectrum of disease from uncomplicated fever to life-threatening dengue shock syndrome (DSS). Although multiple factors influencing dengue outcomes have been studied, the contribution of viral genetic variation to clinical outcomes remains poorly understood. We conducted a viral genome-wide association study (vGWAS) to identify viral variants associated with early viremia and DSS risk in retrospective cohorts in Vietnam (2006–2009).

Methods: We integrated 496 DENV-1 genomes with clinical metadata for vGWAS. Phylogenetic confounding was assessed using a Vietnamese dataset ($n = 917$) and a global dataset ($n = 6,718$). In addition, a human–mosquito dataset was evaluated to assess the ability of variants to persist across host environments. The functional consequences of identified variants were characterized.

Results: The vGWAS identified NS5 residue 565 as significantly associated with early viremia and DSS risk. Viruses carrying arginine (R) or threonine (T) showed higher viremia at DOI 3–4, while R565 was linked to increased DSS risk ($p = 0.025$). These associations remained robust after adjusting for host genetic susceptibility loci, immune status, sex, and age. These variants were distributed across multiple lineage backgrounds, arguing against phylogenetic confounding. Lysine (K565) predominated globally from 1998 to 2021, and human–mosquito passage experiments demonstrated its stability across transmission cycles, supporting compatibility with replication in both hosts. Functionally, R565 exhibited increased NS5 protein stability and accelerated STAT2 degradation compared to K565, indicating enhanced innate immune antagonism.

Conclusion: NS5-565 variation influences dengue viremia and DSS risk through distinct mechanisms involving modulation of innate immune antagonism and replication-associated enzymatic activity. These findings highlight the importance of monitoring functionally distinct viral variants, which may provide insights into viral evolutionary dynamics and their potential impact on disease phenotype.

B-401 NS1 ELISA-based TCID50 test (NSET) using C6/36 cells for estimation of infectious dengue viral load: A promising alternative to focus-forming assay for clinical evaluation of dengue therapeutics

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Background: Dengue is a mosquito-borne disease caused by four dengue virus serotypes (DENV1-4). Productive infection of cultured cells with DENV results in release of viral NS1 protein. This study evaluated the performance and clinical utility of an NS1 ELISA-based TCID50 test (NSET) for infectious dengue viral load estimation.

Methods: The assay involved infecting C6/36 or Vero cell monolayers in 96-well plates with serially diluted serum samples, followed by NS1 detection in culture supernatants on day 7 post-infection using ELISA. Viral titers were calculated by the Reed–Muench method and compared with those obtained by standard viral quantitation methods, focus-forming assay and qRT-PCR.

Results: NSET showed good agreement with focus-forming assay (infectious viral load) and qRT-PCR (total viral load). Among 59 confirmed dengue patient sera, NSET using C6/36 cells showed significantly higher virus detection rate (72.9% versus 47.5%) and viral titers (2.95 versus 2.27 mean log10 TCID50/ml) than Vero cells. Validation studies demonstrated acceptable precision (log10 SD ≤ 0.5), accuracy (log10 bias ≤ 0.5), and strong linearity ($R^2 > 0.95$) across all four DENV serotypes. No cross-reactivity was observed with Japanese encephalitis virus, yellow fever virus, or chikungunya virus.

Conclusion: NSET using C6/36 cells proved to be a sensitive and reliable method for infectious dengue viral load estimation. Its high-throughput, automation-friendly 96-well format and NS1 ELISA endpoint make it a useful alternative to plaque or focus-forming assays, particularly for analyzing clinical samples. The assay shows strong potential for use in clinical evaluation of dengue therapeutics and antivirals.

B-402 Genetic strategies to enhancing chimeric DENV-3/-2 amplification in Vero cells

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Background: The chimeric DENV-3 component of TAK-003, a licensed live attenuated dengue vaccine was constructed by splicing DENV-3 prM and E genes onto the genomic backbone of attenuated DENV-2 PDK53 strain, using restriction enzymes. Limited availability of restriction sites resulted in splicing of only partial wild-type prM and E genes onto DENV-2 PDK53 genome. Here, we compared two chimeric DENV-3/-2 strains, one with partial against another with complete DENV-3 prM/E sequence.

Methods: An infectious clone of DENV-3/-2 chimeric virus, constructed based on published sequence of the chimeric virus used in TAK-003 (hereon referred to as partial DENV-3/-2), as well as another DENV-3/-2 with the full prM and E gene sequence of DENV-3 16562 (hereon referred to as complete DENV-3/-2), were constructed using the Gibson assembly method. Viruses were rescued from the infectious clones in HEK293T cells and expanded in Vero cells.

Results: A single passage of complete DENV-3/-2 yielded 100-fold higher plaque titre (105 PFU/mL) than the partial DENV-3/-2 (103 PFU/mL). Similar findings were made on immunofluorescence microscopy of infected Vero cells. Interestingly, a second passage of partial DENV-3/-2 in Vero cells resulted in 100-fold increase in plaque titre. This increase in plaque titre was associated with two amino acid substitutions in the partial DENV-3/-2 virus – Thr-to-Iie and Ala-to-Val substitutions at position 443 (T443I) and 444 (A444V), on the transmembrane anchor region of the E protein.

Conclusion: Expansion of DENV-3/-2 in Vero cells could benefit from either the use of full length prM and E genes from wild-type DENV-3 16562, or by incorporating T443I and A444V substitutions in the E protein of partial DENV-3/-2.

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B-421 A glutamic acid to lysine substitution on position 203 of the envelope protein attenuates DENV-1 in human cells and Aedes aegypti

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Abstract: Dengue is the most prevalent mosquito-borne viral disease in humans, of which the vaccine development remains challenging due to the incomplete understanding of the molecular basis of viral attenuation. Here, we explored a pair of dengue virus type 1 (DENV-1): the wild-type DENV-1 16007 strain, which was isolated from the blood of a dengue patient, and its attenuated derivative PDK13. PDK13 has been shown to be safe in phase I clinical trial, and poorly infects *Aedes aegypti*, hence posing low to no risk of inadvertent transmission. To identify the genetic determinants of PDK13 attenuation, we constructed infectious clones of wild-type 16007 and attenuated PDK13 via Gibson assembly and used site-directed mutagenesis to generate infectious clones of mutants, each containing a single mutation of PDK13. We found that one single amino acid change from glutamic acid (E) to lysine (K) at position 203 on the envelope (E) protein reduced the plaque size of wild-type 16007 to the same level of attenuated PDK13. Furthermore, similar to PDK13, the E203K mutant was unable to infect *Aedes aegypti* mosquitoes after oral blood feeding. However, E203K substitution was unstable in the 16007 genomic RNA backbone; the lysine residue reversed to the wild-type glutamic acid with serial passage in Vero cells. Collectively, the data suggests E203K as an attenuating mutation, whose stability is dependent on epistasis with other yet to be identified non-attenuating mutations in PDK13.

C-158 Serology alone misclassifies sequential dengue virus infection

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Background: A risk factor for severe dengue is prior dengue virus (DENV) infection, and with the presence of anti-dengue antibodies as the universally accepted standard for determining secondary DENV infection. However, studies of other viruses, such as SARS-CoV-2, have shown that individuals may have detectable T cell responses even without seroconversion. We thus investigated if DENV-specific T cell responses could similarly be detected in DENV-seronegative individuals, as this would fundamentally alter classification of primary/secondary dengue.

Method: We recruited two independent cohorts from Singapore (n = 37; cross-sectional) and Vietnam (n = 49; longitudinally over one-year). Serostatus was determined using anti-dengue IgG ELISA and plaque reduction neutralization testing. T cell responses were assessed using IFN-γ ELISpot and whole-blood cytokine release assay, following stimulation with DENV-derived peptides. Cord blood (n = 7) served as a dengue-naïve control.

Results: At enrollment, 19/37 (Singapore) and 43/49 (Vietnam) individuals were seropositive. DENV-specific T cell responses were detected in 94.7% (n = 18/19; Singapore) and 76.7% (n = 33/43; Vietnam) of seropositive individuals. Remarkably however, DENV-specific T cell responses were also detected in 50% (n = 9/18; Singapore) and 33.3% (n = 2/6; Vietnam) of seronegative individuals. All cord blood controls were negative for T cell responses. Longitudinal analysis of the Vietnam cohort showed that DENV-specific T cell responses significantly expanded over one-year, even among individuals who remained seronegative, suggesting DENV infection without seroconversion.

Conclusions: DENV-specific cellular immunity can be detected in a significant proportion of DENV seronegative individuals. Reliance on serology alone misclassifies sequential dengue infection and has implications on our current understanding of dengue immunopathogenesis.

C-160 Differentiating Humoral Immunogenicity Driven by a Live-Attenuated Tetravalent Dengue Vaccine From Prior Dengue Virus Exposure: Key Highlights of Immunological Advantage of TAK-003 Vaccination

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Background: Dengue virus (DENV) exposure may induce long-term protection against the infecting serotype, sometimes at the expense of systemic inflammation. TAK-003, a live-attenuated tetravalent dengue vaccine, is well tolerated and has been shown to reduce dengue incidence and hospitalization over 4.5 years in the DEN-301 trial (NCT02747927). This exploratory analysis evaluated immunity driven by TAK-003 versus prior DENV exposure.

Methods: Samples from participants in DEN-301 who received 2 doses of TAK-003 (dengue naïve [DN], n=48; dengue exposed [DE], n=48) or placebo (DN, n=12; DE, n=24) were analyzed at baseline, days 120, 270, and 450 for responses targeting envelope/pre-membrane and nonstructural protein 1 of DENV-1–4. Responses included neutralizing antibodies, NS1 IgG, complement-fixing antibodies, avidity, total IgG, IgG1, IgA, and IgM. Biomarkers were compared for magnitude, seroprevalence rates, and valency. Uni-and multivariate methods evaluated antibody profiles, including principal component analysis (PCA).

Results: TAK-003 stimulated multi-typic and diverse humoral immunity in DN participants and boosted existing immunity in DE vaccinees. Kinetics of vaccine-driven immunity differed by prior exposure history, but responses were universally sustained through 1-year post-vaccination. At peak immunogenicity, the valency of responses was comparable between vaccine-driven and preexisting immunity, except for IgM and IgA responses, which were primarily vaccine driven. PCA of the antibody response profile driven by prior dengue exposure and vaccination was comparable.

Conclusion: Our results provide the first comprehensive insight into humoral immunogenicity characteristics of TAK-003, emphasizing similarities and differences from prior DENV exposure, which likely shape the vaccine's safety, efficacy, and immunogenicity profile.

Funding: Takeda

C-179 Antibody-dependent enhancement of dengue virus infection and the effects on host alternative splicing

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Background: Dengue is rapidly expanding due to climate change, increased urbanisation and international travel. While most infections are self-limiting, some infections lead to severe dengue which can be life-threatening. A prominent risk factor for severe dengue is antibody-dependent enhancement (ADE), where cross-reactive antibodies can opsonise dengue virus entry by binding to Fc-gamma-receptors in myeloid cells. Additionally, ADE-mediated infection upregulates expression of RNA splicing genes, many of which are host-dependency factors for dengue virus infection. However, it remains unknown whether ADE-mediated infection can affect host gene splicing, and how these changes may impact dengue virus (DENV) infection.

Methods: Primary monocytes were isolated from a seronegative individual, and infected under mock, unopsonised dengue virus (DENV) or ADE conditions. MobiuSCOPE was used to simultaneously quantify viral and gene transcripts at single cell resolution. The circularisation technology in MobiuSCOPE also provided sensitive detection of splicing events at the single cell level. Bioinformatics analyses was performed using the MARVEL R package. Monocyte subset frequencies, gene expression changes and splicing events were compared between the 3 conditions.

Results: Uniform Manifold Approximation and Projection (UMAP) identified distinct monocyte subsets which can be discriminated by RNA expression of marker genes. The proportion of interferon responsive monocytes was significantly increased under ADE conditions. Spliced junction analyses revealed that more genes were differentially spliced under ADE conditions compared to mock and DENV conditions. Genes that were differentially spliced under ADE conditions also differed from DENV-infection conditions, suggesting that the pathway of DENV infection can affect the splicing landscape. Interestingly, many of these alternatively spliced genes also corresponded with increased gene expression, suggesting a potential role of alternative splicing in regulating gene expression under ADE conditions.

Conclusion: ADE-mediated DENV infection induces differential splicing and transcriptomic responses, providing insights into the molecular processes contributing to DENV pathogenesis under ADE conditions.

C-191 Identifying the impact on NK-cell function of a MICB genetic polymorphism associated with severe dengue

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Background: Early NK-cell dysfunction discriminates patients progressing to severe dengue (SD) from mild dengue, but the mechanisms underlying immune dysfunction remain unclear. Genome-wide association studies (GWAS) identified a single nucleotide polymorphism (SNP) in *MICB* as a susceptibility locus for SD. MICB binds NKG2D expressed on NK/CD8$^+$ T-cells, triggering cytotoxicity. We investigated whether this *MICB* SNP impacts NK-cell responses.

Methods: *MICB* SNP rs3132468 was introduced in K562 cells using CRISPR-Cas9. MICB mRNA and protein expression were assessed using RT-PCR, ELISA, and flow cytometry. Sensitivity of gene-edited K562 cells to NK-cell killing was assessed upon co-culture with NK-92 cells. Samples from 192 Vietnamese dengue patients were genotyped for *MICB* rs3132468 using TaqMan . *Ex-vivo* analyses of patient PBMCs examined the contribution of rs3132468 to NK-cell function and its links to disease outcomes.

Results: The "high-risk" variant of *MICB* rs3132468, associated with SD, leads to decreased MICB mRNA and protein expression in gene-edited K562 cells and renders cells less susceptible to NK-cell killing *in-vitro* . In patients, high-risk *MICB* rs3132468 expression is associated with SD with some features of NK/CD8$^+$ T-cell dysfunction.

Conclusion: Our *in-vitro* findings reveal that *MICB* rs3132468 affects NK-cell cytotoxicity through decreased MICB expression. Consistent with the GWAS results, we demonstrate that *MICB* rs3132468 is associated with SD in Vietnamese patients. Furthermore, we show that *MICB* rs3132468 contributes to shaping NK/CD8$^+$ T-cell responses. Our data suggest that genetic polymorphisms may contribute to immune dysfunction leading to poor viral clearance and increased viremia/inflammation typical of SD.

C-245 Fc-Mediated Antibody Effector Functions Shape Disease Outcome during Secondary Dengue Virus Type 2 Infection

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Background: Our understanding of a protective humoral immune response to dengue virus (DENV) remains limited. Antibodies targeting the envelope (E) protein of DENV have neutralizing potential, but may also exacerbate disease during secondary heterotypic infection. Beyond neutralization, Abs engage Fc receptors to trigger innate immune functions such as antibody-dependent complement deposition (ADCD), antibody-dependent cellular phagocytosis (ADCP), and antibody-dependent cellular cytotoxicity (ADCC). These functions are beneficial but can also induce inflammation. However, our understanding of the temporal evolution of Fc-mediated effector functions during DENV infection, and their contribution to disease severity remains poorly understood. We aimed to characterize the dynamic evolution of antibody Fc-mediated effector functions and assess their association with dengue severity after secondary infection with DENV2 in a Cambodian pediatric cohort.

Methods: We evaluated antibody effector function activities including, Ab-dependent enhancement (ADE), ADCD, ADCP, and ADCC collected from a unique longitudinal cohort with confirmed secondary DENV2 infection during the acute, critical, early recovery, and late recovery phases.

Results: Ab effector functions increased progressively post-infection and declined by two months post-infection, while ADE potency peaked during the early acute phase and decreased in the early recovery. In the acute phase of disease, hospitalized patients exhibited higher ADE and ADCD activities compared to subclinical cases. Finally, the magnitude of ADCD and ADCP, but not ADCC or ADE, correlated to anti-E antibody concentrations.

Conclusion: These findings underscore that the quality and function of Fc-mediated antibody responses, rather than their magnitude, contributes to dengue disease outcomes.

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C-249 The Complement-mediated FRNT Enhances Sensitivity in Measuring Dengue Virus Neutralization Titres

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Background: Dengue virus (DENV) remains a major global public health problem, with limited effective vaccines and no specific treatments. Neutralization assays, including Plaque Reduction Neutralization Test (PRNT) and Focus Reduction Neutralization Test (FRNT), are widely used as correlates of protection in dengue vaccine development. However, these assays often exclude complement system, which enhances antibody function and viral clearance, potentially underestimating protective immunity. This study evaluates the impact of complement to neutralization assays.

Methods: The complement-mediated FRNT (CFNT) was performed by incorporating exogenous active complement source into FRNT assay to account for complement-dependent neutralizing antibodies (CdNAb). NT50 values measure by PRNT, FRNT, and CFNT were evaluated across three groups: PRNT-defined DENV naïve (n=40), monotypic (n=22), and healthy adult donors from endemic-region (n=17). Neutralizing activity was compared across all three assays using both qualitative (NT50<10 as naïve) and quantitative analyses.

Results: NT50 values consistently followed the trend PRNT < FRNT < CFNT across all groups and serotypes. Interestingly, only seven out of 40 (17.5%) and one out of 22 (4.5%) were uniformly identified as naïve and monotypic, respectively, across all assays. While in the endemic group, CFNT have changed immune status of six out of 17 donors (35.3%).

Conclusion: CFNT is the most sensitive assay for measuring DENV neutralization in human serum. The low concordance in identifying naïve samples suggests that conventional assays may underestimate immunity. Adopting higher-sensitivity detection methods is important for the accurate evaluation of vaccines and treatments, as well as improving outbreak surveillance in endemic regions.

C-268 Complement in human serum suppresses antibody-dependent enhancement and potentiates neutralization of dengue virus

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Background: Dengue virus (DENV) infection is a major global health threat, but its immunopathogenesis remains poorly understood. Antibody-dependent enhancement (ADE), in which pre-existing antibodies increase viral infection, is a major concern in DENV immunopathogenesis and vaccine development. While conventional in vitro ADE models are well-established, the role of the complement system in modulating this process remains underexplored. This study investigated how complements in human serum influence DENV infection in the presence of enhancing and neutralizing antibodies.

Methods: Two common cell lines for in vitro ADE models, U937 and K562 cells, were infected with DENV serotype 2. The virus was pre-incubated with various concentrations of dengue antibodies, purified from pooled convalescent serum, under three conditions: culture medium, heat-inactivated human serum, or fresh human serum (as a source of active complement). After 48 hours, infection rates were measured by flow cytometry, and DENV production was quantified by a focus-forming assay.

Results: Both heat-inactivated and fresh human serum significantly reduced DENV infection. In the presence of antibodies, complement activation in fresh serum significantly reduced infection compared to inactive complement in heat-inactivated serum. This effect was especially evident at antibody levels that mediate ADE or only partial neutralization.

Conclusion: Human serum limits DENV infection, and active complement amplifies this neutralizing effect under conditions that typically promote ADE. These findings support incorporating complement into *in-vitro* assessments and motivate validation in primary FcγR/complement receptor-expressing target cells.

C-300 Single-cell viral RNA profiling reveals cell-type–specific infection dynamics during antibody-dependent enhancement of severe dengue

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Abstract: Antibody-dependent enhancement (ADE) exacerbates dengue by increasing dengue virus (DENV) replication and immune dysregulation, yet limited animal models hinder mechanistic insight and vaccine development. We establish an A129 mouse model of ADE-mediated severe dengue using the cross-reactive anti-flavivirus monoclonal antibody 4G2. In DENV-2–infected mice, 4G2 treatment induced an inverse dose–lethality relationship: high doses were protective, whereas low doses increased lethality and disease severity, marked by leukopenia, thrombocytopenia, and elevated viral loads. DENV-2 infection alone was non-lethal. Using liver tissue, probe-based single-cell RNA sequencing with custom DENV-2 genome capture, we mapped cell-type–resolved viral burden and host factors over time. Endothelial cells, Kupffer cells, and hepatocytes were predominantly infected, with highest viral genome copies in endothelial cells. Potential novel cell-type markers —IGFBP1, ZBTB16, and PER1 in liver cells; ARID5A in endothelial cells; and IGFBP7 and SPARC in Kupffer cells—were upregulated in 4G2 group. ADE expanded an angiogenic endothelial subset and coincided with a high–viral-load, matrix-remodeling Kupffer-cells features, implicating macrophage–endothelial crosstalk in vascular pathology. Kupffer-cell responses shifted from interferon-dominated signaling in DENV-2 group to IL-1 signaling in 4G2 group, accompanied by reduced Kupffer-cell abundance and lymphocyte cytotoxicity, consistent with diminished antiviral defense. This model and atlas provide a platform to identify cellular drivers of ADE and evaluate interventions for severe dengue.

C-343 Determining Dengue Serotype-Specific Immunity in Serum Samples: Evaluation of PRNT Alternatives and Automation for Increased Throughput

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Background: The plaque reduction neutralization test (PRNT) remains the gold standard for quantifying dengue-neutralizing antibodies but is limited by low-throughput and manual processing. We evaluated three higher-throughput alternatives – xCELLigence real-time cell analysis (RTCA), MTT-based microneutralization, and the immuno-plaque assay-focus reduction neutralization test (iPA-FRNT) – against PRNT. After identifying iPA-FRNT as the optimal platform, we further optimized ArboDot, an automated foci-counting system.

Methods: All assays were performed on 22 serum samples against a dengue serotype 2 virus (DENV-2). To further assess iPA-FRNT performance, the sample cohort was expanded to 60 samples (30 dengue IgG positive and 30 negative). Automated foci quantification was performed using ArboDot, a custom ImageJ macro-enabling standardized analysis of full 96-well plate images.

Results: iPA-FRNT and xCELLigence RTCA showed the strongest correlation with PRNT 50 titers (R 2 = 0.74 and 0.68, respectively), while the MTT-based assay showed poor correlation (R 2 = 0.47). iPA-FRNT was selected for further validation, demonstrating 100% sensitivity and 93.5% specificity relative to PRNT. To enhance scalability in throughput, automated foci quantification using ArboDot was applied to iPA-FRNT, producing results consistent with manual counting. Performance depended on thresholding and particle size parameters, while contrast optimization ensured consistent FFU/mL values across varying image quality parameters. Overall, automation preserved result interpretation while improving efficiency and throughput.

Conclusion: iPA-FRNT provides a scalable and reliable alternative to PRNT, with high concordance and reduced turnaround time. Integration with ArboDot enhances efficiency and standardization, supporting large-scale applications such as seroprevalence studies where rapid and high-volume sample processing is essential.

C-344 Evaluation of Yellow Fever Virus Serology Assays Against an Orthoflaviviral Co-endemic Background

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Background: Yellow fever (YF) is a vaccine-preventable arboviral disease caused by the yellow fever virus (YFV), an orthoflavivirus alongside dengue (DENV) and Zika viruses. While YFV remains geographically limited to Africa and the Americas, global climate change and human migration patterns threaten to expand its reach. The disease presents diagnostic challenges due to cross-reactive antibodies with other orthoflaviviruses, particularly in endemic regions in Africa where multiple arboviruses co-circulate. Besides the standardised YF IgM serology kit (YF MAC-HD) developed by the United States Centres for Disease Control and Prevention (CDC), several other YFV serology kits are commercially available; however, their performance has not been validated.

Methods: The present study evaluated the performance of six commercially available YFV IgM and IgG assays of two testing platforms, ELISA and indirect immunofluorescence test (IIFT), using 224 febrile samples collected in Ghana, a YFV-endemic country.

Results: All evaluated assays showed moderate to high specificity but low sensitivity. Euroimmun anti-YFV IgM IIFT yielded the highest specificity (100%) with moderate sensitivity of 54.2% compared to virus neutralisation test-confirmed YF MAC-HD ELISA. Abbkine and MyBioSource YFV IgM ELISA showed approximately 50% cross-reactivity with DENV IgM. For YFV IgG detection, all tested kits had low sensitivity (20-45%) but showed acceptable specificity (55-90%), with Euroimmun anti-YFV IgG IIFT giving the lowest false positive rate of 10%.

Conclusion: From this evaluation, commercial YFV serology assays have differing test performances when used in arbovirus endemic settings and serology test results require validation by virus neutralisation test.

C-351 Elevated HLA-DQ expression is associated with high capsid-specific T cell response to yellow fever vaccination that controlled heterologous orthoflavivirus challenge infection in humans

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Background: Neutralising antibodies have long been thought to mediate protection against acute orthoflaviviral infections. We recently showed that in orthoflavivirus-seronegative healthy volunteers vaccinated with live attenuated yellow fever 17D (YF17D) vaccine and challenged with Japanese encephalitis/YF17D chimeric vaccine virus, acute orthoflaviviral infection was controlled to the point of undetectable RNAemia and seroconversion by capsid-specific T cells, independent of neutralising antibodies.

Methods: To understand host immune signatures underpinning T cell response, we profiled whole blood transcriptomics and plasma proteomics.

Results: We found positive enrichment of antigen presentation gene modules in aviremic participants at baseline. Among the leading edge genes, HLA-DQA1 and HLA-DQB1 were most differentially expressed, with higher levels expressed invariantly in aviremic participants compared to viremic participants. Notably, higher baseline expression of HLA-DQ protein was observed in effector memory and TEMRA CD4 + T cells in aviremic participants and negatively correlated with protein levels of VEGFR1 and PGF. PGF binds VEGFR1 to suppress T cell proliferation and promote monocyte activation. Concordantly, lower levels of pro-inflammatory cytokines such as CXCL10, IL6 and IFNg were observed up to day 7 post-vaccination in aviremic participants. Furthermore, HLA-DQ levels positively correlated with CXCL11 and IL7 which have roles in T cell recruitment, proliferation and survival. This was consistent with higher levels of IFNg and granzyme B in aviremic participants on day 10 post-YF17D vaccination.

Conclusion: Our findings add to our recently published data that pre-vaccination immune endotypes may differentiate those that are more likely to develop robust cellular immunity from orthoflaviviral infection/vaccination.

C-352 Reporter Virus Particle Neutralisation Assay for the Quantitation of Yellow Fever Virus-Specific Neutralising Antibodies

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Background: Antigen-specific neutralising antibodies (nAbs) are often measured in vaccine studies, with plaque-reduction neutralisation test (PRNT) as the gold standard. However, PRNT can be labour-intensive, time-consuming, low throughput and depending on the pathogen tested, could require high containment laboratories; use of attenuated strains suffers from inaccuracies due to small plaques. Hence, there is a need to develop alternative neutralisation assays that could circumvent these obstacles. One way is to replace live viruses used in PRNT with reporter virus particles (RVPs). RVPs are antigenically similar to live viruses but have a replication-deficient genome and therefore infection cannot disseminate, allowing RVPs of high-risk pathogens to be used in a BSL-2 laboratory. Furthermore, the subgenomic replicon of RVPs encodes for a reporter luciferase protein that could be used as a standardised and high throughput readout for measuring nAbs.

Method: The Yellow Fever Virus (YFV) RVP neutralisation assay was developed to quantitate YFV-specific nAbs using a luminescence readout. To validate the YFV RVP assay, we evaluated performance specifications including trueness, specificity, repeatability, reproducibility and measurement of uncertainty.

Result: The YFV RVP neutralisation assay demonstrated good intra-assay repeatability and inter-assay reproducibility and trueness with reference to PRNT (<20% coefficient of variation). Furthermore, the YFV RVP neutralisation assay was highly specific, with no cross-reactivity to closely-related flaviviruses including JEV, DENV2, DENV3 or serum matrix components.

Conclusion: This assay would be useful for clinical trials that require a standardised method of evaluating vaccine efficacy and large-scale epidemiological studies measuring seroprevalence.

C-400 Dengue infection elicits durable E-dimer-binding memory B cells responses shaped by infection history and disease severity.

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Abstract: Despite their central role in long-term immunity to dengue infection, the persistence, functional properties and maturation of dengue-binding memory B cells (MBCs) remain poorly defined. The dengue virus (DENV) envelope (E) protein is the major target of the humoral immune response. Here, we characterized soluble E-dimer (sE-dimer)-binding MBCs in a well-defined cohort of patients with hospitalized dengue and their subclinical household contacts, up to one-year post-infection. Flow cytometry and single-cell transcriptomics revealed that hospitalized patients exhibited an enrichment of activated and proliferating sE-dimer-binding B cells at two months post infection compared to subclinical infected cases. By one-year post-infection, sE-dimer-binding MBCs had increased in frequency in both groups. Ex-vivo single-B cell cultures generated 102 monoclonal antibodies (mAbs), one-third of which bound preferentially to the sE-dimer rather than the sE-monomer, indicating selective targeting of conformational epitopes. The most potent DENV2-neutralizing antibodies were sE-dimer specific, DENV2 restricted and primarily derived from subclinical donors, while hospitalized donors showed a higher frequency of serotype cross-neutralizing mAbs, cross-binding sE-monomer/sE-dimer antigens. Secondary infection was associated with increased cross-reactivity and elevated somatic hypermutation rates, suggested germinal center re-entry and further affinity maturation. Together, these findings demonstrate that sE-dimer-binding MBCs are long lasting, occupy distinct B cell subsets, and give rise to antibodies whose breadth and potency are shaped by previous infection history and disease severity. This work provides insight into the dynamics of dengue-binding B cell immunity and informs rational design of E-dimer-based vaccines.

C-409 Serotype-Specific Neutralizing Antibody Responses to Dengue Clinical Outcomes

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Background: Antibody-dependent enhancement (ADE) is a central hypothesis for severe dengue pathogenesis and is conventionally believed to be mediated by cross-reactive, sub-neutralizing antibodies. Dengue vaccines are designed to induce high levels of neutralizing antibodies (nAbs) against the four dengue virus (DENV) serotypes. However, there has been no conclusive evidence that serotype-specific nAbs induced by natural infections are associated with a reduced risk of severe disease.

Methods: We conducted a test-negative design study at the Vung Tau General Hospital in Vung Tau City, Southern Vietnam, from 2020 to 2023. During the study period, we collected serum samples and clinical information from patients suspected of having dengue and laboratory confirmed DENV serotypes. We quantified pre-existing nAbs against all four DENV serotypes using a 50% plaque reduction neutralization test and analyzed their impact on clinical outcomes, including symptomatic infection and hospitalization, using multivariable logistic regression and generalized additive modeling.

Results: We found serotype-specific nAb responses to symptomatic infection and hospitalization. While nAbs conferred protection from symptomatic infection, they were associated with opposing outcomes regarding hospitalization, depending on titer levels and infecting serotypes. Notably, high titers of multi-serotype nAbs were associated with a reduced risk of hospitalization.

Conclusion: We showed that even serotype-specific nAbs have an enhancing effect on hospitalization. Our results suggest that maintaining high titers of nAbs against all four serotypes is crucial for preventing both symptomatic infections and hospitalizations. Our findings refine the current understanding of ADE in dengue pathogenesis and have critical implications for future dengue vaccine strategies.

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C-414 Age-Related Alterations in Humoral Response in Patients with Dengue

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Background: Older adults are at greater risk than young adults of severe dengue. However, how increasing age affect the immune response to dengue virus infection remains to be defined.

Methods: To compare humoral immune responses between old and young dengue patients, we measured DENV-specific antibody, neutralizing activity and antibody-dependent enhancement (ADE in the plasma from older (>=60 years old, n=75) and younger patients (18 to 30 years old, n=75) enrolled at the dengue acute febrile phase with median 3 days of illness and followed up for 3 months.

Results: At enrollment, 111/150 patients were positively detected with DENV-specific IgG. Older patients displayed higher DENV-specific IgA levels ($p<0.0001$). There were no significant differences in neutralizing activity ($p=0.135$) or ADE ($p=0.998$) against the infecting DENV-2 serotype between the two groups. DENV-specific antibody levels were positively correlated with the neutralizing activity but not with the ADE activity. In DENV-2 patients (n=112), virus loads in older compared to younger patients were higher (1.99×10^8 and 2.49×10^7 RNA copies/ml, respectively; $p=0.024$). Viremia was correlated with positively with the ADE activity in both groups, but negatively correlated with the neutralizing activity in older patients.

At 3-month follow-up, DENV-specific antibody levels were comparable between the two groups. However, older compared to younger patients exhibited higher neutralizing antibody levels ($p=0.026$).

Conclusion: Collectively, these preliminary findings provide insight into the differences in humoral immune response to DENV infection in older compared to younger adults, with potential implications for understanding dengue pathogenesis and optimizing vaccine strategies in older populations.

C-434 Heterotypic and Homotypic Neutralizing Responses to DENV-1 in Six-Month-Old Infants: Evidence from Focus Reduction Neutralization Test

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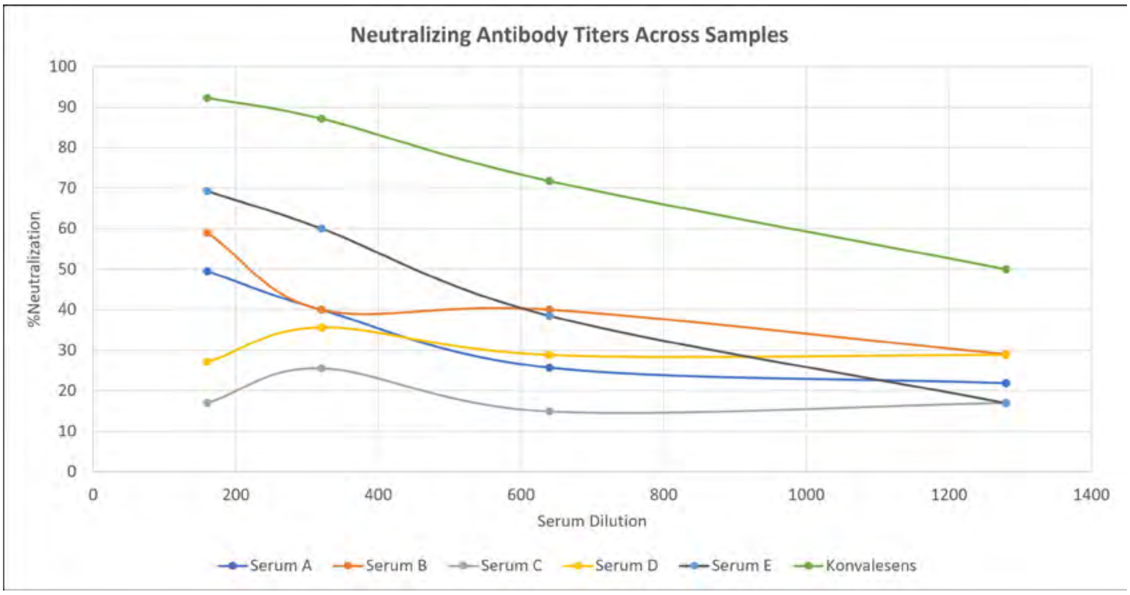
Background: In high-endemic settings such as Indonesia, accurate dengue diagnosis in infants is critical yet challenging, as maternal antibodies may interfere with standard serological assays. Understanding neutralizing antibody profiles in this age group is essential to improve diagnostic accuracy and inform vaccination timing. This study aimed to evaluate DENV-1 neutralizing antibody responses in six-month-old infants with clinical dengue symptoms using FRNT.

Methods: Five infant sera (aged six months) were tested using FRNT against DENV-1, measuring FRNT50 and FRNT90 titers, collected from patients with confirmed DENV-1, DENV-4, and dengue-negative cases. Results were compared against a convalescent-phase serum from a DENV-1-confirmed adult (34 years old, day 7 post-fever onset), as no age-matched convalescent was available.

Results: DENV-1-confirmed infants (Sera A, B) showed low but detectable neutralizing titers (FRNT50: 1/80; FRNT90: 1/10), consistent with early primary infection. The DENV-4 infant (Serum C) demonstrated limited cross-reactive neutralization (FRNT50: 1/40; FRNT90: 1/10). One IgG-positive dengue-negative infant (Serum E) yielded elevated titers (FRNT50: 1/320; FRNT90: 1/20), suggesting maternal antibodies. Serum D showed negligible neutralization. The adult convalescent control showed substantially higher titers (FRNT50: 1/1280; FRNT90: 1/160).

Conclusion: FRNT effectively differentiated active DENV-1 infection, heterotypic cross-reactivity, and maternal antibody presence in six-month-old infants, with notably lower titers than the adult convalescent control, highlighting age-related differences in humoral immunity with implications for infant dengue diagnosis and vaccine strategies.



D-184 Dengue vaccination in Singapore: A modelling study

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Background: Dengue imposes a substantial public health and economic burden in Singapore. Despite sustained vector control efforts, the magnitude and frequency of outbreaks have increased over recent decades. Vaccination has therefore emerged as a promising strategy to complement existing measures. Qdenga (TAK-003), a commercially available dengue vaccine, is recommended by WHO-SAGE for children aged 6–16 years in high-transmission settings. However, translating these recommendations to low-transmission settings like Singapore is not straightforward due to distinct age patterns of dengue burden and the vaccine's complex efficacy profile.

Methods: We developed an age-stratified, multi-serotype compartmental transmission model calibrated to age-specific seroprevalence and surveillance data from Singapore. We projected the impact of introducing a routine vaccination program across different age-targeting strategies under dominant serotype scenarios (DENV-1–4).

Results: Under a 10-year routine vaccination program with 80% coverage, it can avert up to on average 9%, 12%, 7%, and 5% cases in DENV-1–4 dominant serotype scenarios respectively. Hospitalizations can be reduced up to 15% across all scenarios. In Singapore, targeting older age groups is more beneficial than the 6–16-year age group recommended by the WHO-SAGE for high-transmission settings. Vaccinating individuals aged 17–30 years achieves the greatest reduction in cases, whereas targeting those aged 51–70 years leads to the highest reduction in hospitalizations.

Conclusion: Our model-based analysis provides useful insights to support policymakers and public health authorities in designing evidence-based, dengue vaccination strategies in Singapore. The findings also underscore the importance of tailoring dengue vaccination programs to local epidemiological conditions for effective disease control.

D-189 Real-World Safety of a School-Based TAK-003 Dengue Vaccination Program in Indonesian Children: A Prospective Observational Study

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Background: Dengue remains a major public health challenge in Southeast Asia, with Indonesia reporting one of the highest disease burdens globally. Children account for a substantial proportion of dengue-related morbidity and hospitalization. The tetravalent live-attenuated dengue vaccine TAK-003 has demonstrated favorable efficacy and safety in phase III clinical trials, but real-world safety data from large pediatric vaccination programs remain limited.

Objective: To assess the safety and tolerability of two-dose TAK-003 vaccination in a real-world school-based dengue immunization program among children in Kutai Kartanegara Regency, East Kalimantan, Indonesia

Methods: This prospective observational study included children aged 6–12 years receiving two doses of TAK-003 through a school-based vaccination program. Participants were observed for 30 minutes after vaccination for immediate reactions. Parents/caregivers recorded solicited local and systemic adverse events for 28 days using standardized diary cards verified by trained primary health-care workers. Adverse events following immunization (AEFI) were summarized descriptively.

Results: A total of 953 children received the first dose, and 731 completed the second dose. No serious adverse events or vaccine-related hospitalizations were reported. Injection-site pain was the most common local reaction (7.1% after dose 1; 5.0% after dose 2). The most frequent systemic events were fatigue (3.0–3.1%), myalgia (2.5–3.0%), and headache (2.5–2.9%). Overall, AEFI incidence is lower after the second dose (18.6%), and most events were mild and self-limiting.

Conclusion: TAK-003 demonstrated a favorable safety profile and was well tolerated in this real-world school-based program, supporting dengue vaccination in endemic settings.

Keywords: TAK-003; dengue vaccine; AEFI ; children; school-based vaccination

D-192 T-Cell Immunogenicity to TAK-003 in Children and Adults Following Tetravalent Dengue Vaccination: A Comparative Analysis

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Background: TAK-003 is an approved live-attenuated tetravalent dengue vaccine. Phase 3 efficacy was demonstrated in children in dengue-endemic settings. Comparable neutralizing antibody responses in children and adults supported extrapolation of efficacy to adults. As T-cell responses may also contribute to protection against dengue, we assessed TAK-003–induced T-cell responses in baseline seronegative children and adults.

Methods: This exploratory analysis evaluated data from participants who received a 2-dose schedule of TAK-003 on Days 1 and 90 in phase 2 trials (children 4–16 years [n=86], NCT02948829; adults 22–58 years [n=19], NCT02425098) and had a positive T-cell response to peptide pools common to both trials. The peptide pool spanned non-structural (NS) proteins NS1, NS3 and NS5 corresponding to DENV-1,-2,-3 and-4. T-cell interferon-gamma (IFN-γ) enzyme-linked immunospot assay [ELISPOT] was used to analyze T-cell responses. Responses were assessed up to 1 month after dose 2 (Day 120).

Results: At Day 120, the log fold change from baseline in IFN-γ ELISPOT T-cell magnitude against any DENV peptide pool across NS1, NS3 or NS5 did not differ between children and adults ($p=0.413$, two-sided Wilcoxon test). IFN-γ ELISPOT T-cell serotype-specific responses against DENV-1 to-4-matched peptide pools had comparable magnitudes across age groups.

Conclusion: TAK-003 elicited comparable T-cell responses to DENV-1,-2,-3 and-4 in baseline seronegative children and adults. These exploratory findings are consistent with TAK-003-induced comparable humoral immunogenicity across age groups and supports its use in children and adults.

D-196 Envelope protein sequence variation of DENV-3 infections during a phase 3 efficacy study of a live attenuated dengue vaccine

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Background: Dengue disease is caused by four virus serotypes. Takeda's live attenuated tetravalent dengue vaccine (TAK-003) comprises structural proteins from each serotype in an attenuated dengue virus type 2 (DENV-2) backbone. In the Phase III trial DEN-301 (NCT02747927), TAK-003 efficacy was observed against all serotypes in baseline seropositive recipients, varied by serotype in baseline seronegative recipients, with no efficacy against DENV-3 in baseline seronegative recipients and no indication of increased disease severity. The virus envelope (E) protein accumulates intra-serotype genetic diversity, potentially impacting vaccine efficacy.

Methods: This study evaluated the association between antigenic diversity of DENV-3 and outcome of DENV-3 exposure in the DEN-301 trial.

Results: A contemporaneous global picture of DENV-3 population genetics based on E gene sequences from circulating DENV-3 strains in 4 endemic countries, revealed amino acid variations between vaccine and wild-type virus strains/genotypes, that spanned all E protein structural domains. Phylogenetic and regression analysis showed no link between phylogenetic distance, E protein amino acid variation, or burden of E protein genetic diversity, with the outcome of DENV-3 exposure measured by viral load post-infection or dengue hospitalization. TAK-003 driven antibody responses neutralized DENV-3 isolates from regions with DENV-3 infections, similarly to the parental DENV-3 strain.

Conclusion: Antigenic mismatch between vaccine DENV-3 E sequences and the strains causing VCD in the DEN-301 trial is unlikely to be the sole immunological driver for efficacy trends against DENV-3 in seronegative recipients. Post-licensure studies will allow continued surveillance to monitor vaccine performance against the backdrop of DENV sequence diversity and evolution.

D-199 Strategic Implementation and Progress of the Post-Approval Dengue Vaccine Effectiveness Study of TAK-003 Against Hospitalization in Children and Adolescents (DEN-401)

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Background: Takeda's tetravalent dengue vaccine, TAK-003, is approved in >40 countries. The phase 3 DEN-301 (NCT02747927) trial demonstrated overall efficacy but was not powered to assess DENV-3 and DENV-4 in baseline dengue-naïve participants. DEN-401 (NCT06843226), a post-approval study in Southeast Asia, is designed to address these gaps. We present approaches to implement DEN-401 along with study progress.

Methods: DEN-401 is a nested case-control study enrolling ~70,000 children/adolescents. Initiated in 2025, the study will run for ≥3 years. At enrollment, blood samples are collected for all participants to enable later assessment of dengue seropositivity among cases and matched controls. The study seeks to assess TAK-003's effectiveness against hospitalized virologically confirmed dengue, including severe dengue. Participating countries include Thailand (n=35,000; started March 2025), Indonesia (n=30,000; started September 2025), and Malaysia (n=5000; estimated start April 2026).

Study Progress: The study is ongoing, with >80% of the cohort enrolled (as of February 2026). All participants are under active, hospital-based surveillance for ascertainment of hospitalized dengue cases. Status update by country: in Thailand, enrollment is complete (35,000 participants as of December 2025); in Indonesia, 24,022 participants have been enrolled (as of March 16, 2026); and in Malaysia study initiation is planned for April 2026. Vaccination is through public vaccination programs led by country or local public health authorities.

Conclusion: This rigorously designed large study is progressing well from implementation to high-quality data collection through partnerships with health authorities and academics. The results will provide evidence to support decision-making bodies and inform vaccination policy.

Funding: Takeda

D-216 Characterisation of an optimised genome recoded live Zika vaccine candidate

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Background: While the global cases of Zika virus (ZIKV) cases have been declining since the 2015-2016 epidemic, low levels of transmission have persisted in the Americas and Asia. As a WHO priority pathogen with no licensed vaccines or antiviral treatments, ZIKV remains a significant threat, leaving vulnerable populations exposed to potential neurological or teratogenic complications.

Methods: Optimised genome recoding, as opposed to codon pair deoptimization, were used to generate infectious clones and assembled for in vitro screening to identify potential vaccine candidates. Assessment of attenuation was evaluated through intracranial injections in Swiss Webster pups. Protection, immunogenicity, and vertical transmission were evaluation the highly sensitive AG129 and A129 murine models. Crucially, vector competence was also evaluated to validate environmental safety of the vaccine candidate.

Results: Our lead vaccine candidate, VacZen, demonstrated various markers of attenuation in vitro, and absence of neurovirulence in vivo in Swiss Webster pups. Single dose vaccination conferred sterilising protection and elicited robust cellular responses in AG129 mice, and importantly, prevented maternal-fetal transmission in A129 mice. Furthermore, oral challenge in the primary vector, *Ae. aegypti* resulted in zero recovery of the live viruses, confirming a lack of vector competence.

Conclusion: These findings demonstrated the feasibility of an optimised genome recoded live orthoflavivirus vaccine that provides sterilising and maternal-fetal protection. Importantly, absence of vector competence provides a critical ecological safeguard against vaccine strain escape.

D-236 Development of a next-generation live-attenuated DENV2 vaccine strain using genome recoding

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Background: Dengue virus (DENV) poses a major global health burden with no widely effective treatment. Vaccine development is complicated by four antigenically distinct serotypes, requiring balanced serotype-specific immunity, for which live-attenuated vaccines remain most promising, as current chimeric designs produce imbalanced responses.

Methods: This study validates a live-attenuated DENV2 vaccine strain designed by integrating two complementary strategies. First, employment of genome-wide silent mutations to disrupt functional RNA structures and long-range interactions, reducing virus fitness to generate an attenuated vaccine backbone. Second, strategic integration of specific missense attenuating mutations – repurposed from successful orthoflavivirus vaccines – into the recoded backbone, screened for their ability to further enhance attenuation and innate response induction in mammalian cells. A suckling mouse neurovirulence model evaluates in vivo attenuation through intracranial inoculation; while protective efficacy is assessed in adult mice through lethal wildtype DENV2 challenge following immunization, with survival and immune responses measured to determine vaccine-induced protection.

Results: The recoded backbone exhibited reduced plaque size and attenuated replication in mammalian and mosquito cell lines. Addition of a lead missense mutation further suppressed replication and elicited elevated innate interferon responses. In vivo, the candidate strain showed marked attenuation in suckling mice and adult AG129 mice demonstrated strong humoral immune responses, with vaccine-induced neutralizing antibodies protecting against lethal wildtype DENV2 challenge.

Conclusion: This work contributes to DENV vaccine development by offering a novel, dual-strategy live-attenuation approach that enhances safety and innate immunity. The findings support future tetravalent vaccine design, addressing limitations of current candidates and advancing global dengue prevention efforts.

D-251 Long-Term Safety and Cell-Mediated Immunity Before and After Booster of Tetravalent Dengue Vaccine TAK-003 in Healthy Adults in Dengue Nonendemic United States

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Background: The cell-mediated immune (CMI) response likely contributes to long-term protection against dengue. The safety and long-term CMI response following TAK-003 vaccination (2-dose schedule) and a single booster dose were evaluated in healthy adults (18-60 years) in the DEN-303 trial.

Methods: TAK-003 recipients were enrolled in DEN-303 and followed for 36 months post-first dose. At month 36, participants were randomized to receive TAK-003 booster dose or placebo. A CMI subset was evaluated for T-cell responses measured by interferon-gamma (IFN-γ) ELISPOT after dengue virus (DENV) specific peptide pool stimulation at 21, 33 and 36 months post-first dose and 1 and 6 months post-booster. Reactogenicity and booster safety were also evaluated.

Results: Of the 246 DEN-303 enrolled participants, 149 were randomized into the booster phase (TAK-003=74; placebo=75). Fifty participants comprised the CMI subset, with 21 in the booster phase (TAK-003=10; placebo=11). No vaccine related deaths or SAEs occurred during follow up. T-cell responses persisted at 21, 33 and 36 months post-first dose in baseline-seronegative participants, with median magnitudes of IFN-γ/ELISPOT responses to any peptide pool of 696.5 (Q1/Q3=316.0/1421.5), 366.3 (Q1/Q3=122.0/644.5), and 498.8 (Q1/Q3=234.0/1203.0) SFC/million PBMC, respectively. At 1 and 6 months post-booster, median magnitude responses were 420.0 (Q1/Q3=324.0/837.5) and 466.3 (Q1/Q3=70.5/1325.5) SFC/million PBMC, respectively, and in placebo recipients they were 474.5 (Q1/Q3=288.5/1497.0) and 193.0 (Q1/Q3=88.8/300.3) SFC/million PBMC, respectively.

Conclusion: Long-term safety and T-cell immunogenicity of TAK-003 was maintained during 42 months of follow-up, and boosting at 36 months demonstrated modest improvements in durable T-cell responses through the end of the study.

D-264 Development of a non-chimeric live-attenuated Dengue Virus Serotype 3 vaccine candidate

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Background: Dengue virus remains a global threat, with a subset of patients progressing to potentially lethal severe dengue. Despite advances in dengue vaccine development, current chimeric vaccines struggle to achieve balanced protection across all four serotypes. These limitations underscore the need for reliable and rational design approaches for developing non-chimeric live-attenuated vaccines.

Methods: In this study, genome recoding was employed to develop a non-chimeric live-attenuated Dengue Virus Serotype 3 (DENV-3) vaccine strain. This approach introduces numerous synonymous mutations across the viral genome to disrupt key RNA elements, thereby attenuating the virus while preserving the native polyprotein sequence and antigenic epitopes for serotype-specific immunity. In parallel, missense mutations associated with attenuation or immune modulation from existing orthoflavivirus vaccines were evaluated within the recoded backbone. Attenuation was assessed in vitro by plaque phenotype and in vivo using a suckling mouse neurovirulence model. Host interferon responses were evaluated by measuring mRNA expression of interferon-stimulated genes in infected cells.

Results: Attenuation of DENV-3 was demonstrated *in vitro* and *in vivo*. Extensively recoded DENV-3 showed significantly reduced plaque sizes and decreased mortality in intracranially inoculated suckling mice. Introduction of an NS1 mutation within the vaccine backbone not only further improved attenuation in vitro and in vivo, but also enhanced host interferon responses in infected cells.

Conclusion: These findings support the development of a non-chimeric live-attenuated DENV-3 vaccine candidate for potential inclusion in a future tetravalent dengue vaccine and highlights genome recoding as a viable strategy for rational dengue vaccine development.

D-267 An integrative approach to rational engineering of dengue virus-like particles

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Background: Dengue envelope protein dimers (EDE) have been suggested to be important in inducing broadly neutralizing antibodies against all four serotypes of dengue viruses (DENV). With a similar architecture to EDE, DENV virus-like particles (VLPs) are promising vaccine candidates. However, the morphology of DENV VLPs is unstable and heterogeneous in size because they lack a viral genomic core. Since dengue VLPs, like the virion, are enveloped, we suspect that the heterogeneity in VLP morphology is influenced by the interaction of EDE with the lipid bilayer.

Methods: First, the lipid extracted from purified mD2VLPs was subjected to liquid chromatography-tandem mass spectrometry (LC–MS/MS) to determine the lipid composition of VLPs. Guided by the cryo-EM density map of mD2VLP, all-atom (AA) models were constructed through extensive molecular dynamics (MD) simulations to probe the protein-lipid and protein-protein interactions between E and M dimers that govern particle stability. Guided by molecular simulations, site-directed mutagenesis (SDM) was introduced, and a series of experiments was performed to evaluate the VLPs' secretion efficiency, their morphology, and antigenicity.

Results: The lipidome profiling revealed two types of lipids extracted in the highest quantity from purified VLPs: diacylglycerols (DGs) and fatty acids (FAs). To understand how the lipid composition interacts with EDEs, the mutations at critical sites along the E-H1 helix were simulated. The SDM results suggested that both double-and triple-leucine mutant mD2VLPs produced ~2-fold greater secretion in comparison to mD2VLP. 500-ns AA-MD simulations of the double-or triple-leucine mutants of the EDE of mD2VLP in a DG-dominant lipid bilayer revealed a stable and folded E-H1 helix with increased E-H1 lipid interactions. Furthermore, the double-mutant sample exhibits a single size peak and improved antibody accessibility, indicating more uniform particles with clear symmetry.

Conclusions: This work highlights the role of envelope protein-lipid interactions in maintaining VLP stability and yield, guiding engineering of improved VLP-based vaccines.

D-282 Durability of AS01 adjuvant driven effects on T-cell response to vaccination in older adults – lessons for dengue

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Background: There is growing evidence that TAK-003 vaccination protects against dengue through antigen-specific T-cells. As the burden of dengue shifts towards older adults, dengue vaccination in this population may be warranted. However, the response of an aging immune system to vaccination may be blunted. Recently, we and others have found that the first dose of AS01 B-adjuvanted zoster vaccine (Shingrix) alters innate immune pathways to enable strong T-cell responses to the second dose of Shingrix; cellular immunity has been associated with protection from shingles. Herein, we ask whether those who have received Shingrix sustained innate immune reprogramming to enhance immune response to TAK-003 vaccination in older adults.

Methods: Immunocompetent adults (50-65 years old) were enrolled 4 years ago(N=14) to receive 2 doses of Shingrix. Transcriptional profiling was conducted pre-and post-dose 1, as well as 4 years after vaccination. As a control, we also enrolled similar aged adults(N=14) to receive the live attenuated shingles vaccine, Zostavax.

Results: At 60 days after dose 1 of Shingrix, genes in neutrophil-enriched, monocyte-enriched, and TLR-related pathways were reduced in expression, which were associated with higher T-cell response to dose 2. Such reprograming of innate immune genes were not seen in those that received Zostavax. However, at 4 years after vaccination, the expression of these genes reverted to resemble those that received Zostavax, suggesting that the effects of AS01 in enhancing cellular immune response to vaccination is transient.

Conclusion: Prior Shingrix vaccination is unlikely to enhance immunogenicity of TAK-003 in older adults.

D-290 Safety of a Mass Dengue Vaccination Campaign with Qdenga® (TAK-003) in Thailand: Evidence from a Hybrid Active–Passive Surveillance System

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Background: Real-world, post-licensure safety data are essential to inform large-scale dengue vaccination programmes. Following the introduction of Qdenga® (TAK-003) in Thailand, safety monitoring under routine programme conditions remains limited.

Methods: We conducted a multi-site study of adverse events following immunisation (AEFI) during a mass vaccination campaign among children aged 7–10 years in three provinces. A hybrid surveillance system was implemented, comprising active monitoring for 30 minutes post-vaccination in clinical settings and passive reporting of events occurring within 28 days through the national AEFI surveillance system. Incidence rates were calculated per 1,000 doses and summarised by dose, timing, and clinical characteristics.

Findings: 18,690 first doses and 16,884 second doses were administered. AEFI were more frequently reported after the first dose than the second (8·4 vs 3·4 per 1,000 doses). Most events occurred within 7 days of vaccination (75% after dose 1; 44% after dose 2) and were predominantly mild and self-limiting. Systemic and unsolicited events were most commonly reported, while dermatological events were infrequent (1·12 vs 0·30 per 1,000 doses). Immediate reactions under direct clinical observation were infrequent, and no anaphylaxis was identified. Hospitalisation was rare, and all cases recovered without sequel*ae.* No clustering of specific adverse events or unexpected safety patterns was observed, and findings were consistent across sites.

Conclusion: In this large-scale, programmatic, post-licensure setting, Qdenga® demonstrated a favourable safety profile under a hybrid active–passive surveillance system. The absence of serious or unexpected safety signals, including under direct clinical observation, supports the continued implementation of dengue vaccination programmes in endemic settings.

D-302 Clinical Impact of Childhood and Adolescence Dengue Vaccination in Indonesia: A Dynamic Transmission Modeling Approach

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Background: Indonesia is estimated to be among the countries with the highest dengue disease burden in the world. Multiple mathematical models have investigated the potential public health and economic impacts of dengue vaccination in Indonesia. However, many of these models either omitted transmission dynamics or overlooked some key aspects of dengue transmission.

Methods: This study aimed to assess the potential impact of a hypothetical vaccine in Indonesia using a transmission model that accounts for key features known to affect the transmission dynamics of dengue. Across 122,472 scenarios related to vaccine's profile (efficacy, and duration of efficacy) and implementation strategies (vaccination coverage rate, and targeted age of vaccination), we evaluated the potential impact of routine dengue vaccination for children and adolescents (ages 1 – 18 years) and identified the optimal target age of vaccination to avert the maximum number of symptomatic cases.

Results: Across scenarios, vaccinating 1-or 2-year-olds averted the largest proportion of symptomatic cases (3.47%–55.00%, depending on vaccine profile), whereas vaccinating 10–18-year-olds averted the fewest (2.25%–47.50%). We estimated that the median (95% uncertainty interval; UI) number of symptomatic dengue cases prevented by vaccination over a 20-year time horizon following vaccine introduction ranged from 4.9 (95% UI: 1.6–13.6) million to 8.6 (95% UI: 3.5–16.7) million.

Conclusion: These findings indicate that a safe and effective dengue vaccine for all age groups administered to young children could substantially reduce the dengue burden in Indonesia.

D-322 Switching the Lens: Societal vs Payer Value of Introducing TAK-003 into Indonesia's National Immunization Program

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Background: Dengue imposes substantial health and economic burdens in Indonesia. This highlights a need to shift from a narrow healthcare payer perspective to the broad society perspective when evaluating dengue preventions such as vaccination.

Methods: Using a validated static model with dynamic components, we compared no vaccination with four strategies targeting school-aged children: routine vaccination at age 9 (R9) with optional catch-up campaigns at ages 10–12 years (CU10-12), over a 20-year horizon, assuming 80% coverage and a 3% discount rate. Cost-effectiveness was assessed using thresholds of 0.5× and 1× Indonesia's 2024 GDP per capita (USD 4,957).

Findings: Across strategies, TAK-003 reduced symptomatic dengue by 31–34%, hospitalisations by 38–42%, and deaths by 38–42%, averting 1.1–1.3 million DALYs compared with no vaccination. From societal perspective, all strategies were cost saving (net savings USD 721.6–731.5 million), driven by reduced productivity losses (USD 5.246 billion without vaccination vs. USD 2.869 billion [R9CU10-12] and USD 3.191 billion [R9]), and school absenteeism (USD 333.0 million without vaccination vs. USD 169.4 million [R9CU10-12] and USD 189.0 million [R9]). From payer perspective, ICER ranged from USD 1,489 to USD 1,580 per DALY averted (<0.5×GDP). Probabilistic analysis showed 99.9% and 99.7% probability of cost-effectiveness, respectively societal perspective at 0.5xGDP and payer perspective at 1×GDP. One way sensitivity highlighted discounting, severity of second infections, and vaccine price as key drivers.

Interpretation: Whilst under the payer perspective, dengue vaccination is already cost-effective, a societal perspective demonstrated even greater returns with cost savings, supporting inter ministerial financing and timely adoption of TAK 003 in Indonesia's national immunization program.

Funding: Takeda Innovative Medicines

D-324 Evaluation of a Locally Manufactured Dengue Vaccine (Prodenga) in Bangladesh: A Randomized Non-Inferiority Trial Against Butantan-DV

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Background: Dengue virus (DENV) is the most prevalent arboviral infection worldwide, placing over two billion people at risk. Bangladesh has endured recurrent outbreaks since 2000, with the largest burden in 2023, reporting 321,179 cases and 1,705 deaths. Dhaka experiences major epidemics every 3–5 years, predominantly driven by DEN-2 and DEN-3. Despite this, dengue vaccines have not been systematically evaluated in Bangladesh. A locally manufactured vaccine could transform prevention strategies. The Butantan tetravalent live-attenuated vaccine (Butantan-DV), based on NIH's TV003, is licensed in Brazil with proven efficacy. Incepta Pharmaceuticals has developed TV003 under NIH licensure, marketed as Prodenga. Country-specific evidence is essential to support licensure and policy adoption.

Methods: We propose a double-blind, randomised, non-inferiority trial comparing a single subcutaneous dose of Prodenga with Butantan-DV. A total of 3,222 participants will be enrolled in Dhaka across age-deescalating cohorts: adults (18–59 years), adolescents (7–17 years), and children (2–6 years). Each cohort will include 1,074 participants (537 per vaccine arm). The primary immunogenicity endpoint is seroconversion to DEN-2 and DEN-3 at day 28, measured by PRNT. The primary safety endpoint is the incidence of solicited adverse events and serious adverse events through day 28.

Objectives:

1. To compare the immunogenicity of Prodenga and Butantan-DV in terms of serotype-specific seroconversion.
2. To assess safety by comparing adverse events between vaccine arms.

Expected Impact: This trial will provide critical country-specific data to support approval of Prodenga in Bangladesh. Findings will inform integration into outbreak response, endemic control, and the national Expanded Programme on Immunisation (EPI). A locally manufactured, affordable dengue vaccine offers a cost-effective solution for Bangladesh and potentially for broader regional and global use.

D-325 Exploiting the Clec9A targeting vaccine platform to develop a safe and effective DENV vaccine

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Objectives: Dengue envelope domain III (EDIII) is a leading subunit vaccine candidate, shown to induce strongly neutralising and predominantly serotype-specific antibodies, though it is weakly immunogenic. We have explored a dendritic cell-targeting vaccine approach to deliver EDIII to the cDC1 dendritic cell subset via Clec9A receptor. This study investigates the humoral and cellular EDIII-specific immune responses and protective efficacy elicited by this vaccination approach in immune competent mice that are either dengue naïve or with pre-existing DENV immunity.

Methods:

- Prime-boost regimen: 5-6 weeks old BALB/c mice were subcutaneously immunised twice, 1 month apart, with Clec9A-EDIII adjuvanted with poly I:C.
- Pre-existing DENV2 immunity was generated by the sc. administration (twice at 2-week interval) of live DENV adjuvanted with Addavax.
- DENV2 challenge: MAR1-5A3 was injected in BALB/c mice 1 day prior to DENV2 infection in immunised mice 2 weeks after boosting
- Immune assays: Systemic anti-EDIII Ab and neutralising Ab were monitored via ELISA and PRNT respectively. Systemic EDIII-specific B and T cell responses were quantified via ELISPOT and flow cytometry.

Results: A homologous prime-boost immunization regimen with Clec9A-EDIII induced sustained anti-EDIII IgG titres and DENV2-specific neutralising antibody titres up to 12 months post-boost. Clec9A-EDIII immunisation also generated EDIII-specific spleen T fh cell response and poly-functional CD4 + T cells. In mice with pre-existing DENV2 immunity, a single dose immunization with Clec9A-EDIII boosted the neutralising Ab response to titres that were comparable to those obtained upon homologous prime-boost regimen in naïve animals. Clec9A-EDIII was able to reduce viremia and viral load in DENV2 infected mice.

Conclusions: These promising results support that the Clec9A targeting approach may overcome the weak immunogenicity of EDIII vaccine antigen and advance its clinical development.

D-339 Replacing human with engineered dengue virus 5' and 3' untranslated regions dispense with chemically-modified nucleosides in RNA vaccines

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Background: mRNA vaccines are highly effective as proven during the outbreak, while limited by innate immune activation and associated reactogenicity, even with the utilization of chemically modified nucleosides. Dengue viruses (DENV) have evolved untranslated regions (UTRs) that regulate host RNA sensing and immune responses. This study investigated whether engineered DENV UTRs could replace chemical nucleoside modifications in RNA vaccine design to improve safety while maintaining immunogenicity.

Methods: We engineered chimeric mRNAs using DENV-4 5' and 3' UTRs with eGFP or SARS-CoV-2 spike protein coding sequences. mRNAs were synthesized without chemical nucleoside modifications and formulated into lipid nanoparticles. Expressions of different constructs were assessed in multiple cell lines like HEK293T and A549 using flow cytometry. Immunogenicity was evaluated in BALB/c mice through intramuscular vaccination with mRNA-LNP, measuring spike-specific neutralizing antibodies, T cell responses, and serum cytokine levels at various timepoints.

Results: The engineered DENV4-D2VR construct showed enhanced protein expression compared to human UTR controls in vivo. In murine studies, the DENV-derived mRNA induced robust spike-specific neutralizing antibodies and T cell responses comparable to conventional mRNA vaccines. Critically, inflammatory cytokine responses (IL-1α, IL-1β, IL-6, TNF-α) and interferon responses (IFN-α2, IFN-λ2, IFN-γ, CXCL9) were significantly reduced compared to human UTR constructs, while maintaining protective immunity levels. In addition, this construct maintained production of subgenomic flaviviral RNA, demonstrating preserved dengue-derived regulatory functions.

Conclusion: This study provides a cost-effective strategy for RNA vaccine development. The engineering RNA vaccines with DENV UTRs have displayed immunological effectiveness and reduced innate immune responses without nucleoside modification.

D-365 Immunogenicity and safety of TAK-003 coadministration with yellow fever, hepatitis A, and 9-valent human papillomavirus vaccines: clinical trial evidence and post-marketing findings

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Background: TAK-003 has demonstrated efficacy and a favorable safety profile. Coadministration of TAK-003 with other vaccines can facilitate integration of dengue vaccination into immunization programs and travel medicine. Coadministration studies with yellow fever (YF-17D), hepatitis A virus (HAV), and human papillomavirus (9vHPV) vaccines have been conducted. We present an integrated cross-platform analysis of these data with postmarketing surveillance findings on TAK-003 with other vaccines.

Methods: Immunogenicity and safety findings from TAK-003 coadministration studies with YF-17D(NCT03342898), HAV(NCT03525119), and 9vHPV(NCT04313244) were reviewed in a side-by-side cross-platform comparison. Postmarketing data span 3 years (February 2023-February 2026).

Results: Noninferiority of immune responses to partner-vaccines was demonstrated in all 3 studies: yellow fever seroprotection was 99.5% with YF-17D and 99.1% with concomitant YF-17D+TAK-003; hepatitis A seroprotection was 97.1% with HAV and 98.7% with concomitant HAV+TAK-003; 9vHPV immune responses were noninferior for all 9 HPV types with concomitant 9vHPV+TAK-003 versus 9vHPV alone. TAK-003 immunogenicity was maintained across combinations, populations and settings. Safety findings were consistent with the known profiles of TAK-003 and partner-vaccines; no vaccine-related serious adverse events were reported. Since launch, ~24.4 million TAK-003 doses have been distributed globally. In Takeda's global safety database, 9241 postmarketing cases for TAK-003 were identified; ~ 6% reported administration of ≥1 other vaccine, with no new important safety findings.

Conclusion: Across the 3 vaccine combinations and settings, TAK-003 consistently preserved partner-vaccine immune responses, maintained immunogenicity, and was well-tolerated. Postmarketing surveillance identified no new safety concerns, and together, these data support TAK-003's integration into routine immunization programs and travel medicine .

Funding: Takeda.

D-366 Engineering an Attenuated Human Cell-Adapted Dengue Virus Type 3

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Background: The four dengue viruses (DENV-1 to-4), although belonging to the same genus, show different replicative characteristics in vitro. Unlike the other three DENVs, DENV-3 can be difficult to propagate in mammalian cells, making mechanistic studies challenging and possibly even limit cost-effective manufacturing of dengue vaccines. We recently reported a DENV-3 clinical isolate, DENV3/TZK/2016 (D3/TZK), isolated from the urine of an immunosuppressed allograft renal transplant recipient with prolonged DENV infection, that showed adaptation to mammalian and human cells. We explore herein its potential as a genomic template for deriving attenuated DENV-3 with useful propagative properties.

Methods: Infectious clones of wild-type D3/TZK and mutant derivatives carrying prM-S29V, NS1-G53D and NS2B-I114T were generated by site-directed mutagenesis followed by Gibson assembly. Virus genome stability and viral replication kinetics were assessed in mammalian cells.

Results: D3/TZK replicated to higher levels in vero cells as compared to another clinical DENV-3 isolate, derived from the blood of a Singapore-based dengue patient (D3/SG/05K863DK1/2005). Introduction of previously characterised, mechanistically-defined attenuating mutations, namely prM-S29V, NS1-G53D and NS2B-I114T into D3/TZK backbone generated mutants that remained stable with serial passaging. These mutants also showed accelerated replication kinetics and IFNb response in Huh7 cells, similar to DENV-2 PDK53, a component of the licensed TAK-003 tetravalent dengue vaccine.

Conclusion: D3/TZK, could be a prototypic, human-adapted DENV-3 for studying dengue pathogenesis, and as genetic template for live attenuated vaccine development.

D-394 A qualitative study of sentiments on dengue vaccination amongst stakeholders in Singapore

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Background: Despite extensive vector control measures, Singapore is still susceptible to dengue outbreaks due to low population immunity that paradoxically stems from this success. Therefore, alternative prevention measures like vaccination are an important consideration. We aimed to explore sentiments on upcoming dengue vaccines among stakeholders involved in the evidence-to-policy process for opinions on integrating a dengue vaccine in national programs.

Methods: We conducted 19 semi-structured interviews with academics, clinicians and policy staff who work on dengue. The abductive thematic approach was used for analysis.

Results: Participants suggest that the need for a dengue vaccine in Singapore is diminished by the low burden and success of vector control including newer measures like Project Wolbachia which could render vaccines unlikely to achieve cost-effectiveness as a national program, with most participants postulating that a dengue vaccine would end up in the private route first. The shadow of Sanofi's Dengvaxia causing antibody dependent enhancement is a major concern that trickles down to the expectations for upcoming vaccines, Takeda's Qdenga and MSD's V181, highlighting an especially cautious approach to decisions surrounding Qdenga. The decision process to introduce a vaccine is non-linear and complex, involving different stakeholders at each stage and several essential criteria used were identified. In the evidence-to-policy process, SSHSPH is said to be a key influencer with strong connections and collaborations with policy.

Conclusion: There is a need for a multi-pronged approach to control dengue, considering both vector-based approaches and pharmaceutical interventions. While Singapore is highly technocratic in decision-making, there is room for improvement to consider emerging evidence, and awareness for collaboration amongst academia and policy.

D-399 Dengue Vaccination Sentiment in the General Public

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Background: Despite exemplary vector control that brought the A. aegypti population to extremely low levels, dengue remains a prominent vector-borne disease in Singapore. Its low population immunity compared to endemic counterparts renders the population highly susceptible. As promising vaccines come onto the market, understanding of public sentiment can guide future integration of vaccination to complement the national control strategy.

Methods: 1,500 members of the general public aged ≥21 years old were surveyed on their sentiments on the local dengue situation, control measures and acceptance for various characteristics in a dengue vaccine. Logistic regression was conducted to examine factors associated with vaccine acceptance in those <60 and ≥60 years old.

Results: Willingness to accept a dengue vaccine decreased from 75.2% (95%CI: 69.1% - 80.5%) in the 21-29 years old to 49.8% (95%CI: 43.8% - 55.8%) in those ≥65 years old. Perceiving responsibility to get vaccinated for dengue was the most significant determinant regardless of age group. Within the confidence domain, trusting the dengue vaccine recommended by the Ministry of Health was associated with greatest odds of vaccine acceptance, followed by recommendation by their doctors and government leaders. Within the complacency domain, believing a vaccine was necessary to prevent dengue was consistently significantly associated with greater odds of vaccine acceptance.

Conclusion: Instilling a sense of collective responsibility, building confidence in the healthcare system and public health authorities, and understanding the necessity of vaccine in preventing dengue are important in future communications to encourage uptake of dengue vaccine.

D-418 Three Years of Post-Marketing Experience with Takeda's Dengue Vaccine – A Safety Data Review

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Background: TAK-003, a live-attenuated tetravalent dengue vaccine, was launched in February 2023 and is approved in >40 countries. As dengue vaccination expands globally, post-marketing surveillance is critical to characterize TAK-003 real-world safety and identify rare or unexpected events beyond clinical trials. We present a descriptive analysis of TAK-003 post-marketing safety data collected over a period of 3 years since launch.

Methods: A descriptive analysis was performed on 3 years of post-marketing safety data extracted from Takeda's Global Safety Database (data-lock February 18, 2026). Anaphylaxis cases were defined as meeting Brighton Collaboration (BC) Diagnostic Certainty Levels 1-3.

Results: Approximately 24.4 million TAK-003 doses have been distributed globally, with the largest volume in Brazil (~17 million doses) where national immunization programs target children aged 10-14 years. At data lock, 9,241 cases reporting 24,293 adverse events following immunization (AEFIs) were recorded. Demographics showed a median age of 14 years (range: 6 weeks-112 years), and 48.6% were female. Vaccine coadministration was recorded in ~6 % of cases. Most AEFIs were non-serious (91.5%) and most frequent included pyrexia, headache, myalgia, rash, and injection site reactions. Serious AEFIs (8.5%) included hypersensitivity-related and anxiety-related/vasovagal events, and dengue fever; there were no TAK-003-related deaths. There were 113 anaphylaxis cases, none with fatal outcome; 48% occurred within 15 minutes and 97% after Dose 1. Anaphylaxis rates remained within published global vaccine rates (1-10 cases per million doses).

Conclusion: Over 3 years of post-marketing surveillance and 24.4 million doses distributed, no new important safety risks emerged, confirming the favorable benefit-risk profile of TAK-003 consistent with clinical trials.

D-420 Operational and Scientific Challenges in Dengue Vaccine Clinical Trials: A Global Implementation Perspective

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Background:

Dengue is a rapidly expanding mosquito-borne viral disease causing an estimated 100–400 million infections annually, with nearly half of the world's population at risk. Between 2020–2050, dengue is projected to impose a global economic burden of approximately INT$306 billion, with Southeast Asia expected to bear the highest impact. Rising transmission driven by climate change, changing rainfall patterns, and population mobility highlights the urgent need for effective vaccine development strategies.

Methods:

An implementation-oriented narrative review was conducted using WHO reports, peer-reviewed literature, and experiential insights from the management of large-scale dengue clinical development programs were synthesized to identify barriers influencing dengue vaccine clinical development and trial operations strategies.

Results:

Global dengue incidence reached record levels in 2024, with >14 million reported cases and ~10,000 deaths worldwide. Since 2010, over 190 dengue-related clinical trials have been initiated globally. Based on experience from dengue vaccine and treatment trials involving >25,000 participants, major operational challenges included delayed diagnosis, seasonal outbreak variability, surveillance limitations, rapid resource mobilization, cross country coordination challenges and long-term participant retention. Key scientific barriers included co-circulation of four dengue serotypes, heterogeneity in immune responses, antibody-dependent enhancement (ADE), lack of standardized endpoints, and underreporting affecting vaccine efficacy assessment.

Conclusion:

Dengue clinical trials require adaptive, globally coordinated strategies to address both operational and scientific challenges. Strengthening surveillance systems, harmonizing clinical endpoints, and implementing participant-centered trial approaches on community engagement to enhance recruitment and retention will be critical to accelerating the development of dengue vaccines with acceptable benefit /risk profile worldwide.

D-422 TAK-003 (Qdenga) and DENV-3: could a dengue controlled human infection model decipher the challenge of protection in seronegative individuals?

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Background: TAK-003 (Qdenga, Takeda Vaccines) is a tetravalent live-attenuated dengue vaccine based around a DENV-2 backbone for each of the four strains. Despite overall efficacy of TAK-003 against dengue fever, there is significant variation in efficacy for non-DENV-2 serotypes with particular concern surrounding DENV-3.

Methods: A systematic review of the published literature was performed to analyse DENV-3-specific immunogenicity, vaccine efficacy (VE) and effectiveness of TAK-003.

Results: A PubMed search identified 201 articles, of which 23 were included in the systematic review.

DENV-3 geometric mean titres were 1.7log10 and 0.9log10 lower than for DENV-2 at day 30 and day 120 respectively, but comparable to DENV-1 and DENV-4. Cross-reactive T-cell responses developed against DENV-3 but the relative magnitude was significantly lower than for DENV-2.

VE against DENV-3 in the pivotal TIDES trials among seropositive recipients was 52.3% (95% CI, 36.7–64.0) but −15.5% (95% CI, -108.2–35.9) in the seronegative. This lack of VE in seronegative individuals appeared in the first year post-vaccination (–38.7% (95%CI, –335.7 -55.8)).

Real-world data demonstrated vaccine effectiveness of 61.7% (95%CI, 39·9–75·6) for symptomatic dengue and 67.5% (95% CI, 43·4–81·3) for hospitalised disease. Assessment of effectiveness against DENV-3 was limited by small numbers.

Conclusion: Possible reasons for reduced VE in DENV-3 include DENV-2 antigenic dominance, waning of DENV-3-specific neutralising antibodies and suboptimal cell-mediated immunity. While further studies of real-world vaccine effectiveness are important for determining whether protection against severe dengue is preserved, natural infection studies are an efficient tool for yielding a mechanistic understanding.

E-124 Exploring Fascinating Potential: Repurposing Embelin Derivatives for Dengue Treatment

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Background: Dengue remains a major global health threat, with the WHO projecting a ten-fold increase in reported cases globally between 2000 & 2019, rising from 500,000 to 5.2 million. Since the beginning of 2025, over 4.5 million cases dengue cases and over 3 000 dengue-related deaths have been reported. Despite its increasing incidence and potential to progress into severe disease, effective antiviral therapies are lacking. This study aimed to identify potential anti-dengue agents by designing and evaluating embelin-derived compounds targeting essential viral proteins.

Methods: A library of 370 repurposed drugs was screened against major dengue targets, including the Envelope protein, NS2B-NS3 protease, NS3 helicase, NS5 RNA-dependent RNA polymerase, and NS5 methyltransferase. Molecular docking using Auto Dock Vina 1.5.6 identified multi-target inhibitors, ADMET predictions evaluated pharmacokinetics and toxicity, and molecular dynamics simulations assessed protein–ligand complex stability. Designed compounds will next undergo synthesis and in vitro validation through cytotoxicity testing, anti-dengue assays, and qRT-PCR.

Results: Docking analysis identified 7 repurposed drugs exhibiting strong binding affinities toward all selected dengue targets. These compounds displayed consistent interaction patterns, including significant hydrogen bonding and aromatic interactions. ADMET evaluation suggested acceptable pharmacokinetic profiles, and MD simulations confirmed stable protein–ligand complexes. These insights enabled the optimization of embelin-based structures with promising antiviral potential.

Conclusions: This study highlights the potential of repurposed embelin as multi-target dengue inhibitors. The integration of molecular docking, interaction analysis, ADMET evaluation, and MD simulations forms a strong basis for developing antiviral candidates. Upcoming synthesis and biological testing will further determine the therapeutic promise of these designed embelin derivatives.

E-129 Health-Related Quality of Life Among Patients Hospitalized with Dengue Fever in Bangladesh

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Background: Dengue is an increasing public health concern in Bangladesh, yet its impact on health-related quality of life (HRQoL) remains poorly characterised. Following a substantial rise in dengue cases in 2024, we assessed HRQoL among hospitalised dengue patients and examined associated factors.

Methods: This observational study included hospitalised dengue patients in Bangladesh. HRQoL was measured using the EQ-5D-3L instrument. Multivariable regression models were used to identify demographic, socioeconomic, and clinical factors associated with EQ-5D-3L index and EQ-VAS scores.

Results: Among 490 patients (median age 27 years), most were aged under 40 years (79%), male (80%), and urban residents (73%). Dengue Group B accounted for 70% of cases. A high proportion reported problems with mobility (86%), self-care (80%), usual activities (85%), pain/discomfort (89%), and anxiety/depression (82%). The mean EQ-5D-3L index score was 0·46 (SD 0·38), and the median EQ-VAS score was 50 (IQR 30–60). Patients with severe dengue (Group C) had markedly poorer HRQoL than those with Group A disease (index 0·12 vs 0·62; VAS 28·8 vs 41·0; $p<0·001$). Older age (≥60 years) and comorbidities were associated with significantly lower HRQoL. Male patients reported higher EQ-VAS scores than females, while urban residents reported lower self-rated health than rural residents. Dengue severity, age, and comorbidities remained independent predictors of HRQoL in multivariable analyses.

Conclusions: Dengue substantially impairs HRQoL among hospitalised patients in Bangladesh, particularly in older adults, those with severe disease, and those with comorbidities. Targeted, patient-centred interventions are needed to mitigate this burden. in resource-constrained settings.

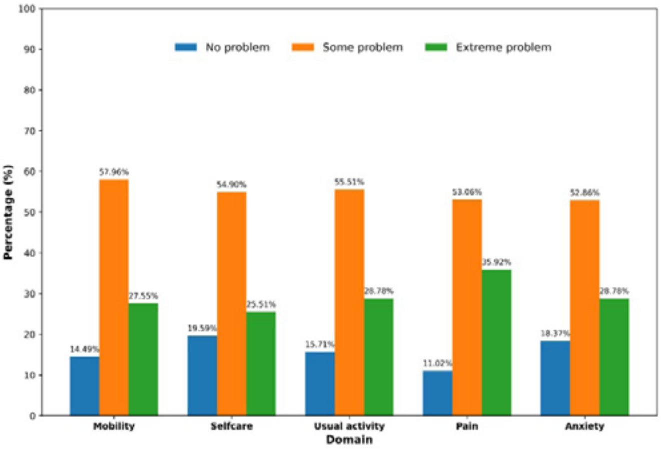

Figure 1: Frequency of reported problems by dimensions of QoL

E-132 A diagnostic conundrum of a falsely invalid dengue NS1 antigen immunochromatographic assay result in a patient with dengue fever: an explanation and a simple solution

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Background: The patient presented with 4 days of classical symptoms of dengue fever. Immunochromatographic assay (IMC) is widely used due to its simplicity and rapid time-to-result. For test to be valid, the control line (C-line) must be present. However, in this case the C-line was not visible in the NS1-Ag cassette but visible in the IgM/IgG test, and a strong NS1 Ag-line was visible.

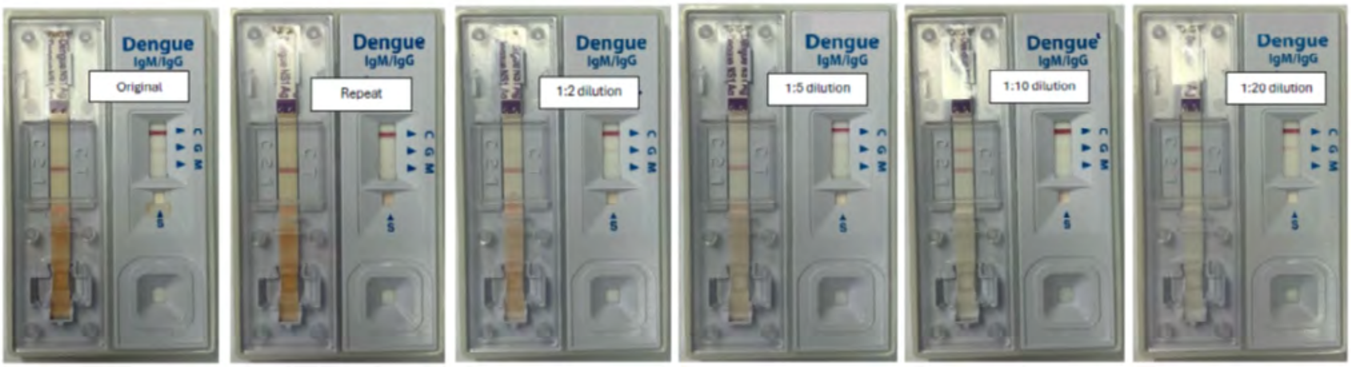
Methods: Repeat test was performed to exclude technical error and faulty cassette. Subsequently, to trouble-shoot, serum was serially diluted with PBS and retested. An ELISA test was also performed.

Results: The C-line became visible when serum was serially diluted and its intensity increased with higher serum dilutions. The presence of NS1-Ag was confirmed using ELISA method. Multiple factors could result in this phenomenon:

1. Procedural errors, such as defective kit, or reading of results outside of recommended time. This was excluded by repeat test adhering to proper procedures with the same result.
2. Unidentified interfering substances in serum. However, the test was valid for IgM/IgG cassette.
3. High NS1-Ag concentration depleted free anti-dengue NS1 gold-conjugated antibody resulted in:
   (a) formation of T antibody-NS1-gold conjugate immunocomplex at T-line, preventing the flow of gold-conjugated antibody to C-line;
   (b) reduction of binding affinity between C-line’s anti-gold conjugate antibody and NS1-gold conjugate complex compared to free gold-conjugated antibody.

The effects of points 3a & b could be reduced with sample dilution.

Conclusions: Hook effect at very high antigen concentration resulting in false negative is well-documented for IMC. However, the effect of analyte concentrations on C-line is lesser known. While IMC test result without C-line is to be interpreted as invalid, an accompanying visible T-line should warrant further examination. High concentrations of antigen, outside the working range of the assay, could falsely diminished the presence of C-line. Through serum dilution, this rendered the test as valid, providing critical and useful information for patient management.



E-138 Defining the clinical utility of dengue RT-iiPCR for rapid and accurate diagnosis

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Background: Rapid molecular diagnostics are critical for timely dengue virus (DENV) detection, especially in resource-limited settings. Reverse transcription-insulated isothermal polymerase chain reaction (RT-iiPCR) enables sample-to-answer amplification without thermocyclers. While this platform was previously validated, its diagnostic performance against contemporary viral genotypes and, critically, across different host immune statuses remains largely undefined. We assessed a DENV iiPCR assay against quantitative real-time reverse transcription PCR (qRT-PCR) during the 2023 outbreak in southern Taiwan.

Methods: Acute-phase sera (n = 185) from febrile patients were tested by qRT-PCR, pan-DENV iiPCR, IgM/IgG ELISAs, and serotype-specific RT-PCR/iiPCR. Diagnostic performance was evaluated with qRT-PCR as a reference. Subgroup analyses examined effects of days post-symptom onset (PSO), immune status (primary vs secondary infection), and serotype on iiPCR sensitivity.

Results: Pan-iiPCR achieved 88.4 % sensitivity and 100 % specificity versus qRT-PCR. Sensitivity peaked within 3 days PSO (96.8 %) and in primary infections (95.0 %) but declined after day 3 (53.3 %) and in secondary infections (82.2 %). Combining pan-iiPCR with IgM testing raised sensitivity to ≥99 % beyond the viremic window. iiPCR correctly typed 83.5 % (71/85) of DENV-1 and 94.3 % (66/70) of DENV-2. Because pan-iiPCR served as the screening step, 18 RT-PCR–positive specimens were pan-iiPCR negative and therefore did not proceed to iiPCR serotyping.

Conclusions: iiPCR enables rapid early-phase detection and is useful when paired with serology. However, reduced sensitivity in low-viremia and secondary infections, as well as incomplete serotyping, limit standalone use. Primer optimization and integration with IgM testing may enhance outbreak utility.

E-147 Severe dengue-Plasmodium falciparum malaria coinfection in a traveller returning to Malaysia from Nigeria: A Case Report

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Introduction: Dengue fever and malaria co-infection has been rarely reported, with an estimated pooled prevalence of up to 4.2%–7.5% among febrile patients. We report a rare case of severe malaria and dengue co-infection in a traveller returning from Nigeria to Malaysia.

Case Presentation: A 50-year-old Malay male presented with a five-day history of fever with chills, arthralgia, myalgia and gastrointestinal symptoms following a three-month stay in Nigeria. At the emergency department, he was alert but hypotensive, thus requiring fluid resuscitation and admission to the intensive care unit. The initial blood parameters showed a haemoglobin of 11.2 g/dL, a platelet count of 37 x 10 9 /L, a haematocrit of 32.5%, a prothrombin time (PT) of 15.9 seconds, and a creatinine level of 155 U/L. Dengue IgM was positive, but negative for IgG and NS1. Blood film for malaria parasites (BFMP) showed a Plasmodium falciparum count of 34,798 parasites/µL. The patient was treated for severe malaria with intravenous artesunate (168 mg daily) for five days alongside supportive care for dengue with warning signs. The third BFMP was negative for parasitemia. He was discharged uneventfully.

Discussion: Dengue and malaria may be clinically indistinguishable, thus leading to delayed or misdiagnosis of the co-infection. This case exemplifies both the diagnostic challenge and management of co-infection, as severe dengue complicates severe malaria, which manifests concurrently as shock, coagulopathy, and renal impairment.

Conclusion: This case warrants a high index of suspicion for co-infection in travellers returning from high-burden areas to ensure timely intervention.

E-149 Unveiling the Hidden Risk of Cardiac Involvement in Dengue Fever: A Critical Cross-Sectional Study

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Background: Dengue is the fastest-spreading mosquito-borne viral disease globally and can lead to serious complications, including liver failure, acute kidney failure, disseminated intravascular coagulation, encephalopathy, myocarditis, and hemolytic uremic syndrome. Early assessment of cardiac involvement in dengue is crucial to avoid life-threatening consequences. Objectives: The study aimed to assess cardiac dysfunction in children with dengue and to correlate cardiac features with the severity of dengue infection.

Methods: This was a cross-sectional analytical study conducted in the Department of Pediatrics, DMIHER, Sawangi, Wardha. Patients were categorized into three groups: dengue without warning signs, dengue with warning signs, and severe dengue. Each patient underwent detailed history-taking, clinical examination, and laboratory tests, including complete blood count, electrolytes, liver, and kidney function tests. Cardiac function was assessed using 2D Echo and Troponin I, with statistical significance set at $p < 0.05$.

Results: A total of 142 children with a mean age of 85.32 ± 48.34 months were enrolled in the study. Cardiac involvement was observed in 8% of patients based on clinical signs, with 30.98% showing abnormal ECG findings and 39.43% presenting elevated CK-MB levels. Abnormal ECG findings included sinus bradycardia, sinus arrhythmia, right bundle branch block, sinus exit block, left bundle branch block, ST depression, and ST-T wave changes. A reduced ejection fraction was noted in 16.19% of cases. ECG changes were observed in 15% of cases, and some also had abnormal 2D echocardiography findings. Sinus arrhythmia was the most common ECG abnormality, while mild pericardial effusion was the predominant echocardiographic finding. Elevated cTn-I levels and abnormal ECHO findings were associated with prolonged hospital stays.

Conclusion: Cardiac involvement, such as myocarditis and arrhythmias, is common in dengue and requires comprehensive evaluation using ECG, echocardiography, and cardiac biomarkers. Early cardiac assessment is crucial for effective management.

E-161 Direct costs of dengue in the East Asia and Pacific region: A systematic literature review

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Background: Dengue poses a growing public health challenge. We synthesized evidence on the direct costs of dengue across East Asia and Pacific (EAP) countries.

Methods: We systematically searched EMBASE and PubMed during 01/01/2014–01/23/2025. We extracted and summarized data for direct medical costs (DMC) and other cost components by country, healthcare setting, and age. Costs were standardized to 2025USD.

Results: Of 146 eligible references, 42 reported on DMC. At national level, mean DMC in Thailand for an outpatient episode was $196 and for a hospitalization was $369–$785, while mean DMC for all care types in Taiwan was $517 per case. Across care settings, mean DMC per episode for outpatient care were lowest at $10 in Thailand and highest at $56 in Cambodia, while mean DMC per episode for hospitalization were lowest at $113 in Vietnam and highest at $547 in Indonesia. When compared across ages, hospitalization costs per episode for pediatrics were higher than adults ($145 for <15 years vs $98 for ≥15 years) in Vietnam, while hospitalization and outpatient costs in adults exceeded pediatric costs ($121 vs $100 for hospitalization; $11 vs $8 for outpatient) in Thailand. In a study conducted in Taiwan, the mean DMC per case among the elderly (≥75 years) was $1,731, the highest observed among all age groups examined.

Conclusion: Direct costs of managing dengue is substantial in EAP region. DMC varied significantly by country, healthcare setting, and age. Dengue prevention and control efforts are needed to curtail these costs.

E-170 Multicenter Evaluation of a Single-Device Dengue Antibody/Antigen Rapid Test for Simultaneous Detection of NS1, IgM, and IgG.

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Background: Dengue continues to pose a significant global health burden in tropical and subtropical regions, where early and accurate diagnosis is essential for effective clinical management and outbreak control. Although rapid diagnostic tests (RDTs) are widely used at the point of care, their performance remains variable. Objectives: To evaluate the diagnostic accuracy of the ASSURE Dengue Ab/Ag Rapid Test across multiple settings using reference ELISAs and commercially available CE-marked RDTs, supported by independent multicenter clinical evaluations.

Methods: A multicenter evaluation was conducted across Singapore, India, and Bangladesh. In Singapore, 430 characterized serum/plasma samples (141 positive, 289 negative) were tested against Panbio ELISAs and compared with SD Standard Q Dengue Duo. In India, 300 prospective samples were evaluated against Panbio ELISAs. In Bangladesh, 85 retrospective samples were assessed against a combination of reference RDTs, ELISAs, and PCR assays.

Results: In Singapore, the ASSURE Dengue Ab/Ag Rapid Test achieved 100% sensitivity (141/141) and 100% specificity (289/289), significantly outperforming SD Standard Q Dengue Duo (sensitivity 46.81%, specificity 99.31%). In India, the test demonstrated complete concordance (100%) with Panbio ELISAs across NS1, IgM, and IgG markers. In Bangladesh, NS1 antigen detection remained consistently robust (sensitivity 100%, specificity 88.14–96.00% depending on comparator), while antibody detection showed lower sensitivity (IgM 45.45%, IgG 42.50%) but maintained high specificity (91.07–100%).

Conclusion: The ASSURE Dengue Ab/Ag Rapid Test demonstrated superior and consistent diagnostic performance across diverse clinical settings compared with CE-marked RDTs and ELISAs, particularly for NS1 antigen detection. These findings support its use as a reliable point-of-care diagnostic tool for early dengue infection, with strong applicability in both controlled and real-world settings.

E-178 Primary versus secondary acute dengue infection, incidence and characterization between A&E and inpatient admissions in a single healthcare tertiary center in Singapore.

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Background: Dengue is a common mosquito-borne infection and secondary infection is associated with greater severity. It is endemic in Singapore, with high disease burden and periodic outbreaks.

Objectives: We determine the incidence and characteristics of acute primary (PD) and secondary (SD) dengue in A&E and admitted patients in a tertiary hospital, which has not previously been well described.

Methods: In our hospital, a rapid-immunochromatographic-assay is used for A&E patients (with short turn-around time for admission decisions); and an EIA for inpatients (better performance). Laboratory and clinical data from 2023 were analysed.

Results: In A&E, 15.5% (of 1530) were positive for acute dengue. 52.5% were PD (average age 47.1yrs vs 56.8yrs for SD) out of which 55.2% required admission (vs 73.45% for SD). In those who were dengue neg, 75.16% never had dengue while 9.28% were previously exposed. For inpatients, 810 Ag±IgM EIA tests were requested, 10.1% had acute dengue. 47 with acute infection had IgG results available, where 14.9% had PD (average age 49.1, vs 72.1 for SD). The dengue classification by different age groups and location are presented in Figure 1. Figure 2 summarizes the presenting signs and symptoms in PD and SD. Of note, those with SD had higher frequency of marked thrombocytopenia and abnormal liver function tests.

Conclusions: We presented data of patients in A&E and ward admissions with acute dengue. A smaller proportion of inpatients had PD, compared to those seen in A&E, likely reflecting the greater severity of illness in secondary dengue.

Figure 1: Dengue classification by different age groups and locations.

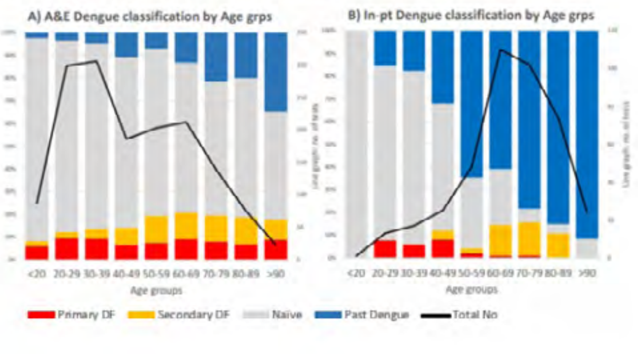
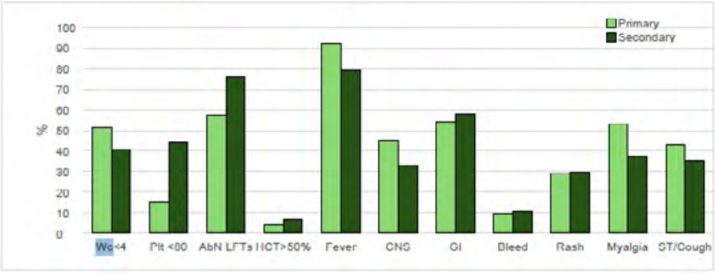


Figure 2: Overall presenting signs & symptoms of patients with primary and secondary dengue.



E-182 Serum total sialic acid in critical phase improves prediction of dengue hemorrhagic fever

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Background: Endothelial glycocalyx disruption plays a key role in dengue pathogenesis. Total sialic acid (TSA), a potential marker of glycocalyx shedding, may reflect disease severity. However, its relationship with systemic inflammation and clinical outcomes remains unclear.

Methods: We analyzed a cohort of 79 patients from the 2014–2015 dengue outbreaks in Taiwan. Total sialic acid and cytokines were measured during the critical phase. Correlations with cytokines were assessed using Spearman analysis. Associations between TSA and disease severity, including dengue hemorrhagic fever (DHF), severe thrombocytopenia (platelet <20,000/μL), bleeding, and plasma leakage, were evaluated using Mann–Whitney U test. Multivariable logistic regression and receiver operating characteristic (ROC) analysis were performed to identify independent predictors of DHF and evaluate discriminatory performance.

Results: Serum TSA was significantly higher in patients with DHF (p=0.020) and severe thrombocytopenia (p=0.027), with consistent but non-significant trends in bleeding and plasma leakage. TSA showed no significant correlation with IL-6, IL-1β, IL-8, or TNF-α. In multivariable analysis, TSA remained independently associated with DHF after adjustment for age (aOR=1.017, 95% CI 1.001–1.032, p=0.038). ROC analysis demonstrated modest discrimination for TSA alone (AUC=0.661), which improved substantially when combined with age (AUC=0.816).

Conclusion: Total sialic acid is an independent and clinically relevant biomarker of dengue severity, distinct from cytokine-mediated inflammation. Its combination with age significantly improves prediction of DHF, supporting a role for glycocalyx-related pathways in dengue pathogenesis and risk stratification.

E-185 Predicting the Timing of Plasma Leakage in Dengue Hemorrhagic Fever: A Retrospective Study

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Background: The precise timing of plasma leakage in Dengue Hemorrhagic Fever (DHF) is often difficult to determine. However, accurate identification of its onset is critical for guiding fluid management during the critical phase. This study aimed to develop a predictive model to estimate the timing of plasma leakage.

Methods: A retrospective observational study was conducted in Colombo, Sri Lanka, including 185 adult DHF patients (June–December 2025). Plasma leakage timing was determined using Pack Cell Volume (PCV) and radiological criteria. The final model was developed using multiple linear regression.

Results: Nearly half developed plasma leakage on days 4–5, with the remainder showing early or delayed onset. No significant associations were found with demographics, comorbidities, or presenting symptoms with leaking onset time. Admission CRP and sodium showed weak associations, while liver function tests showed none. Time to lowest white blood cell (WBC) count ($r = 0.779$, $p < 0.001$) and platelet count ($r = 0.758$, $p < 0.001$) strongly correlated with leakage timing. Faster declines in platelets ($r = -0.687$) and WBC ($r = -0.582$) were associated with earlier leakage. Multivariable analysis identified time to lowest WBC, time to lowest platelet count, and nadir platelet count as independent predictors, explaining 67.8% of variance (adjusted $R^2 = 0.678$).

Conclusion: This study highlights the importance of trend-based monitoring in DHF. The proposed model enables estimation of plasma leakage onset and supports timely fluid management. These findings provide a foundation for developing dynamic clinical prediction tools incorporating serial laboratory trends.

E-186 Dynamic Original and Modified Pan-Immune-Inflammation Values (PIV & mPIV) for Predicting Disease Progression in Adults with Dengue

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Background: Dengue is a dynamic illness with an initial febrile phase followed by critical and recovery phases. Ability to predict disease progression during febrile phase aids in management. We evaluated whether a dengue-adapted modified pan-immune-inflammation value (mPIV) improves risk stratification compared with the previously published PIV and neutrophil-to-lymphocyte ratio (NLR).

Methods: We analyzed a retrospective cohort of adults with laboratory-confirmed dengue from 2005–2008 (ARDENT), excluding patients with dengue hemorrhagic fever or dengue shock syndrome (DHF/DSS) at enrolment. PIV [(neutrophils×platelets×monocytes)/lymphocytes] counts and mPIV [(neutrophils×monocytes)/(platelets×lymphocytes)] were calculated longitudinally up to illness day 10 before DHF/DSS onset. Predictive performance was evaluated using generalized estimating equations, mixed-effects logistic regression, and time-dependent Cox models, adjusted illness day, age, gender, ethnicity, Charlson score, and day-specific AUC-ROC.

Results: Overall, 1,621 (22%) patients progressed to DHF/DSS. Log(PIV) and log(mPIV) demonstrated opposing, phase-specific associations: higher log(PIV) was associated with lower risk, while higher log(mPIV) predicted increased risk. Log(PIV) performed the best during early febrile phase, with peak performance on day 2 (AUC 0.819, 95%CI: 0.709–0.929), surpassing log(mPIV) and log(NLR). Log(mPIV) performed better discrimination later in illness (day 5 AUC 0.684, 95%CI: 0.652–0.717), while log(NLR) consistently underperformed.

Conclusions: Leveraging on routine daily complete blood count, in adult dengue PIV can serve as a valuable predictor during early febrile phase. The mPIV has slight advantage over PIV as illness progresses with corresponding declining platelet counts. All 3 indices provide AUCs close to 0.7, reflecting their value and more research to further refine easily accessible biomarkers on day-to-day practice.

DELEGATES' ABSTRACTS

E-188 Aspartate aminotransferase-to-platelet ratio index for prediction of severe dengue: an observational study from Bangladesh

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Background: During epidemics of dengue, early identification of severe cases is essential for optimum management. The objective of our study was to evaluate the predictive value of the aspartate aminotransferase-to-platelet ratio index (APRI) at admission for identifying severe dengue.

Methods: This observational study included adult patients with laboratory-confirmed dengue admitted to two tertiary hospitals in Dhaka, Bangladesh, between July 2023 and December 2024. Severe dengue was defined according to WHO 2009 criteria. Multivariable logistic regression was used to examine the association of warning signs and APRI with severe dengue. Model performance was assessed using pseudo-R^2, receiver operating characteristic (ROC) curves, area under the curve (AUC), Brier score, and integrated discrimination improvement (IDI). Diagnostic accuracy measures were calculated for warning signs, APRI, and their combinations.

Results: Among 1,077 patients, 92 (8.5%) developed severe dengue. Warning signs were present in 45% cases. In multivariable analysis, warning signs (aOR 15.26, 95% CI 7.59–35.01) and APRI (aOR 1.10 per unit, 95% CI 1.08–1.13) were independently associated with severe dengue. Adding APRI improved model fit (pseudo-R^2 0.13 to 0.23) and discrimination (ΔAUC 0.08, 95% CI 0.03–0.13), with IDI 0.10 (95% CI 0.05–0.15). Warning signs showed high sensitivity (0.87) but moderate specificity (0.59), whereas APRI ≥5.97 showed lower sensitivity (0.54) but higher specificity (0.89). Using both together increased sensitivity to 0.97, while requiring both improved specificity to 0.95.

Conclusion: APRI at admission improves prediction of severe dengue beyond clinical warning signs and may support early risk stratification during outbreaks.

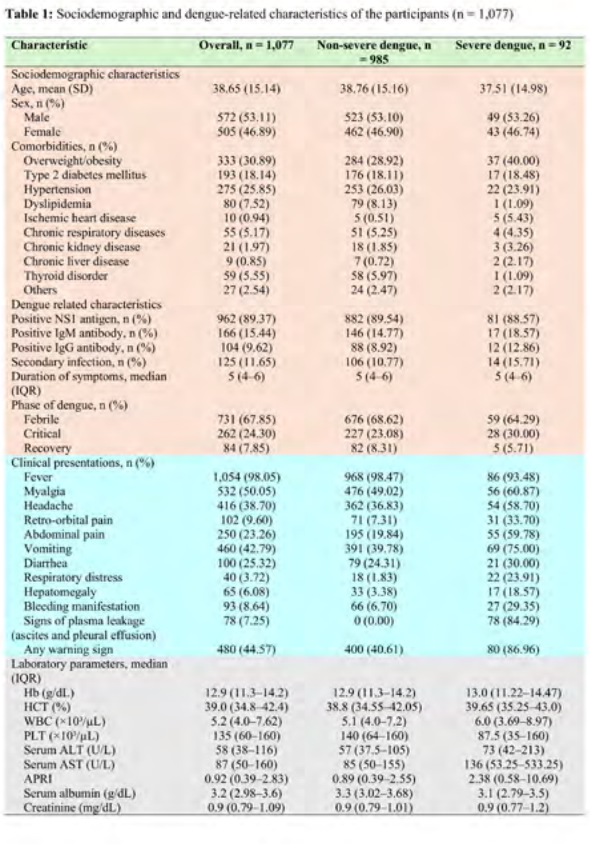

Table 1: Sociodemographic and dengue-related characteristics of the participants (n = 1,077)

Characteristic	Overall, n = 1,077	Non-severe dengue, n = 985	Severe dengue, n = 92
Sociodemographic characteristics			
Age, mean (SD)	38.65 (15.14)	38.76 (15.16)	37.51 (14.98)
Sex, n (%)			
Male	572 (53.11)	523 (53.10)	49 (53.26)
Female	505 (46.89)	462 (46.90)	43 (46.74)
Comorbidities, n (%)			
Overweight/obesity	333 (30.89)	284 (28.92)	37 (40.00)
Type 2 diabetes mellitus	193 (18.14)	176 (18.11)	17 (18.48)
Hypertension	275 (25.85)	253 (26.03)	22 (23.91)
Dyslipidemia	80 (7.52)	79 (8.13)	1 (1.09)
Ischemic heart disease	10 (0.94)	5 (0.51)	5 (5.43)
Chronic respiratory diseases	55 (5.17)	51 (5.25)	4 (4.35)
Chronic kidney disease	21 (1.97)	18 (1.85)	3 (3.26)
Chronic liver disease	9 (0.85)	7 (0.72)	2 (2.17)
Thyroid disorder	59 (5.55)	58 (5.97)	1 (1.09)
Others	27 (2.54)	24 (2.47)	2 (2.17)
Dengue related characteristics			
Positive NS1 antigen, n (%)	962 (89.37)	882 (89.54)	81 (88.57)
Positive IgM antibody, n (%)	166 (15.44)	146 (14.77)	17 (18.57)
Positive IgG antibody, n (%)	104 (9.62)	88 (8.92)	12 (12.86)
Secondary infection, n (%)	125 (11.65)	106 (10.77)	14 (15.71)
Duration of symptoms, median (IQR)	5 (4–6)	5 (4–6)	5 (4–6)
Phase of dengue, n (%)			
Febrile	731 (67.85)	676 (68.62)	59 (64.29)
Critical	262 (24.30)	227 (23.08)	28 (30.00)
Recovery	84 (7.85)	82 (8.31)	5 (5.71)
Clinical presentations, n (%)			
Fever	1,054 (98.05)	968 (98.47)	86 (93.48)
Myalgia	532 (50.05)	476 (49.02)	56 (60.87)
Headache	416 (38.70)	362 (36.83)	54 (58.70)
Retro-orbital pain	102 (9.60)	71 (7.31)	31 (33.70)
Abdominal pain	250 (23.26)	195 (19.84)	55 (59.78)
Vomiting	460 (42.79)	391 (39.78)	69 (75.00)
Diarrhea	100 (25.32)	79 (24.31)	21 (30.00)
Respiratory distress	40 (3.72)	18 (1.83)	22 (23.91)
Hepatomegaly	65 (6.08)	33 (3.38)	17 (18.57)
Bleeding manifestation	93 (8.64)	66 (6.70)	27 (29.35)
Signs of plasma leakage (ascites and pleural effusion)	78 (7.25)	0 (0.00)	78 (84.29)
Any warning sign	480 (44.57)	400 (40.61)	80 (86.96)
Laboratory parameters, median (IQR)			
Hb (g/dL)	12.9 (11.3–14.2)	12.9 (11.3–14.2)	13.0 (11.22–14.47)
HCT (%)	39.0 (34.8–42.4)	38.8 (34.55–42.05)	39.65 (35.25–43.0)
WBC (×10³/µL)	5.2 (4.0–7.62)	5.1 (4.0–7.2)	6.0 (3.69–8.97)
PLT (×10³/µL)	135 (60–160)	140 (64–160)	87.5 (35–160)
Serum ALT (U/L)	58 (38–116)	57 (37.5–105)	73 (42–213)
Serum AST (U/L)	87 (50–160)	85 (50–155)	136 (53.25–533.25)
APRI	0.92 (0.39–2.83)	0.89 (0.39–2.55)	2.38 (0.58–10.69)
Serum albumin (g/dL)	3.2 (2.98–3.6)	3.3 (3.02–3.68)	3.1 (2.79–3.5)
Creatinine (mg/dL)	0.9 (0.79–1.09)	0.9 (0.79–1.01)	0.9 (0.77–1.2)

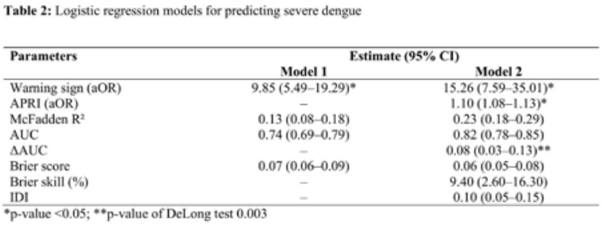

Table 2: Logistic regression models for predicting severe dengue

Parameters	Estimate (95% CI)	
	Model 1	Model 2
Warning sign (aOR)	9.85 (5.49–19.29)*	15.26 (7.59–35.01)*
APRI (aOR)	–	1.10 (1.08–1.13)*
McFadden R^2	0.13 (0.08–0.18)	0.23 (0.18–0.29)
AUC	0.74 (0.69–0.79)	0.82 (0.78–0.85)
ΔAUC	–	0.08 (0.03–0.13)**
Brier score	0.07 (0.06–0.09)	0.06 (0.05–0.08)
Brier skill (%)	–	9.40 (2.60–16.30)
IDI	–	0.10 (0.05–0.15)

*p-value <0.05; **p-value of DeLong test 0.003

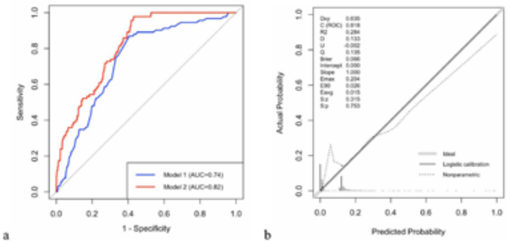

Figure 1: Discrimination and calibration of predictive models for severe dengue. (a) Receiver operating characteristic (ROC) curves comparing the base model with WHO warning signs and the extended model including APRI, (b) Calibration plot of the extended model showing agreement between predicted and observed risk across deciles.

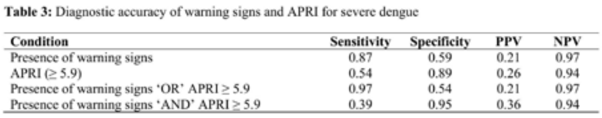

Table 3: Diagnostic accuracy of warning signs and APRI for severe dengue

Condition	Sensitivity	Specificity	PPV	NPV
Presence of warning signs	0.87	0.59	0.21	0.97
APRI (≥ 5.9)	0.54	0.89	0.26	0.94
Presence of warning signs 'OR' APRI ≥ 5.9	0.97	0.54	0.21	0.97
Presence of warning signs 'AND' APRI ≥ 5.9	0.39	0.95	0.36	0.94

E-194 Associations of PTX3 and C5a with Aminotransferases and Disease Severity during the Acute Phase of Secondary Dengue Infection: A Multicenter Study in Indonesia

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Background: Hepatic involvement is common during acute dengue, but the relationship between complement-linked innate mediators and liver enzyme abnormalities in secondary dengue remains unclear. We evaluated plasma Pentraxin 3 (PTX3) and complement component 5a (C5a) during acute secondary dengue and examined associations with aminotransferases and disease severity.

Methods: This multicenter study included patients with acute secondary dengue classified as dengue fever (DF) or dengue hemorrhagic fever (DHF). PTX3 and C5a were measured in EDTA plasma collected during the acute phase. Their associations with aspartate aminotransferase (AST), alanine aminotransferase (ALT), and disease severity were analyzed. Discriminatory performance of AST and ALT for DHF was assessed using area under the curve (AUC).

Results: PTX3 and C5a levels were higher than in healthy controls, but neither differed significantly between DF and DHF. In contrast, AST and ALT were significantly higher in DHF than in DF ($p<0.05$ and $p<0.001$, respectively). However, both transaminases showed only modest ability to discriminate DHF, with AUCs of 0.628 for AST and 0.670 for ALT. The optimal thresholds were 85 IU/L for AST (sensitivity 58.6%, specificity 64.3%) and 62 IU/L for ALT (sensitivity 51.7%, specificity 78.5%). PTX3 correlated moderately with AST ($r=0.542$) and ALT ($r=0.358$), whereas C5a correlated weakly with AST ($r=0.279$) and was not associated with ALT.

Conclusion: PTX3 showed a stronger association with aminotransferase elevation than C5a during acute secondary dengue. Although AST and ALT were higher in DHF, their limited discriminatory performance suggests they are insufficient as stand-alone markers of severity.

E-203 Pre-clinical detection of diagnostic biomarkers to differentiate dengue haemorrhagic fever

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Background: Dengue fever (DF) is a significant cause of acute febrile illness; timely identification of patients who progress to dengue haemorrhagic fever (DHF) is challenging. We aim to identify biomarkers to differentiate possible DHF early.

Methods: mRNA was extracted from the peripheral blood mononuclear cells of DF and DHF patients during the febrile stage to measure the expression levels of selected genes by quantitative polymerase chain reaction. Biomarkers (Interleukin-10 (IL-10), Ras Association Domain Family Member 5 (RASSF5) were selected to identify a different severity predictor in the acute stage of dengue.

Results: From an ongoing study, 71 samples were analysed, including 17 controls, 46 DF and 8 DHF. IL 10 median was 0.2315 (IQR 1.31) in DF and 6.7997 (IQR 84.21) in DHF. The distribution of IL-10 and RASSF5 was non-normal (Shapiro–Wilk $p < 0.001$). In IL-10, a statistically significant difference among the groups was observed (Kruskal–Wallis $H = 7.123$, $p = 0.028$). In pairwise comparisons, significantly higher IL-10 levels than DF were observed in DHF ($p = 0.025$). In RASSF5, the median was 0.2196 (IQR 1.37) in DF and 7.0467 (IQR 56.5) in DHF. No statistically significant difference among the groups was observed in RASSF5 (Kruskal–Wallis $H = 2.453$, $p = 0.293$).

Conclusion: IL-10 was significantly elevated in DHF compared to DF, suggesting its potential role as a marker of disease severity. This may be useful as a potential biomarker for the clinical prognosis of severe dengue. Further studies are needed to confirm the findings with a larger cohort. .

E-207 NS1 antigenemia extends the virological window for dengue therapeutic evaluation

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† These authors contributed equally to this work

Background: Dengue virus (DENV) infection causes major morbidity and approximately 40,000 deaths annually, yet no licensed antiviral exists. Early-phase trials rely on plasma DENV RNA, but RNAemia declines rapidly after presentation, narrowing the window for therapeutic assessment. Secreted nonstructural protein 1 (NS1) persists longer and has been linked to viral replication and some severity markers, suggesting value as a complementary biomarker.

Methods: We quantified NS1 and virological markers in (i) DENV-2-infected hepatocytes sampled over 48 h, (ii) 103 adults with dengue in the placebo arm of a randomized ivermectin trial, and (iii) 210 children with confirmed dengue in Thailand. We assessed correlations between NS1 and viral RNA or infectious titers, compared clearance times, and examined associations with WHO 1997 dengue fever (DF) and dengue hemorrhagic fever (DHF).

Results: In hepatocytes, NS1 area under the curve (AUC) correlated with infected-cell counts ($r=0.992, p<0.001$), and infectious titers ($r=0.858, p=0.006$). In adults, AUC-NS1 and AUC-RNA were moderately correlated ($r=0.407, p=0.015$), with no difference in AUC-NS1 between DF and DHF ($p=0.535$). In children, AUC-NS1 was higher in DHF than in DF ($p=0.005$), whereas AUC-NS1 and AUC-RNA were not correlated ($r=0.090, p=0.503$). NS1 clearance exceeded RNA clearance by about 1 day in adults (6.62 vs 4.96 days) and children (5.78 vs 4.41 days) (both $p<0.001$).

Conclusion: NS1 persists beyond RNAemia and reflects viral burden *in vitro* and in adults, supporting its use as a complementary biomarker for early dengue therapeutic evaluation. Variability by age and clinical phenotype highlights the need for standardized quantitative assays and subgroup-specific analyses.

E-215 Evaluation of Amplicon Sequencing Protocols for Dengue Virus Genomic Surveillance

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Background: Amplicon-based next-generation sequencing has become a widely adopted approach for viral genome sequencing. The performance of available amplicon sequencing protocols tends to vary on different Dengue virus (DENV) lineages. In the present study, we therefore, evaluated serotype-specific and pan-serotype protocols (DengueSeq) using locally circulating DENV lineages to determine their applicability for DENV genomic surveillance.

Methods: DengueSeq primer panels were modified to improve the coverage of untranslated regions of DENV genome. Serotype-specific and pan-serotype protocols were evaluated using a genetically diverse panel of DENV-1-4 isolates (n=17). Each isolate was sequenced at three concentrations (low, medium and high RNA loads; Cq 21–35) by using Illumina 150 PE technology.

Results: Pan-serotype panel (98.6%) and serotype-specific panels (97.9%) achieved comparable average genome completeness at 10× depth of coverage. However, the pan-serotype approach showed relatively low genome coverage in DENV-1 (95.6%) and DENV-4 (94.9%) at low concentrations but outperformed the serotype-specific approach in DENV-2 and DENV-3 (99.7% average completeness) across all dilutions. Genome coverage gaps mainly occurred at low virus concentrations, suggesting that low template loads likely caused the dropouts.

Conclusion: Both serotype-specific and pan-serotype approaches are appropriate to generate complete DENV genomes. These two approaches provide flexibility in choosing the most suitable protocol for arbovirus surveillance programmes. Specifically, the pan-serotype approach provides time and cost savings by eliminating prior serotype determination and allows the concurrent detection of mixed-serotype infections. The findings emphasize the importance of validating the existing protocols for local DENV diversity before implementing them for DENV genomic surveillance.

E-224 Urinary Proteins as Prognostic Biomarkers of Severe Dengue

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Background: Dengue is the most prevalent global arboviral infection, and numbers are projected to increase with a warmer climate. While most cases are mild, 2–5% will progress to develop severe complications. Current methods to stratify patients at risk of severe dengue rely on the WHO 2009 dengue guidelines; while sensitive, they lack specificity, which can result in unnecessary hospitalisation during large dengue outbreaks. Reliable prognostic biomarkers that are deployable across various healthcare settings are urgently needed.

Methods: In a prospective dengue cohort, we quantified urinary proteins, neutrophil gelatinase-associated lipocalin (NGAL) and soluble urokinase plasminogen activator receptor (suPAR), by ELISA. A total of 319 urine samples were evaluated: 113 in the febrile phase, 102 in the critical phase, 74 in the recovery phase, and 30 from healthy controls. Disease severity was classified using the WHO 2009 classification.

Results: Urinary NGAL and suPAR were significantly higher in dengue cases compared to controls, and levels increased with progressive severity in the febrile and critical phases. In the febrile phase, the AUROC to stratify those at risk of severe dengue was 0.88 for urinary NGAL and 0.79 for urinary suPAR. Urinary NGAL at a cut-off value of 3.5 ng/ml yielded a sensitivity of 0.99 and specificity of 0.74, whereas suPAR at a cut-off of 13.4 ng/ml demonstrated a sensitivity of 0.65 and specificity of 0.93.

Conclusion: Febrile phase urinary NGAL and suPAR demonstrated good prognostic value for identifying those at risk of severe dengue. Further studies are needed to validate these findings.

E-225 Clinical performance evaluation of a high-throughput, automated dengue NS1 antigen assay for diagnosis of acute dengue infection

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Background: Dengue virus is a mosquito-borne flavivirus with four distinct serotypes; infection by one serotype does not confer cross-protective immunity against the others. The dengue virus NS1 protein is detectable in blood during early disease, making it a reliable marker for prompt diagnosis. The Elecsys® Dengue Ag assay detects the NS1 antigen of all dengue serotypes using a fully automated platform. This study evaluated the performance of the assay in individuals with confirmed disease and determined its specificity in endemic and non-endemic cohorts.

Methods: The relative specificity and positive percent agreement (PPA) of the Elecsys Dengue Ag assay were based on comparisons with the Vidas Dengue NS1 Ag assay and Euroimmun Dengue Virus NS1 ELISA, respectively. Diagnostic sensitivity was assessed against dengue RNA detection by PCR. PPA and diagnostic sensitivity were evaluated in samples from individuals at different stages after symptom onset. Specificity was analysed in samples presumed to be dengue-negative from blood donors from endemic or non-endemic regions.

Results: The PPA in PCR-positive samples was 98.76% (95% CI: 96.41-99.74, n=241). Specificity was 100% (95% CI: 99.75-100.00, n=1497) and 99.91% (95% CI: 99.49-100.00, n=1099) in samples from endemic and non-endemic areas, respectively. The assay also demonstrated a diagnostic sensitivity of 94.90% (95% CI: 91.44-97.26, n=255) in PCR-positive samples.

Conclusion: The Elecsys Dengue Ag assay demonstrated strong agreement with the comparator assays, including high sensitivity during acute infection and excellent specificity in diverse populations, thus providing a rapid (18-minute), high-throughput, clinically relevant means for timely dengue diagnosis and outbreak management.

E-226 Clinical performance of a fully automated assay for detection of anti-dengue IgM antibodies in late acute and recent dengue infections

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Background: Accurate and timely diagnosis of dengue virus (DENV) infections is essential for disease management. Anti-DENV IgM antibodies appear within 3-5 days post-symptom onset and remain detectable for months, making them useful for identifying recent or late acute infections. The Elecsys® Dengue IgM assay is a fully automated immunoassay for qualitative detection of IgM antibodies for diagnosing acute or recent DENV infection. This study evaluated its diagnostic performance compared with established commercial assays across defined cohorts using frozen plasma or serum samples.

Methods: Diagnostic sensitivity was assessed using follow-up samples from PCR-confirmed symptomatic patients taken ≤45 days post-PCR confirmation. Relative sensitivity was assessed using IgM-positive samples based on comparator assays (Euroimmun and Tecan Dengue IgM ELISA). Specificity was assessed in samples from presumed dengue-negative populations in endemic and non-endemic regions.

Results: The Elecsys Dengue IgM assay demonstrated higher diagnostic sensitivity (86.78%; 95% CI: 79.42-92.25%; n=121) than the comparator assay (69.42%; 95% CI: 60.39-77.47%). Its relative sensitivity in IgM-positive plasma and serum samples was 100% (95% CI: 95.75-100.00%; n=85). Its relative specificity in presumed-negative samples from endemic and non-endemic regions was 94.61% (95% CI: 93.33-95.70%; n=1483) and 99.18% (95% CI: 98.45-99.62%; n=1096), respectively.

Conclusion: The Elecsys Dengue IgM assay outperformed the comparator and demonstrated 100% relative sensitivity in IgM-positive serum and plasma samples. It also demonstrated high specificity in samples from endemic and non-endemic regions. These results support the value of the Elecsys Dengue IgM assay in detecting DENV-specific IgM antibodies to facilitate clinical management and public health surveillance.

E-234 Dengue serotype and its association with clinical severity: a retrospective study in a tertiary hospital in Kuala Lumpur

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Background: Dengue remains a major public health challenge in Malaysia, where all four dengue virus (DENV) serotypes co-circulate and influence disease severity. This study aimed to determine the distribution of circulating dengue serotypes and evaluate their association with disease severity, clinical manifestations, and laboratory parameters among patients in a tertiary hospital in Kuala Lumpur.

Methods: A retrospective study was conducted at Hospital Kuala Lumpur from March 2023 to August 2024. Dengue NS1 antigen-positive samples submitted to the National Public Health Laboratory for serotyping via multiplex real-time polymerase chain reaction (PCR) were included. Demographic, clinical, and laboratory data were extracted from medical records. Associations between serotypes and clinical outcomes were analysed using Chi-square or Fisher's exact test for categorical variables, and Kruskal–Wallis or one-way ANOVA for continuous variables.

Results: A total of 126 dengue cases were analysed. DENV-2 was the predominant serotype (68.3%), followed by DENV-4 (11.9%), DENV-1 (10.3%), and DENV-3 (9.5%). Most patients had dengue with warning signs (69.0%), while 27.0% developed severe dengue. Severe dengue occurred most frequently in DENV-2 infections; however, no significant association was found between serotype with disease severity and clinical manifestations. The platelet count, aspartate aminotransferase and alanine aminotransferase were statistically significant. DENV-4 infections showed pronounced thrombocytopenia, whereas DENV-3 infections demonstrated higher transaminase levels.

Conclusion: DENV-2 was the dominant serotype and accounted for most severe dengue cases. Variations in platelet counts and transaminase levels suggest differences in clinical profiles, underscoring the importance of continuous dengue serotype surveillance for epidemiological monitoring and clinical risk assessment.

E-238 Endemicity Matters: A 6-Year Retrospective Investigation of Clinical Outcomes and Severity Markers in a Multi-National Dengue Cohort

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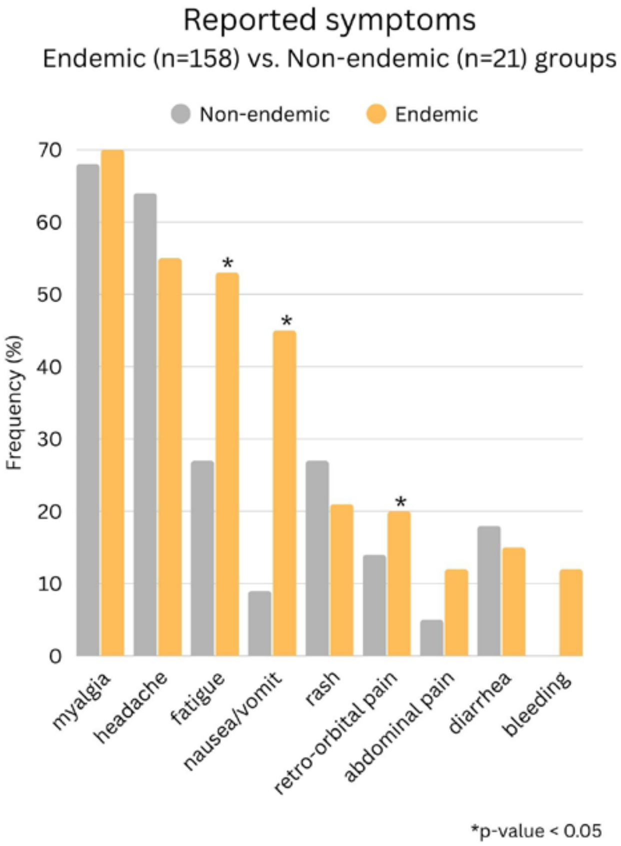
Background: Data on dengue infections among foreigners in specialized tropical clinics remains scarce. This study evaluated clinical presentations, severity markers, and seasonal patterns of laboratory-confirmed dengue among foreign nationals visiting the Fever Clinic at the Hospital for Tropical Diseases, Bangkok.

Methods: This retrospective review (Jan 2020–Dec 2025) of 179 foreign nationals with laboratory-confirmed dengue (NS1, IgM, or PCR) compared clinical and laboratory parameters between endemic and non-endemic cohorts.

Results: 179 cases were identified representing 22 countries (mean = 29 years; 43% male). All participants presented with fever. Incidence peaked in November (50% aged 21–30). While 21 (12%) originated from non-endemic regions, most reported recent Southeast Asian travel (mean = 1.5 months). Mean illness duration was 3.8 days. Primary symptoms were myalgia (71%), headache (55%), and fatigue (50%); myalgia was the most frequent complaint in non-endemic patients (68%). Bleeding was exclusive to endemic patients ($p < .05$). Endemic cases showed significantly higher frequencies of retro-orbital pain, fatigue, and nausea ($p < .05$). Overall, 57% required hospitalization. Endemic status was significantly associated with higher admission rates (62.7% vs. 33.3%; $p = .024$) and lower mean platelet counts (Mean Difference:-33,282 cells/mm^3; 95% CI:-66,206 to-358; $p = .048$). No significant differences were observed in Hb, WBC, or liver enzymes ($p > .05$).

Conclusion: Although clinical presentations are similar across cohorts, endemic travelers face higher severity and significantly higher admission rates. A high suspicion for severe progression is necessary for all patients, especially during post-monsoon peaks.



E-239 Ongoing Chikungunya Virus Transmission went Under-Recognized in a Setting with a High Burden of Dengue

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Background: North Sumatra is an Indonesian province with high-burden for dengue, reporting a rolling 5-year average of ±6000 cases annually. In contrast, the Indonesian Ministry of Health reported no chikungunya in North Sumatra in 2019-2024, then in 2025 reported a large chikungunya outbreak. This study describes evidence for ongoing chikungunya transmission in a highly dengue-endemic context, and presents the first published whole genome chikungunya virus (CHIKV) sequences from North Sumatra.

Methods: Chikungunya detection was performed on suspected dengue patients from Medan, North Sumatra using RT-PCR and IgG/IgM rapid test. Sera were also tested for dengue using RT-PCR, IgM rapid test, and indirect IgG ELISA. Whole genome sequencing was conducted to identify CHIKV genotype and potential mutations.

Results: Of 300 samples, there were 24 (8%) chikungunya and 167 (56%) dengue cases. Ten CHIKV samples were sequenced, identified as Asian genotype, and all had E1-K211E mutations associated with increased adaptation to *Aedes aegypti* . Serology testing showed 197 (66%) samples with positive dengue IgG only, 3 (1%) with positive CHIKV IgG only, and 58 (19%) positive for both.

Conclusion: There is active co-circulation of DENV and CHIKV in Medan, North Sumatra despite official case reports reporting only dengue and no chikungunya in 2019-2024. These 2023-2024 CHIKV IgG findings suggests partial population immunity; susceptible individuals remain, permitting ongoing transmission, demonstrated by chikungunya outbreak in 2025. In settings with multiple co-circulating arboviruses, it's important to have integrated surveillance using multiplexing molecular-based diagnostics, and genomic sequencing for monitoring mutations with outbreak potential.

E-258 The burden of additional Dengue Infection Detected by Dengue IgM Capture ELISA in Cebu, Philippines

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Background: Dengue diagnosis varies by timing of infection, with NS1 antigen and RT-PCR detecting early-phase cases, while IgM serology identifies infections in the later stage. Reliance on early diagnostic tests alone may underestimate the disease burden, underscoring the importance of incorporating IgM detection to improve surveillance and epidemiologic assessment. We aimed to evaluate the proportion of febrile children with negative dengue NS1 and RT-PCR, but with detectable anti-DENV IgM by serologic testing. Methodology: We analyzed acute and convalescent paired sera collected from children presenting with an acute febrile illness as part of an observational study (ClinicalTrials.gov, NCT03465254) conducted in Cebu, Philippines. A total of 314 paired samples that were dengue RT-PCR-and NS1-negative were tested for anti-DENV IgM by enzyme-linked immunosorbent assay (Panbio™ Dengue IgM Capture ELISA).

Results: Out of 314, 33 (10.51%) of acute samples were dengue IgM positive. Among these, 26 (76.47%) of the paired convalescent samples had detectable dengue IgM. The median age was 11 years old (IQR=4), ranging from 9 to 13 years old. The majority of children with detectable anti-DENV IgM were clinically diagnosed as dengue (32, 96.97%), and were more likely to present with nausea and vomiting (p=0.018) and anorexia (p=0.041).

Conclusion: Our findings show that anti-DENV IgM ELISA identified an additional 11% of dengue cases despite negative NS1/RT-PCR. This reflects expected limitations of early diagnostic assays and the importance of incorporating serologic testing to capture infections presenting in the later phase of dengue illness.

E-271 Comparison of clinical, hematological, and cytokine profiles between dengue and severe dengue patients in Dhaka, Bangladesh

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Background: Dengue remains a major public health concern in Bangladesh. Cytokine responses are central to dengue pathogenesis and may help distinguish disease severity. This study compared the clinical, hematological, and cytokine profiles of dengue and severe dengue patients and evaluated their ability to differentiate between the two groups.

Methods: A cross-sectional study was conducted at Bangladesh Medical University and DNCC Dedicated COVID-19 Hospital, Dhaka, involving 85 serology-confirmed dengue patients categorized into dengue (n=25) and severe (n=60) dengue patients according to WHO 2025 criteria. Clinical features, hematological parameters, and cytokines (GM-CSF, MIP-1β, IL-4, IL-6, IL-10) were measured. ROC curve analysis was performed to assess the discriminatory performance of cytokines.

Results: In the overall study population, 58.8% were male, with a mean age (mean±SD) of 38.58±16.46 years. Bodyache (44.7%), headache (35.3%), and fever (32.9%) were the most prevalent symptoms. Diabetes mellitus (15.3%) and hypertension (11.8%) were the most common comorbidities. In the laboratory profile, platelet count and neutrophil percentage were significantly decreased, whereas hematocrit, WBC count, lymphocyte percentage, and alanine transaminase were elevated in the severe dengue patients. Comparing cytokines, IL-4, GM-CSF, and MIP-1β were decreased, whereas IL-6 was elevated in severe dengue patients ($p<0.05$). ROC curve analysis revealed that IL 4 (AUC=0.78, $p<0.05$) and MIP 1β (AUC=0.93, $p<0.05$) strongly differentiate the dengue patient group. Conversely, IL 6 (AUC=0.85, $p<0.05$) showed a strong ability to distinguish severe dengue patients.

Conclusion: Distinct clinical and cytokine patterns were observed between severity groups, indicating their potential utility in early severity assessment and warranting larger cohort validation.

E-274 Psychometric evaluation of a novel patient-reported Dengue Virus Daily Diary (DENV-DD) measuring illness intensity

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Background: Dengue remains a significant global health concern, but few measures exist to assess the trajectory and intensity of dengue-associated signs/symptoms from the patient perspective. This study evaluated the psychometric properties of the Dengue Virus Daily Diary (DENV-DD), a novel patient-reported outcome measure assessing dengue symptom intensity and disease burden.

Methods: The draft DENV-DD, developed per regulatory guidance, was administered to febrile individuals aged 8-65 years in an observational study across two South-East Asian dengue-endemic countries. Laboratory-confirmed dengue participants (n=81) completed the diary for 28 days. Dengue negative participants (n=29) completed 14 days. Concurrent measures supported psychometric evaluation. Dengue positive data were used to evaluate item performance, dimensionality, reliability, validity, ability to detect change, and score interpretation of the DENV-DD. Dengue negative data supported known-groups comparisons.

Results: Confirmatory factor analysis supported a single total symptom score. Internal consistency was very strong (Cronbach's alpha=0.90) and test-retest reliability across a 3-day interval was moderate-strong (intraclass correlation coefficients ≥0.68). Construct validity showed moderate correlations with concurrent measures (r=0.39-0.52) and significant between groups differences by health states ($p<0.001$) and dengue infection status ($p=0.017$). Ability to detect change was demonstrated by greater score improvements in improved versus stable participants. Assessment of meaningful score regions suggested the total score could be split into distinct severity ranges.

Conclusion: The DENV-DD is a reliable and valid PRO measure assessing the trajectory and intensity of dengue-associated signs/symptoms in outpatient settings. This tool may be useful in observational and clinical research settings to assess disease burden and impact of interventions on reducing illness intensity.

E-275 Timely Detection of Critical Phases and Shock in Dengue Fatalities: Findings from an Annual Dengue Death Review in Sri Lanka, 2024

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Background: Sri Lanka has been successful in reducing the dengue case fatality rate by improving patient care. Key improvements include timely recognition of the critical phase, early detection of shock, and judicious fluid management. We analysed fatal dengue cases to assess whether the critical phase and shock were accurately identified and whether fluid replacement was appropriately administered.

Methods: All dengue-related deaths reported in 2024 in Sri Lanka were reviewed, using data from clinical records and adjudicated by an expert review panel. Key variables considered were admission details, detection of warning signs, critical-phase timing, recognition of shock, commencement of critical-phase monitoring, and the panel's retrospective assessment of the adequacy of rate and type of fluid management. Available-case denominators were used throughout.

Results: Among the 24 fatalities, 10 (41.7%) cases were already in the critical phase or shock on admission. Another seven (29.16%) subsequently developed leaking or shock during ward stay. Documentation of warning signs was inadequate in 5/24 (20.8%). Among evaluable cases, specific dengue monitoring chart initiation was delayed in 12/20 (60.0%) and shock recognition in 12/18 (66.7%). Early fluid management was identified as inadequate in 9/20 (45.0%). Delayed recognition of significant bleeding was noted in 14/16 (87.5%), which resulted in delayed blood transfusion in 13/16 (81.2%).

Conclusion: These findings suggest that opportunities remain to further enhance the timely recognition of shock and bleeding in dengue patients. Improving the timely detection of shock, appropriate monitoring, and fluid management may lead to better clinical outcomes and further reduction of case fatalities.

E-276 Bedside serial ultrasound versus haematocrit rise as plasma leakage criteria in dengue haemorrhagic fever: a retrospective analysis from National Institute of Infectious Diseases (NIID), Sri Lanka

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Background: WHO SEARO criteria for Dengue Haemorrhagic Fever (DHF) consider evidence of plasma leakage as the defining criterion: haematocrit/packed cell volume (PCV) rise ≥10-20% from baseline, evidence of pleural effusion or ascites clinically or on imaging or presence of hypoalbuminemia/hypoproteinaemia. We compared the proportion of confirmed DHF patients meeting following plasma leakage criteria: PCV ≥10%, PCV ≥20%, and serial bedside ultrasound (USS) free fluid detection.

Methods: We conducted a retrospective analysis of dengue admissions to the NIID, Sri Lanka, during 2023–2024 and the second quarter of 2025. Serologically confirmed patients (NS1 antigen or dengue IgM positive) with a final diagnosis of DHF (determined retrospectively) and available USS and PCV data were included.

Results: Of 875 confirmed dengue admissions, 344 (39.3%) were classified as DHF. USS was performed in all 344 and detected free fluid (ascites and/or pleural effusion) in 330 (95.9%). PCV data were available in 324 (94.2%): PCV rise ≥10% was present in 150 (46.3%) and ≥20% in only 43 (13.3%). Among the 324 with both tests, PCV ≥10% alone would miss 168 (51.9%) USS-confirmed leakage cases; PCV ≥20% criterion would miss 270 (83.3%). Only 8 (2.5%) and 3 (0.9%) patients had PCV ≥10% or ≥20% respectively without USS-detectable free fluid.

Conclusion: Bedside ultrasonography (USS) significantly outperforms haematocrit (PCV) monitoring for detecting plasma leakage in DHF. Relying solely on PCV thresholds misses over half of patients as PCV may be confounded with factors such as bleeding. Consequently, serial bedside USS is an indispensable diagnostic tool for timely, accurate DHF classification

E-294 Clinical Features, Diagnostic Pitfalls, and Outcomes of Neonatal Dengue at a Tertiary Children's Hospital in Vietnam

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Background: Neonatal dengue is an uncommon but important diagnosis in endemic settings because it can mimic neonatal sepsis or immune thrombocytopenia. This study aimed to describe the clinical features, laboratory findings, and outcomes of neonatal dengue.

Methods: We conducted a retrospective descriptive study of neonates aged <28 days with laboratory-confirmed dengue admitted to Children's Hospital 1, Ho Chi Minh City, Vietnam, from 2012 to 2018. Diagnosis was based on dengue NS1 antigen and/or IgM ELISA. Maternal perinatal history, neonatal clinical features, laboratory results, treatment, and outcomes were reviewed.

Results: Thirty-two neonates were included. All mothers had confirmed dengue in the perinatal period; the median interval between maternal fever onset and delivery was-1 day (IQR,-2 to 2). At referral, 25.0% were misdiagnosed with neonatal sepsis and 12.5% with immune thrombocytopenia. Median age at fever onset was 5 days and at diagnosis was 7 days. Petechiae (87.5%) and hepatomegaly (75.0%) were common. Most cases (81.2%) were dengue with warning signs; none progressed to severe dengue. Platelet counts decreased from 97,111 ± 37,826/mm^3 (days 1–3) to 30,100 ± 5,749/mm^3 (days 4–6). NS1 positivity reached 94.4% when tested within the first 3 days. Blood cultures were negative in all cases; one neonate required platelet transfusion and no deaths occurred.

Conclusion: Neonatal dengue should be suspected in febrile neonates born to mothers with perinatal dengue, particularly with petechiae, hepatomegaly, thrombocytopenia, negative cultures, and low inflammatory markers. Early recognition may reduce misdiagnosis and unnecessary antibiotic use.

E-306 Intramuscular Anti-D Immunoglobulin for Dengue-Associated Thrombocytopenia: A Preliminary Clinical Study

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Background: Dengue fever frequently leads to thrombocytopenia, posing significant risks of bleeding and clinical complications. Currently, no specific therapy exists beyond supportive care and platelet transfusions. Intravenous Anti-D immunoglobulin is effective in immune thrombocytopenic purpura (ITP) but is not readily available in India. This study explores the feasibility and safety of intramuscular (IM) Anti-D as a novel intervention for dengue-associated thrombocytopenia.

Methods: Seven patients with serologically confirmed dengue infection and platelet counts between 50,000–90,000/µL were enrolled. Each received a single IM dose of Anti-D immunoglobulin (300 mcg) with standard supportive care. Platelet counts, clinical outcomes, and adverse events were monitored for 7 days post-administration

Results: The mean baseline platelet count was 74,200/µL (range 60,000–88,000). Following IM Anti-D administration, all patients demonstrated stabilization or an upward trend in platelet counts within 72 hours. None required platelet transfusion. No serious adverse effects or hemolytic reactions were observed. Supportive care requirements remained unchanged.

Conclusion: This is the first clinical exploration of intramuscular Anti-D immunoglobulin in dengue-associated thrombocytopenia. Findings from this small cohort suggest feasibility, safety, and potential benefit in stabilizing platelet counts. Larger, controlled studies are warranted. If validated, this approach could offer an accessible therapeutic option in dengue-endemic, resource-limited regions.

Keywords: Dengue, Thrombocytopenia, Anti-D Immunoglobulin, Intramuscular, Novel therapy, LMIC

E-350 Post-Dengue Syndrome: A Chronic Sequelae of Dengue Infection-A Prospective Study in Pakistani Cohort

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Background: Dengue fever is a major global health concern, particularly in tropical and subtropical regions, yet the long-term effects of infection, known as post-dengue syndrome (PDS), remain insufficiently studied. This study aimed to evaluate the prevalence of persistent symptoms following dengue infection and their association with disease severity within a Pakistani cohort.

Methods: Conducted at Mayo Hospital in Lahore, this observational cohort study tracked **104** dengue-infected patients aged 11 years and older over a six-month period. Persistent symptoms were defined as those persisting for more than 14 days post-infection.

Results: The study revealed that 84 patients (81%) experienced persistent symptoms, with myalgia (86%), generalized weakness (82%), and fatigue (76%) being the most frequently reported. Patients classified with **severe dengue (Dengue Hemorrhagic Fever [DHF] Grades 1-3)** had significantly higher odds of developing persistent symptoms compared to those with non-severe dengue (Dengue Fever [DF]). Multivariable analysis indicated that patients with severe dengue were 17.7 times more likely to report persistent symptoms ($P < 0.001$). Additionally, rheumatic symptoms during the acute phase were strongly associated with the likelihood of long-term sequelae (a OR = 3.89, 95% CI: 1.17–13.0, $P = 0.027$). Cognitive symptoms, such as memory impairment, were infrequent, affecting only 3.6% of the cohort.

Conclusion: These findings emphasize the significant burden of persistent symptoms following dengue infection and highlight the necessity for improved long-term care strategies, particularly in dengue-endemic regions like Pakistan.

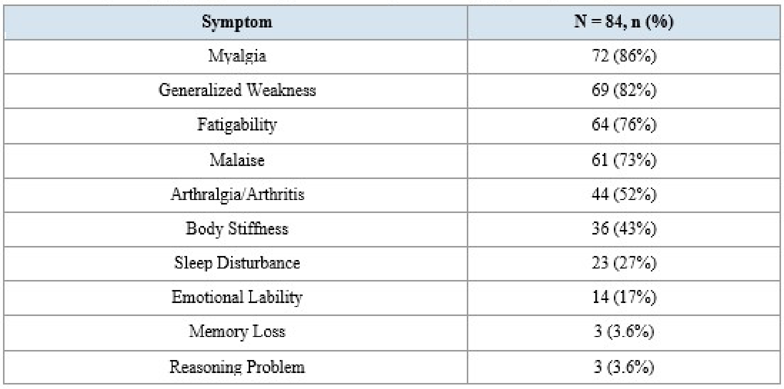

Table 2: Frequency of symptoms in patients with persistent symptoms (N = 84)

Symptom	N = 84, n (%)
Myalgia	72 (86%)
Generalized Weakness	69 (82%)
Fatigability	64 (76%)
Malaise	61 (73%)
Arthralgia/Arthritis	44 (52%)
Body Stiffness	36 (43%)
Sleep Disturbance	23 (27%)
Emotional Lability	14 (17%)
Memory Loss	3 (3.6%)
Reasoning Problem	3 (3.6%)

E-363 Point-of-Care Prediction of Severe Dengue Using the Non-Structural Protein–Thrombin Complex (NST): From Biomarker Discovery to Clinical Deployment

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Background: Timely identification of patients at risk for severe dengue is a major unmet need in endemic regions, where outbreaks overwhelm healthcare systems. Existing clinical and laboratory markers lack sufficient accuracy in the early febrile phase. We evaluated the non-structural protein–thrombin complex (NST) as a novel, mechanistically relevant biomarker for early risk stratification and its translation into a rapid point-of-care test.

Methods: In this retrospective diagnostic–prognostic study, 162 acute-phase patients (Day 0–7) were enrolled, including 102 confirmed dengue cases and 60 non-dengue controls. NST was quantified using ELISA and a newly developed rapid colorimetric strip (NST-STRIP) with a portable reader. Diagnostic accuracy and severity prediction (WHO 2009 classification) were assessed using ROC analysis and multivariable models adjusting for key confounders.

Results: NST-ELISA achieved near-perfect discrimination for dengue infection (AUC = 1.000), while NST-STRIP maintained excellent performance (AUC = 0.967). For early prediction of severe dengue, NST-STRIP outperformed conventional markers (AUC = 0.905 vs. platelet 0.848). Integration of NST-ELISA, NST-STRIP, and platelet count significantly improved sensitivity to 90.7% (OR = 27.8). The NST-STRIP demonstrated high reproducibility (CV <5%) and strong quantitative correlation with ELISA (r = 0.99), with stable performance across fever days.

Conclusions: NST represents a clinically actionable biomarker that bridges pathophysiology and real-world application. The rapid NST-STRIP enables bedside risk stratification within minutes, offering a scalable solution for outbreak settings and transforming early dengue management from reactive to predictive.

E-368 Dengue-related maculopathy, a serious but misregarded complication of dengue: One-year follow-up of 62 patients in a cohort study.

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Background: Dengue is defined as severe when patients exhibit severe plasma leakage, severe bleeding and/or severe organ involvement. Here, we present a large cohort of patients with a poorly documented organ injury, namely dengue-related maculopathy (DRM).

Material and methods: We assessed a prospective cohort built during the 2021 dengue epidemic on Réunion Island. Patients who consulted with ocular symptoms in the aftermath of a confirmed dengue episode were screened, and we only enrolled patients with confirmed maculopathy by optical coherence tomography. Patients were followed for one year.

Results: Sixty-two patients were enrolled: the median age was 34.5 years [26-41.3], and women were predominant (n=42/62, 68%). Patients were classified as non-severe dengue with warning signs in 43% (n=27/62), and as severe dengue in 6% (n=4/62) of them. Ocular symptoms occurred within 7 days IQR [6-8] after onset of dengue, frequently upon waking-up (n=31/50, 62%), were mainly bilateral (n=39/62, 63%), and consisted mostly of blurred vision (n=42/60, 70%) and scotoma (n=39/61, 64%). From the 124 examined eyes, 95 presented DRM. At baseline, the best corrected visual acuity (BCVA) was less than 85 ETDRS (Early Treatment Diabetic Retinopathy Study) in 41% (n=38/93) of the eyes. At the one-year follow-up visit, 36 patients reported persistent ocular symptoms (mainly scotoma, 53%), affecting working for 27% (n=14/52) and/or driving for 20% (n=10/50) of them.

Conclusion: DRM can lead to long-term ocular symptoms. Clinicians and ophthalmologists should be aware of this condition, to recognize it and to advise patients on its prognosis.

E-373 Dengue Encephalitis

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Abstract: Dengue fever is a common arboviral infection in tropical regions, typically presenting with fever, rash, myalgia, and hemorrhagic manifestations. Neurological complications such as dengue encephalitis are rare but increasingly recognized. We report a case of dengue encephalitis in a 4-year-old female child from northeastern India, highlighting the diagnostic challenges and clinical course of this uncommon presentation. The child presented with a high-grade fever of eight days' duration, associated with vomiting, headache, a generalized tonic-clonic seizure, and altered sensorium. On examination, she was febrile, tachycardic, and hypotensive with petechial rash and signs of early shock. Neurological evaluation revealed impaired consciousness without meningeal signs. Laboratory investigations showed thrombocytopenia, leukopenia, elevated liver enzymes, and hyponatremia. Cerebrospinal fluid analysis revealed lymphocytic pleocytosis with elevated protein. Serological testing confirmed dengue infection with positive IgM antibodies in both serum and cerebrospinal fluid, while other infectious causes such as Japanese encephalitis, herpes encephalitis, malaria, and typhoid were excluded. During hospitalization, the patient developed bleeding manifestations and progressed to dengue shock syndrome. She was managed in the intensive care unit with supportive therapy, including intravenous fluids, blood products, and anticonvulsants. The patient showed gradual clinical improvement and was discharged without neurological deficits after two weeks.

This case emphasizes that dengue encephalitis, although rare, should be considered in children presenting with fever and neurological symptoms in endemic regions. Early recognition and exclusion of other causes of encephalitis are essential for appropriate management. A high index of suspicion is crucial to avoid misdiagnosis and ensure timely supportive care, which can lead to favorable outcomes even in severe presentations.

E-396 Myeloperoxidase Promotes Gut Tight Junction Breakdown in Clinical Dengue

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Background: Increased intestinal permeability in dengue is associated with severe complications. The breakdown of gut tight junctions mediated by neutrophil-derived factors has been documented in inflammatory bowel diseases but has not yet been reported in dengue. In this study, we investigated the role of myeloperoxidase (MPO) in gut tight junction breakdown among a cohort of dengue-positive adults.

Methods: Plasma samples were collected from 97 adult dengue patients (39 with dengue without warning signs [D*w*WS], 45 with dengue with warning signs [DWS], and 13 with severe dengue [SD]) during the febrile, critical, and recovery phases. Samples were assayed for markers of intestinal injury (Trefoil factor 3, TFF3), gut tight junction integrity (Zonula Occludens-1 and Caludin5) and neutrophil MPO using serological assays.

Results: During the febrile and critical phases, all measured proteins were elevated in dengue patients compared to controls, returning to baseline levels in the recovery phase. SD patients exhibited greater tight junction breakdown and injury, and higher MPO levels compared to DWS and DwWS patients. MPO levels positively correlated with intestinal injury and tight junction disruption, suggesting its role in mediating gastrointestinal injury in dengue.

Conclusion: In adults with dengue, increased intestinal permeability is associated with MPO-mediated disruption of tight junctions. Targeting MPO may represent a potential therapeutic strategy.

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E-397 Multiplex RT-PCR For Simultaneous Diagnosis of Dengue & Chikungunya Co-Infection in Sri Lanka

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Background: In Sri Lanka, dengue (DENV) and chikungunya (CHIKV) occur regularly, with periodic increases in cases straining healthcare services. Diagnosis in many settings still relies on antigen-based tests, which may vary across infection stages. Molecular methods provide greater sensitivity and specificity, particularly in early illness, and enable reliable detection of circulating viral strains.

Methodology: Serum samples (n=11) from patients with acute febrile illness (1–5 days post-onset) were analysed using multiplex RT-PCR for DENV serotypes and CHIKV. Results were compared with NS1 antigen testing.

Results: Multiplex RT-PCR detected DENV in 8/11 (72.7%) (95% CI: 39.0–94.0), CHIKV in 5/11 (45.5%) (95% CI: 16.7–76.6), and co-infection in 2/11 (18.2%) (95% CI: 2.3–51.8). DENV-2 was the predominant serotype (6/8), followed by DENV-4 (2/8).

NS1 positivity was 7/11 (63.6%) (95% CI: 30.8–89.1), with three RT-PCR-positive cases missed by NS1. RT-PCR quantification cycle (Cq) values ranged from 16.95–39.99 for DENV and 27.72–39.52 for CHIKV, with lower values in early infections (days 3–4), consistent with active viraemia.

Clinical features, including arthralgia, myalgia, vomiting, and joint pain, were non-specific across mono- and co-infections.

Conclusion: This study provides molecular evidence of DENV–CHIKV co-infections in Sri Lanka and demonstrates that multiplex RT-PCR improves early detection compared to NS1-based assays, supporting integration of multiplex molecular diagnostics into routine clinical management and surveillance in endemic settings.

E-406 Point-of-care IgG as a Predictive Marker of Dengue Clinical Outcomes

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Background: Dengue IgG seropositivity is commonly interpreted as a marker of secondary infection and increased disease severity. We aimed to reassess its association with clinically significant deterioration using real-world electronic health record data.

Methods: We conducted a retrospective cohort study across six public hospitals in Singapore, including patients presenting to the Emergency Department or admitted between 1 January 2023 and 31 December 2025 with clinically diagnosed dengue. Patients with laboratory-confirmed dengue (NS1 antigen or PCR positive) and IgG results from a rapid dengue duo diagnostic test were included. The primary outcome was a composite of severe or higher-acuity illness: ICU/HDU admission, in-hospital mortality, peak NEWS2 ≥5, or fluid accumulation. Multivariable logistic regression was used to adjust for age, sex, ethnicity, and Charlson Comorbidity Index.

Results: Among 4,832 patients, 1,425 (29.4%) were IgG-positive and 854 (18.0%) met the composite outcome. Severe illness was independently associated with increasing age (adjusted OR [aOR] 1.13 per 10-year increase; 95% CI 1.08–1.19), male sex (aOR 0.78; 95% CI 0.67–0.91), Indian ethnicity (aOR 1.38; 95% CI 1.08–1.75), and higher Charlson Comorbidity Index (Charlson 1–2: aOR 1.76; 95% CI 1.42–2.17; Charlson ≥3: aOR 2.48; 95% CI 1.75–3.50). Despite being older and having greater comorbidity burden, IgG-positive patients had lower odds of severe illness after adjustment (aOR 0.62; 95% CI 0.52–0.74).

Conclusion: Contrary to conventional assumptions, dengue IgG seropositivity was associated with lower risk of severe illness. Further studies needed to evaluate performance in secondary dengue and clarify disease pathogenesis in older adults.

E-408 Fluid Management in Dengue Fever – Is Hospital-at-Home a Safe Alternative to Inpatient Care?

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Background: Effective vector control has paradoxically reduced dengue herd immunity in Singapore, shifting the disease burden toward older adults with multi-comorbidities. This demographic faces heightened risks of severe disease, prolonged hospitalisation, and increased resource utilisation, necessitating novel care models to optimise outcomes and manage healthcare capacity.

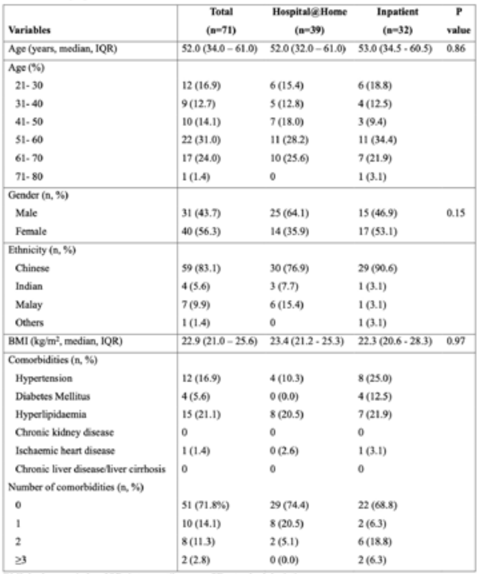
Objective: To evaluate the safety and performance of a Hospital-at-Home (H@H) model compared with traditional inpatient care for haemodynamically stable adult dengue patients at a Singapore tertiary hospital.

Methods: This retrospective cohort study included laboratory-confirmed dengue patients (NS1 antigen or PCR positive) hospitalised between June 2022 and March 2024. Eligible patients were haemodynamically stable per the managing physician. Exclusion criteria comprised haemodynamic instability, non-resolving warning signs, major advanced unstable comorbidities, and immunocompromised status. H@H-enrolled patients were compared with inpatients who declined participation. Baseline demographics, fluid balances, and clinical outcomes were abstracted from electronic records.

Results: We evaluated 39 H@H patients and 32 inpatients; 43.7% were male, 31.0% were aged 51–60, 28.2% had ≥1 comorbidity, and 69.0% presented without warning signs. Median recovery day did not differ significantly between groups (7 vs. 8 days). Nine patients progressed to severe dengue (2 severe transaminitis, 1 gastrointestinal bleeding). Six H@H patients developed plasma leakage with hypotension requiring home intravenous (IV) fluid boluses; 5 were managed at home, while 1 preferred return-to-hospital (RTH). Another H@H patient had an RTH for a rheumatoid arthritis flare; both recovered well. No high-dependency/intensive-care transfers or 30-day mortality occurred. H@H patients received significantly shorter IV fluid durations (2 vs. 4 days), whereas a higher proportion of inpatients received excessive IV fluids (84.4% vs. 56.4%). Overall, H@H saved 84 hospital bed days.

Conclusion: Clinically stable adult dengue patients, including those with multi-comorbidities, can be safely managed under the H@H model to optimise limited hospital bed capacity. H@H has since become an established care pathway in our institution.

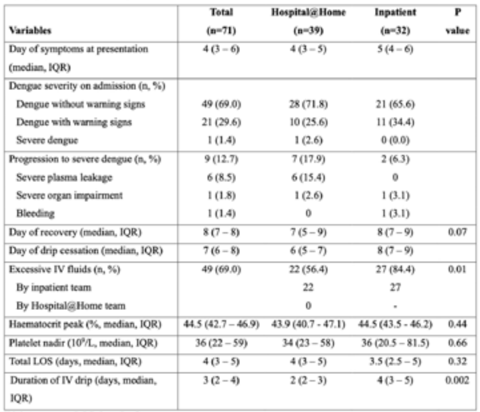
Table 1: Demographics



Variables	Total (n=71)	Hospital@Home (n=39)	Inpatient (n=32)	P value
Age (years, median, IQR)	52.0 (34.0 – 61.0)	52.0 (32.0 – 61.0)	53.0 (34.5 - 60.5)	0.86
Age (%)				
21- 30	12 (16.9)	6 (15.4)	6 (18.8)	
31- 40	9 (12.7)	5 (12.8)	4 (12.5)	
41- 50	10 (14.1)	7 (18.0)	3 (9.4)	
51- 60	22 (31.0)	11 (28.2)	11 (34.4)	
61- 70	17 (24.0)	10 (25.6)	7 (21.9)	
71- 80	1 (1.4)	0	1 (3.1)	
Gender (n, %)				
Male	31 (43.7)	25 (64.1)	15 (46.9)	0.15
Female	40 (56.3)	14 (35.9)	17 (53.1)	
Ethnicity (n, %)				
Chinese	59 (83.1)	30 (76.9)	29 (90.6)	
Indian	4 (5.6)	3 (7.7)	1 (3.1)	
Malay	7 (9.9)	6 (15.4)	1 (3.1)	
Others	1 (1.4)	0	1 (3.1)	
BMI (kg/m^2, median, IQR)	22.9 (21.0 – 25.6)	23.4 (21.2 - 25.3)	22.3 (20.6 - 28.3)	0.97
Comorbidities (n, %)				
Hypertension	12 (16.9)	4 (10.3)	8 (25.0)	
Diabetes Mellitus	4 (5.6)	0 (0.0)	4 (12.5)	
Hyperlipidaemia	15 (21.1)	8 (20.5)	7 (21.9)	
Chronic kidney disease	0	0	0	
Ischaemic heart disease	1 (1.4)	0 (2.6)	1 (3.1)	
Chronic liver disease/liver cirrhosis	0	0	0	
Number of comorbidities (n, %)				
0	51 (71.8%)	29 (74.4)	22 (68.8)	
1	10 (14.1)	8 (20.5)	2 (6.3)	
2	8 (11.3)	2 (5.1)	6 (18.8)	
≥3	2 (2.8)	0 (0.0)	2 (6.3)	

BMI: body mass index, IQR: interquartile range, SD: standard deviation

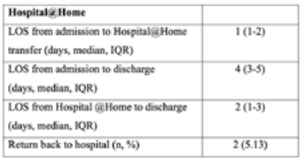
Table 2: Clinical Characteristics



Variables	Total (n=71)	Hospital@Home (n=39)	Inpatient (n=32)	P value
Day of symptoms at presentation (median, IQR)	4 (3 – 6)	4 (3 – 5)	5 (4 – 6)	
Dengue severity on admission (n, %)				
Dengue without warning signs	49 (69.0)	28 (71.8)	21 (65.6)	
Dengue with warning signs	21 (29.6)	10 (25.6)	11 (34.4)	
Severe dengue	1 (1.4)	1 (2.6)	0 (0.0)	
Progression to severe dengue (n, %)	9 (12.7)	7 (17.9)	2 (6.3)	
Severe plasma leakage	6 (8.5)	6 (15.4)	0	
Severe organ impairment	1 (1.8)	1 (2.6)	1 (3.1)	
Bleeding	1 (1.4)	0	1 (3.1)	
Day of recovery (median, IQR)	8 (7 – 8)	7 (5 – 9)	8 (7 – 9)	0.07
Day of drip cessation (median, IQR)	7 (6 – 8)	6 (5 – 7)	8 (7 – 9)	
Excessive IV fluids (n, %)	49 (69.0)	22 (56.4)	27 (84.4)	0.01
By inpatient team		22	27	
By Hospital@Home team		0	-	
Haematocrit peak (%, median, IQR)	44.5 (42.7 – 46.9)	43.9 (40.7 - 47.1)	44.5 (43.5 - 46.2)	0.44
Platelet nadir (10^9/L, median, IQR)	36 (22 – 59)	34 (23 – 58)	36 (20.5 – 81.5)	0.66
Total LOS (days, median, IQR)	4 (3 – 5)	4 (3 – 5)	3.5 (2.5 – 5)	0.32
Duration of IV drip (days, median, IQR)	3 (2 – 4)	2 (2 – 3)	4 (3 – 5)	0.002

IV: intravenous; LOS: length of stay

Table 3: Hospital@Home performance metrics



Hospital@Home	
LOS from admission to Hospital@Home transfer (days, median, IQR)	1 (1-2)
LOS from admission to discharge (days, median, IQR)	4 (3-5)
LOS from Hospital @Home to discharge (days, median, IQR)	2 (1-3)
Return back to hospital (n, %)	2 (5.13)

E-413 Modeling the kinetics and magnitude of dengue viral biomarkers: a systematic review and meta-analysis

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Background: Dengue virus (DENV) infections are commonly assessed using viral load (VL) or soluble NS1 antigen (sNS1) from blood samples of patients. Higher levels of both biomarkers has been associated with disease progression. The kinetics of these biomarkers is dependent on patient serostatus and infecting serotype — although results have been inconsistent due to heterogeneity in study time-points and population characteristics. In this systematic review and meta-analysis (Prospero Study CRD420251072509), we collated individual-level sequential VL and sNS1 data from published studies to characterize the magnitude and kinetics of both biomarkers whilst accounting for population heterogeneities.

Methods: Inclusion was dependent on reporting at least two sequential VL and sNS1 measurements from human serum or plasma, reported in unit time (e.g., days of symptoms/illness), in English language publications. From 2,687 publications, we identified 52 unique studies for analysis. Biomarker kinetics were modelled using a meta-regression approach with random effects at the individual and study level.

Results: Biomarker magnitude and kinetics was assessed across viral serotype, patient serostatus, age and disease severity. Both biomarkers cleared faster in secondary infections when compared to primary infections. VL kinetics varied by serotype and age. NS1 levels varied by serotype, while the clearance of NS1 varied by age (-0.57, 95% CrI: -0.92 – -0.21). Although neither biomarker differed in clearance rate by disease severity – VL levels were lower in non-severe cases (-0.58, 95% CrI: -0.90 – -0.25).

Conclusion: These findings provide insight into dengue biomarker kinetics across populations, with implications for diagnosis, disease monitoring, and timing of anti-viral therapeutic interventions.

E-429 Epidemiological and clinical characteristics of dengue infections among hospitalized children in a tertiary hospital in Malaysia

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Background: Dengue is a major global public health threat and an important cause of pediatric hospitalization in endemic settings such as Malaysia. This study aimed to describe the demographic and clinical characteristics of hospitalized children with dengue and identify factors associated with severe disease.

Methods: We conducted a retrospective observational study among children hospitalized with laboratory-confirmed dengue at Hospital Tuanku Ja'afar Seremban between January 2023 to December 2025. Cases were categorized as non—severe or severe dengue based on the WHO 2009 dengue classification. Demographic, clinical, laboratory, and outcome data were analyzed.

Results: A total of 337 children were included, of whom 29 (8.6%) had severe dengue. The median age was 7.3 years (IQR 4.0–9.9) with 53.1% were male. Children with severe dengue were older children than those with non-severe dengue (8.6 vs 7.1 years, $p=0.04$). Clinical features associated with severe dengue included lethargy (72.4% vs 28.2%, $p=0.001$), abdominal pain (55.2% vs 29.2%, $p=0.004$), tender hepatomegaly (24.1% vs 0.3%, $p<0.001$), shock (96.6% vs 0.3%, $p<0.001$), and reduced urine output (44.8% vs 21.4%, $p=0.004$). Plasma leakage with pleural effusion and ascites was more common in severe dengue (both $p<0.001$). Severe dengue was also associated with higher hematocrit and alanine aminotransferase levels, lower platelet count and albumin levels, increased PICU admission, oxygen requirement, and longer hospital stay (all $p<0.001$). No mortality occurred.

Conclusion: Severe pediatric dengue occurred in approximately one in twelve hospitalized children and was associated with features of plasma leakage, abdominal symptoms, lethargy, laboratory derangements, and greater healthcare utilization.

E-432 A Mathematical Model for Platelet Kinetics in Dengue Infection

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Background: Thrombocytopenia is a hallmark hematological abnormality in dengue and is associated with disease progression. It is driven by both reduced platelet production and increased peripheral destruction through viral and immune-mediated mechanisms. A mechanistic mathematical model that integrates current knowledge of platelet kinetics with new data on platelet aging in dengue offers a promising approach to better characterise thrombocytopenia in dengue.

Methods: Published literature on platelet kinetics and existing mathematical models, both general and dengue-specific, was reviewed to inform the model development. Platelet dynamics were represented using a transit compartmental model. Published longitudinal data on platelet count and immature platelet fraction in dengue were used for model calibration.

Results: The final model comprised 12 main compartments and 6 parameters, incorporating thrombopoiesis, platelet maturation from immature to mature circulating forms, and the feedback regulation linking circulating platelet counts to thrombopoiesis. The model reproduced published trajectories of platelet count and immature platelet fraction in dengue with good agreement. The model could also be fitted to individual patient data within a nonlinear mixed-effects framework.

Conclusion: This model will provide a clinically relevant framework for describing platelet dynamics in dengue. It may contribute to the improvement in prediction of platelet recovery and dengue outcomes, and support identification of surrogate endpoints for early-phase therapeutic studies.

E-435 Kinetics and Clinical Utility of Platelet Indices in Dengue Infection: A Systematic Review

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Background: Dengue is a major arboviral disease with a wide spectrum of clinical manifestations. Thrombocytopenia is a key feature across all severity categories; however, platelet count alone has limited value for clinical management. This review evaluated current evidence on the kinetics and clinical utility of platelet indices, including mean platelet volume (MPV), platelet distribution width (PDW), plateletcrit (PCT), platelet-large cell ratio (P-LCR), and immature platelet fraction (IPF), in dengue diagnosis, prognosis, and case management.

Methods: Original studies reporting reporting quantitative platelet index data in dengue patients were identified from Embase, PubMed, Scopus, and Web of Science without language or date restrictions. Screening and data extraction were conducted independently by two reviewers, with disagreements resolved by a third reviewer. Study quality was assessed using a modified CASP checklist.

Results: Of 3,503 unique records screened, 58 studies were included. Most were cross-sectional studies in adult populations examining associations between platelet indices, platelet count, and dengue severity. Platelet count was positively correlated with PCT, but negatively correlated with MPV, PDW, and P-LCR. Across studies, IPF peaked 24-48 hours before platelet recovery, and an IPF threshold of 10% was suggested to predict the platelet recovery within 72 hours and prevented unnecessary platelet transfusion. However, the overall quality of available evidence was low due to poor reporting as well as bias-prone study design and data analysis.

Conclusion: Platelet indices may offer complementary clinical value beyond platelet count, but robust prospective longitudinal studies are needed to characterise their kinetics and confirm their role in dengue care.

F-142 Evaluating the robustness of *Wolbachia* incompatible-insect technique and introgression under future climate change scenarios

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Incompatible-insect technique (IIT) and introgression are two biotechnologies encompassing the introduction of *Wolbachia*-infected mosquitoes to reduce dengue transmission. Introgression releases mosquitoes infected with “virus-blocking” strains of *Wolbachia*. However, IIT releases only *Wolbachia*-infected male mosquito to induce cytoplasmic incompatibility when they mate with wildtype female mosquito, resulting in non-viable offspring to reduce the mosquito population. Current evidence suggests high entomological and epidemiological effectiveness of these technologies, yet, climate-change may mediate these effects. Here, we evaluated the long-term robustness of these technologies under future climate-change scenarios. We compiled publicly available datasets on *Aedes* abundance across regions the globe, historical and projected climatic conditions in these regions and conducted experiments to test the thermal effects on *Wolbachia*-infected mosquitoes. Climatically-driven entomological models were developed and calibrated using Bayesian approaches to model observed *Aedes* population dynamics and infer area-specific climate-driven variation in mosquito life-history traits. We back-inferred historical mosquito abundances and projected mosquito abundance in future climate-change scenarios and then simulated the counterfactual implementation of IIT or introgression.

We find that *Aedes* populations are projected to increase in all regions across all climate-change scenarios from 2050–2100 even under high heat conditions in the absence of interventions. IIT can suppress wild-type populations effectively across all future scenarios and in high heat conditions. However, under the introgression approach, *Wolbachia* prevalence is compromised in warmer temperatures and periods of low precipitation. Findings demonstrate strong evidence that IIT can be a robust vector control tool and introgression may falter under high heat conditions.

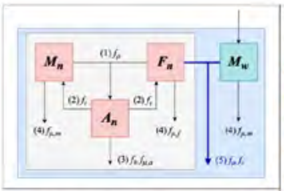

Figure 1. Diagram of climatically driven entomological model.

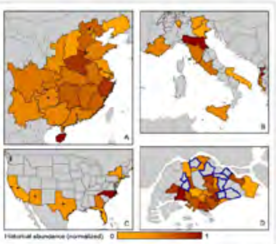

Figure 2. Historical mosquito abundance by region in relative density

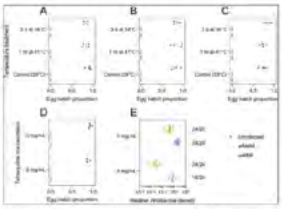

Figure 5. *Wolbachia*-induced cytoplasmic incompatibility remains robust to extreme temperatures and suppression through antibiotic treatment.

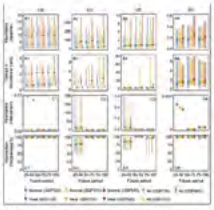

Figure 6. Abundance projections with corresponding intervention effectiveness (IE) under different future climate scenarios.

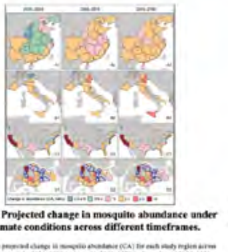

Figure 3. Projected change in mosquito abundance under future climate conditions across different timeframes.

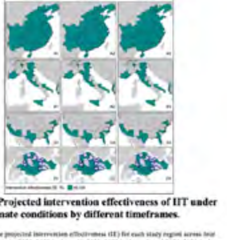

Figure 4. Projected intervention effectiveness of IIT under future climate conditions by different timeframes.

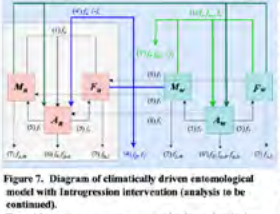

Figure 7. Diagram of climatically driven entomological model with Introgression intervention (analysis to be continued).

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F-171 Effects of Urban Land Use on mosquito larvae abundance in Phnom Penh, Cambodia

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Background: Urbanization and environmental change are widely recognized as major drivers of mosquito ecology and arbovirus transmission. Cambodia, and particularly Phnom Penh, has experienced rapid urbanization that may have contributed to the proliferation of anthropogenic habitats favorable to mosquito vectors. However, the influence of urban land-use patterns on larval mosquito diversity and breeding habitat ecology remains poorly understood in this urban setting. Therefore, this study aimed to investigate how urban land use shapes larval mosquito ecology in Phnom Penh, the capital city of Cambodia.

Methods: Larval surveys were conducted in 2025 across 20 sites representing five land-use classes, in four urban zones, themselves divided according to two level of urban centrality. Larvae and environmental variables were collected using a line-transect sampling approach during both the dry and rainy seasons.

Results: A total of 40,343 mosquitoes belonging to 14 were identified, including 10 of medical importance. Dengue vectors were highly dominant (87%), comprising *Aedes aegypti* (83%) and *Aedes albopictus* (4%), with significantly higher abundance during the rainy season. Japanese encephalitis (JE) vectors accounted for 15% of collections, mainly *Culex quinquefasciatus* (10%), while malaria vectors were rare (<1%). Neither urban land use nor urban centrality showed had a significant effect on the relative density of larval mosquitoes, including dengue and JE vectors. Dengue vectors were not significantly associated with the measured environmental factors, whereas JE vectors were significantly associated with water type, pH, and temperature recorded 21 days prior to collection. Although the highest number of larvae was collected from plastic containers, metal containers were identified as the most productive breeding habitats.

Conclusion: In Phnom Penh, urban mosquito ecology appears to be driven primarily by container availability, seasonality, and temperature rather than land-use classification. Given that plastic containers substantially increase arbovirus vector densities, targeted source reduction of these habitats is critical for effective vector control.

F-172 Sustained Reduction of Dengue in an Industrial Mining Operation in Papua, Indonesia: A Four-Year Integrated Vector Management Success (2022–2025).

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2 Global Medical Services, Freeport McMoran Inc, USA

Background: Industrial workforces in hyper-endemic tropical regions face disproportionate dengue risk. In Papua, Indonesia, both occupational and community exposure drive transmission among workers. We present a four-year operational evaluation of a comprehensive dengue control program at a large industrial site, assessing Integrated Vector Management (IVM) outcomes.

Methods: A longitudinal operational evaluation was conducted using routine epidemiological, entomological, laboratory, and programme implementation data collected between 2022 and 2025. Interventions included *aedes* larvae monitoring across operational zones, larviciding of permanent water-holding containers; emptying of temporary ones; Adult *Aedes* surveillance used Prokopack aspirators with laboratory identification and dengue virus testing; drainage maintenance, indoor and space spraying, and personal repellent distribution.

Results: Dengue incidence declined by 77%, from 434 cases (15.4 per 1,000 workforce) in 2022 to 103 cases (3.5 per 1,000) in 2025, despite stable rainfall and consistent surveillance. Poisson regression confirmed a significant declining trend (IRR = 0.63 per year, $p < 0.001$), representing 37% average annual reduction. In 2025, entomological surveillance identified 620 *Aedes* mosquitoes from 18,611 collected; dengue virus positivity among 405 tested *Aedes* samples was 8.6%, with DENV-2 predominant. Insecticide susceptibility testing showed 100% *Aedes albopictus* mortality, confirming rotational efficacy. Larval source management averted emergence of thousands of mosquitoes. However, 84% of cases were imported from outside jobsite (Timika), indicating transmission pressure beyond program boundaries.

Conclusion: Integrated vector surveillance, systematic larval reduction, and environmental management drove major incidence declines in this occupational setting. Sustained IVM offers a viable model for dengue prevention in high-risk endemic industrial environments.

F-201 Uncovering the Root Causes of Dengue Hemorrhagic Fever (DHF): Findings from a Community Diagnosis in Kendal Regency, 2024

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Background: Community diagnosis in Kendal Regency identified DHF as a priority health problem, with the highest CFR (7.7) in Central Java in 2023 and cases rising from 375 to 999 by 2024.

Methods: Root cause identification employed a cross-sectional study design. The sampling technique used was purposive random sampling, with a total of 104 respondents. The samples were DHF patients within the working areas of Boja I and Rowosari I Health Centers in 2024. Data were collected through structured interviews and observations and analyzed descriptively.

Results: The results of the community diagnosis revealed several contributing factors to dengue incidence were not covering water storage containers (57.7%), not overturning water containers (62.5%), not cleaning potential water-holding items inside or outside the house (53.8%), not checking for larvae (59.6%), not planting mosquito-repellent plants (83.7%), not installing wire mesh on house ventilation (70.2%), the habit of hanging clothes (50%) and keeping windows open in the morning or evening (83.7%). Environmental factors comprised the presence of breeding places (67.3%) and the high House Index (18.3%). Social factors were also identified, including the absence of routine community clean-up activities (55.8%), lack of support from community leaders (65.4%), and the absence of health education or counseling on PSN 3M Plus (61.5%).

Conclusions: Dengue fever is a priority public health problem in Kendal Regency, with the identified root causes including behavioral factors, environmental factors, and healthcare service-related factors Keywords: Community diagnosis, DHF, behavior, environmental

F-204 Comprehensive Analysis of Insecticide Resistance and VGSC Gene Mutations in *Aedes aegypti* Mosquitoes in Bangladesh

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Arboviral diseases such as dengue, chikungunya, and yellow fever pose significant public health challenges globally. In Bangladesh, dengue control primarily relies on targeting the main vector, Ae. aegypti, through insecticides.

This study evaluated insecticide resistance in Aedes aegypti, focusing on pyrethroids, organophosphates, and carbamates used in Bangladesh, and analyzed V1016G and F1534C voltage-gated sodium channel mutations associated with pyrethroid resistance. Adult mosquitoes (field-reared F0 and laboratory-reared F1) from Dhaka and Chattogram were tested using WHO susceptibility tube bioassays, and molecular assays were conducted to detect target-site resistance.

Recommended doses of all pyrethroids (deltamethrin, etofenprox, alphacypermethrin, and permethrin) showed resistance against Ae. aegypti in both cities. Among the 3 tested concentrations of deltamethrin (0.05%, 0.25%, and 0.5%), only a 10-fold higher concentration (0.5%) shows 99±0.25% knockdown effects against Dhaka city (F_1) Ae. aegypti, where the population of Chattogram city was less than 98%. The carbamate insecticide bendiocarb (0.1% & 0.5%) also showed resistance in both cities. Conversely, malathion 5% (organophosphates) was found to be the only susceptible insecticide (mortality >98%) against dengue vector mosquitoes both in Dhaka (F_0, F_1) and Chattogram (F_0, F_1). The gene sequencing data analysis showed that resistant samples had mutations F1534C and V1016G, along with a number of other point mutations.

The study emphasizes the importance of integrated mosquito management (IMM), including the application of modern tools, to reduce dengue in Bangladesh.

F-210 Heterogeneous suppressive effect of *Wolbachia* incompatible insect technique coupled with sterile insect technique across time and historical *Ae. aegypti* abundance-using distributional synthetic controls

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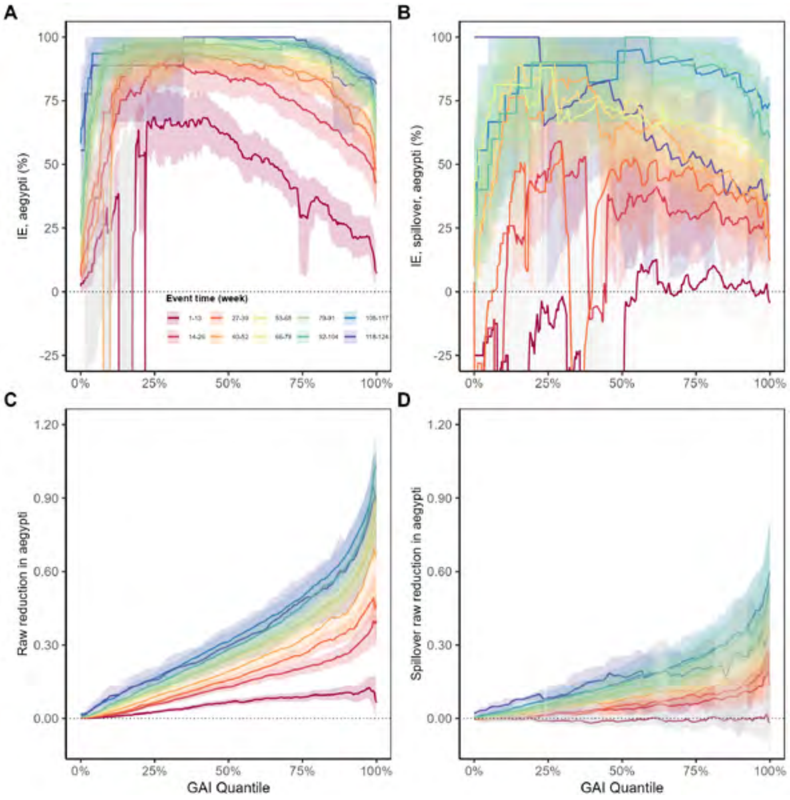
Background: The incompatible insect technique coupled with sterile insect technique (IIT-SIT) is a promising vector control technique to suppress the *Aedes aegypti* population. However, few studies have examined the treatment effect heterogeneity within treated areas. We conducted a quasi-experimental study using distributional synthetic controls to quantify heterogeneous treatment effects across time-since-intervention using trap-level surveillance mosquito abundance, examine the trends of mosquito elimination in intervened locations and determine treatment effect heterogeneity in the areas adjacent to treated areas.

Method: We analyzed an *Ae. aegypti* population surveillance dataset collected from surveillance traps in Singapore between 2019 and 2022. Distributional synthetic control method was applied to 91 intervened sectors to construct their counterfactual mosquito abundance distributions, and treatment effects were quantified as relative improvements in empirical mosquito abundance distributions compared with the counterfactual ones.

Result: The average sector intervention effectiveness increased from 24.04% (95% CI: 16.61– 30.85%) to 86.08% (95% CI: 82.89% – 88.78%) during treatment, indicating substantial temporal heterogeneity. The maximum effectiveness difference among quantiles of the mosquito abundance distribution decreased from 61.33% to 29.62%, suggesting reduced spatial heterogeneity during intervention. Spillover effectiveness in areas adjacent to intervened sectors increased from -1.29% (95% CI: −14.67% – 10.24%) to 78.08% (95% CI: 72.36% – 83.24%). The percentage of traps with no mosquitoes increased by 33.01% (95% CI: 29.50% – 36.57%) after two-year intervention.

Conclusion: These findings demonstrate substantial spatial and temporal heterogeneity in the suppressive effects of IIT-SIT on *Ae. aegypti* mosquito abundance.



F-214 Differentiation of *Wolbachia* strains for the monitoring of *Wolbachia-Aedes* suppression strategy.

Ming Hao CHUA[1], Danna Cruz ONG[1], Carmen KOO[1], Chee Seng CHONG[1], Milly Choi[1], Cheong Huat TAN[1], Judith Chui Ching WONG[1], Shuzhen SIM[1], Lee Ching NG[1], Hapuarachchige Chanditha HAPUARACHCHI[1], Surya Pavan YENAMANDRA[1]

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Background: *Wolbachia*-based suppression of *Aedes aegypti* has proven effective in reducing dengue burden in Singapore. In this approach, the counter impacts of inadvertent releases of *Wolbachia-Aedes* females are mitigated by sterilizing them through irradiation prior to release. Nevertheless, monitoring of field-caught females for *Wolbachia* strains remains critical for early detection and potential source tracing of *Wolbachia-Aedes* establishments at intervention sites. Therefore, this study aimed to develop a real-time quantitative PCR (RT-qPCR) assay for the rapid detection and differentiation of *Wolbachia* strains.

Methods: High confidence, strain-specific single nucleotide polymorphisms (SNP) were identified by genome-wide comparison of w AlbB-E, w AlbB-T and w AlbB-V *Wolbachia* strains used in Singapore. A triplex real-time polymerase chain reaction assay (RT-qPCR) was developed using locked nucleic acid probes capturing three strain-specific SNPs. The triplex assay was further evaluated to determine its operational applicability.

Results: Initial evaluations using 135 *Ae. aegypti* specimens positive for each *Wolbachia* strain demonstrated 100% strain specificity for the selected SNPs. The optimized triplex assay was highly sensitive (limit of detection: 10 copies per reaction). Further evaluation of the assay with 15 laboratory-reared female *Ae. aegypti* infected with each *Wolbachia* strain and 55 field-caught *Wolbachia-Aedes* specimens confirmed the accurate detection and strain differentiation by the newly developed assay.

Conclusion: This study developed a sensitive and high-throughput RT-qPCR assay that is customizable to differentiate *Wolbachia* strains to strengthen post-release monitoring and quality control of *Wolbachia*-based mosquito control programmes in dengue-endemic regions.

F-232 Epidemiological effectiveness of *Aedes*-borne disease vector control interventions: a living systematic review and meta-analysis

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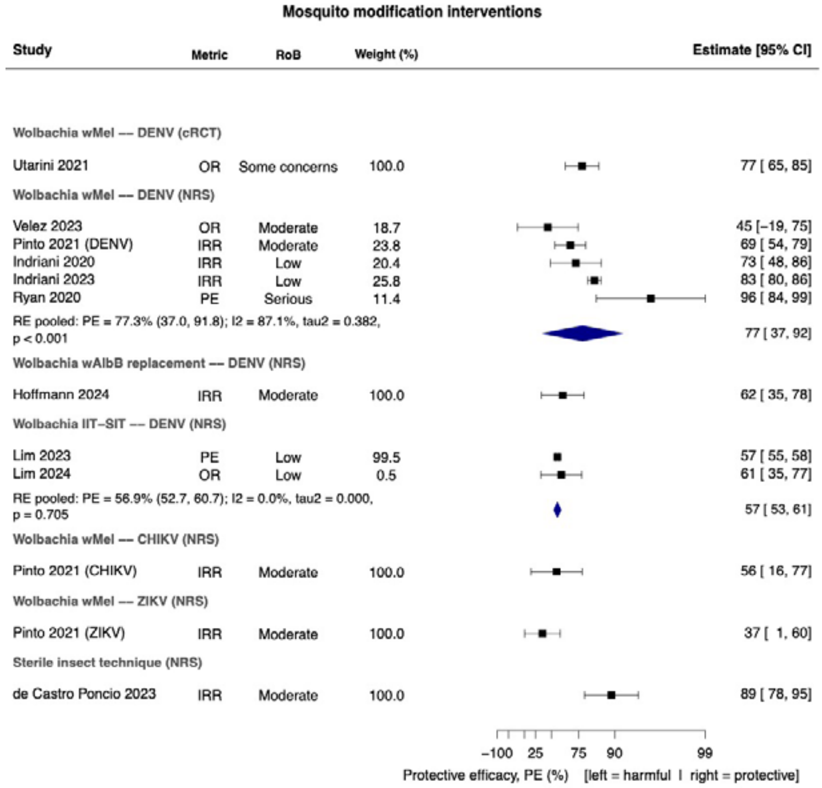
2. National Centre for Infectious Diseases, Singapore
3. SingHealth Duke-NUS Academic Medical Centre, Singapore

Background: *Aedes*-borne diseases have evolved from geographically confined tropical diseases to significant global health threats. With limited theurapeutic options, vector control remains the primary prevention strategy, yet the epidemiological evidence underpinning these interventions has never been assessed across all intervention classes and study designs. This living systematic review and meta-analysis assessed epidemiological effectiveness of *Aedes* control interventions and the robustness of their effect estimates by evaluating their trial designs.

Methods: Following PRISMA guidelines, EMBASE, PubMed, Web of Science, and Scopus were searched from inception to June 6, 2025 for studies evaluating the epidemiological effectiveness of *Aedes*-borne disease control interventions, excluding modelling and laboratory articles. Reviewers (TWI, MXW, JYC) independently extracted information from eligible studies and assessed risk-of-bias using RoB2 and ROBINS-I. Random-effects meta-analyses were performed, with the certainty-of-evidence evaluated through GRADE. This living review is registered with PROSPERO (CRD420251060653).

Results: Of 2279 studies screened, 62 studies spanning 19 countries were included. Non-randomised studies contributed the majority of completed epidemiological evidence, and endpoint definitions were highly heterogeneous across intervention types. Mosquito modification contributed the largest body of evidence (22 studies), with all completed evaluations reporting reductions in disease endpoints. Pooled protective efficacy for w Mel *Wolbachia* replacement against dengue was 77% (95%CI 37–92;5 studies). The remaining intervention classes were informed by fewer and smaller studies, shorter observation periods (median 27 months), and less consistent protective effects. Over half of the studies were at serious-to-critical risk-of-bias, and GRADE certainty was very low for 25 of 46 outcome-level assessments.

Conclusion: While most interventions showed protective signals, only mosquito modification strategies showed a robust evidence base for sustained epidemiological impact at city-scale. Evidence for most other intervention classes remains sparse, methodologically weak, and of very low certainty, highlighting gaps for control policy and future trial design.



Random−effects model (REML + HKSJ). Weights are within−subgroup RE weights. PE = (1 − ratio) x 100%.

F-248 Post-Release Assessment of *Wolbachia* Establishment and Dengue Virus Circulation in *Aedes* mosquito Populations in Vientiane, Lao PDR

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2. National Center Laboratory and Epidemiology

Background: Dengue remains a major public health concern in Lao PDR, particularly in urban areas such as Vientiane. *Wolbachia*-based mosquito replacement has been introduced as a complementary strategy to reduce virus transmission. In Lao PDR, implementation is led by the Ministry of Health with partners; however, post-release evaluation remains essential.

Methods: From January 2026, *Aedes* mosquitoes were collected every two months from *Wolbachia* release sites in Vientiane and control sites in Vang Vieng. Mosquitoes were morphologically identified and tested for *Wolbachia* and flavivirus using PCR. Dengue case data from the MOH will be used for future comparison with entomological and virological findings.

Preliminary results: A total of 12,021 mosquitoes were collected from release and control sites, with *Aedes aegypti* comprising 2.96% (n=356), *Aedes albopictus* 0.45% (n=55), *Aedes* spp. 0.13% (n=16), Armigeres spp. 0.5% (n=60), and Culex spp. 96% (n=11,534). Among *Aedes aegypti*, *Wolbachia* was detected in release sites (75.5%, 40/53) but not in control sites (0%, 0/30). Flavivirus detection was lower in release sites (7.3%, 8/110) than in control sites (26.7%, 8/30). Sanger sequencing of PCR-positive samples identified insect-specific flaviviruses, with no evidence of dengue virus or other human-pathogenic flaviviruses detected.

Perspective: This study provides provide early evidence of *Wolbachia* establishment in *Aedes aegypti* populations in release areas, supporting *Wolbachia*-based vector control in Vientiane. The absence of dengue virus may reflect seasonal variation and low transmission during sampling. Continued monitoring and integration with epidemiological data are needed to assess dengue transmission.

F-272 The MSF experience with *Wolbachia* for dengue reduction in Tegucigalpa, Honduras

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3 Médecins sans frontières, Operational Center, Geneva Switzerland.

4 World Mosquito Program, Medellín, Colombia.

Background: The *Wolbachia* method, developed by the World Mosquito Program (WMP), involves inserting *Wolbachia* bacterium into female *Ae. Aegypti* mosquitos, which is passed on to their offspring and prevents transmission of arboviruses in subsequent generations. Médecins Sans Frontières (MSF) implemented this intervention during 2023-24 by incubating and releasing *Wolbachia*-carrying mosquitoes into the community of El Manchen, Honduras.

Methods: Between June-July 2023, MSF conducted sensitization activities to inform the community on the release of *Ae. aegypti* mosquitoes containing *Wolbachia* . *Ae.aegypti* ovum capsules inoculated with *Wolbachia* were imported from Colombia. Mosquitoes were incubated locally and later released at 1,200 predetermined points from August 2023 to February 2024. Containers located within 52 households supported weekly releases. Weekly monitoring of *Wolbachia* was conducted during the release period through September 2025. Epidemiological, entomological, and qualitative data were collected to assess community perspectives and impact.

Results: Entomological results suggest that *Wolbachia* became established in the local A. *aegypti* population in El Manchén, with a prevalence of 97.8% by June 2025. Epidemiological monitoring suggest that El Manchén was significantly less impacted by the 2024 dengue outbreak following implementation, with a 28.8% reduction in incidence compared to control areas ($p<0.01$). High community acceptance of *Wolbachia* was documented despite challenges. Participants highlighted MSF's proximity and collaborative approach as key contributors to acceptability and emphasized the potential of community involvement to support sustainable dengue prevention strategies.

Conclusion: Results suggest that with strong community participation and financial investment, *Wolbachia* may be a feasible and effective strategy against dengue in Honduras.

F-280 Successful implementation and establishment of *Wolbachia* in Vientiane Capital, Lao PDR

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4 Division of Communicable Disease Control, Vientiane Capital Health Department, Laos
5 World Mosquito Program

Background: Dengue is a significant public health threat in the Lao PDR, with Vientiane Capital experiencing the highest burden and recurrent outbreaks. Conventional control measures have not prevented sustained transmission. In response, a *Wolbachia*-carrying *Aedes aegypti* replacement program was implemented. We describe the implementation and establishment outcomes in Vientiane Capital.

Methods: Releases of *Wolbachia* (wAlbB) infected *Aedes aegypti* by village health volunteers were conducted from August 2025 to January 2026 across 25 km^2, approximately 153,000 people. Implementation was coordinated among Save the Children, World Mosquito Program and the Ministry of Health, the Department of Communicable Disease Control, with support from provincial and district authorities and community leaders. Community engagement included village loudspeakers, radio, community visits, and social media.

Results: An estimated 60 million *Wolbachia*-infected mosquitoes were released at a rate of 2.5 million per week. At the end of the release period, the *Wolbachia* frequency increased up to 89% prevalence, indicating a good establishment in the Vientiane environment. Community engagement led to strong acceptance (over 94%). Key implementation lessons included the importance of inclusive engagement strategies, strong multi-level government support, consistent mosquito production and release quality to minimize contamination, and effective coordination between field and rearing teams. Monitoring of *Wolbachia* prevalence is ongoing.

Conclusion: Initial results show encouraging signs of *Wolbachia* establishment in Vientiane Capital. This approach is suitable for similar urban dengue-endemic settings in Asia. Ongoing entomological and epidemiological monitoring is underway, and scale-up to the remaining urban areas of Vientiane and four provinces.

F-286 Operational Implementation and Establishment of *Wolbachia* in Dili, Timor-Leste

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Background: Timor-Leste regularly experiences dengue outbreaks which place significant pressure on the health system. In 2025, the Ministry of Health and its partners implemented the *Wolbachia* replacement program whereby *Wolbachia*-infected *Aedes aegypti* mosquitoes were released in an effort to reduce dengue transmission. We describe the implementation of this program in Dili, Timor-Leste.

Methods: *Wolbachia*-infected *Ae. aegypti* were released weekly over a 24-week period from August 2025 across approximately 20km2 comprising 240,000 people. The program was led by the Ministry of Health with Menzies School of Health Research, Action on Poverty, and the World Mosquito Program. We describe key operational components including mosquito production, release logistics, quality control, *wolbachia* prevalence in mosquitoes and community engagement. *Wolbachia* establishment was monitored through routine entomological surveillance.

Results: *Wolbachia* establishment increased over the release period, reaching 55%-69% prevalence. Over 40 million *Wolbachia*-infected mosquitoes were released at an average rate of 84,731 per km2/week. Key lessons highlighted the importance of well-controlled mosquito rearing conditions. Environmental and infrastructure constraints included contamination, temperature instability, and equipment limitations. Logistics and implementation challenges required flexible release strategies. Community awareness, acceptance, trust and access to release points were made possible by continuous community engagement and stakeholder participation with local authorities, health professionals and government.

Conclusion: *Wolbachia* implementation in Dili indicates early signs of establishment with community engagement paramount; ongoing entomological and epidemiological surveillance is planned and will be critical to confirm stability and assess impact. These findings can inform scale-up in similar resource-constrained and dengue-endemic settings.

F-292 Long-Term Impact of *Wolbachia*-Infected Mosquito Releases on Dengue Seroprevalence in Children: Evidence from Yogyakarta, Indonesia

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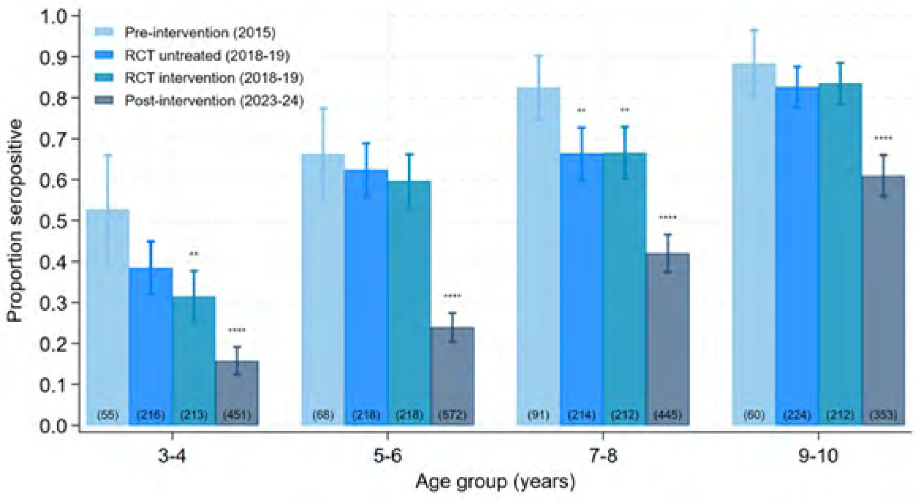
Background: Dengue virus (DENV) remains a major public health challenge in Indonesia, particularly in densely populated urban areas. In Yogyakarta, a cluster-randomized controlled trial (CRCT) evaluated a biocontrol strategy using *Wolbachia* pipientis-infected *Aedes aegypti*. Releases were conducted from March to December 2017 in intervention clusters and from October 2020 to January 2021 in former control areas, enabling phased, city-wide establishment. While reductions in dengue incidence have been demonstrated, evidence on long-term population-level transmission remains limited. This study assessed changes in dengue seroprevalence following *Wolbachia* deployment.

Methods: We conducted a comparative seroepidemiological analysis using age-stratified samples from dengue test-negative participants in the AWED trial (2018–2019) and an enhanced surveillance study (2023–2024), alongside pre-intervention baseline data (2015). The analysis focused on children aged 3–10 years, consistently represented across all periods. Differences in seroprevalence were assessed using age-stratified Mantel–Haenszel chi-square tests.

Results: Dengue seroprevalence in children aged 3–10 years declined from 73% pre-intervention (2015) to 34% post-intervention (2023–2024) (Mantel–Haenszel $\chi^2 = 155.8$, $p < 0.0001$). Reductions were greatest in younger children, reflecting higher exposure during the post-intervention period, but remained significant across all age groups. Declines were already evident during 2018–2019, when approximately half of the city had been treated, particularly among children aged ≤4 years in treated areas.

Conclusion: Citywide *Wolbachia* deployment in Yogyakarta is associated with substantial and sustained reductions in dengue transmission, evidenced by declining seroprevalence. Integration of seroepidemiological, clinical, and genomic data will be essential for understanding durability and broader epidemiological implications of this intervention.



F-320 Cost-effective release adjustment of *Wolbachia* suppression technique coupled with sterile insect technique in Singapore

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Aedes-borne diseases are spreading due to climate change and urbanization. Combining the incompatible insect technique (IIT) with the sterile insect technique (SIT) effectively reduces *Aedes* populations, but optimizing release strategies for cost-effectiveness remains a challenge due to the need for sex-sorting and regular long-term releases. This study demonstrated an adaptive release strategy leveraging high resolution nationwide vector surveillance system with the release intensity adjusted based on wildtype female mosquito abundance. Using a random forest model, we nowcasted mosquito abundance with 70% accuracy in prescribing correct release strategy, guiding release adjustments tested over two years in high-rise residential areas (n = 393,236 residents, 8 sites). Results show maintenance of mosquito suppression despite reduced release intensity. Scaled up to nationwide coverage, the release adjustment strategy makes the IIT-SIT programme more cost-effective through a 49% reduction in intervention cost per year, reducing the cost per DALY averted from US$112,200 to US$ 54,800, and an increase in the benefit-cost ratio from 1.142 to 2.90.

F-327 Development and Implementation of a Digital Interface with Associated Functions to Monitor the Weekly Institutional Source-Reduction Mosquito Control Activities in Western Province, Sri Lanka

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Background: Dengue is a major public health burden in Sri Lanka, with the Western Province reporting nearly 50% of cases. Median notifications exceed 35,000 annually, with 51,552 cases recorded in 2025. Without direct agent control, vector-control remains the primary strategy. Given the 7–10-day mosquito lifecycle, weekly source-reduction is essential. Because institutional breeding indices are often higher than homes, a simple, sustainable monitoring mechanism was identified as an urgent health system need.

Methods: Following a needs assessment and expert stakeholder consultations, a zero-cost digital interface was developed for the Western Province. This platform includes data entry tools, a dashboard, and a visualizer aligned with national recommendations. Endorsed by the Provincial-Dengue-Task-Force, the system provides Medical-Officer-of-Health (MOH) offices and administrative bodies with direct access to data from all institutions specifically under their purview. This facilitates localized oversight, ensuring transparent field activities across the entire province.

Results: Digital platform provided a structured, transparent method for real-time tracking and accountability, achieving 100% coverage among government health institutions, schools and MOH offices. Institutions are officially advised to enter data every Friday, enabling stakeholders to monitor progress routinely and during review meetings. Qualitative feedback highlights the innovation’s feasibility and its potential utility for managing other mosquito-borne conditions like Chikungunya.

Conclusion Digital tools can be effectively bridging monitoring and accountability gaps in routine vector-control programmes. By integrating with existing activities at zero cost, long-term sustainability is assured. This initiative promotes a culture of responsibility and data-driven decision-making.

F-332 Evaluating the Impact of Urban Landscape on Mosquito Species Occurrence and Disease Vulnerability in Dhaka

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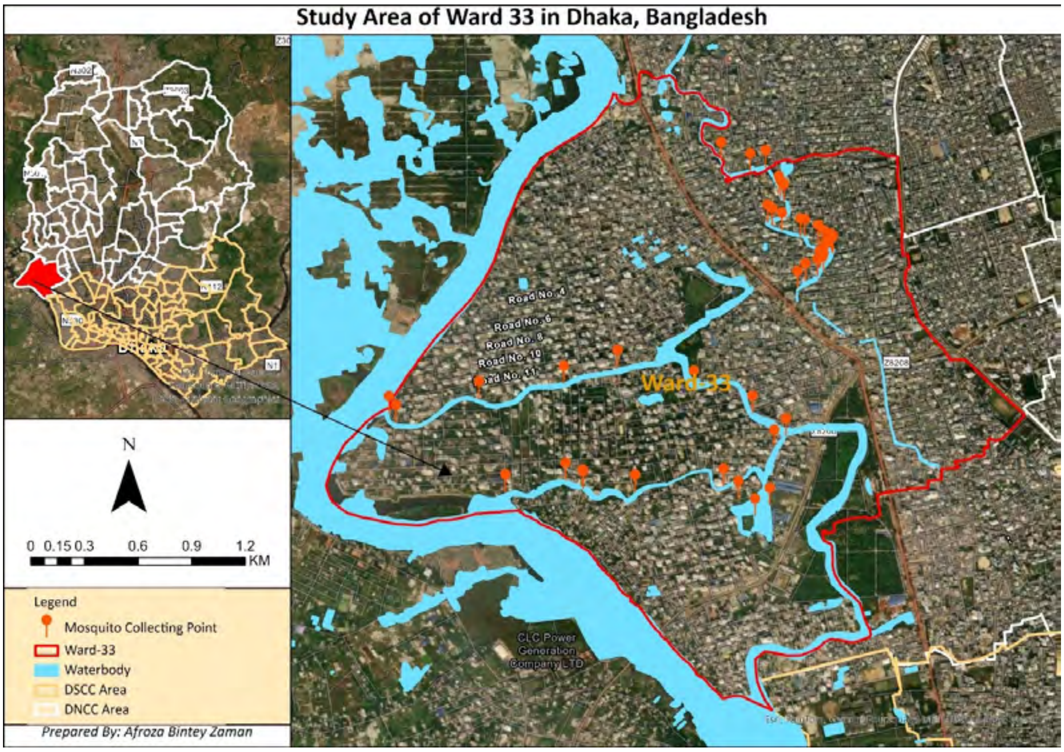
Bangladesh is highly vulnerable to mosquito-borne diseases, driven by the widespread availability of mosquito breeding habitats in both natural and artificial water sources. In Dhaka, rapid and unplanned urbanization, coupled with poor waste management, has facilitated the proliferation of breeding sites in drains, sewage systems, abandoned plots, slums, and stagnant water bodies, thereby increasing the risk of vector-borne disease transmission.

This study assessed mosquito species occurrence and evaluate associated disease risk in Dhaka North. Breeding habitats were identified through judgmental sampling, and geographic coordinates were recorded using a GPS application. Larval and pupal samples were collected using standard dipping techniques, and density (larvae and pupae per dip) was recorded. Samples were transported to the IRES at Jahangirnagar University and identified morphologically.

A total of 3,903 mosquitoes (adults, larvae, and pupae) were collected from 41 locations, including 777 adults, of which 445 were female. *Culex quinquefasciatus* was the dominant species, present in 93% of sites, while co-occurrence with *Anopheles vagus* was observed in 7% of locations, indicating elevated transmission risk. High-risk areas based on mosquito density included Mohammadia Housing Ltd., Novodoi Housing, and Ramchandrapur, while combined density and sex ratio analysis identified Ramchandrapur, Bosila, and Novodoi as the most vulnerable. Spatial analysis integrating field data with the Detailed Area Plan (DAP) identified high-risk buffer zones within 200–400 m of breeding sites, covering 9,431 structures.

These findings highlight the need for integrated urban planning, routine surveillance, and targeted vector control strategies to reduce mosquito proliferation and mitigate disease risk in Dhaka.



F-334 Assessing effectiveness of *Wolbachia* IIT-SIT program in dengue risk reduction in low-rise residential areas

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The epidemiological effectiveness and efficacy of *Wolbachia*-based incompatible insect technique coupled with sterile insect technique (IIT-SIT) in high-density, high-rise residential areas in Singapore is well-characterized. In this study, we reported the effectiveness of *Wolbachia* IIT-SIT on reducing of *Aedes aegypti* abundance and dengue risk in low density and low-rise residential estates. *Wolbachia* IIT-SIT interventions commenced in EW 17 2022 in Marine Parade and further expanded to other low-rise residential estates up until EW9 2024 encompassing more than 26,000 households and a total area of 8 km 2 . We utilized corrected Gravitrap *Aedes aegypti* index (GAI), a measure of *Ae. aegypti* abundance adjusted for the sample degradation, and a nationally representative test-negative database to quantify the IIT-SIT's effectiveness in these estates. *Wolbachia* releases in low-rise residential estates reduced *Ae. aegypti* abundance by up to 98.3% (95% CI: 98.1%-98.5%), using synthetic control method, and reduced dengue risk by 78% (95% CI: 64-86) after 12 months of sustained releases using matching framework with logistic regression. Protective effectiveness remained similar in subgroup analysis by years, sex groups, and age groups. *Wolbachia* IIT-SIT program was shown to be effective in reducing dengue vector abundance and dengue risk in low-rise residential estates of Singapore. Despite differences in the habitats in low-rise residential estates the results were similar to results observed in high-rise, high-density studies previously conducted in Singapore, suggesting applicability of the program to low-rise residential settings

F-335 Estimating the effectiveness of *Wolbachia* incompatible insect technique coupled with sterile insect technique (IIT-SIT) in reducing dengue hospitalizations

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Dengue is an arboviral disease that presents public health challenges in tropical and subtropical countries. *Wolbachia* incompatible insect technique coupled with sterile insect technique (IIT-SIT) involves the release of male *Wolbachia*-infected *Aedes aegypti* mosquitoes to suppress wild-type *Ae. aegypti*. In this study, we investigated the effectiveness of *Wolbachia* IIT-SIT in reducing dengue hospitalizations, as a measure of severe dengue, via emulation of a cluster-randomized controlled test negative trial (cRCT) conducted in Singapore. We used nationally representative healthcare claims and dengue surveillance data to construct a dataset of individuals tested for suspected dengue infection with dengue hospitalization status. We also leveraged the setting of a well characterized cRCT of *Wolbachia* IIT-SIT conducted from 2022–2024 comprising total of 724,428 residents. We then emulated a cRCT which took dengue hospitalization as the outcome of interest and estimated odds ratios comparing the odds of dengue hospitalisation between *Wolbachia*-exposed and unexposed individuals suspected of dengue infection. The individuals' characteristics were well balanced between the arms. 7,958 and 9,759 dengue tests were done with 210 (2.6%) and 661 (6.8%) dengue hospitalizations recorded in intervention and control arms respectively. In intention-to-treat analysis, there was an overall protective effectiveness (PE) of 68% –73% 3 to 12 months of *Wolbachia* exposure against dengue hospitalizations. The estimated PE remained fairly constant across all exposure durations and were replicated across all age (PE range: 53% – 85%) and sex (PE range: 44% – 81%) subgroups except for young individuals aged 0–20 years old. We also observed higher PE in oldest age group (PE range: 75% – 85%) compared to younger age groups (PE range: 53% – 67%). *Wolbachia* IIT-SIT can be highly effective in reducing dengue hospitalizations and can be integrated in vector control programmes to reduce the healthcare burden associated with *Aedes*-borne diseases.

F-342 Space Spraying Strategies for Effective Management of *Aedes* Mosquitoes

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Background: Space spraying via ultra-low-volume application, aerosol sprays and thermal fogging remains a critical intervention for adult mosquito control during dengue outbreaks and high-density infestations. Given the potential development of insecticide resistance, we evaluated current space spray practices against local *Aedes* populations in Singapore to ensure continued efficacy.

Methods: Bioassays were conducted using field-derived *Aedes* mosquitoes with mortality assessed 24 hours post-exposure. Pyrethroid-based household aerosol products were evaluated using Peet Grady Chamber (PGC) tests, followed by simulated field trials with targeted direct spray and non-targeted application (5 sec spray around the room). For thermal fogging validation, Actellic® 50EC (organophosphate-based), diluted in oil or water, was tested against mosquitoes placed in both exposed and concealed positions.

Results: The top three household aerosol products from the PGC test (>80% mortality) achieved 100% knockdown and mortality in simulated field trial using targeted application. However, poor efficacy was observed for non-targeted application (38.4-63.2% knockdown, 9.5-79.4% mortality). For thermal fogging, the oil-diluted formulation showed 97.6-100% mortality, performing significantly better than the water-diluted formulation (73.5-89.7% mortality) at exposed positions ($p<0.05$). At concealed positions, mortality was 66.8-85.4% and 35.3-57.2% for oil-diluted and water-diluted formulations, respectively.

Conclusion: Pyrethroid- and organophosphate-based space spraying products remain effective when applied using established techniques. However, mosquitoes in concealed locations remain difficult to control, and higher efficacy can be achieved through targeted indoor aerosol spray and oil-diluted thermal fogging. This study emphasises the need for continuous efficacy monitoring and the integration of complementary strategies within an integrated vector management framework.

F-345 Beyond Transinfection: Challenges in Generating Alternative *Wolbachia-Aedes* Strains

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Background: Developing alternative *Wolbachia-Aedes aegypti* strains is crucial for long-term sustainability of *Wolbachia* suppression programmes. Current large-scale implementations rely primarily on *w*AlbB and *w*Mel strains, creating vulnerability to potential programme failure. Alternative strains are needed to mitigate established *Wolbachia* populations from unintentional releases and provide heat-tolerant options for tropical deployment. However, transinfection via embryo microinjection often yields strains with unpredictable fitness or pathogen-blocking traits. Methods We characterised two novel *Wolbachia-Aedes aegypti* lines with a Singapore genetic background- *w*Mal-SG (transinfected from *Aedes* malayensis) and *w*Pip-SG (transinfected from Culex molestus). We evaluated key phenotype traits essential for operational performance: maternal transmission efficiency, cytoplasmic incompatibility, fitness parameters including egg viability and quiescent egg storage capacity, *Wolbachia* stability in stored eggs, and pathogen-blocking efficacy against dengue (DENV2, DENV3), chikungunya, and Zika viruses.

Results: Both strains exhibited complete maternal transmission and strong cytoplasmic incompatibility. However, these advantages were offset by severe fitness penalties: *w*Pip-SG exhibited rapid loss of quiescent egg viability (declining to <20% after one month vs >80% for controls) and progressive loss of *Wolbachia* infection in stored eggs. *w*Mal-SG demonstrated reproductive self-incompatibility with significantly reduced egg viability in self-crosses compared to outcrosses. Neither strain effectively blocked dengue, chikungunya, and Zika infection, with salivary gland viral titres comparable to wild-type controls.

Conclusion Neither the *w*Mal-SG nor *w*Pip-SG strains meet the operational requirements for large-scale field deployment due to significant fitness costs and the absence of an effective pathogen-blocking phenotype. These findings underscore the complex biological challenges inherent in developing viable *Wolbachia-Aedes aegypti* strains and further highlight the critical need for continued strain development to ensure programme sustainability and resilience in *Wolbachia*-based vector control strategies.

F-354 AI-Driven Insights: Automated 2D Mosquito Flight Path and Interaction Analysis Using a Single-Camera System.

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Background: Mosquito behaviour and mosquito-mosquito interactions serve as direct measures of mating success, fitness and competitive performance. However, tools for quantifying these behaviours in routine cage studies remain limited, as current image-based approaches often require complex setups, specialized camera systems, and extensive post-processing of recorded data. Leveraging recent advances in artificial intelligence (AI), we developed a streamlined single-camera system for automated monitoring of mosquito behaviour under standard cage conditions.

Methods: Flight activities within the cage are recorded using a fixed camera under uniform illumination. The video is subsequently processed using an AI-based detection and 2D tracking approach to follow individual mosquitoes and reconstruct their trajectories. These extracted 2D trajectories are then further analysed to derive behavioural measures such as flight activity, movement patterns, and interaction-related events.

Results: The system enables continuous tracking of mosquito flight activity, reconstructs complete 2D flight trajectories, and detects interaction events between individuals. It generates consistent behavioural outputs in an automated manner, including spatiotemporal metrics such as active flight duration and quiescence, speed and directional movement. The system can track multiple mosquitoes simultaneously, with performance dependent on video quality. Requiring only a single camera and uniform illumination, the setup is straightforward to deploy and facilitates high throughput repeatable experiments.

Conclusion: This system provides a practical approach for capturing mosquito behavioural data that is otherwise difficult to obtain using conventional tools. Its minimal hardware requirements, direct analytical outputs, and ease of deployment make it suitable for diverse applications in vector biology research and routine quality control assessments.

F-369 Scaling up the Sterile Insect Technique (SIT) against Aedes albopictus in France through automation and industrialized mass rearing

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Background: In mainland France, Aedes albopictus represents both a major biting nuisance and an emerging public health threat. Although arboviruses such as dengue are not yet endemic, imported cases are increasing annually and can lead to autochthonous transmission. In 2025, more than 800 autochthonous chikungunya cases were reported, linked to an epidemic in Réunion Island. The Sterile Insect Technique (SIT), deployed by Terratis, requires large-scale mosquito production, making automation essential in a high labor-cost context.

Methods: Terratis developed automated larval rearing systems with scalable functionalities, including robotic food preparation and delivery, water injection, and direct egg hatching in racks. Larger adult cages minimizing manual handling were introduced. Pupae are sex-sorted using the Wolbaki system. A mosquito dispenser capable of storing up to 400,000 chilled males and releasing field doses of approximately 1,000 active males was also developed.

Results: Production reached 1.5 million males per week in a 220 m² facility operated by six full-time staff. Automation enables multi-day food preparation and repeated daily feeding, reducing manual intervention to larva/pupa collection, transport to sorting, and tray washing. This capacity supports coverage of 500 hectares across multiple cities in France, achieving up to 50% induced egg sterility during the first mosquito season. The current facility has a maximum capacity of 2.5 million males per week.

Conclusion: Terratis is scaling up toward a new facility targeting 40 million males per week, building on existing automation technologies.

F-377 Enhancing Urban Aedes Surveillance with Spatial, Mobility, and Weather Variances

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Background: Effective control of Aedes mosquitoes, the dengue vectors, requires robust surveillance systems. However, current gravitrap systems often yield very few or even zero captured mosquitoes even in areas with moderate mosquito densities, leading to potential underestimation of Aedes populations. This issue may be particularly pronounced in settings with substantial spatio-temporal fluctuations in mosquito activity, such as Taiwan and Hong Kong. We aimed to enhance gravitrap surveillance by leveraging evidence from spatial modeling and behavioral and weather-related covariates, thereby improving risk detection sensitivity and predictive accuracy.

Methods: Using gravitrap data, we first combined auto-logistic models (Markov Random Fields) and disease mapping models to account for spatial dependencies and improve prediction of Aedes risk index (high, moderate, and low). Second, we used Google human mobility indices and weather conditions (total rainfall and mean temperature) along with Aedes abundance and applied distributed lag nonlinear models to assess the impacts of human mobility, rainfall, and temperature on mosquito abundance during the COVID-19 pandemic.

Results: The proposed auto-Markov gravitrap index improved sensitivity through enhanced spatio-temporal risk prediction and cross-validation performance in Taiwan. Furthermore, we found that reduced residential mobility, indicating less time spent at home, was significantly associated with increased mosquito abundance in Hong Kong, while rainfall and temperature demonstrated substantial nonlinear lagged effects.

Conclusion: Our findings demonstrate that gravitrap surveillance can be strengthened by incorporating spatio modeling approaches and behavioral determinants, leading to more sensitive and accurate detection of Aedes risk in urban environments. This potentially supports more cost-effective dengue prevention strategies.

F-379 Impact of Physical Vector Control Intervention on Dengue Fever in Honduras: A Bayesian Structural Time Series Analysis

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Background: Dengue fever remains a major public health crisis in Honduras. In July 2024, a multi-pronged, environmentally sustainable physical vector control intervention was implemented across nationwide healthcare facilities. This study evaluates the impact associated with this multi-pronged intervention on the incidence of dengue.

Method: We employed a Bayesian Structural Time Series model to construct a robust synthetic counterfactual of expected dengue cases. Utilizing weekly incidence data from January 2014 to January 2025, the model isolated the true intervention signal from endogenous infectious momentum and high-frequency seasonal cycles. A Bayesian Spike-and-Slab prior evaluated biological meteorological lags, and an indicator for the 'Morazánico week' national holiday.

Results: During the post-intervention period, the model estimated a 69.9% relative reduction in actual weekly dengue cases compared to the counterfactual. The posterior probability of an intervention effect was 97.24% ($p = 0.0276$). Extensive in-time placebo tests confirmed this decline was not a natural epidemic burnout. Notably, the holiday covariate exhibited a significant negative coefficient, reflecting an artificial dip in surveillance reporting due to reduced healthcare-seeking behavior.

Conclusion: The implementation of the physical vector control intervention was associated with an unprecedented and sustained decline in dengue transmission in Honduras, likely by disrupting high-viremia nosocomial amplification hubs. These results provide evidence for policymakers to sustain this environmentally friendly intervention as a core component of Integrated Vector Management (IVM) programs in Latin America.

F-386 Field implementation of public health prevention, protection, and promotion interventions against dengue fever in Timor-Leste

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Background: Dengue disproportionately affects weaker, resource-poor health systems. Although top-down chemical or biological interventions exist, vulnerable groups limited by opportunity or cost rely on reducing transmission and early diagnosis. Timor-Leste experiences high dengue risks, where a major outbreak in 2022 confirmed 5658 cases and an ongoing outbreak in 2026 confirmed 4230 cases. This study assessed the impact of preventive intervention to suppress dengue transmission.

Methodology: This study aimed to improve community physical protection using dengue prevention kits in health facilities and schools across 14 municipalities (mosquito lamps, insecticide-treated bed nets (ITBNs), sticky traps, rapid diagnostic tests (RDTs), and education materials), targeting detection, protection, and awareness. Monthly trends in national reported cases were analysed from 2022 until after the 2024 intervention (July 2024).

Results: 2,608 lamps, 85,515 RDTs, 92,014 traps and 2,514 ITBNs were distributed starting from January 2024. Segmented regression analysis of weekly percentage change in dengue cases comparing 2 outbreak periods before and after the intervention (2020 Jan – 2022 Mar and 2024 Jan – 2026 Mar) found that the monthly percentage increase in dengue cases during the 2026 outbreak (84.29%) was 54.93% less than the increase during the previous 2022 outbreak (187.03%). The percentage of national cases reported from the capital reduced from 75.8% in 2023 to 68.2% in 2025 following subnational use of RDTs.

Conclusion: Suppressed case propagation showed effective dengue prevention, protection, and promotion interventions in Timor-Leste during an outbreak. Reduction in the proportion of cases reported from the capital indicates redirection of central resources and increased capacity for subnational management. Communities with weak resources face concurrent and protracted crises, with little resources for hazard-mitigation. Providing low-cost, low-tech, and community-actionable dengue protection is the cornerstone of sustainable health improvements.

F-392 Evaluating the long-term effectiveness of imperfect Wolbachia interventions in preventing arboviral disease: the potential role of immune dynamics

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Background: After release of *Wolbachia* (*w*Mel)-infected *Aedes aegypti* in Rio de Janeiro, Brazil, dengue risk reduction varied over time and was not significant during epidemic transmission in 2024. To explore mechanisms underlying variations in effectiveness, we simulated dengue dynamics following *w*Mel introduction.

Methods: We simulated dengue transmission using a SEIR–SEI framework, modeling *w*Mel introduction as a reduction in effective infectious mosquitoes and testing varying introgression and immunity scenarios. Intervention effects were estimated by comparing simulated incidence at an introgression level against an otherwise identical simulation with 0% introgression.

Results: Simulations showed larger incidence reductions in populations near endemic equilibrium susceptibility compared to highly susceptible populations. In some scenarios, yearly incidence was transiently higher with *w*Mel introduction than without, as large outbreaks deplete susceptibles in no-intervention scenarios while transmission continues for longer under partial *w*Mel introgression. Cumulative incidence was always lower after *w*Mel introduction regardless of introgression level.

Conclusion: *w*Mel effectiveness is context-dependent and may be difficult to detect in settings with high susceptibility, incomplete introgression, or high spatial heterogeneity in transmission risk, such as Rio de Janeiro. Settings where larger risk reductions have been observed may reflect higher, more uniform introgression and populations closer to endemicity, rather than differences in biological efficacy. Therefore, longer observation periods and addressing time-varying confounding and effect modification by population immunity may be needed, and cumulative incidence metrics may more reliably estimate intervention impact. Generalizing *w*Mel effectiveness estimates across settings will require attention to how immunity, introgression, and transmission risk differ between them.

F-407 The Intervention for Dengue Epidemiology in Malaysia (iDEM) Trial: Measuring the Effectiveness and Impact of Integrated Vector Management on Urban Dengue Incidence

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Background: The iDEM study was a non-blinded cluster-randomised controlled trial conducted in Kuala Lumpur and Putrajaya. The study was to evaluate whether preventive IVM could reduce dengue incidence and Aedes density in urban settings.

Methodology: High-risk low- and medium-cost high-rise residential areas with recurrent outbreaks were enrolled. Of 329 eligible sites, 280 were randomised: 139 (intervention) and 141 (routine control). The intervention comprised targeted outdoor residual spraying, autodissemination devices, and community engagement. The primary outcome was dengue incidence from the national surveillance system, supplemented by entomological monitoring (*Aedes* indices), insecticide resistance testing, and acceptability assessments.

Results: The intervention did not significantly reduce overall dengue incidence compared with the routine control. Post-hoc analyses suggested reductions in dengue cases within outbreak clusters (29%) and hotspot area (49%), indicating possible benefit in targeted high-transmission setting. Entomological indicators showed modest non – significant reductions, highlighting the known difficulty of correlating vector indices directly with dengue transmission. The mean adult *Aedes* density was 4% lower in the intervention arm that in the control arm but not statistically significant (p=0.86). Species-specific analysis showed a 7% decrease (p=0.78) in *Ae. aegypti* adult density and larval density showed declined, but not significant (8%, p=0.60). Insecticide resistance levels against deltamethrin remained stable (<40% for knockdown and mortality). Importantly, the intervention did not increased insecticide resistant to deltamethrin.

Conclusion: Although proactive IVM did not significantly reduce overall dengue incidence or *Aedes* density, it may still be beneficial in outbreak and hotspot settings The study period coincides with the Covid-19 pandemic, during which movement restriction and altered human behavior may have influenced dengue transmission dynamics and reduced the ability to detect intervention effects.

F-415 Translating Singapore's Dengue SARIMA Forecasts into Weekly Risk Signals for Targeted Vector Control

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Background: Dengue continues to impose a substantial public-health burden across Asia. While intensive interventions such as Wolbachia have proven effective, their cost and operational intensity can limit continuous deployment. This study develops an early-warning system that converts SARIMA forecasts into interpretable risk signals to support more targeted allocation of limited resources.

Methods: Weekly dengue case data from Singapore (2012–2022; MOH/NEA weekly bulletins) were modelled using SARIMA. A SARIMAX extension additionally incorporated lagged temperature, humidity, wind and warm-day share as leading indicators. The fitted models were validated using walk-forward backtesting across origins between 2014 and 2022. To support operational use, the dashboard allows users to set a weekly case threshold, which then converts each weekly forecast probability of exceeding a user-set threshold into Low, Medium and High risk bands.

Results: The SARIMA$(3,1,0)(0,1,0)_{52}$ model was selected as the most suitable model, producing well-calibrated forecasts with 0.80 prediction-interval coverage, with 80% of observed weekly case counts falling within the model's 80% forecast intervals. The accompanying risk bands helped distinguish elevated-risk weeks from quieter periods, providing an interpretable intervention signal alongside the point forecasts.

Conclusion: Layering threshold-based weekly risk bands onto a SARIMA forecast produces an interpretable early-warning tool with calibrated uncertainty and operationally useful outbreak detection. This supports pre-positioning Wolbachia releases and routine vector-control into flagged weeks, enabling more targeted allocation where year-round intensive deployment is infeasible.

Surveillance warning dashboard

Making NEA's model operational

With live dengue data, the surveillance dashboard will use dengue activity as a proxy to identify weeks where risk of outbreaks is more likely to exceed a threshold for intervention.

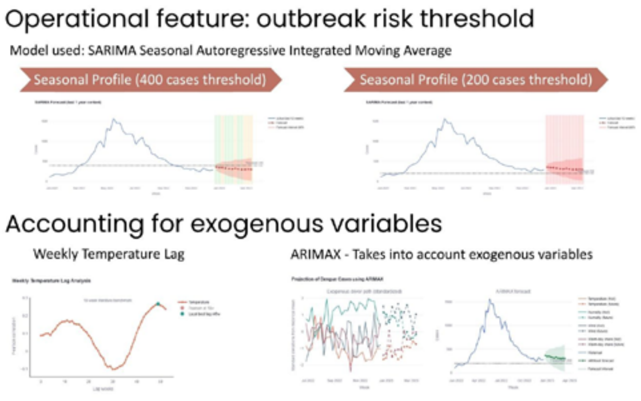
Dashboard Flags Risk

When the threshold has a high probability of crossing threshold, the dashboard flags that period as higher risk, supporting coordination with NEA for more efficient seasonal allocation of Wolbachia releases.

Why Wolbachia

NEA's Wolbachia pilot achieved 98% suppression of Ae. aegypti populations and 88% reduction in dengue incidence at trial sites. Diderichsen et al. noted Zika, transmits through the same Aedes aegypti vector, hence suppression confers a corresponding reduction in Zika transmission risk.

Using seasonality to drive insights



Operational feature: outbreak risk threshold

Model used: SARIMA Seasonal Autoregressive Integrated Moving Average

Accounting for exogenous variables

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F-439 Optimizing Sugar and Blood Feeding to Boost Egg Yield in Aedes aegypti Mass Rearing

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Background: Mass-rearing of Aedes mosquitoes is a core operational component of population suppression or replacement programmes, where the ability to produce high-quality mosquitoes at scale is critical for efficiency, cost-effectiveness, and long-term sustainability. A key operational challenge involves optimizing egg production within adult colony cages under intensive rearing conditions. This study evaluated the effects of increased sucrose feeding surface area and blood meal volume on fecundity within our mosquito production system.

Methods: Egg yield was estimated using an in-house pattern-matching protocol developed for ovistrip analysis. Two sucrose delivery methods with different feeding surface areas were evaluated. The original method used two 50ml Falcon tubes fitted with sponges, providing a total sucrose solution surface area of about 6 cm² while the modified method used a round container with cotton, which increased the total sucrose solution surface area to about 28 cm². In addition, the effect of increased blood meal provision was assessed by increasing the total blood volume provided across three feeding sessions from 104 mL to 108 mL.

Results: Compared to the original method, the expanded sucrose feeding setup increased egg yield by 4%, likely due to improved nutritional access and enhanced adult longevity. Notably, increasing the total blood meal volume by only 4 mL resulted in a disproportionate 15% increase in egg yield. The most significant gains were observed when combining the new sucrose setup with increased blood provision, which generated a synergistic 41% increase in egg production per cage.

Conclusion: These findings indicate that both sucrose accessibility and blood meal volume are drivers of egg production, with blood availability exerting a more pronounced effect on overall output. Optimizing these feeding parameters is essential for maximizing facility throughput and improving the cost-efficiency of mass-rearing operations.

G-162 A systematic review to assess humanistic and societal burden of dengue in East Asia and Pacific region

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Background: Dengue is a major global health problem, posing substantial burden. We synthesized evidence on humanistic and societal impact of dengue for patients and their caregivers in East Asia and Pacific (EAP) countries.

Methods: We systematically searched EMBASE and PubMed during 01/01/2014–01/23/2025 with prespecified inclusion/exclusion criteria for dengue in EAP. We extracted data for school-days and workdays lost, health-related quality of life (HRQoL), and disability-adjusted life years (DALYs).

Results: Of 146 eligible references, 4 reported on school-days lost, 5 on workdays lost, 4 on HRQoL, and 12 on DALYs. In five endemic countries, mean school-days loss of 3.8-5.6 days was reported for hospitalized children, while 0.7-2.6 days were reported for outpatients. Overall, patient workday loss ranged from 6.6–7.8 days. Overall mean caregiver workday loss ranged from 0.3–3.3 days, while a Vietnam study reported mean caregiver workday loss of 7.6 days for hospitalized patients. A Philippines study reported elevated depressive (13.3% vs 3.5%) and anxiety symptoms (34.2% vs 16.2%) in pediatric in-patients vs controls. A Taiwan study reported higher incidence of depressive disorders among dengue patients vs controls (273.93 vs 223.81 per 100,000 person-years). In Vietnam, mean EuroQol-5D-5L score was 0.66, indicating a significant reduction in HRQoL. DALYs for dengue ranged from 9.15 (Cook Islands) to 647,505.72 (Indonesia) in 2019.

Conclusion: There is limited data on humanistic burden of dengue in EAP with significant heterogeneity among studies. Although some studies reported sizable patient and caregiver burden, further research is needed to better understand this burden.

G-169 Barriers to Dengue Vaccine Uptake in International Travelers: A Mixed-Methods Study

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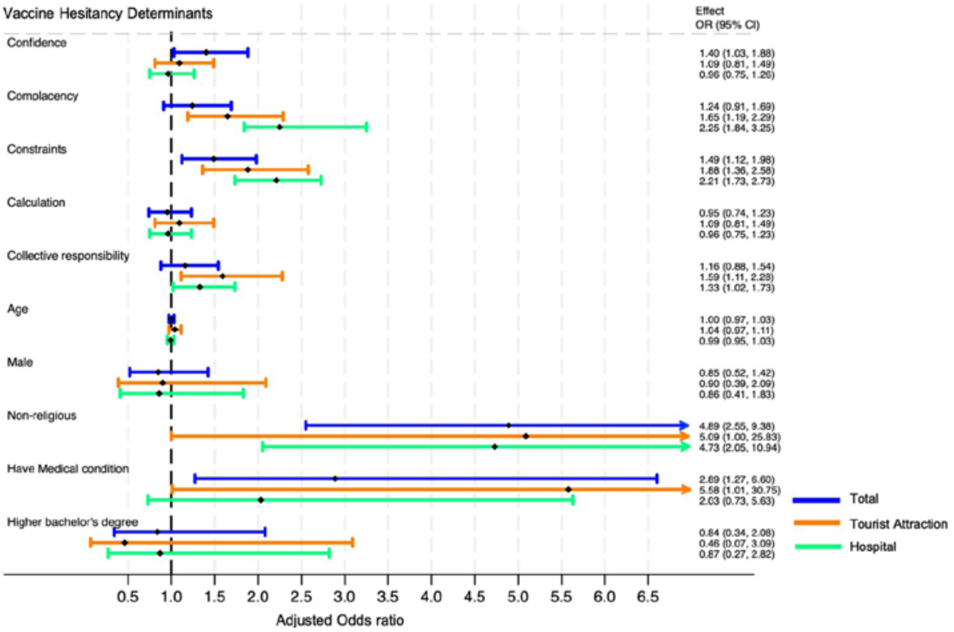
Background: Dengue poses a growing threat to international travelers, yet vaccine uptake remains limited due to inconsistent guidelines and psychological barriers. This study provides key strategies into psychological barriers and determinants of hesitancy, which may guide future strategies once global dengue vaccination guidelines for travelers are established and widely adopted.

Methods: We conducted a mixed-methods study from May 2024 to March 2025 in Bangkok, Thailand, assessing vaccine hesitancy among 429 international travelers using the 5C model and thematic analysis of interviews.

Results: The prevalence of dengue vaccine hesitancy was higher than previous literature. Dengue vaccine acceptance was 36.8%, with non-religious affiliation (adjusted odds ratio [aOR]: 4.89; 95% CI: 2.55–9.38), higher confidence, and lower perceived constraints significantly associated with acceptance (Figure1). Non-acceptors reported significantly higher levels of complacency and constraints, and lower collective responsibility scores (all $p < 0.001$). Travelers often underestimated dengue risk and cited logistical challenges and vaccine accessibility as barriers. Trust in healthcare providers, especially from endemic regions, influenced decisions, while collective responsibility was less relevant.

Conclusion: High dengue vaccine hesitancy among travelers highlights the need for healthcare providers to enhance vaccine confidence and address complacency. Improving vaccine accessibility and aligning schedules with travel plans may reduce barriers and support uptake once global guidelines are established.



G-235 Training frontline physicians for zero dengue deaths by 2030: a scalable national education model from Sri Lanka

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Background: Dengue remains a major public health challenge in Sri Lanka, with more than 50,000 cases reported annually. The national dengue case fatality rate (CFR) declined from 1% in 2009 to 0.11% by 2018 but subsequently plateaued. In 2022, the National Institute of Infectious Diseases introduced a two-week mandatory training programme on clinical dengue management for first-year postgraduate trainees in internal medicine, integrated into the national physician training programme.

Methods: The programme included one week of theory-based teaching including pathophysiology, fluid management, bedside assessment, and ultrasound-guided decision-making in dengue using interactive case discussions. Second week consisted of supervised small-group ward-based training with focused reviews of critically ill and fatal dengue cases. Evaluation was conducted using pre-and post-training assessments and structured participant feedback.

Results: Between 2022 and 2026, 314 trainees completed the programme. Overall, 95% rated it as either excellent or good. More than two-thirds gave top-tier ratings for lectures, bedside sessions, and case discussions. Qualitative feedback indicated improved confidence in recognising warning signs, managing fluid therapy, and using haematocrit and ultrasound to guide bedside decisions. Coinciding with this, the national dengue CFR declined from 0.094% (72 deaths) in 2022 and 0.069% (62 deaths) in 2023 to 0.048% (24 deaths) in 2024 and 0.054% (28 deaths) in 2025—an overall reduction of 42%.

Conclusion: A structured, practice-oriented dengue training programme delivered through a specialised centre was feasible, well-accepted, and associated with strengthened physician capacity to improve dengue care. This model offers a scalable, cost-effective educational strategy that could be adapted across Southeast Asia.

G-241 Implementing an Integrated Urban Dengue Preparedness and Response Model in Chattogram, Bangladesh: An Implementation Science Approach

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Background: Dengue poses a growing public health threat in Bangladesh, with recurrent outbreaks affecting densely populated urban areas. Chattogram City has experienced increasing transmission driven by rapid urbanisation, suboptimal vector control, and gaps in surveillance and response capacity. Following the 2023 epidemic and in alignment with national priorities, Médecins Sans Frontières (MSF) initiated the Chattogram Urban Dengue Response Project to strengthen preparedness through an integrated, multisectoral approach. This abstract describes the implementation model and early operational experience to inform urban dengue response strategies in resource-constrained settings.

Methods: A phased implementation approach was initiated from October 2025 in dengue hotspot areas identified with local authorities. Three priority urban hotspot areas were selected, targeting high-risk populations. The intervention integrates five components: community engagement, vector control support, surveillance strengthening, capacity building, and operational research. The project was designed through a multi-stakeholder workshop guided by MSF's dengue strategic framework, reflecting sustained engagement. Early implementation focuses on stakeholder engagement, site prioritisation, recruitment of multidisciplinary teams, and alignment with Ministry of Health and municipal priorities. Data are derived from routine programme monitoring.

Results: Early implementation enabled identification and prioritisation of three dengue hotspot areas and establishment of partnerships with key governmental and municipal actors. A multi-stakeholder design process informed programme structure and alignment with national strategies. Core components—including surveillance strengthening, community outreach, and vector control support—are being operationalised, with initial systems for data collection and coordination established. Recruitment of multidisciplinary teams is ongoing. Early experience demonstrates feasibility of phased implementation in complex urban settings, while highlighting challenges related to coordination, evolving data systems, and gradual scale-up.

Conclusion: An integrated, partnership-driven dengue response model is feasible in complex urban settings and supports alignment with national priorities. Early experience underscores the importance of co-design with authorities and phased implementation. This approach may inform dengue preparedness strategies in similar endemic, resource-constrained contexts.

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G-253 Perception of climate and awareness of infectious diseases in Cambodia

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Background: Climate change is reshaping the distribution and intensity of vector-borne diseases, yet public awareness of climate-health linkages remains poorly documented in tropical, climate-vulnerable settings. In Cambodia, where dengue and other mosquito-borne diseases (MBD) represent a major public health burden, understanding population perceptions is critical to designing effective communication and prevention strategies.

Methods: We conducted a nationwide cross-sectional study using a mixed-methods approach across Cambodia. The quantitative component enrolled adults aged 18 and above from 4,160 households across 104 villages and 12 districts in Phnom Penh, collecting data on climate perceptions and infectious disease awareness. The qualitative component was conducted among 754 stakeholders to explore in greater depth the understanding of climate-health linkages and drivers of health-seeking behaviour.

Results: Dengue and malaria were widely known (99.2%, 97.0%), followed by chikungunya and Japanese encephalitis (78.3%, 68.3%), while Zika was poorly known (15.6%). Females understand better the dengue's transmission mode than males, and the recognition of MBD risks from floods was associated with dengue knowledge and varied by geography ($p<0.001$). General climate awareness—such as noticing rising temperatures—is significantly associated with better understanding of climate impacts on mosquito populations and human health ($p<0.001$). Despite this, knowledge of climate drivers of mosquito-and water-borne diseases remained low.

Conclusion: The findings reveal a critical disconnect in understanding climate-driven infectious diseases risks, despite showing high climate awareness. Targeted health communication strategies linking climate signals to specific disease threats are urgently needed to strengthen community preparedness in Cambodia and similar settings.

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G-305 From Awareness to Prevention: Enhancing Dengue Prevention through Multicultural Community Engagement Strategy in the Sultanate of Oman.

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Background: Dengue remains a significant emerging disease and public health issue in Oman, particularly among Asian migrants, influenced by environmental factors and health literacy gaps. This study evaluated a multicultural community engagement intervention aimed at disrupting the mosquito life cycle and assessing knowledge, attitudes, and practices (KAP) related to dengue prevention in Salalah.

Method: From March 2025 to March 2026, a total of 888 participants from diverse nationalities (Omani, Bangladeshi, Indian, and Pakistani) were surveyed, and 1496 individuals from the community were mobilized for weekly vector control led by community leaders and embassy and counselor representatives. Mosquito repellent and preventive bed nets were distributed in high-risk zones. Dengue cases are compared with intervention and non-intervention areas. KAP measured in percentages.

Result: Zero dengue cases in the intervention area compared to 16 cases in the non-intervention area, with individuals in intervention zones exhibiting significantly higher KAP scores. Only 5% of participants recognized *Aedes aegypti*'s biting times, and while 71.3% had heard of dengue, 48% demonstrated high knowledge, with 52.8% engaging in strong preventive practices. Factors affecting KAP levels included nationality, education, residence area, and occupation, highlighting Asian migrants with lower education as particularly vulnerable.

Conclusion: Dengue prevention has turned into a social responsibility. Ongoing community-leading weekly mosquito control activities and culturally relevant multi-language health education, supported by community and embassy leaders, are crucial for effective dengue prevention in a multiculture context. Additionally, equitable distribution of resources and increasing dengue awareness in workplaces and community forums are essential for migrants.

Intervention impact - GIS Mapping of the dengue cases –(red HOME –indicate dengue cases). GREEN RECTANGLE –Intervention area – ZERO cases were reported

G-331 Understanding community-level barriers to dengue control in Cebu, Philippines

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Background: Addressing the challenges in combating dengue is multifaceted and extends beyond clinical disease management. This report aims to describe the challenges identified by various stakeholders in Cebu Province, Philippines in relation to dengue prevention and control.

Methods: A stakeholders' meeting was conducted in Cebu City last March 2024. The meeting was attended by 113 invited healthcare workers (i.e. nurses, physicians, program managers) from the Department of Health Region 7 office, provincial health office and health centers, government hospitals, and private clinics. We analyzed transcripts from structured group discussions using thematic analysis. AI-assisted coding tools (ChatGPT) were utilized for initial clustering, followed by manual validation and refinement by the investigators to ensure contextual accuracy. The challenges were clustered into themes and sub themes. We further analyzed the sub themes which arose during the breakout session.

Findings: Four themes were identified: (1) governance, (2) health system, (3) community and patient-level behavior, and (4) environmental and social determinants. Under governance, the primary challenges were low budget allocation, political issues, inadequate community support, and weak intersectoral collaboration. Health system barriers included gaps in surveillance, challenges in clinical diagnosis and management and weak vector strategies. On behavior, stakeholders cited poor health-seeking behaviors, vaccine hesitancy and misconceptions. Finally, socioeconomic and environmental factors included low education attainment and the impact of climate change.

Conclusion: The systematic identification of these barriers by various stakeholders, especially at the community-level, provides critical insights for enhancing existing dengue prevention and control strategies in Region 7.

G-361 Evaluation of the Enhanced Dengue 4S Campaign in the Philippines: A mixed-methods implementation research protocol

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INTRODUCTION: Dengue remains a major global public health concern, with recurring outbreaks despite sustained vector control efforts. In the Philippines, the Department of Health (DOH) implemented the Dengue 4S Strategy in 2012—Search and destroy breeding sites, secure self-protection, seek early consultation and support fogging/spraying only in hotspot areas—later enhanced in 2020 to incorporate broader vector-borne disease control and strengthened community engagement. However, there has been no comprehensive evaluation of its effectiveness and implementation at scale. This study, commissioned by the DOH and to be conducted by the ICHHD, aims to assess the effectiveness and implementation of the Enhanced 4S Strategy in selected dengue-endemic areas.

METHODS: This study employs a Hybrid Type 1 Effectiveness-Implementation Design using mixed methods. Quantitative analysis will utilize interrupted time series (ITS) of routine dengue surveillance data. Household surveys (n=1,268) will assess knowledge, attitudes and practices (KAP). Qualitative data will be collected through key informant interviews and focus group discussions. Data will be analyzed using regression modeling and thematic analysis guided by the RE-AIM Framework.

RESULTS: This study will generate estimates of changes in dengue incidence trends associated with the Enhanced 4S strategies, alongside measures of community compliance and implementation fidelity. Preliminary outputs include composite indicators of 4S adherence, identification of implementation gaps, and comparative insights across urban and rural settings.

CONCLUSION: This study will generate evidence on the effectiveness and real-world implementation of a national dengue prevention strategy. Findings will inform policy refinement, strengthen community-based interventions, and provide a basis for improving the implementation of the strategy nationwide.

G-364 Why Communities Remain Vulnerable to Dengue: A Qualitative Study of Socio-Environmental Determinants in Gampaha District, Sri Lanka

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Background: Dengue has become a persistent public health concern in Sri Lanka. Although reliant on vector-borne transmission, the dengue epidemiology is often shaped by non-biological determinants. This study aimed to examine socio-environmental determinants influencing dengue risk vulnerability and their effect on the adoption of sustainable preventive behaviours among urban communities in Sri Lanka.

Methods: This qualitative study was conducted as part of a cluster-randomised clinical trial of a spatial repellent intervention (Mosquito-Shield™) for dengue prevention in an endemic district. Eight focus group discussions were conducted, each with 6-8 participants, including males and females. Participants were purposively selected from four study clusters (intervention and control arms), comprising community leaders and youth (12–16 years) enrolled in the cRCT cohort. Data were transcribed verbatim in local languages, translated into English, and analysed using thematic analysis.

Results: Strong social integration and routine community activities, such as evening sports, religious events, social welfare initiatives, and neighbourhood gatherings, encourage people to occupy outdoor public spaces during peak mosquito hours, including roadsides, playgrounds, community centres, and religious venues. Flooding from unplanned urbanisation is a key contributor to seasonal dengue risk. Human-driven environmental conditions, including poor waste management, obstructed drainage, and water accumulation, increase the probability of mosquito breeding sites within community spaces. Poor attitudes towards dengue prevention, risk tolerance, and negative experiences with public service delivery, including unreliable waste collection, undermine proactive dengue prevention behaviours.

Conclusion: Dengue prevention extends beyond individual-level behavioural change. Effective control requires proactive actions, reduced environmental degradation, and strong institutional support.

G-390 Public Attitudes to a Dengue Controlled Human Infection Programme in Singapore

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Background: Controlled human infection (CHI) studies have been used in the USA to accelerate the development of dengue vaccines and therapeutics.

Methods: We conducted a cross-sectional survey among adults in Singapore between December 2024 and October 2025. We assessed knowledge of dengue, awareness of challenge studies, trust in oversight, perceived risks and benefits, willingness to participate, and compensation preferences.

Results: Among 107 participants (median age 49.0 years; 56.1% >45 years; 89.7% with prior dengue infection), only 14.0% reported prior awareness of challenge studies. Dengue knowledge was moderate to high, with correct responses across knowledge items ranging from 63.6% to 97.2%. After reading a dengue CHI scenario, 86.0% agreed individuals should be allowed to participate, and 67.3% agreed or strongly agreed such studies should take place. Perceived trust of scientists (80.3%) and ethics committees (86.0%) was high. Risk of serious side effects was the dominant concern, ranked among the top three factors by 92.5%. While 79.4% agreed participants should be paid, expectations were widely dispersed: 15.9% favoured ≤SGD100/day, 11.2% supported >SGD400/day, and 13.1% declined to state a preference. SGD250/day was the most frequently selected option (16.8%), without a majority. Younger participants more often reported payment would influence participation ($p<0.01$), whereas older participants emphasised social considerations ($p<0.01$).

Conclusion: Despite limited baseline awareness and a survey population that would not be expected to be eligible for a dengue challenge study, respondents were broadly supportive. Compensation preferences were highly heterogeneous; a controlled human infection community advisory group has been formed to further explore this and related questions.

G-417 Beyond the Science: Educating and Engaging Communities on Wolbachia Technology in Singapore

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Background: Since 2016, Singapore has conducted a multi-phased field study involving the release of male Wolbachia-carrying Aedes aegypti mosquitoes to suppress wild Aedes aegypti populations. Given longstanding public messaging on the importance of eliminating mosquitoes, releasing mosquitoes into the community is inherently counter-intuitive to residents. A structured community engagement and education framework was therefore adopted to build public understanding, trust, and acceptance of the project.

Methods: Stakeholder engagement was organised around four foundational pillars: education, consultation, involvement, and feedback. Strategies included community meetings, door-to-door visits, educational materials, and social media campaigns, designed to be inclusive, transparent, and collaborative. To assess public acceptance and identify knowledge gaps, sentiment surveys were conducted across multiple modes — online, face-to-face street surveys, and door-to-door household surveys, at key intervals throughout the project.

Results: Community surveys conducted in 2016, 2019, and 2022 consistently demonstrated high levels of awareness, trust, and acceptance among residents at study sites and the broader public, with 96% of residents either expressing support or remaining neutral towards the project. Survey findings were used to refine public communications and education campaigns, enabling targeted messaging to address identified knowledge gaps and misinformation.

Conclusion: Effective community education and engagement is a critical enabler of novel vector control programmes. Singapore's experience demonstrates that a structured, consultative engagement approach can successfully build public acceptance of counter-intuitive interventions. These findings offer useful insights for the design of dengue education programmes accompanying the deployment of emerging vector control technologies in other settings.

H-168 Rising Dengue in an Unplanned City: Policy Implications for Vector Control and Disease Prevention

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Dengue is an escalating public health challenge in Bangladesh, driven by favorable ecological conditions, unplanned urbanization, and high population density. The disease is primarily transmitted by *Aedes aegypti* and *Aedes albopictus*. Despite ongoing control efforts, recurrent outbreaks indicate critical gaps in surveillance, vector control, and early warning systems.

Dengue data, seasonal patterns, outbreak peaks, and vector indices were analyzed, alongside container productivity and habitat characteristics. Dengue incidence has increased steadily over recent years, with major outbreaks in 2019, 2022, and 2023. The largest outbreak in 2023 recorded 321,179 cases and 1,705 deaths. In 2025, Bangladesh reported 102,861 dengue-related hospitalizations, with males representing 62.5% and the highest burden among young adults aged 21–30 years. The actual disease burden is substantially higher, as many hospitals do not report cases, and numerous patients receive treatment at home, highlighting significant underreporting.

Transmission consistently peaks during the monsoon season (August–November), coinciding with increased vector density due to favorable breeding conditions. Container productivity analysis identified flooded floors (42.27%), basement parking (16.8%), and drums (14.74%) as the primary breeding sites, collectively producing nearly 74% of dengue vectors. Current interventions rely on larvicides (Temephos, Novaluron) and adulticides (Deltamethrin, Malathion), but fragmented surveillance and inconsistent application reduce their effectiveness.

These findings emphasize the urgent need to strengthen vector surveillance, establish climate-based early warning systems, implement IVM, prioritize high-productivity breeding sites, and engage communities. Enhanced data-driven decision-making and consistent evidence-based interventions are essential for sustainable dengue prevention in Bangladesh and other tropical megacities facing similar challenges.

H-261 Development of National Preparedness Self-Assessment Toolkits for Arboviral Diseases: An Evidence-based Approach for Countries

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Background: Understanding countries' preparedness and response capacity for arbovirus outbreaks is essential. A 2021 WHO survey identified major gaps in all African countries surveyed. In 2024, we conducted a self-assessment preparedness-analysis in Burkina Faso, Cameroon, Côte d'Ivoire, and Tanzania under the Resilience Against Future Threats initiative. As existing tools require updating, we developed a toolkit to guide governments in systematically identifying context-specific, evidence-based interventions.

Methods: We reviewed literature on toolkits for determining arbovirus preparedness. Building on this evidence, we created a framework outlining the toolkit's purpose, workplan development, and steps for conducting national self-assessments, providing countries with a structured process for evaluating arbovirus preparedness capacities.

Results: The toolkit development for arbovirus preparedness assessment process consists of three phases. Phase 1 (planning) focuses on team formation, creation of terms of reference (TORs), tool development, and stakeholder engagement. It includes five TORs plus templates for budget estimates and work plans. Phase 2 (implementation) covers data collection through desk reviews, stakeholder interviews, self-assessment surveys, rapid analysis, and workshops, using six instruments. Phase 3 (analysis and reporting) involves synthesizing key findings, writing the report and policy brief, and preparing dissemination materials for national stakeholders.

Conclusion: The national preparedness self-assessment toolkit helps countries systematically adapt approaches to their contexts for combating arbovirus threats. This approach can also guide development of similar tools across other health domains.

H-321 Impact of COVID-19 Policies on the Post-pandemic Resurgence of Dengue Fever in Southeast Asia and Latin America

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Background: Dengue fever, one of the most widespread mosquito-borne diseases, declined markedly during the early COVID-19 pandemic due to lockdowns and reduced mobility. However, the sharp resurgence in 2023 raised concerns about the long-term epidemiological effects of pandemic-era measures. This study examines the sustained impact of COVID-19 public health policies on dengue transmission across seven high-burden countries in Southeast Asia and Latin America.

Methods: Monthly dengue cases and COVID-19 policy indices from January 2020 to December 2023 were analyzed in seven countries with ≥2,000 dengue cases in 2020. Based on the Oxford COVID-19 Government Response Tracker (OxCGRT), countries were grouped as Strict COVID-Control (SCC: Singapore, China) or Less Strict COVID-Control (LSCC: Indonesia, Argentina, Brazil, Colombia, Mexico). Generalized linear models assessed lagged effects of the Stringency Index and policy sub-components, adjusting for climate and reporting bias.

Findings: Dengue cases declined by 41.3% (95% CI: 36.2–46.5; $p < 0.001$) in 2020 relative to pre-pandemic levels. In LSCC countries, public information and vaccination policies were significantly associated with reduced dengue incidence ($p < 0.001$), suggesting indirect protective effects of COVID-19-related awareness measures. In SCC countries, economic interventions showed mixed effects: debt relief reduced dengue risk ($\beta = -0.783$; $p = 0.003$), while income support increased it ($\beta = 0.583$; $p = 0.003$).

Interpretation: COVID-19 policies exerted lasting, heterogeneous effects on dengue transmission. Strengthening communication, vector control, and vaccination in LSCC settings, and maintaining vigilance and integrated surveillance in SCC settings, are crucial for sustainable dengue preparedness.

I-217 In Vitro and In Vivo Evaluation of Obeldesivir Against Dengue Virus Serotype 2

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Background: Obeldesivir, a nucleoside analogue with broad-spectrum antiviral activity, is a promising candidate for repurposing against dengue virus. Given the continued burden of dengue, particularly from dengue virus serotype 2 (DENV-2), this study aimed to evaluate the in vitro and in vivo efficacy of obeldesivir as a repurposed antiviral candidate.

Methods: In vitro assessment of obeldesivir was performed using an immunofluorescence assay and a plaque reduction assay to determine antiviral activity. The effect of obeldesivir on cell viability was evaluated using an ATP-based cell viability assay. For in vivo evaluation, AG129 mice were infected with DENV-2 and treated orally with obeldesivir at 30 and 60 mg/kg twice daily for three days. Mosnodenvir (10 mg/kg) was included as a positive control. Viral RNA levels in plasma, liver, and spleen were quantified on day 4 post-infection using RT-qPCR.

Results: Obeldesivir demonstrated promising in vitro antiviral activity, with an EC_{50} of less than 10 µM and a selectivity index greater than 10. In vivo, treatment resulted in significant antiviral effects; however, viral RNA reduction was limited to less than 1 log compared to vehicle-treated control mice. In contrast, mosnodenvir achieved more than 1 log viral RNA reduction.

Conclusion: Obeldesivir shows encouraging in vitro and moderate in vivo activity against DENV-2, supporting its potential as a repurposed antiviral candidate. Further optimization of dosing or combination strategies may enhance its therapeutic efficacy.

I-243 Distinct Antiviral Kinetics and Immunomodulatory Profiles of Moxidectin and Ivermectin Against Dengue Virus in Human Hepatocytes

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Background: Moxidectin (MOX) and ivermectin (IVM), repurposed antiparasitic agents, have demonstrated antiviral activity against dengue virus (DENV); however, their time-dependent effects and impact on host immune responses remain unclear. We compared the antiviral kinetics and immunomodulatory profiles of MOX and IVM in human hepatocytes.

Methods: Immortalized human hepatocyte cells were infected with DENV-2 and treated with 5 μM MOX or IVM. Antiviral activity from 2–48 h post-infection was assessed by focus-forming unit assay, NS1 ELISA, and NS3 Western blot. Host antiviral gene expression at 48 hours was measured by qRT-PCR, and cytokine production was analyzed using a multiplex assay.

Results: Both MOX and IVM reduced DENV infection by more than 50% from 18 h onward while maintaining viability above 80%. MOX exerted stronger early antiviral activity, showing greater reduction of NS1-positive cells at 24 h than IVM (59% vs 35%) and lower NS3 protein levels. MOX also more effectively reduced extracellular virion production at 21 h. In contrast, IVM showed greater inhibition at 48 h, indicating a more sustained antiviral effect. At later time points, both compounds reduced extracellular virions and secreted NS1. Both drugs suppressed pro-inflammatory mediators, including IL-8, TNF-α, RANTES, and IP-10. Only IVM upregulated IFNAR1 and RIG-I expression, and IP-10 suppression was more pronounced with IVM.

Conclusion: MOX and IVM exhibit distinct but potentially complementary anti-DENV effects in human hepatocytes. MOX acts earlier during infection, whereas IVM provides more sustained inhibition and enhances interferon-associated signaling, supporting further evaluation of both agents as repurposed dengue therapeutics.

I-296 Barriers to enrollment in Dengue fever antiviral trials – lessons from a Phase 2a study

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Background: Recruitment has been challenging in a Phase 2a multi-center, randomized, controlled study of EYU688, an oral dengue NS4B inhibitor, in adult patients with dengue fever (NCT06006559).

Methods: A multidisciplinary team performed a root cause analysis of barriers to enrollment and prioritized mitigation measures.
Causes for low enrollment:

- Lower case-load in the 2025 dengue season compared to 2024.
- Challenges to conduct full screening within 48 hours after symptom onset.
- Baseline laboratory values indicate advanced disease in some cases.
- Limited sensitivity of the NS1 rapid diagnostic test (RDT) for screening. More sensitive tests are often not timely available.
- Protocol-mandated hospitalization for 5 days limits patients' willingness to participate. Home nursing as an alternative is not accepted in some countries.
- Regulatory and operational hurdles limit site initiation during outbreaks.

Prioritized mitigation measures:

- Enhance accountability and focus between trial leadership and local project management.
- Community-centered recruitment strategies, e.g. patient referral through satellite clinics and public health partnerships, and screening of household contacts.
- Positive NS1 antigen ELISA was added to inclusion criteria.
- Logistic and legal hurdles to home nursing were addressed.
- Increased engagement with sites and investigators, fostering trust-building and best-practice sharing.
- Feasibility assessments for new sites take the above-mentioned challenges into account.

Results: The qualitative and quantitative impact of these measures on recruitment will be reported at the congress.

Conclusions: Insights into the success of mitigation measures inform future antiviral treatment studies and help optimize the development roadmap for effective and safe treatments.

I-329 Elucidating the Molecular Mechanisms of Schizophyllum commune Against Dengue Virus Infection via Transcriptomic Analysis

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Background: Intraperitoneal administration of Schizophyllum commune aqueous extract (ScASE) confers protection against DENV2 infection in AG129 mice, highlighting its potential as an anti-dengue therapeutic. This study investigated the antiviral mechanisms of ScASE using high-throughput RNA sequencing to analyze the host transcriptome.

Methods: RNA was extracted from the spleens of mock-infected, DENV2-infected, and ScASE-treated (500 mg/kg, 2x IP, 4 days) DENV2-infected AG129 mice. mRNA libraries were constructed and sequenced. Sequence reads were aligned to Mus musculus reference genome (GCF_000001635.27_GRCm39). Differentially expressed genes (DEGs) were identified using the criteria $|\log2FC| \geq 1$ and Q-value ≤ 0.05. These DEGs were analysed using Gene Ontology (GO), KEGG databases, and protein-protein interaction (PPI) networks.

Result: Transcriptomic analysis identified 1365 DEGs common to both infection and treatment groups. ScASE treatment upregulated 833 genes and downregulated 513 genes. PPI network analysis identified Il1b and Il12b as central nodes for the upregulation of the cytokine-cytokine receptor interaction pathway, serves as a molecular messenger for the inflammatory defence response. These genes also key components of C-type lectin receptor signalling pathway, likely mediating the cellular uptake of proteoglycans the active compound in ScASE. Conversely, protein processing in endoplasmic reticulum pathway a critical site for dengue virus replication showed the highest level of suppression, with 40 genes significantly downregulated in ScASE-treated mice.

Conclusion: This study elucidates the molecular pathways governing the anti-dengue activity of ScASE, specifically the dual action of boosting innate immune signalling while suppressing the endoplasmic reticulum-associated machinery required for viral replication.

R-123 A role for sphingosine-1-phosphate analogues in dengue shock?

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Background: Dengue shock (DS) is characterised by profound vascular leakage through a disrupted endothelium. Current management relies on intravascular volume replacement, highlighting the need for targeted endothelial therapies. Sphingosine-1-phosphate (S1P) is a bioactive sphingolipid that maintains endothelial integrity by preserving the glycocalyx and adherens junctions. Low S1P levels are associated with severe dengue. We investigated associations between S1P and its plasma carrier apolipoprotein-M (ApoM) with clinical outcomes in adults with DS.

Methods: We conducted a prospective observational study of adults with DS at the Hospital for Tropical Diseases, Ho Chi Minh City. Plasma S1P and ApoM were measured at enrolment (≤24h of shock diagnosis), 48h, and hospital discharge. Associations were assessed with pulmonary vascular leak (lung ultrasound), SOFA score, ICU admission, ventilation, vasopressors, haemofiltration, time to discharge, and in-hospital mortality.

Results: Among 135 patients (median 26years; median SOFA 7; 34 ICU admissions; 5 deaths), each two-fold increase in ApoM at enrolment was associated with reduced odds of death (OR0.20), ICU admission (OR0.18), ventilation (OR0.35), vasopressors (OR0.20), and haemofiltration (OR0.19); lower SOFA score (β–0.70); faster discharge (HR1.42); and earlier IV-fluid cessation (HR1.30) (all $p<0.05$). Higher S1P levels were associated with reduced mortality (OR0.09), organ support, lower SOFA score (β–1.0), faster discharge (HR1.95), and reduced pulmonary vascular leak (r–0.23) (all $p<0.05$).

Conclusion: Low S1P and ApoM are strongly associated with pulmonary vascular leakage, organ failure severity, longer hospitalisation, and mortality in DS. As S1P signalling is pharmacologically modifiable, the ApoM/S1P axis represents a promising therapeutic target for dengue-associated vascular leakage.

R-133 Integrating global dengue surveillance to give new insights into climatic drivers, growth trends and outbreak forecasting

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Background: Routine dengue surveillance data form the backbone of outbreak response, burden estimation and early warning systems. However, fragmented reporting, missing data and uneven global coverage obscure long-term trends and limit the ability to link observed dynamics to climatic drivers or to build transferable forecasting systems. Recent advances in global surveillance synthesis and modelling provide an opportunity to reassess what routine data can reveal about dengue’s expansion and predictability.

Methods: We integrate results from multiple global analyses of dengue surveillance and risk, combining harmonised case reporting databases, Bayesian spatio-temporal gap-filling models, climatic regression analyses and comparative forecasting frameworks. Monthly dengue incidence time series were reconstructed for over 140 countries since 1990 and analysed alongside large-scale climate variability to characterise long-term growth, seasonal and multiannual dynamics, and limits to predictability across diverse transmission settings.

Results: Gap-filled surveillance data reveal sustained exponential growth in reported dengue cases globally, with the most rapid increases occurring in regions of recent emergence. Seasonal and multiannual epidemic cycles have intensified over time, with increasing synchrony across countries, consistent with a growing influence of large-scale climatic drivers. Despite this, forecasting skill remains highly heterogeneous, with strong performance in some endemic settings but limited transferability across regions.

Conclusion: Together, these studies demonstrate how improving the completeness and interpretability of routine dengue surveillance transforms its value for understanding transmission drivers, benchmarking forecasting systems and evaluating intervention impact. Integrated surveillance analytics are essential for translating climatic risk into reliable, policy-relevant dengue early warning and control strategies.

R-165 Mechanistic insights into dengue virus-induced reprogramming of innate immune response

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Background: Prior infection with dengue virus (DENV) has been found to reprogram baseline innate immune gene expression, particularly in monocytes, that alters the host response to live attenuated dengue vaccination and likely also subsequent DENV infection. However, mechanisms underlying this innate immune reprogramming remain unknown.

Methods: We applied an integrated multi-omic approach combining ATAC-seq and RNA-seq to characterize DENV-induced chromatin and transcriptional reprogramming in human monocytes. Comparative analysis between dengue-seropositive and seronegative individuals identified epigenetic signatures, which were further validated using locus-specific chromatin accessibility assays and quantitative real-time PCR in an ex vivo model of innate immune reprogramming.

Results: Prior DENV exposure was associated with a significantly more compact chromatin landscape in monocytes from dengue-seropositive individuals compared with seronegative individuals. Differentially accessible regions were enriched at loci related to immune response, cell death, epigenetic regulation, and metabolic pathways, suggesting a regulatory program that promotes inflammatory responses while supporting cell survival. Validation in ex vivo reprogrammed monocytes confirmed these chromatin alterations and their impact on corresponding gene transcription. Notably, these chromatin alterations were associated with a trained immune response, characterized by increased pro-inflammatory cytokine expression following secondary DENV infection in reprogrammed cells. Upstream mechanisms, including histone modifications and metabolic changes, are currently under investigation.

Conclusion: Prior DENV exposure induces a trained immunity-like program in monocytes that shapes host innate immune response to a subsequent infection. These findings provide new insights into DENV immunobiology and may inform future vaccine and antiviral strategies.

R-195 Prior Zika virus imprints subsequent dengue virus neutralizing antibodies by skewing the repertoire of antibody-secreting cells

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Background: Zika virus (ZIKV) and dengue virus serotypes 1-4 (DENV1-4) co-circulate, eliciting cross-reactive antibodies that may worsen dengue immunopathology. Surprisingly, we found that primary ZIKV infection doubles the risk for subsequent severe dengue compared to primary DENV.

Methods: We examined how prior ZIKV versus DENV1 infection differently modulates subsequent DENV2 immunity. Using single-cell sequencing, we defined the B cell receptor (BCR) repertoire of antibody-secreting cells (ASCs) during acute DENV2 infection from children with primary DENV2 (n=1; reference), secondary DENV1-DENV2 (n=2), or secondary ZIKV-DENV2 (n=3) cases.

Results: Remarkably, ZIKV-DENV2 ASCs were dominated (33-50%) by a single clonotype in all three cases, showing convergent selection and limited pathways to DENV2 recognition, whereas DENV1-DENV2 ASCs were diverse. ZIKV-DENV2 ASCs showed more mutations than DENV1-DENV2, indicating selection pressure on ZIKV-primed immunity. Subgroups of the ZIKV-DENV2 clonotype were classified based on BCR amino acid motifs and tested as monoclonal antibodies, revealing that the majority did not neutralize DENV2 (the infecting virus) and only ~10% potently neutralized DENV2. Cryo-EM demonstrated that this ZIKV-DENV2 clone targeted the conserved flavivirus fusion loop and envelope dimer:dimer interface. Mass spectrometry analysis showed that this clonotype continued to dominate serum DENV2-IgG months after infection. The ZIKV-DENV2 clonotype and late-convalescent sera preferentially neutralized the Asian-American over Cosmopolitan DENV2 genotype, indicating a lasting serological imprint of lower breadth.

Conclusion: Primary ZIKV infection skews the repertoire of ASCs responding in subsequent DENV2, diminishing the quality of neutralizing antibodies compared to prior DENV1. Thus populations with distinct sequences of infections may acquire DENV-neutralizing antibodies differently.

R-262 Is homotypic reinfection a key feature of endemic DENV settings?

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Background: Immunity following infection with the four dengue virus serotypes (DENV1-4) remains difficult to define. Reports of individuals being reinfected with the same serotype challenge the paradigm that infection induces lifelong homotypic immunity. However, the frequency of these events and their importance for shaping immune profiles remain unknown.

Methods: Here, we used data from three cohorts (N = 4,268 total participants) in two highly endemic settings (Cebu, Philippines, and Kamphaeng Phet, Thailand), which included long-term follow-up of individuals (mean follow-up of 8.8, 1.9, and 5.0 years). These data allowed us to elucidate age-specific patterns of infection and immunity, and to quantify individual long-term antibody titer dynamics following infection. We formulated mathematical models to explain these patterns, allowing for the possibility of progressive loss of immunity to homotypic reinfection.

Results: At the individual level, we found that, in the absence of subsequent infection, antibody titers exhibit a steady long-term decay following incident infections (half-life of 7-8 years), with the rate of decay slowing with increasing age. At the population level, incorporating homotypic reinfection was required to explain the age-specific dynamics of infection and immunity observed in our cohorts. We estimated that in highly endemic settings such as the Philippines, 60% of individuals have been homotypically reinfected by the age of 40 years.

Conclusion: Our findings highlight homotypic reinfections as a key feature of endemic DENV settings and suggest that vaccines mimicking natural infection might not be expected to provide lifelong protection against infection.

R-291 Stepwise approach for Dengue Vaccine Introduction to National Immunization program in Thailand

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Background: Dengue remains a high-burden, climate-sensitive threat in Thailand, with >105,000 cases reported in 2024 despite sustained vector control. The National Vaccine Institute (NVI), in close collaboration with the Department of Disease Control (DDC), led a stepwise strategy to translate scientific evidence into national immunization policy via the Advisory Committee on Immunization Practices (ACIP).

Methods: We conducted a comprehensive policy and implementation analysis integrating national surveillance, multi-stakeholder consultations, health economic evaluation, operational feasibility analyst, Phase IV study data, and vaccine manufacturing feasibility assessments. A stepwise, evidence-informed framework synthesized epidemiologic, economic, operational, and social evidence to guide ACIP decision-making.

Results: Health economic evaluation revealed that Dengue vaccine (TAK-003) reduces cases but requires price negotiation due to high costs, while *Wolbachia*-based intervention offers a more cost-effective alternative for Thailand. Dengue vaccine has been considered as a priority to the national immunization program and further need comprehensive evidence of effectiveness against type 3, 4. Thus, Phase IV study has been implemented in children aged 7–10 years and revealed of feasibility and scalability with high community acceptance at 65% of vaccination. Building on these findings, application of the B.R.A.V.E. framework (Burden awareness, Recommendation clarity, Active education, Vaccine confidence, and Equitable access) translated evidence into actionable policy, program delivery, and strategic communication. Concurrently, multi-stakeholder engagement facilitated cross-level alignment, strengthening implementation coherence and supporting long-term sustainability.

Conclusion: Thailand's experience demonstrates a stepwise, multidisciplinary model for dengue vaccine introduction. This model provides actionable, generalizable insights to inform evidence-based immunization policy and decision-making in dengue-endemic settings.

R-338 Strategic Deployment of wMelM-SG for Suppression of *w*AlbB-SG populations established in the field

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Background: The Incompatible Insect Technique (IIT) relies on continuous deployment of male *Wolbachia*-infected *Aedes aegypti* mosquitoes to suppress vector populations for effective dengue control. However, unintentional release of fertile females, due to sex sorting limitations led to establishment of *Wolbachia-Aedes* population in the field. This rendered the suppression effect of IIT ineffective and resulted in a resurgence in mosquito populations comprising both *Wolbachia*-infected and wild type populations. Use of sterile insect technique (sterilisation of males with radiation) was unsuccessful in controlling the population. Study demonstrated use of an alternative *Wolbachia* strain (*w*MelM-SG) and environmental management to successfully target and suppress the established *w*AlbB-SG population.

Method: Singapore-outcrossed *w*MelM-SG line was established by introgressing *w*MelM-infected *Ae. aegypti* into local *Ae. aegypti* genetic background, producing phenotypically optimised strains suitable for large-scale deployment. Prior to release, male *w*MelM-SG were treated with low dose X-ray to render any contaminating female infertile. Mosquito population levels were monitored using the Gravitrap index derived from Singapore's national *Aedes* vector surveillance network. Breeding activity of the established *w*AlbB-SG population was monitored using ovitraps deployed. Detection and quantification of *w*AlbB was performed using a multiplex real-time qPCR assay targeting the *w*AlbB *wsp* gene. Field-established *w*AlbB-SG population were distinguished from any contaminating females using Whole Genome variant profiling. Robots were used to identify potential breeding sites in secondary rooftop.

Results: Deployment of *w*MelM-SG cum environmental management successfully suppressed the established *w*AlbB-SG population. After one year of intervention, established *w*AlbB-SG population was no longer detected in Gravitrap or ovitrap collections.

Conclusion: Alternative *Wolbachia* strains offer effective contingency strategies for managing strain establishment events, particularly in complex scenarios where conventional approaches may not achieve the desired outcome for suppression. These findings provide important insights for risk mitigation and ensure long-term resilience of *Wolbachia* suppression programmes.

R-385 Anakinra for dengue patients with hyperinflammation: a phase II double-blind randomized-controlled trial

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Background: Patients with dengue and hyperinflammation are at higher risk of worse clinical outcomes. Interleukin-1 blockade using anakinra has demonstrated efficacy in other acute viral conditions, suggesting potential utility for patients at risk of severe dengue.

Methods: We conducted a randomized double-blind placebo-controlled phase II trial of anakinra in patients ≥ 12 years old, diagnosed with dengue with warning signs or severe dengue, and having serum ferritin >2000ng/ml (NCT05611710). Participants received either anakinra or placebo for 4 days. The primary endpoint was the change in mSOFA score (delta mSOFA) over 4 days. Secondary endpoints included safety and laboratory measurements.

Results: 157 participants were enrolled: 69(44%) female, median age 32 years (range: 12-70). 103/157(65%) patients were randomized at day 5 of illness. 82(52%) had dengue with warning signs and 75(48%) severe dengue. Median mSOFA score at enrolment was 4 (range: 1 - 9). Mean delta mSOFA over 4 days was 1.18(±1.47) overall, 0.99(±1.44) in dengue with warning signs and 1.39(±1.50) in severe dengue. A total of 449 adverse events (54 serious) was recorded – mostly attributable to dengue, primarily thrombocytopenia, neutropenia, dengue shock and respiratory failure due to fluid overload. 98% AEs resolved by discharge or day 30 follow-up. **There were no deaths. The full unblinded data will be presented at the conference.**

Conclusion: This is the first biomarker-guided trial of immunomodulation in dengue. Results will provide critical evidence for a novel therapeutic approach with potentially major impact on dengue management.