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# Asymptomatic humans transmit dengue virus to mosquitoes

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**Three-quarters of the estimated 390 million dengue virus (DENV) infections each year are clinically inapparent. People with inapparent dengue virus infections are generally considered dead-end hosts for transmission because they do not reach sufficiently high viremia levels to infect mosquitoes. Here, we show that, despite their lower average level of viremia, asymptomatic people can be infectious to mosquitoes. Moreover, at a given level of viremia, DENV-infected people with no detectable symptoms or before the onset of symptoms are significantly more infectious to mosquitoes than people with symptomatic infections. Because DENV viremic people without clinical symptoms may be exposed to more mosquitoes through their undisrupted daily routines than sick people and represent the bulk of DENV infections, our data indicate that they have the potential to contribute significantly more to virus transmission to mosquitoes than previously recognized.**

mosquito experimental infection | Cambodia | *Aedes aegypti* | human-to-mosquito transmission | dengue

With 3.97 billion people living in 128 countries currently at risk for infection, dengue viruses (DENV-1 to -4) cause more human morbidity and mortality worldwide than any other arthropod-borne virus (1, 2). *Aedes aegypti* mosquitoes are the primary vectors of DENV throughout the tropics (3). Dengue prevention relies on the control of *Ae. aegypti* populations, which is failing in most parts of the world due to lack of resources, lack of political will, and/or ineffective implementation (4).

Virus transmission from infected humans to mosquitoes is a critical step in dengue epidemiology, but due to logistical constraints it has been directly examined only in a handful of studies to date (5). In initial experimental infections of human volunteers during the 1920s (6, 7), the onset of clinical symptoms occurred 4–9 d after virus inoculation by mosquito bite (8). DENV-infected humans were infectious to mosquitoes from 2 d before to 2 d after the onset of symptoms, and *Ae. aegypti* fed on viremic people were able to transmit virus to another person after at least 11 d of extrinsic incubation (8). Results from later studies indicated that, for naturally infected people with clinically apparent dengue, the duration of detectable viremia was on average 4–5 d after the onset of symptoms, but could range from 2 to 12 d (9, 10). Investigators in Vietnam fed *Ae. aegypti* directly on 208 symptomatic, hospitalized dengue patients and reported that the probability of successful human-to-mosquito DENV transmission was coincident with the kinetics of viremia (11). Dengue patients were infectious up to 5 d after the onset of symptoms, which generally corresponded with “defervescence” (11).

All previous studies on human-to-mosquito DENV transmission were limited to people with overt illness and did not consider sub-clinical infections. An estimated 300 million of the total 390 million DENV infections per year are clinically inapparent or mildly

symptomatic, i.e., no illness that disrupted a person’s daily routine (1). Following Grange et al. (12), we use “inapparent” or “sub-clinical” interchangeably to denote infections confirmed by virus detection or seroconversion, but with insufficient symptoms to be detected by existing surveillance systems and health care providers. “Asymptomatic” refers to a confirmed DENV infection in the complete absence of reported or detected symptoms. Inapparent human DENV infections are a potentially important component of the overall burden of dengue because they can serve as a previously unrecognized source of mosquito infection (12). Epidemic transmission of DENV associated with low viremia levels and mild illness has been reported (13). It has long been assumed, but not empirically verified, that people with inapparent infections fail to infect mosquitoes because they do not reach sufficiently high viremia levels (5). This assumption is based on the observation that disease severity is positively correlated with the magnitude of DENV viremia (10, 11, 14). To our knowledge, the only study that quantified viral RNA levels in a limited number of asymptomatic DENV infections in humans did not detect a significantly lower viremia (15), but infectiousness to mosquitoes was not evaluated. The aim of the present study was to document variation in DENV infectiousness of naturally infected humans across the spectrum of disease manifestations, including fully asymptomatic infections, and to verify the assumption that people with inapparent infections are not infectious to mosquitoes.

## Significance

**Our work provides evidence that people who are infected with dengue virus without developing detectable clinical symptoms or prior to the onset of symptoms are infectious to mosquitoes. At a given level of viremia, symptom-free people were markedly more infectious to mosquitoes than clinically symptomatic patients. Our results fundamentally change the current paradigm for dengue epidemiology and control, based on detection of dengue virus-infected cases with apparent illness.**

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Next, we examined the human, virological, and entomological factors that were associated with infectiousness to mosquitoes. In multivariate regression analyses, both viremia level and disease category were consistently and significantly associated with the likelihood of mosquito infection (Table 1). Conversely, infection immune status (primary, secondary, or indeterminate status), age, and EIP were not significant predictors of successful mosquito infection. A significant effect of serotype and gender was only detected for one mosquito feeding method, but not both, which may be due to the fact that the cohorts of individuals involved in each mosquito feeding method were not exactly the same.

Our data confirmed that the level of viremia is one of the most important determinants of human infectiousness to mosquitoes (11). The amount of detectable DENV RNA in participants' plasma (expressed in cDNA copies per milliliter) ranged from 1.61 to 10.1 log<sub>10</sub> cDNA copies per mL of plasma across all study participants (mean ± SE: 6.17 ± 0.14). The observed magnitude of viremia was not associated with age, gender, DENV serotype, or immune status. It was, however, significantly different between disease categories (*SI Appendix, Table S1*). Viremia level measured in people with asymptomatic infections (mean ± SE: 4.75 ± 0.39 log<sub>10</sub> cDNA copies per mL) was lower on average than in people with presymptomatic (mean ± SE: 6.74 ± 0.25 log<sub>10</sub> cDNA copies per mL) or symptomatic (mean ± SE: 6.12 ± 0.17 log<sub>10</sub> cDNA copies per mL) infections. Because viremia level depends on when it was measured during the course of infection (Fig. 14), we also compared the average viremia level of asymptomatic infections with that of people who developed symptoms, stratified by day of illness. The average viremia level of asymptomatic infections did not differ from viremia levels observed 2–3 d before or 5–8 d after the onset of symptoms. It was, however, significantly lower than between –1 and 4 d of illness. Thus, the average DENV viremia level of asymptomatic infections corresponded to the magnitude of viremia observed during the early and late viremic period of people who develop symptoms. To confirm that the dynamic nature of the viremic phase (Fig. 14) did not confound our time-independent analysis, we repeated the multivariate regression analysis with temporal stratification of disease categories. Although the effect of viremia level decreased, overall results did not change when symptomatic people were split into groups of 0–2, 3–4, and 5–8 d of illness (*SI Appendix, Table S5*). Asymptomatic DENV-infected people were always significantly more infectious than symptomatic people, with the exception of group 0–2 d of illness, which was marginally insignificant for indirect feeding. Presymptomatic DENV infections

did not differ significantly from asymptomatic infections (*SI Appendix, Table S5*).

Viremia levels measured by qRT-PCR and expressed, like in this study, as cDNA copy numbers are generally well correlated with infectious titers, but should be interpreted with caution. The number of infectious virus particles measured by the mosquito inoculation technique can be 2–5 logs lower, depending on the virus strain, cell type used, level of viremia, host immune response, and several other factors such as handling and storage conditions of viremic blood sample (21). RT-PCR detects RNA from infectious viruses, but also from immature virions and defective particles. On the other hand, five participants with undetectable DENV viremia by qRT-PCR were infectious to mosquitoes. This further highlights the limited correlation between infectious titer and concentration of viral RNA in plasma. It also suggests that the amount of virus might differ between venous blood (used to measure viremia) and capillary or venule blood (imbibed by mosquitoes) and/or between plasma and whole blood. As previously reported, it is also possible that the high sensitivity of the mosquito infection model may help to detect low levels of viremia that are below the limit of detection by qRT-PCR, but are actually sufficient to infect mosquitoes (21). In our multivariate analysis (Table 1), factors other than the amount of viral RNA in plasma (e.g., serotype and disease category) contributed to differences in participant infectiousness.

Strikingly, asymptomatic and presymptomatic infections were associated with increased overall probability of mosquito infection, independently of viremia level measured as cDNA copy numbers. Asymptomatic and presymptomatic DENV infections did not differ significantly from each other (direct:  $P = 0.430$ ; indirect:  $P = 0.496$ ). Dose–response scatterplots revealed that asymptomatic and presymptomatic infections were more infectious to mosquitoes than symptomatic infections at any given viremia level (Fig. 2). By direct feeding, the 50% mosquito infectious doses [95% confidence interval (CI)] were 5.31 (4.81–5.80), 5.68 (5.30–6.00), and 7.21 (7.05–7.36) log<sub>10</sub> viral cDNA copies per mL of plasma in the asymptomatic, presymptomatic, and symptomatic categories, respectively. By indirect feeding, the corresponding estimates were 5.68 (5.14–6.55), 5.97 (5.55–6.33), and 7.78 (7.59–7.99), respectively.

We analyzed viral loads in the wings and legs of infected mosquitoes because they are positively correlated with DENV in *Ae. aegypti* saliva and thus mosquito transmission potential (20). The strongest predictor of viral loads in positive mosquitoes was human viremia, followed by disease category and DENV serotype

**Table 1. Multivariate regression analysis of successful human-to-mosquito DENV transmission**

Factor	Direct feeding		Indirect feeding	
	OR (95% CI)	<i>P</i> value	OR (95% CI)	<i>P</i> value
Serotype	N.S.			
DENV-1			3.66 (1.76–7.63)	<0.001
DENV-2			1.74 (0.72–4.19)	0.213
DENV-4			Ref.	
Gender	N.S.			
Male	2.08 (1.07–4.04)	0.032		
Female	Ref.			
Viremia, +1 log <sub>10</sub> copies/mL	2.05 (1.64–2.56)	<0.001	1.81 (1.52–2.16)	<0.001
Disease category				
Asymptomatic	10.05 (1.76–57.51)	0.010	6.72 (1.90–23.9)	0.003
Presymptomatic	4.84 (2.02–11.58)	<0.001	4.19 (1.94–9.05)	<0.001
Symptomatic	Ref.		Ref.	

Minimal adequate model based on marginal logistic regression of mosquito infection status. DENV-3 was excluded due to small sample size. Direct and indirect feedings are analyzed separately as indicated in the table heading. Test statistics for the full model are in *SI Appendix, Table S2*. CI, confidence interval; N.S., not significant; OR, odds ratio; Ref., reference level.



other arboviruses with a high proportion of inapparent infections such as yellow fever virus (30).

Global efforts to reverse the increasing burden of dengue disease will require more than overcoming the lack of resources, lack of political will, or ineffective intervention implementation. Equally important will be an improved understanding and application of influential features of virus transmission dynamics. It is our hope that changing views about how people with inapparent and mild DENV infections contribute to transmission will improve the theory of DENV transmission dynamics, lead to innovation in outbreak detection and response, and refine assessment of new prevention strategies.

## Materials and Methods

**Ethics Statement.** This study was approved by the Cambodian National Ethics Committee for Health Research (Protocol 063NECHR) and by the Institut Pasteur Ethics Board for European Projects. A participant's enrollment was subject to obtaining written consent signed by the participant or by a legal representative for participants under 16 y of age.

**Study Participants.** Patients presenting with acute dengue-like illness between June and October of 2012 and 2013 were enrolled at Kampong Cham City Provincial Hospital and at two district hospitals of the Kampong Cham province (SI Appendix, Fig. S2). This province is ~120 km northeast from Phnom Penh, the capital of Cambodia, where the Institut Pasteur in Cambodia (IPC) is located. Participant inclusion criteria were as follows: (i) age  $\geq 2$  y (age  $\geq 4$  y for direct mosquito feeding); (ii) axillary temperature  $>38.0$  °C; (iii) two or more of the following symptoms: headache, retroorbital pain, muscle pain, joint pain, rash, and any bleeding; and (iv) written informed consent from the participant or a legal representative for participants under 16 y of age.

DENV infection of hospitalized patients was confirmed by NS1 antigen detection using a commercial rapid diagnostic test (for details, see *Dengue Diagnosis and Classification* below) followed by qRT-PCR on the plasma sample obtained during the acute febrile phase of disease (SI Appendix, Fig. S3) (31). Patients with a confirmed DENV infection by NS1 antigen detection and/or qRT-PCR were considered dengue index cases (DICs) that initiated geographic cluster investigations. Cluster participants were enrolled from family members at the DIC's household as well as from people living in houses within a 200-m radius of the DIC's home or in the 20 closest houses when the population density of the area exceeded the logistical capacity of the field team. Cluster participants were aged from 2 to 40 y and lived in villages located within 30 km from the provincial hospital (SI Appendix, Fig. S2). Cluster participants or representative for the participants under 16 y of age provided a written informed consent before enrollment. Exclusion criteria were as follows: (i) pregnancy or breastfeeding; (ii) symptoms inconsistent with dengue and obvious nondengue acute infection (e.g., otitis media, pneumonia, meningitis); or (iii) known chronic illness.

**Clinical Data and Blood Collection.** DICs and cluster participants were examined during sequential visits as shown in SI Appendix, Figs. S3 and S4. At each visit, data were collected using a standardized questionnaire designed for either hospitalized patients or cluster participants.

For hospitalized patients, three blood samples were collected: shortly after hospital admission during the febrile acute phase (visit 1), at the time of defervescence (visit 2), and during the convalescent phase at hospital discharge (visit 3), which in general corresponded to days 3–5 of hospitalization. The severity of the disease was assessed according to the 1997 World Health Organization (WHO) criteria using clinical, biological, and paraclinical examination data recorded at admission and throughout the entire hospitalization period (32).

To screen cluster participants for DENV infection, home visits were conducted within 24 h after DIC identification [home visit 0 (HV0)] and then again at day 2 (HV2) and day 7 (HV7) during 2012. In 2013, only HV0 and then a visit 4 d later (HV4) were conducted (SI Appendix, Fig. S4).

Blood samples drawn during visits were sent with ice packs to IPC within 5–10 h for laboratory diagnosis. Blood samples were collected in tubes with EDTA anticoagulant, and volume drawn was adapted according to participant weight: 3.0 mL for children below 20 kg of weight and 5.0 mL for individuals over 20 kg.

**Cluster Investigation Participant Follow-Up.** Once confirmed positive for DENV infection, cluster investigation participants were visited at different time points depending on their clinical presentation. Cluster participants with any dengue-like clinical symptoms described above, at any point in their observation period, were considered as symptomatic cases and those who did not report or present any symptom during examination in the follow-up period

were classified as asymptomatic individuals. The participant was classified as symptomatic if any symptoms appeared or were reported by the participant or their caregiver during the follow-up period or if the participant or their caregiver reported antipyretic drug intake.

Symptomatic cluster participants were visited immediately after confirmation of DENV infection at three time points: day 0 (D0), D2, and D7. A longer and closer monitoring was conducted in the asymptomatic group at D0, D1, D2, D3, D4, D5, D6, D7, and D10 (SI Appendix, Fig. S4). During each daily visit, a blood sample was collected and a standard questionnaire was administered regarding current symptoms or history of symptoms during at least 2 consecutive days for the last 7 d including dengue-like symptoms (headache, retroorbital pain, muscle pain, joint pain, rash, and any bleeding), body temperature, and intake of an antipyretic drug. D0 of the cluster investigation follow-up usually corresponded to the second day after the participant was enrolled (at HV0) due to the time required for blood sample transportation to IPC and subsequent laboratory confirmation.

**Dengue Diagnosis and Classification.** Blood samples collected at admission (visit 1) of hospitalized patients were tested for DENV NS1 antigen by SD BIOLINE Dengue Duo rapid diagnostic kit (Standard Diagnostic) according to the manufacturer's recommendations. This test was performed by well-trained nurses at the patient's bedside and the result was confirmed at IPC by DENV RNA detection in the same blood sample using a serotype-specific multiplex qRT-PCR method (31). The qRT-PCR had a limit of detection of 0.5–3 plaque-forming units (PFU) and 5–10 cDNA copies per 20- $\mu$ L reaction, depending on the serotype (31). To screen for additional DENV infections among household members and neighbors, blood samples that were collected at HV0, HV2, HV7 (2012), or HV0 and HV4 (2013) were tested by qRT-PCR at IPC. Results were communicated to the field team on a daily basis to initiate cluster investigations, perform mosquito feedings when required, and ensure the follow-up of cluster participants. DENV viremia was expressed as cDNA copy number per milliliter of plasma.

Serological tests were performed on sera collected during the acute and convalescent phase of the infection in both symptomatic and asymptomatic groups for detection of antibodies against DENV. Because of potential cross-reactivity among flaviviruses, all specimens were tested for both anti-DENV and anti-Japanese encephalitis virus (JEV) using an in-house IgM capture ELISA (MAC-ELISA) and hemagglutination inhibition (HI) assay as previously described (33, 34). Primary or secondary immune status of DENV infections was determined by HI test according to WHO criteria (32).

**Aedes aegypti for Human-to-Mosquito Transmission Experiments.** Wild immature stages of *Ae. aegypti* were repeatedly collected at ~2-mo intervals at different locations in Kampong Cham province from areas where the study participants resided. All *Ae. aegypti* females that were used in human-to-mosquito DENV transmission experiments were from laboratory-reared F<sub>2</sub> or F<sub>3</sub> generations derived from F<sub>1</sub> parental females that tested negative for DENV, JEV, and chikungunya virus (CHIKV) by virus-specific RT-PCR and for other potential flaviviruses by pan-flavivirus RT-PCR (31, 35–37).

Briefly, field-caught *Ae. aegypti* larvae (F<sub>0</sub>) were pooled, reared in distilled water, and fed on commercial dry fish food. Following emergence, adult mosquitoes were fed twice weekly directly on immobilized mice and maintained on cotton soaked with 10% (wt/vol) sugar solution in an environmental chamber with 12:12 light/dark hours, at 27 °C, and 70% relative humidity. F<sub>1</sub> eggs were collected on paper towels lining oviposition cups placed in the cages. The F<sub>1</sub> generation was reared as described above, and F<sub>1</sub> adults were kept in cages containing males and females. F<sub>1</sub> females were provided blood meals for multiple gonotrophic cycles over a period of 30 d. At the end of this period, surviving F<sub>1</sub> adults were removed and freeze-killed. F<sub>1</sub> adults that died before 30 d were also collected for testing. All F<sub>1</sub> mosquitoes were sorted by sex in a Petri dish placed on ice, pooled into vials of 10 mosquitoes (male and female) per vial, and homogenized. Extracted RNA was tested for DENV, JEV, CHIKV, and other flaviviruses (31, 35–37).

Eggs from cages that included only F<sub>1</sub> females and that tested negative for all tested viruses were hatched and reared to produce F<sub>2</sub> and F<sub>3</sub> adults for experimental feeding as described above. Nulliparous female *Ae. aegypti* of the F<sub>2</sub> and F<sub>3</sub> generations were used in human-to-mosquito transmission experiments.

**Experimental Exposure of *Ae. aegypti* to DENV Viremic Blood.** Following confirmation of DENV infection, each study participant was asked, or through his/her legal guardian, to participate in human-to-mosquito transmission experiments by direct and/or artificial membrane (indirect) feeding methods (SI Appendix, Fig. S5). Written informed consent was provided for all enrolled participants. Both hospitalized patients (DICs) and cluster participants were involved in mosquito feedings (SI Appendix, Fig. S6).

For direct feeding, two mesh-covered 500-mL paper cups, each containing 25 female 5- to 9-d-old *Ae. aegypti* that had been starved for 24 h, were placed on

the participant's legs for 5 min. A nurse monitored participants for 30 min for any side effects and was prepared to advise the participant to seek treatment if fever or any other symptoms occurred in the following 2 wk. Antihistamine cream was applied to the sites of mosquito bites to relieve itchiness.

For indirect feeding, venous blood was drawn from the participant into a tube with EDTA anticoagulant within 30 min after direct mosquito feeding. Briefly, 3.0 mL of whole blood was thoroughly mixed with 30  $\mu$ L of 10 mM ATP used as a phagostimulant, and the remaining blood was kept to quantify DENV RNA by qRT-PCR. Approximately 1.5 mL of mixture was loaded into two glass feeders maintained at 37 °C by a connected heated water source. Two mesh-covered 500-mL paper cups, each containing 25 female 5- to 9-d-old *Ae. aegypti* that had been starved for 24 h, were placed under the feeders for 30 min to allow blood feeding through a piece of desalted porcine intestine used as a membrane.

After direct or indirect feeding, mosquitoes were cold anesthetized at 4 °C for 10–15 min and sorted on a Petri dish placed on ice. Unfed or partially fed females were discarded. Only fully engorged females were transferred to a new 500-mL paper cup and maintained in an environmental chamber maintained in a bio-safety level 2+ facility with 12:12 light/dark hours, at 27 °C, and 70% relative humidity for ~2 wk. EIP ranged from 10 to 19 d, but for most participants (92%) surviving females were harvested between 13 and 16 d after blood feeding. Variation in EIP was taken into account in the statistical analyses.

**DENV Detection in Mosquitoes.** When harvested for processing, mosquitoes were freeze-killed, and their legs and wings were separated from the rest of the body with sterile forceps and, for each mosquito, placed individually in a vial containing 500  $\mu$ L of sterile PBS with 10% (vol/vol) FCS and 15–20 ceramic beads. The mixture was homogenized using a MagNA Lyser Instrument (Roche Life Science Thailand, catalog no. 03358976001) at 6,500 rpm for 50 s. Viral load in individual mosquito body parts was measured by qRT-PCR and the results expressed as cDNA copy number per milliliter of legs and wings suspension (31).

**Statistical Analyses.** All analyses were based on the final cohort of 181 infected human participants including 13 asymptomatic, 42 presymptomatic,

and 126 symptomatic people. Analyses of mosquito infection data were performed separately for direct and indirect feeding methods. Detectable plasma viremia levels were  $\log_{10}$ -transformed and analyzed with an analysis of variance. The proportion of infected mosquitoes was analyzed as a function of the covariates using marginal logistic regression models. Dose–response curves and 50% mosquito infectious dose estimates were derived from the logistic regression coefficients. Because of the small size of the asymptomatic cohort, dose–response curves could not be further stratified within each disease category. Viral load in infected mosquitoes was  $\log_{10}$ -transformed and analyzed with a generalized linear mixed model that included the random effect of the participant and fixed effects of other covariates. Full models were reduced to minimal adequate models by backward elimination of nonsignificant terms in a stepwise fashion. Dispersion was estimated from the data, and *P* values were obtained with *F* statistics. All statistical analyses were performed in GenStat (38).

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- Bhatt S, et al. (2013) The global distribution and burden of dengue. *Nature* 496(7446):504–507.
- Brady OJ, et al. (2012) Refining the global spatial limits of dengue virus transmission by evidence-based consensus. *PLoS Negl Trop Dis* 6(8):e1760.
- Lambrechts L, Scott TW, Gubler DJ (2010) Consequences of the expanding global distribution of *Aedes albopictus* for dengue virus transmission. *PLoS Negl Trop Dis* 4(5):e646.
- Morrison AC, Zielinski-Gutierrez E, Scott TW, Rosenberg R (2008) Defining challenges and proposing solutions for control of the virus vector *Aedes aegypti*. *PLoS Med* 5(3):e68.
- Carrington LB, Simmons CP (2014) Human to mosquito transmission of dengue viruses. *Front Immunol* 5:290.
- Siler JF, Hall MW, Hitchens AP (1926) Dengue: Its history, epidemiology, mechanism of transmission, etiology, clinical manifestations, immunity, and prevention. *Philipp J Sci* 29:1–302.
- Simmons JS, St. John JH, Reynolds FHK (1931) Experimental studies of dengue. *Philipp J Sci* 44:1–247.
- Nishiura H, Halstead SB (2007) Natural history of dengue virus (DENV)-1 and DENV-4 infections: Reanalysis of classic studies. *J Infect Dis* 195(7):1007–1013.
- Gubler DJ, Suharyono W, Tan R, Abidin M, Sie A (1981) Viraemia in patients with naturally acquired dengue infection. *Bull World Health Organ* 59(4):623–630.
- Murgue B, Roche C, Chungue E, Deparis X (2000) Prospective study of the duration and magnitude of viraemia in children hospitalised during the 1996–1997 dengue-2 outbreak in French Polynesia. *J Med Virol* 60(4):432–438.
- Nguyet MN, et al. (2013) Host and viral features of human dengue cases shape the population of infected and infectious *Aedes aegypti* mosquitoes. *Proc Natl Acad Sci USA* 110(22):9072–9077.
- Grange L, et al. (2014) Epidemiological risk factors associated with high global frequency of inapparent dengue virus infections. *Front Immunol* 5:280.
- Gubler DJ, Suharyono W, Lubis I, Eram S, Gunarso S (1981) Epidemic dengue 3 in central Java, associated with low viremia in man. *Am J Trop Med Hyg* 30(5):1094–1099.
- Vaughn DW, et al. (2000) Dengue viremia titer, antibody response pattern, and virus serotype correlate with disease severity. *J Infect Dis* 181(1):2–9.
- Duong V, et al. (2011) Clinical and virological factors influencing the performance of a NS1 antigen-capture assay and potential use as a marker of dengue disease severity. *PLoS Negl Trop Dis* 5(7):e1244.
- Yoon IK, et al. (2012) Underrecognized mildly symptomatic viremic dengue virus infections in rural Thai schools and villages. *J Infect Dis* 206(3):389–398.
- Mammen MP, et al. (2008) Spatial and temporal clustering of dengue virus transmission in Thai villages. *PLoS Med* 5(11):e205.
- Endy TP, et al. (2011) Determinants of inapparent and symptomatic dengue infection in a prospective study of primary school children in Kamphaeng Phet, Thailand. *PLoS Negl Trop Dis* 5(3):e975.
- Gordon A, et al. (2013) The Nicaraguan pediatric dengue cohort study: Incidence of inapparent and symptomatic dengue virus infections, 2004–2010. *PLoS Negl Trop Dis* 7(9):e2462.
- Lambrechts L, et al. (2012) Dengue-1 virus clade replacement in Thailand associated with enhanced mosquito transmission. *J Virol* 86(3):1853–1861.
- Choy MM, Ellis BR, Ellis EM, Gubler DJ (2013) Comparison of the mosquito inoculation technique and quantitative real time polymerase chain reaction to measure dengue virus concentration. *Am J Trop Med Hyg* 89(5):1001–1005.
- Rathakrishnan A, et al. (2012) Cytokine expression profile of dengue patients at different phases of illness. *PLoS One* 7(12):e52215.
- Liebman KA, et al. (2014) Determinants of heterogeneous blood feeding patterns by *Aedes aegypti* in Iquitos, Peru. *PLoS Negl Trop Dis* 8(2):e2702.
- Stoddard ST, et al. (2013) House-to-house human movement drives dengue virus transmission. *Proc Natl Acad Sci USA* 110(3):994–999.
- Christofferson RC, Mores CN (2011) Estimating the magnitude and direction of altered arbovirus transmission due to viral phenotype. *PLoS One* 6(1):e16298.
- Pongsiri A, et al. (2014) Differential susceptibility of two field *Aedes aegypti* populations to a low infectious dose of dengue virus. *PLoS One* 9(3):e92971.
- Coffey LL, et al. (2009) Human genetic determinants of dengue virus susceptibility. *Microbes Infect* 11(2):143–156.
- King AA, Ionides EL, Pascual M, Bouma MJ (2008) Inapparent infections and cholera dynamics. *Nature* 454(7206):877–880.
- Fraser C, Riley S, Anderson RM, Ferguson NM (2004) Factors that make an infectious disease outbreak controllable. *Proc Natl Acad Sci USA* 101(16):6146–6151.
- Chastel C (2011) [Asymptomatic infections in man: A Trojan horse for the introduction and spread of mosquito-borne arboviruses in non-endemic areas?] *Bull Soc Pathol Exot* 104(3):213–219. French.
- Hue KD, et al. (2011) Validation of an internally controlled one-step real-time multiplex RT-PCR assay for the detection and quantitation of dengue virus RNA in plasma. *J Virol Methods* 177(2):168–173.
- WHO/TDR (1997) *Dengue Hemorrhagic Fever: Diagnosis, Treatment, Prevention, and Control* (World Health Organization, Geneva), 2nd Ed.
- Vong S, et al. (2010) Dengue incidence in urban and rural Cambodia: Results from population-based active fever surveillance, 2006–2008. *PLoS Negl Trop Dis* 4(11):e903.
- Clarke DH, Casals J (1958) Techniques for hemagglutination and hemagglutination-inhibition with arthropod-borne viruses. *Am J Trop Med Hyg* 7(5):561–573.
- Shirato K, Miyoshi H, Kariwa H, Takashima I (2005) Detection of West Nile virus and Japanese encephalitis virus using real-time PCR with a probe common to both viruses. *J Virol Methods* 126(1–2):119–125.
- Pastorino B, et al. (2005) Development of a TaqMan RT-PCR assay without RNA extraction step for the detection and quantification of African Chikungunya viruses. *J Virol Methods* 124(1–2):65–71.
- Scaramozzino N, et al. (2001) Comparison of flavivirus universal primer pairs and development of a rapid, highly sensitive heminested reverse transcription-PCR assay for detection of flaviviruses targeted to a conserved region of the NS5 gene sequences. *J Clin Microbiol* 39(5):1922–1927.
- VSN International (2011) GenStat for Windows (VSN International, Hemel Hempstead, UK), 15th Ed.