

## Original Article

# Molecular typing of dengue virus in Mizoram, Northeast India

Christine Vanlalbiakdiki Sailo<sup>1</sup>, Souvik Ghatak<sup>1</sup>, Subbarayan Sarathbabu<sup>1</sup>, Girija Shankar Bariha<sup>1</sup>, Ayan Majumder<sup>1</sup>, Abhinav Singh<sup>1</sup>, Ralte Lalremruata<sup>2</sup>, Eric Zomawia<sup>3</sup>, Benjamin Lalrinpuia<sup>4</sup>, Lalfak zuali<sup>1</sup>, John Zothanzama<sup>1</sup>, Nachimuthu Senthil Kumar<sup>1</sup>

<sup>1</sup> Department of Biotechnology, Mizoram University, Aizawl, Mizoram, India

<sup>2</sup> Department of Microbiology, Synod Hospital, Durtlang, Aizawl, Mizoram, India

<sup>3</sup> Hospital and Medical Education, Department of Health and Family Welfare, Government of Mizoram, Aizawl, India

<sup>4</sup> Department of Physiology, Zoram Medical College, Falkawn, Mizoram, India

#### Abstract

Introduction: Dengue is an emerging vector-borne public health threat and characterization at the molecular level is important for proper management of the disease. The aim of the study is to examine the diversity of the dengue viral serotypes from a hilly mountainous region of Northeast India.

Methodology: Thirty-six blood samples that were positive for dengue virus IgM antibodies identified by the enzyme-linked immunosorbent assay (ELISA) method were collected and quantified for the IL6 gene expression by using reverse transcriptase polymerase chain reaction (RT-PCR).

Results: All the patients had dengue hemorrhagic fever (DHF); 12 samples had a monotypic infection and 14 samples had dual infection with various dengue virus (DENV) serotypes; one sample had triple infection with DENV-1, DENV-2, and DENV-3.

Conclusions: This study identified DENV-1 as the major serotype in the state of Mizoram and it is the first report on the molecular typing of the dengue virus from the hilly mountainous state located in the Indo-Burma region bordering Myanmar and Bangladesh.

Key words: dengue; serotypes; co-infection; moist tropical; Northeast India.

J Infect Dev Ctries 2022; 16(10):1637-1642. doi:10.3855/jidc.16137

(Received 24 November 2021 – Accepted 21 June 2022)

Copyright © 2022 Sailo *et al.* This is an open-access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

#### Introduction

Dengue is an Aedes mosquito-borne viral disease that has spread worldwide and the dengue haemorrhagic fever (DHF) has become a lethal disease in Asian and Latin American countries [1]. Redengue with emergence of altered clinical manifestations and severity is linked to change in epidemiology as well as a shift in the infection from young children to adults [2]. There are four antigenically unique serotypes of the virus (DENV-1, DENV-2, DENV-3, and DENV-4) [3] with vast geographic distribution and with high epidemic activity. DHF and dengue shock syndrome (DSS) are key public health issues [4,5,6,7]. Hence, it is important to study the serotype of the dengue virus in different climatic zones to fully understand the etiology of the disease.

Primary infection can induce lifetime protective immunity to a single serotype with only transient protection against the other three serotypes. Seroepidemiological reports show that secondary infection can be a major risk factor for DHF and DSS through antibody-dependent enhancement [8].

It is important to determine the DENV serotypes from different climatic zones for epidemiological and diagnostic investigations. The incidence of dengue is continually increasing globally and the serotype varies based on geographical region. Between 1990 to 2017 there was an increase in the number of cases (from 23.2 to 104.7 million), as well as age-standardized incidence rate (431.6 to 1371.3 per 100000 population) [9].

The state of Mizoram is a part of the Indo-Burma biodiversity hotspot in the eastern Himalayan range with an average annual rainfall of 2,100-3,500 mm, temperature ranging from 11 to 29 °C, and is in the moist tropical to subtropical climatic zone [10]. Mizoram is one of the eight Northeastern India (NEI) states and shares geographical boundary with Myanmar and Bangladesh. Among the NEI states, DENV activity has been documented from Assam [11], Arunachal Pradesh [12], Nagaland [13], and Manipur [11,14]., Dengue incidence cases have been increasing in NEI and this may be due to an increase in population, urbanization, and poor waste management [15]. Different serotypes along with coinfections have been reported in NEI. DENV2 and DENV3 were detected in Mizoram [15]. This study was undertaken using molecular typing to examine the diversity of the dengue virus serotypes in blood samples in Mizoram.

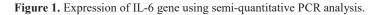
### Methodology

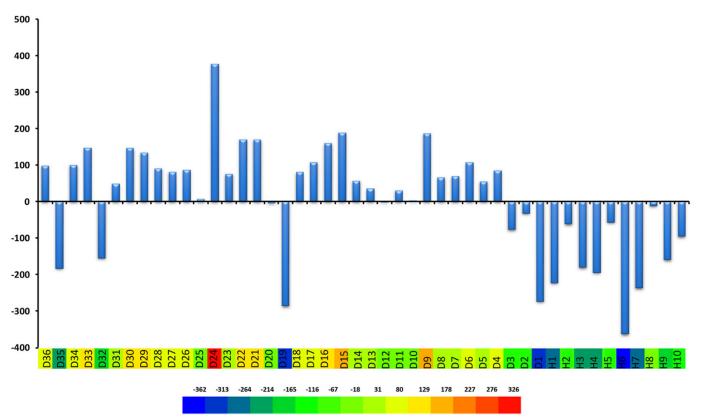
#### Ethics

Ethical clearance was obtained from Institutional Human Ethical Committee, Mizoram University (MZU/IHEC/2017/004 dated 31 August 2017).

#### Sampling and total RNA from blood sample

Blood samples were collected from dengue patients in Synod Hospital, Durtlang, Mizoram, Northeast India. All the patients exhibited DHF and were IgM positive (Supplementary Table 1). The red blood cells (RBCs) were lysed using a hypotonic buffer (ammonium bicarbonate and ammonium chloride; Himedia, Thane West, India) and the lymphocytes were separated. Three volumes of Red Blood Cells (RBC) lysis buffer was added to the blood sample, vortexed and inverted 5 minutes, and centrifuged (Eppendorf 5415R, Hamburg, Germany) at 2000 g for 10 minutes. The pellet was further treated with RBC lysis buffer and mixed well, centrifuged 2-3 times until a clean white pellet was obtained. The pellet was resuspended in 1 mL of TRIzol (ThermoFisher, Waltham, USA) and 10 µL proteinase K (10 mg/mL stock; Himedia, Thane West, India). The sample was vortexed 5 times for 30 seconds for lysis, with 5 minute incubation in ice in each interval. Next, 200 µL of chloroform was added, mixed well by vortexing, and centrifuged at 15,000 g (at 4 °C) for 10 minutes, and the supernatant was transferred to a fresh tube containing equal volumes (1:1) of chilled isopropanol (Merck, Kenilworth, USA) and incubated at -20 °C overnight, followed by centrifugation at 10,000 g at (4 °C) for 20 minutes. The pellet was washed in 70% ethanol containing DEPC treated water, followed by centrifuging at 10,000 rpm for 10 minutes. The pellet was air-dried and suspended in 30 µL RNAse-free MilliQ water; the purity and concentration were determined by quantitative spectrophotometric assay (Cary UV-visible spectrophotometer, Agilent Technologies, Santa Clara, USA). The total RNA was checked using denaturing agarose gel and Qubit (Eppendorf, Hamburg, Germany) [16].





Densitometric analysis of intensity of each amplified PCR product using Image J software. X- axis: Sample number; Y axis: relative mRNA expression.

#### cDNA Preparation and PCR amplification

First-strand cDNA synthesis was carried out (Revert Aid kit, Thermo Scientific, Waltham, USA) and specific primers were used for the amplification of the DENV serotypes. The standard 20  $\mu$ L PCR reactions were performed (125 nM of each primer, 10× PCR buffer, 1.5 mM MgCl<sub>2</sub>, 1U *Pfu* DNA polymerase, 0.5 mM dNTP) for 35 cycles with appropriate annealing temperatures (Supplementary Table 2) [17].

### Semi-quantitative reverse transcriptase PCR (RT-PCR)

Total cellular RNA (5  $\mu$ g) was used for each reverse transcription reaction for the synthesis of the first-strand cDNA. Primers targeting exons 4 and 5 of IL6 (5'-CCAGCTATGAACTCCTTCTC-3' and 5'-GCTTGTTCCTCACATCTCTC-3') and exons 1 and 3 of  $\beta$ -actin (5'-ACCATGGATGATGATGATGATGATGCC-3' and 5'- ACATGGCTGGGGGTGTTGAAG-3') were used

Table 1. PCR based serotypic pattern of dengue in Mizoran	n.
---	----

Sample	DENV 1.1/ DENV 1.2 / DENV 2.1 / DENV 2.2 /
No.	DENV 3 / DENV4
	Infectious type (mono/multi serotype)
D1	S3
D2	-
D3	S1.2/S2.1
D4	-
D5	S1.1/S2.1/S2.2
D6	S1.2/S2.1/S3
D7	S2.2/S3
D8	S1.2/S3
D9	S1.2/S2.1
D10	S1.2/S2.1/S3
D11	-
D12	-
D13	S2.2/S3
D14	S2.1
D15	S1.2/S3
D16	S1.2
D17	S1.2/S3
D18	S1.2
D19	S1.2
D20	S1.2
D21	S1.2
D22	S1.1/S1.2
D23	S1.2
D24	S1.2
D25	S1.2
D26	-
D27	S1.2/S2.1
D28	S1.2/S2.1
D29	S1.2
D30	S1.1
D31	S1.2/S2.1
D32	S1.2
D33	S1.1/S1.2/S2.1/S2.2
D34	S2.2
D35	-
D36	-

[18]. The PCR program was 35 cycles consisting of 94  $^{\circ}$ C for 30 seconds, 1-minute at the annealing temperature using a touchdown protocol (4 cycles each at 62  $^{\circ}$ C and 60  $^{\circ}$ C; 30 cycles at 58  $^{\circ}$ C), and 72  $^{\circ}$ C for 5 minutes. Polyacrylamide gel (10%) electrophoresis and ethidium bromide staining were used to visualize the products [19,20].

### Densitometric analysis

The banding patterns and molecular mass of the RT-PCR results were analyzed using Syngen G-Box gel image analysis software (Sacramento, CA, USA) and ImageJ ver. 1.53 (https://imagej.nih.gov/ij/).

### Results

### Identification of expression of IL-6 from blood samples

Twenty-six samples showed positive amplification of the IL-6 gene, out of which 11 samples had intensity between 100-200 RFU. The intensity of D24 was more than 300 RFU which indicates higher expression of IL-6 when compared with the other positive samples (Figure 1).

### Detection of serotypes from blood samples

PCR amplification of the dengue patient's DNA showed that DENV Serotype 1 (1.1 and 1.2) were absent in 12 samples (D1, D2, D4, D7, D11 to D14, D26, D34 to D36) and the serotype 1.2 was present in 23 Samples (D3, D6, D8 to D10, D15 to D25, D27 to D29, D31 to D33). Samples D5, D22, D30 and D33 have serotype 1 (1.1) of DENV.

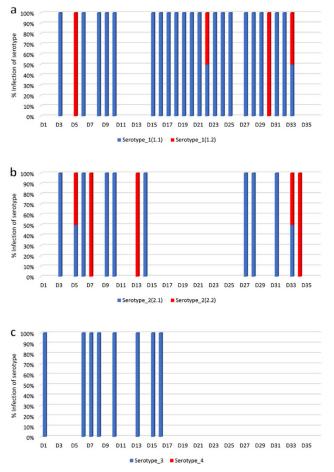
PCR amplification of the samples showed that D3, D6, D9, D10, D14, D27, D28 and D31 were DENV-2.1 positive and samples D7, D13 and D34 were DENV-2.2 positive. The samples D5 and D33 also showed positive amplification in both DENV-2.1 and 2.2. Serotype-DENV 3 was detected in samples D1, D6, D7, D8, D10, D13, D15 and D17 and serotype DENV 4 was not detected in any sample (Supplementary Figure 1). Most of the DENV infections in patients who were 4-40 years of age were multi serotype infections (Table 1, Figure 2).

### Discussion

Identification of DENV serotypes is important for informed planning of community health programs as the incidence of the disease is increasing. DENV serotypes 1 and 4 were reported from India in 1964 [26,27] and serotype 3 was reported in 1968 [28]. Simultaneous infections with DENV serotypes were detected in 2006 in New Delhi, India [29]. Mizoram, is situated in the southernmost part of Northeast India at an altitude of 500-2157 m. The state experiences wet summers (18–33 °C) and dry winters (11–24 °C) influenced by the southwest monsoon [30] and has become a dengue-endemic zone with outbreaks of DF and DHF. Dengue is now gradually spreading and establishing in the rural and urban areas of Mizoram, as well as in other parts of Northeast India, and there is monitoring of serotypes using molecular detection. Consequenty there are few reports on the spread of dengue as an epidemic or sporadic outbreaks in the region.

Several factors are associated with dengue incidences and their spread including rainfall, temperature, humidity and host immunity; however, it has been reported that temperature has the strongest effect on its transmission [26]. A study on the

**Figure 2.** Graphical representation for the detection of DENV serotypes.



**a.** presence of serotype DENV (1.1 & 1.2); **b.** samples D3, D6, D9, D10, D14, D27, D28, D31 are DENV-2.1 positive, samples D7, D13, D34 are DENV-2.2 positive and samples D5, D33 are both DENV-2.1 and 2.2 positives; **c.** Presence and absence of Serotype DENV in Samples D1, D6, D7, D8, D13, D15, D16. DENV 3 with 100% efficiency and there is no presence of Serotype-4.

meteorological data of Mizoram between 1979-2003 revealed an average annual increase of 0.08% in relative humidity, a 20.45 mm increase in annual rainfall and a ~0.1 °C increase in temperature (since 2007). These climatic factors may have facilitated the rise of dengue cases in the state by favoring the growth of its vector *Aedes aegypti* [27]. Therefore, study of serotypes that are predominant in the state may help develop effective prevention and mitigation strategies.

In the present study, all the blood samples reacted to the dengue IgM antibody. The highest number of dengue cases were detected in the age group 20-40 years, followed by the group 10-20 years (Supplementary Table 1). Although fewer samples of suspected dengue cases were detected during the monsoon season (June to October) in Mizoram, most of the samples were positive for dengue IgM antibody by the ELISA method. The dengue cases started in June and peaked in November. This is the monsoon or postmonsoon period and the stagnant waters are favored for the breeding of vector mosquitoes, *Aedes* sp. and their relative abundance is 5–222 larvae/10 dips/m<sup>2</sup> [10].

Semi-quantitative RT-PCR was performed for molecular detection with the 36 positive samples; out of these, 26 samples were IL-6 positive involving DENV 1, DENV 2, and DENV 3. DENV 1 and 2 were predominant in the samples, some samples (D3, D6, D9, D10, D27, D28, D31, and D33) had dual infections with DENV 1 and DENV 2. These samples with dual infection were IgM reactive and IL-6 positive (Figure 1). The samples D7 and D13 had the dual infection of DENV 2 and DENV3, and D8, D15, and D17 samples had a dual infection of DENV1 and DENV3 (Table 1) and they were IgM reactive and IL-6 positive. D10 amplified against DENV1, DENV 2, and DENV 3 and also contained IgM antibody and IL-6. The presence of viral RNA along with IgM antibody may be due to successive infection and IgM production due to the initial infection, as is evident by the intensity of the IL-6 bands (Figure 1). The level of IL-6 was found to be significantly elevated in the severe form of dengue fever [28,29]. In the present study we found an upregulation of the IL-6 expression and all the cases were only IgM positive which indicates primary infection. The downregulation or limited upregulation in a few patient samples may be because they were initial infections. IL-6 shows an increased level of secondary infection (IgM and IgG positive) compared to primary infection (IgM positive) [29].

DHF was found in all the patients with multiple dengue serotypes and was mainly found among the adults (20-40 years) and younger age groups which may be due to the non-exposure of all serotypes of DENV in them. Although multiple DENV serotypes have been found, further monitoring is needed to determine its endemic nature in the state of Mizoram.

Earlier studies have reported dengue in the Northeastern States including Manipur and Arunachal Pradesh [11]. The first incidence of dengue-like fever was reported at ten different localities of the Aizawl district in Mizoram between August and December 2016. The mosquito (*Aedes aegypti*) was the potential disease-causing vector species from the 11 localities of the Aizawl district in Mizoram. There was no preference toward gender or age groups and the study revealed a high density of vector mosquitoes [30].

This study adds to the report on co-circulation of the DENV serotypes from the Mizoram state [15]. The region is still remote, and with the increasing migration of the population towards urban areas, there is a great dependency on water resources. This also leads to more pockets of water bodies in urban settings generating new breeding grounds for the dengue viral hosts [25]. The DENV serotypes may evolve into new serotypes with higher severity and infectivity and will depend on the climatic conditions and environmental changes. The present study highlights the importance of continuous monitoring of DENV using molecular typing to understand the circulation and presence of the various serotypes in the Northeastern Indian states, as distinct genotypes were found which may be associated with different clinical outcomes and could be used for designing effective mitigation strategies [30].

#### Conclusions

This study identified DENV-1 as the main serotype. There is a need for molecular typing and systematic monitoring of the serotypes in relation to environmental alterations and geographic regions. This study also highlights the need for large-scale sampling and identification of the *Aedes* mosquito species across geographical boundaries.

#### Acknowledgements

The authors thank the Department of Biotechnology (DBT), New Delhi for the infrastructural facility at the Advanced Level State Biotech Hub, Mizoram University (BT/NER/143/SP44475/2021).

#### References

 World Health Organization (2017) Dengue and severe dengue. Available: http://www.who.int/mediacentre/factsheets/fs117/en/.

 Accessed: 15 April 2019.
Lee KS, Lai YL, Lo S, Barkham T, Aw P, Ooi PL, Tai JC, Hibberd M, Johansson P, Khoo SP, Ng LC (2010) Dengue

- Hibberd M, Johansson P, Khoo SP, Ng LC (2010) Dengue virus surveillance for early warning, Singapore. Emerg Infect Dis 16: 847-849.
- Henchal EA, Putnak JR (1990) The dengue viruses. Clin Microbiol Rev 3: 376-396.
- 4. Halstead SB, Cohen SN (2015) Dengue hemorrhagic fever at 60 years: early evolution of concepts of causation and treatment. Microbiol Mol Biol Rev 79: 281-291.
- Srivastava VK, Suri S, Bhasin A, Srivastava L, Bharadwaj M (1990) An epidemic of dengue haemorrhagic fever and dengue shock syndrome in Delhi: a clinical study. Ann Trop Paediatr 10: 329-334.
- World Health Organization (1999) Strengthening implementation of the global strategy for dengue fever and dengue haemorrhagic fever, prevention and control. Report of the informal consultation, 18–20 October 1999, WHO HQ, Geneva. Available: https://apps.who.int/iris/handle/10665/66186. Accessed: 15 April 2019.
- 7. Gubler DJ (1998) Dengue and dengue hemorrhagic fever. Clin Microbiol Rev 11: 480-496.
- Shukla R, Ramasamy V, Shanmugam RK, Ahuja R, Khanna N (2020) Antibody-dependent enhancement: a challenge for developing a safe dengue vaccine. Front Cell Infect Microbiol 10: 572681.
- Zeng Z, Zhan J, Chen L, Chen H, Cheng S (2021) Global, regional, and national dengue burden from 1990 to 2017: a systematic analysis based on the global burden of disease study 2017. eClinicalMedicine 32: 100712.
- Vanlalruia K, Senthilkumar N, Gurusubramanian G (2014) Diversity and abundance of mosquito species in relation to their larval habitats in Mizoram, North Eastern Himalayan region. Acta Trop 137: 1-18.
- 11. Dutta P, Khan SA, Borah J, Mahanta J (2012) Demographic and clinical features of patients with dengue in northeastern region of India: a retrospective cross-sectional study during 2009-2011. J Virol Microbiol: 1-11.
- 12. Khan SA, Dutta P, Topno R, Soni M, Mahanta J (2014) Dengue outbreak in a hilly state of Arunachal Pradesh in northeast India. Scientific World J: 1-6.
- 13. Dutta P, Mahanta J (2013) Potential vectors of dengue and the profile of dengue in the north-eastern region of India: an epidemiological perspective. Dengue Bull 30: 234-242.
- Khan SA, Dutta P, Borah J, Chowdhury P, Doloi PK, Mahanta J (2013) Dengue outbreak in an Indo-Myanmar boarder area: epidemiological aspects and risk factors. Trop Biomed 30: 451–458.
- Chetry S, Khan SA, Dutta P, Apum B, Medhi PS, Saikia DC, Temsu T, Mawii L, Marak BC (2019) Dengue virus serotypes and genotypic characterization from northeast India. J Med Virol 91: 918-927.
- Ghatak S, Sanga Z, Pautu JL, Kumar NS (2015) Coextraction and PCR based analysis of nucleic acids from formalin-fixed paraffin-embedded specimens. J Clin Lab Anal 29: 485-492.
- 17. Gijavanekar C, Añez-Lingerfelt M, Feng C, Putonti C, Fox GE, Sabo A, Fofanov Y, Willson RC. (2011) PCR detection of

nearly any dengue virus strain using a highly sensitive primer 'cocktail'. FEBS J 278: 1676-1687.

- Vennema H, de Bruin E, Koopmans M. (2002) Rational optimization of generic primers used for Norwalk-like virus detection by reverse transcriptase polymerase chain reaction. J Clin Virol 25: 233-235.
- Gerard GF, D'Alessio JM (1993) Reverse transcriptase (EC 2.7.7.49): the use of cloned maloney murine leukemia virus reverse transcriptase to synthesize DNA from RNA. Methods Mol Biol 16: 73–93.
- Sambrook J, Russell DW (2001) Molecular cloning: a laboratory manual. 3rd ed. New York: Cold Spring Harbor Laboratory Press. 2028 p.
- Myers RM, Varkey MJ, Reuben R, Jesudass ES (1970) Dengue outbreak in Vellore, southern India, in 1968, with isolation of four dengue types from man and mosquitoes. Indian J Med Res 58: 24–30.
- 22. Carey DE, Myers RM, Reuben R (1964) Dengue type 1 and 4 viruses in wild-caught mosquitoes in South India. Science 143: 131–132.
- Myers RM, Carey DE, Rodrigues FM, Klontz CE (1964) The isolation of dengue type 4 virus from human sera in South India. Indian J Med Res 52: 559–565.
- 24. Bharaj P, Chahar HS, Pandey A, Diddi K, Dar L, Guleria R, Kabra SK, Broor S (2008) Concurrent infections by all four dengue virus serotypes during an outbreak of dengue in 2006 in Delhi, India. Virol J 9: 1.
- Zomuanpuii R, Hmar CL, Lallawmzuala K, Hlimpuia L, Balabaskaran Nina P, Senthil Kumar N (2020) Epidemiology of malaria and chloroquine resistance in Mizoram, northeastern India, a malaria-endemic region bordering Myanmar. Malar J 19: 95.
- 26. Mordecai EA, Cohen JM, Evans MV, Gudapati P, Johnson LR, Lippi CA, Miazgowicz K, Murdock CC, Rohr JR, Ryan SJ,

Savage V, Shocket MS, Stewart Ibarra A, Thomas MB, Weikel DP (2017) Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models. PLoS Negl Trop Dis 11: e0005568.

- 27. Karuppusamy B, Sarma DK, Lalmalsawma P, Pautu L, Karmodiya K, Nina PB (2021) Effect of climate change and deforestation on vector borne diseases in the north-eastern Indian state of Mizoram bordering Myanmar. J Clim Chang Health 2: 100015.
- 28. Sirichan Chunhakan, Punnee Butthep, Sutee Yoksan, Kanchana Tangnararatchakit, and Ampaiwan Chuansumrit (2010) Vascular leakage in dengue hemorrhagic fever is associated with dengue infected monocytes, monocyte activation/exhaustion, and cytokines production. Int J Vasc Med 2: 23-27.
- 29. Varghese A, Thomas T, Oommen S, Mathew A, Philip T (2019) Assay of proinflammatory cytokines (IL-6, IFN  $\gamma$ , TNF $\alpha$ ) and its correlation with disease severity in dengue fever. Int J Contemp Med 6: 2454-7379.
- Pautu L, Pachuau Z, Lalmalsawma, Zoramthara (2017) Report of first dengue outbreak in Aizawl, Mizoram, northeast India: Epidemiological and entomological surveillance and observations. Science Vision 17: 61-68.

#### **Corresponding author**

Nachimuthu Senthil Kumar, PhD Professor, Department of Biotechnology, Mizoram University, Aizawl – 796 004, Mizoram, India Tel: +91- 9436352574 Email: nskmzu@gmail.com

**Conflict of interests:** No conflict of interests is declared.

## Annex – Supplementary Items

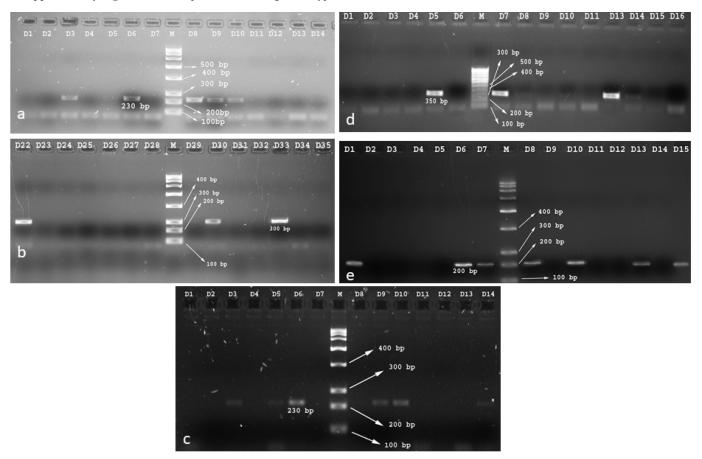
Supplementary	Table 1. Lis	st of samples of	collected for d	lengue viral	characterization.

Case No.	Age of the patients (years)	Diagnostic test
D1	32	IgM positive
D2	36	IgM positive
D3	38	NS-1 & IgM positive
D4	10	IgM positive
D5	7	NS-1 & IgM positive
D6	14	IgM positive
D7	17	NS-1 & IgM positive
D8	32	IgM positive
D9	36	IgM positive
D10	26	IgM positive
D11	31	NS-1 & IgM positive
D12	38	NS-1 & IgM positive
D13	5	IgM positive
D14	16	IgM positive
D15	23	IgM positive
D16	35	NS-1 & IgM positive
D17	10	IgM positive
D18	4	IgM positive
D19	17	IgM positive
D20	56	IgM positive
D21	46	NS-1 & IgM positive
D22	27	IgM positive
D23	63	IgM positive
D24	29	IgM positive
D25	6	IgM positive
D26	19	IgM positive
D27	28	IgM positive
D28	43	IgM positive
D29	14	IgM positive
D30	48	IgM positive
D31	28	NS-1 & IgM positive
D32	25	IgM positive
D33	26	IgM positive
D34	51	IgM positive
D35	37	IgM positive
D36	8	IgM positive

Supplementary Table 2. Primers used for the serotyping of dengue virus.

Primer	Primer Sequence (5'-3')	Annealing temperature	<b>Extension time</b>
DNV.1.1	F- CAGACTAGTGGTTAGAGGAGA	47 °C	40 seconds
DIN V.1.1	R- GGAATGATGCTGTAGAGACA	47 C	
DNV.1.2	F- CAAACCATGGAAGCTGTACG	58 °C	30 seconds
DIN V.1.2	R- TTCTGTGCCTGGAATGATGCT	58 C	50 seconds
DNV.2.1	F- CAACCATGGAAGCTGTACG	56 °C	40 seconds
DIN V.2.1	R- CATCATGAGACAGAGCGAT		
DNV.2.2	F- TTCCAACAAGCAGAACAACAT	58 °C	30 seconds
DINV.2.2	R- TTCTGTGCCTGGAATGATGCCT		
DNV.3	F- ATATGCTGAAACGCGTGAG	57 °C	40 seconds
DINV.5	R- CATCATGAGACAGAGCGAT		
DNV.4	F- TTCCAACAAGCAGAACAACAT	58 °C	30 seconds
DINV.4	R- GCTACAGGCAGCACGGTTT	38 C	50 seconds

Supplementary Figure 1. PCR amplification of dengue serotypes.



Agarose gel showing the presence of the dengue serotypes: **a.** DENV1 - 230 bp product; **b.** DENV1 - 300 bp product; **c.** DENV2- 230 bp product; **d.** DENV2 - 350 bp product; **e.** DENV3 - 200 bp product