1. Project title: “Comprehensive study on virus quasi-species and vascular permeability factors in severe dengue infection in humans for innovative epidemic and clinical managements”

2. Joint Research period:

- **Japan Team**: January 1, 2014 – March 31, 2017
- **Philippine Team**: January 1, 2015 – December 31, 2017
- **Vietnam Team**: January 1, 2014 – December 31, 2016

3. Research Team:

**Japan Team**
Funding period: April 1, 2014 – March 31, 2017
Total Funded Amount (JPY): 46,260,000

<table>
<thead>
<tr>
<th>Japan Team</th>
<th>Name</th>
<th>Position</th>
<th>Affiliation</th>
<th>Role in the project</th>
</tr>
</thead>
<tbody>
<tr>
<td>PI</td>
<td>Futoshi Hasebe</td>
<td>Professor</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Conception of the project, project implementation and, report writing</td>
</tr>
<tr>
<td>Collaborator</td>
<td>Kouichi Morita</td>
<td>Professor</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Conception of the project, virological analysis</td>
</tr>
<tr>
<td>Collaborator</td>
<td>Meng Ling Moi</td>
<td>Associate Professor</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Serologic and molecular analysis</td>
</tr>
<tr>
<td>Collaborator</td>
<td>Corazon C Buerano</td>
<td>Visiting Professor</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Virus isolation and detection, gene sequence and analysis</td>
</tr>
<tr>
<td>Collaborator</td>
<td>Takeshi Nabeshima</td>
<td>Assistant Professor</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Viral genome analysis using next generation sequencer</td>
</tr>
<tr>
<td>Collaborator</td>
<td>Shigeru Tajima</td>
<td>Chief Scientist</td>
<td>Institute of Tropical Medicine, Nagasaki University</td>
<td>Design and construction of recombinant dengue viruses.</td>
</tr>
</tbody>
</table>

Total number of participants including students: 14
### Philippine Team

**Funding period:** January 1, 2015 – December 31, 2017  
**Total Funded Amount (PhP):** 14,762,100.10

<table>
<thead>
<tr>
<th>Name</th>
<th>Position</th>
<th>Affiliation</th>
<th>Role in the project</th>
</tr>
</thead>
<tbody>
<tr>
<td>Filipinas F. Natividad, PhD/Mark Pierre S. Dimamay, PhD</td>
<td>Retired Head/Associate Director</td>
<td>St. Luke’s Medical Center (SLMC)</td>
<td>International and national Linkages</td>
</tr>
<tr>
<td>Maria Luisa G. Daroy, RCh, MS, DPAM</td>
<td>Scientist</td>
<td>SLMC</td>
<td>Project implementation and overall supervision; report-writing</td>
</tr>
<tr>
<td>Maria Terese A. Dimamay, PhD</td>
<td>Scientist</td>
<td>SLMC</td>
<td>Supervision of laboratory experiments, technical training and vascular permeability experiments; report writing</td>
</tr>
<tr>
<td>Ronald R. Matias, PhD</td>
<td>Sr. Res. Scientist and Director</td>
<td>SLMC &amp; United Laboratories, Inc.</td>
<td>Protocol development and laboratory supervision</td>
</tr>
<tr>
<td>Cynthia A. Mapua, MSPH</td>
<td>Associate Director</td>
<td>SLMC</td>
<td>Database development and data analysis</td>
</tr>
<tr>
<td>Edith S. Tria, MD</td>
<td>Head</td>
<td>External Affairs, San Lazaro Hospital</td>
<td>Coordination of patient recruitment, sample and data collection</td>
</tr>
</tbody>
</table>

Total number of participants: 14-16

### Vietnam Team

**Funding period:** January 1, 2014 – December 31, 2016  
**Total Funded Amount (VND):** 2,780,000,000

<table>
<thead>
<tr>
<th>Name</th>
<th>Position</th>
<th>Affiliation</th>
<th>Role in the project</th>
</tr>
</thead>
<tbody>
<tr>
<td>Le Thi Quynh Mai</td>
<td>Vice Director</td>
<td>National Institute of Hygiene and Epidemiology (NIHE)</td>
<td>Project implementation and overall supervision</td>
</tr>
<tr>
<td>Nguyen Thi Thu Thuy</td>
<td>Chief</td>
<td>Arbovirus Laboratory, NIHE</td>
<td>Serologic analysis, virus isolation</td>
</tr>
<tr>
<td>Nguyen Thi Nam Lien</td>
<td>Head</td>
<td>Department of Microbiology, Hue Central Hospital</td>
<td>Coordination of patient recruitment, sample and data collection</td>
</tr>
<tr>
<td>Nguyen Kim Phuong</td>
<td>Head</td>
<td>Department of Microbiology, 108 Military Hospital</td>
<td>Coordination of patient recruitment, sample and data collection</td>
</tr>
<tr>
<td>Le Thanh Nhan</td>
<td>Head</td>
<td>Department of International Research Collaboration and Education, Nhidong Hospital No.1</td>
<td>Coordination of patient recruitment, sample and data collection</td>
</tr>
<tr>
<td>Nguyen Nhat Cam</td>
<td>Director</td>
<td>Hanoi Preventive Medicine Center</td>
<td>Coordination of patient recruitment, sample and data collection</td>
</tr>
</tbody>
</table>

Total number of participants including students: 20
4. **Summary of the joint research** (up to 4 pages for section 4. to 6. including figures. Please note that information described in this report should only be disclosable.)

The research outputs are summarized as follows:

**A. Determination of the virus serotype, genotype and genomic sequences of epidemic DEN strains in the Philippines and Vietnam**

In Vietnam, determination of DENV serotypes, genotypes and genomic sequences and virological characterization were done for the virus strains isolated during the 3 year period of research (Table 1) and also for DENV from serum samples collected as far back as 2008.

<table>
<thead>
<tr>
<th>Year</th>
<th>No. of Serum Samples</th>
<th>NS1 (+)</th>
<th>Virus detection Results of Real time PCR / Virus isolation</th>
</tr>
</thead>
<tbody>
<tr>
<td>2014</td>
<td>953</td>
<td>ND*</td>
<td>DENV-1: ND/ C-57**, V-33***; DENV-2: 36 / C-4, B-3****; DENV-3: 107 / C-9, B-21; DENV-4: 6 / C-2, B-1</td>
</tr>
<tr>
<td>2015</td>
<td>911</td>
<td>207</td>
<td>6 / C-2, B-1</td>
</tr>
<tr>
<td>2016</td>
<td>1736</td>
<td>418</td>
<td>0 / 0</td>
</tr>
<tr>
<td>Total</td>
<td>3600</td>
<td>625</td>
<td>7 / C-19, V-5, B-2; 27 / C-32, V-17, B-13; 89/C-112, V-4, B-8</td>
</tr>
</tbody>
</table>

*ND: not done, ***C: number of virus isolates in C6/36 cell line, ***V: no. of virus isolates in Vero cell line, ****B: no. of virus isolates in BHK Fcγ cell line

The outputs of the work were published as listed in Annex 1. We would like to mention that in 2013, a large DENV outbreak occurred with 204,661 clinical cases in central Vietnam. During the dengue season, September–December 2013, a total of 1532 collected blood samples were screened by dengue NS1 Ag ELISA in Hue central hospital. Out of the 702 samples positive by NS1 Ag ELISA, 501 samples were positive by serotype specific real time – reverse transcription (RT)-PCR method. As a result, DENV-4 was the dominant serotype (245 cases, 48.9%), followed by DENV-1 (141 cases, 28.1%), DENV-3 (63 cases, 12.6%) and the last DENV-2 (52 cases, 10.4%) (Takamatsu Y, et al. J. Clin Virol 66; May 2015,24-26). None of dengue negative specimens showed Chikungunya and other flavivirus such as Zika virus positive by RT-PCR (data not shown).

We reported a case of dengue encephalitis caused by DENV3 genotype III in a male patient with atypical symptoms of DENV infection in Hai Phong, Vietnam in 2013. The virus isolated from the cerebrospinal fluid of this case-patient was closely related...
to DENV3 genotype III strains isolated from serum of two other patients, who manifested classical dengue in the same year and residing in the same area as the case-patient. It is noteworthy to mention that in 2013, DENV3 genotype III was detected for the first time in Vietnam (Minh Huong Phu Ly et. al. J. Clin Virol 2015 Sep;70:93-96) (Fig.1). Currently, the virological and biological characteristics of the CSF and serum isolates are being determined by using nucleotide sequence and virological analyses.

The Philippine team counterpart received the allocated grants starting from fiscal year (FY) 2015. Thereafter, 1,745 sera were collected from 1,290 dengue-suspected patients between 2015-2017 in Manila, Philippines. 893 were enrolled as outpatients and 397 as inpatients. Virus isolation and virological characterization of these samples was performed. Below are some outputs (Tables 2 and 3):

| Table-2. Laboratory test results of samples for Filipino outpatients enrolled in e-ASIA JRP |
|---|---|---|---|
| Year | Number of samples collected | Anti-DENV IgM (ELISA) | Realtime RT-PCR (Alm et al. 2014, serum &/or ICF) |
| 2015 | 437 | 82/435 | 178/431 |
| 2016 | 256 | 23/256 | 86/255 |
| 2017 | 200 | 1/155 | 56/200 |
| Total | 893 | 106/846 | 320/886 |

379 samples were DENV(+) by realtime RT-PCR, with the most prevalent serotype being DENV-1 (34%) in 2015, DENV-3 (40% and 64.3%) in 2016 and 2017. Four specimens from 2017 showed co-infection with DENV-1&3. 98 (25.9%) specimens were unserotypeable using both conventional and realtime RT-PCR methods.

Fig. 2 Distribution of DENV serotypes in 2015-2017 in two Metro Manila hospitals.

| Table-3. Distribution of dengue serotypes in the Philippines by using realtime RT-PCR. |
|---|---|---|---|---|---|
| Serotype | 2015 | 2016 | 2017 | Total (%) |
| DENV-1 | 52 | 17 | 10 | 79 (20.8) |
| DENV-2 | 35 | 21 | 2 | 58 (15.3) |
| DENV-3 | 32 | 34 | 23 | 89 (23.5) |
| DENV-4 | 34 | 14 | 3 | 51 (13.5) |
| DENV-1&3 | 0 | 0 | 4 | 4 (1.06) |
| Unserotypeable | 38 | 47 | 13 | 98 (25.9) |
| Total | 191 | 133 | 55 | 379 |
As of December 2016, a total of 678 serum and plasma samples were sent from the Philippines as part of the e-Asia JRP project in NEKKEN. These samples included outpatient and inpatient samples from 537 individual patients. From IgM and IgG capture ELISA experiments, 62.3% of outpatient samples and 45.7% of inpatient samples were found to be of secondary infection. The serotype distribution of DENV in these samples was 20.7% (n=29) DENV1, 20.0% (n=28) DENV2, 18.6% (n=26) DENV3, and 18.6% (n=26) DENV4 with one sample having coinfection from DENV3 and DENV4. Thirty (30) of the samples were unsertypeable. Interestingly, there have been an increase in the percentage of DENV4 patients. Phylogenetic analyses of the envelope region of the DENV4 demonstrated that the isolated DENV4 belongs to genotype II, and is closely related to those DENV4 strains circulating in South East Asia. DENV4 isolated from the Philippines demonstrated a mixture of 2 different strains with mutations in the E-protein hinge region Thr-58-Ile. Further studies would be needed to determine the role of the mutations in the changing epidemic DENV patterns in the Philippines.

**Fig. 3** Phylogenetic tree based on the envelope gene sequence of selected DENV-4 isolates

**B. Analysis of DENV quasispecies and factors associated with vascular permeability to determine the mechanism of severe dengue**

In FY2014, amino acid mutations of the NS4B region, which are hypothesized to be associated with host adaptability in mosquito (C6/36) and mammalian cells (Vero) in DENV-1 was determined. Using the limited dilution method, 3 phenotypes of DENV quasispecies were successfully isolated from a single patient. Additionally, by using a DENV-1 infectious plasmid clone with same mutations introduced into the NS4B region, studies to determine the biological functions of the virus protein are currently being performed.

Clinical samples (blood and or ascites or pleural effusions) were obtained starting August 2015 from patients at Children Hospital No. 1 (Ho Chi Minh, Southern Vietnam) where annually, a high number of severe dengue patients are treated. Clinical samples were...
obtained from 154 patients with different degrees of disease severity and the samples were analyzed for correlation with disease severity. All specimens were serologically analyzed to differentiate primary from secondary infection and tested by real time RT-PCR for dengue virus serotyping. Seventy three out of 154 samples were found positive by real time RT-PCR (DENV-1: 35, DENV-2: 15, DENV-3: 2, DENV-4: 20, DENV-1&2 mix infection: 1). Correlation between disease severity and infection status (primary or secondary infection) and dengue virus serotype were determined (Fig.2, Fig.3). Unexpectedly, many severe dengue cases were found in primary infection (34%). DENV-2 might be more virulent compare with other serotypes.

All real time RT-PCR positive specimens were directly analyzed by next generation sequencer, Ion Proton, and subjected to virus isolation using different cell lines. Only 1 virus strain (No.69) was isolated from a DSS patient. Four mixed infection cases were found by analysis using Ion Proton (No.49 & 69: DENV-1 &4, No.176: DENV-2 & 4, No.204: DENV-1 & 2) (Fig.4). Several sequence variants were found in DENV-1 and DENV-2 (Fig.5). For the determination of correlation between disease severity and sequence variants there is a need to analyze samples from more severe dengue cases.
On the Philippine side, inpatient samples were used to study the mechanism of vascular permeability and molecular factors associated with it. Current results showed a significant increase in the in vitro vascular permeability (P≤0.05) during the acute phase of DV infection, which gradually decreased to baseline levels during the critical and convalescence phases (Fig. 6A and B). A delay in onset of vascular permeability was seen among patients with warning signs versus patients without warning signs. Interestingly, the kinetics of transforming growth factor beta (TGF-beta) showed a significantly decreased level during the acute phase and gradually increased to normal baseline levels at the critical and convalescence phases (P≤0.0001). Significantly lower concentrations were found among the patients with warning signs versus those without warning signs during the acute and critical phases of DV infection (data not shown). In this study, we believe that TGF-beta and possibly other molecular host factors play an important role in the immune mechanism of increased vascular permeability in severe DV infection, as indicated by our inhibition assay in vitro (data not shown).

C. Determination of DENV antibody neutralizing titer to predict DENV epidemics

In collaboration with the Preventive Medicine Center, Hanoi, samples from 100 residents (healthy individuals) were collected before and after the 2015 outbreak in Hanoi, and the levels of anti-DENV IgM and IgG antibodies were determined by using an in-house ELISA assay. The antibody seroconversion rates, and data on primary and secondary infection among the residents of Hanoi have been obtained. The serum samples were sent to the Institute of Tropical Medicine, Nagasaki University for further analyses on the levels of neutralizing antibodies by using the Fc gamma R-
expressing BHK cells. We were able to establish PRNT for all serotypes of dengue viruses and also for Zika virus. We faced Zika virus outbreak in Vietnam and the Philippines in 2016. Dengue viruses and Zika virus belong to the same family Flaviviridae, therefore it is difficult to differentiate by using ordinary serologic tests such as IF test, IgG-ELISA and IgM-capture ELISA. However we can detect and titrate each virus specific antibody by PRNT method. The first Zika virus infection case and microencephaly cases caused by Zika virus infection in Vietnam were identified by our study members. The introduction of PRNT method was very significant for research on flavivirus infections, especially dengue or Japanese encephalitis in endemic countries.

5. Outputs and Anticipated Outcomes of Joint Research
5-1 Scientific achievements and implemented activities of the joint research
1. Establishment of electronic dengue database
2. Dengue biobank of serum/plasma, virus cultures, and viral nucleic acids
3. Analyses of dengue virus factors – DENV cultures, RNA/cDNA, serotype/genotype
4. Analyses of human host factors – anti-DENV IgM, vascular permeability, cytokines
5. Complete genome sequences of dengue virus isolates by NGS
6. Development of molecular protocols: real-time RT-PCR, vascular permeability assay, modified PRNT, NGS & bioinformatics

5-2 Synergistic effects of the international joint research
1. Training in advanced technologies and protocols
2. Exchange of information and ideas on dengue epidemiology of national and regional significance
3. Close collaboration in preparation of results for publication and presentation.

5-3 Broader impacts including contribution to society
1. Data gathered provide baseline information for implementation of dengue vaccination program by Philippine government
2. Integration of research efforts with other dengue projects within the group and with other groups.

5-4 Development and sustainability of the cooperation
1. Japan (Nagasaki University), Philippines (SLMC, PCHRD) and Vietnam have expressed willingness to continue collaborative research on dengue.

6. Future Goals and Plan of Activities after the project period
1. Continuation of research focus on viral and host factors of dengue severity
2. Whole RNA genome sequencing of dengue virus isolates (virome?)
3. Development of rapid diagnostics for dengue
4. Molecular epidemiology and biostatistics for in silico modelling

7. Recommendations and Comments to the Program
It is indeed a very good opportunity to study dengue virus infection among the 3 countries—Japan, Philippines and Vietnam. We could make a network for the exchange of information and specimens and collaborate research work on infectious diseases. The study period is not long enough, however we got 3 government-financed foreign students—1 student from Philippines and 2 students from Vietnam—to help us in the project. Therefore, we are still able to continue to work on the study subjects. We are aware that at least for one recent e-ASIA JRP project between Japan and two other foreign countries, financial funding is from Japan side only and the other partner countries do not provide cash but only manpower and support in kind. So some budget in Japan side should be flexible for use especially for the arrangement of sample collection.

Annex: List of Scientific Achievements and Implemented Activities of the Joint Research

(Please lists only achievements that are relevant to e-ASIA JRP)

1 Original Publications (All Authors’ Names, Title, Journal Name, Volume, Page, Year, DOI)


2.1-2 Maria Luisa G. Daroy and Filipinas F. Natividad, Report on the dengue situation in the Philippines, Ryoujyun Hall (Nagasaki University), 09 May 2014, Oral presentation.

2.1-3 Takeshi Nabeshima, Application of the next generation sequencer, e-ASIA JRP Dengue Project Kickoff Meeting, Ryoujyun Hall (Nagasaki University), 09 May 2014, Oral presentation.

2.1-4 Corazon C. Buerano, Vascular permeability assay, e-ASIA JRP Dengue Project Kickoff Meeting, Ryoujyun Hall (Nagasaki University), 09 May 2014, Oral presentation.

2.1-5 Futoshi Hasebe. Dengue and Dengue Research in Vietnam. Scientific Workshop to Explore e-ASIA Research Collaboration Opportunities Focused on Emerging Infectious Disease and Cancer priorities in South East Asia and Pacific Rim (Convened in Conjunction with the e-ASIA JRP Board Meeting) Inya Lake Hotel, Yangon, Myanmar, 13-14 August 2015, Oral presentation.


2.1-9 Meng Ling Moi, Overview of e-Asia research project in Japan, e-ASIA JRP Dengue Project Annual Meeting, St. Luke’s Medical Center, (Quezon City Philippines), 16 November 2015, Oral presentation by Skype.

2.1-10 Takeshi, Nabeshima, Strategies for the investigation of viral diseases with next generation sequencer, e-ASIA JRP Dengue Project Annual Meeting, St. Luke’s Medical Center, (Quezon City Philippines), 16 November 2015, Oral presentation by Skype.


2.1-21 Maria Terrese A. Dimamay, Increased vascular permeability in Filipino patients during the course of dengue virus infection, e-ASIA JRP Seminar and Final Meeting in Vietnam, 2016, Library, National Institute of Hygiene and Epidemiology, 22 November 2016, Oral presentation.

2.1-22 Satoshi Shimada, Clinical observation on dengue virus infection in Ho Chi Minh City, Vietnam 2016, Library, National Institute of Hygiene and Epidemiology, 22 November 2016, Oral presentation.

2.1-23 Takeshi Nabeshima, Transcriptome analysis of severe dengue clinical samples, Library, National Institute of Hygiene and Epidemiology, 22 November 2016, Oral presentation by Skype.

2.1-24 Meng Ling Moi, Implications of dengue cross-reactive antibodies in flavivirus endemic areas: the past, the present and the future, Library, National Institute of Hygiene and Epidemiology, 22 November 2016, Oral presentation by Skype.


2.1-26 Mark Anthony Luz. フィリピンにおいて流行するデングウイルスの血清型、遺伝子型及びウイルス遺伝子の特性解析．サイエンスアンゴラ.東京.2017年11月
Organization of workshops, seminars, symposia, etc. (Organizer, Title of Event, Date, Location, Number of Participants, etc.)

a. e-ASIA JRP Japan team, e-ASIA JRP Dengue Project Kickoff Meeting, 09 May 2014, Ryojun Hall (School of Medicine, Nagasaki University), 25 participants.
b. e-ASIA JRP Philippine team, e-ASIA JRP Dengue Project Annual Meeting, 16 November 2015, St. Luke’s Medical Center, (Quezon City Philippines), 19 participants.
c. e-ASIA JRP Vietnam team, e-ASIA JRP Seminar and Dengue Project Final Meeting, National Institute of Hygiene and Epidemiology (Hanoi, Vietnam), 22 November 2016, 24 participants.

Researcher exchanges including students (Description of Exchange, Destination, Duration, etc.)

**[Japan Team]**

a. Maria Terrese Alonzo, Analysis of dengue patient samples, St Luke’s Medical Center (Quezon City, Philippines), 17 February-10 March 2014.
b. Kouichi Morita, Meeting for sample collection from dengue patients in the Philippines, St Luke’s Medical Center (Quezon City, Philippines), 12-15 November 2014.
c. Moi Meng Ling, Meeting for the analysis of dengue patient serum samples by modified plaque reduction neutralization assays and for other laboratory experiments, National Institute of Hygiene and Epidemiology (Hanoi, Vietnam), 23-26 May 2015.
d. Futoshi Hasebe, Meeting for sample collection from dengue patients and sample analysis, St Luke’s Medical Center (Quezon City, Philippines), 31 May-3 June 2015.
e. Satoshi Shimada, Observation of clinical treatment and medical care method for dengue patients at St Luke’s Medical Center and San Lazaro Hospital (Quezon, City and Manila, Philippines), 15-21 November 2015.
g. Moi Meng Ling, Conduct of a training course for modified plaque reduction neutralization assays and other laboratory experiments for differentiation of dengue and Zika virus infection in Vietnam in collaboration with WHO Vietnam office. National Institute of Hygiene and Epidemiology, 08-19 August 2016.
h. Satoshi Shimada, Observation of clinical treatment and medical care method for severe dengue patients in Children Hospital No.1 (Ho Chi Minh City, Vietnam), 04 September-17 November 2016.
i. Phu Ly Minh Huong, Clinical data analysis and collection of samples from severe dengue patients in Children Hospital No.1 (Ho Chi Minh City, Vietnam), 02-27 October 2016.

**[Philippine Team]**

a. Mark Anthony Luz – Monbusho scholarship under the PhD programme, Dept. of Virology (Institute of Tropical Medicine, Nagasaki University), from Oct 2015.
b. Maria Terresse S. Dimamay, PhD – conduct of training and research on vascular permeability assays, Dept. of Virology (Institute of Tropical Medicine, Nagasaki University), 07-19 June 2016, 06-31 March 2017.
c. Lady-Anne S. Pangilinan – training on modified plaque reduction neutralization assays and other laboratory experiments Department of Virology (Institute of...
Tropical Medicine, Nagasaki University), 05-25 July 2015.

d. John Paul Llido – training on modified plaque reduction neutralization assays and other laboratory experiments, Department of Virology (Institute of Tropical Medicine, Nagasaki University), 05-25 July 2015.

[Vietnam Team]
a. Bui Thu Thuy – Monbusho scholarship under the PhD programme, Department of Virology (Institute of Tropical Medicine, Nagasaki University), from April 2014.
b. Nguyen Co Thach – Monbusho scholarship under the PhD programme, Department of Virology (Institute of Tropical Medicine, Nagasaki University), from Oct 2016,
c. Tran Thi Nha, Meeting for sample collection, Vietnam, 30 September to 04 October 2014.
e. Do Phuong Loan, Analysis of dengue patient samples, Department of Virology (Institute of Tropical Medicine, Nagasaki University), 04 November to 01 December 2014.
f. Nguyen Ngoc Linh, Analysis of dengue patient samples, Department of Virology (Institute of Tropical Medicine, Nagasaki University), 08 November-05 December 2014.

5 Number of patent applications : None

6 Awards: None

7 Others (Including agenda of workshop, photos of research teams, meetings, and etc.)
e-ASIA JRP DENGUE PROJECT ANNUAL MEETING
16 November 2015, St. Luke’s Medical Center, Quezon City, Philippines

e-ASIA JRP DENGUE PROJECT ANNUAL/FINAL MEETING
22 November 2016, National Institute of Hygiene and Epidemiology, Hanoi, Vietnam

e-ASIA JRP DENGUE PROJECT ANNUAL/FINAL MEETING
22 November 2016, National Institute of Hygiene and Epidemiology, Hanoi, Vietnam