

**P0077**

**Paper Poster Session**

**Emerging and pre-emerging viruses**

### **Characteristics of dengue outbreak in Dar es Salaam - Tanzania, 2014**

Silvia Meschi<sup>1</sup>, Francesco Vairo<sup>2</sup>, Leonard Mboera<sup>3</sup>, Pasquale De Nardo<sup>4</sup>, Ndekya Oriyo<sup>3</sup>, Susan Rumisha<sup>3</sup>, Fabrizio Carletti<sup>5</sup>, Athanas Mhina<sup>3</sup>, Francesca Colavita<sup>5</sup>, Paola Zaccaro<sup>5</sup>, Serena Quartu<sup>5</sup>, Elibariki Mwakapeje<sup>6</sup>, Concetta Castilletti<sup>7</sup>, Maria Rosaria Capobianchi<sup>\*8</sup>, Antonino DI Caro<sup>9</sup>, Emanuele Nicastrì<sup>4</sup>, Mwele Malecela<sup>3</sup>, Giuseppe Ippolito<sup>2</sup>

<sup>1</sup>*National Institute for Infectious Diseases Inmi Irccs L. Spallanzani, Laboratory of Virolog, Rome, Italy*

<sup>2</sup>*National Institute for Infectious Diseases Inmi Irccs L. Spallanzani, Department of Epidemiology, Rome, Italy*

<sup>3</sup>*National Institute for Medical Research Nimr, Dar Es Salaam, Tanzania*

<sup>4</sup>*National Institute for Infectious Diseases Inmi Irccs L. Spallanzani, Clinical Department, Rome, Italy*

<sup>5</sup>*National Institute for Infectious Diseases Inmi Irccs L. Spallanzani, Laboratory of Virology, Rome, Italy*

<sup>6</sup>*Ministry of Health and Social Welfare, Dar Es Salaam, Tanzania*

<sup>7</sup>*National Institute for Infectious Diseases Inmi Irccs L. Spallanzani, Virology Laboratory, Rome, Italy*

<sup>8</sup>*Istituto Nazionale Per Le Malattie Infettive "Lazzaro Spallanzani", Rome, Italy*

<sup>9</sup>*National Institute for Infectious Diseases Lazzaro Spallanzani, Rome, Italy*

**Background:** The incidence of dengue has grown dramatically around the world in recent decades. One recent estimate indicates 390 million dengue infections per year, of which 96 million manifest clinically. In East Africa, dengue infection has been reported in Somalia, Djibouti, Comoros, United Republic of Tanzania and Kenya. To our knowledge, in 2014 Tanzania experienced the largest dengue fever outbreak documented to date, with all cases occurring in or originating from Dar es Salaam. We report the main findings of the outbreak investigation in order to better define the epidemiological, clinical and virological characteristics of the outbreak.

**Material/methods:** The investigation involved all three districts of Dar es Salaam, namely Kinondoni, Ilala and Temeke and included both urban and peri-urban areas in each district. During the month of June, all consecutive patients with fever of  $> 37.5$  °C for less than 7 days attending the outpatient department at seven selected health facilities were tested with rapid test for malaria (mRDT) and dengue virus (dRDT). Demographic, environmental and clinical data were collected using a structured questionnaire and informed consent was signed by participants to the study. Dengue virus (DENV) specific real time RT-PCR and conventional RT-PCR were performed on dRDT positive serum samples in order to identify the serotype and genotype. Complete envelope gene was sequenced and phylogenetic analysis was performed.

**Results:** DENV infection was present in 101 (20.9%) of 483 enrolled patients, whereas 9 (1.9%) patients were IgG positive, indicating past infection. The incidence reached a peak during the mid of June and decreased towards the end of the month. Patients aged > 15 years had a 2-fold increase in the odds of infection ( $p=0.029$ ). Warning signs were frequent in patients with DENV infection (41.6%,  $p=0.006$ ) and three patients met criteria for severe dengue. Sixty-two patients with DENV infection tested positive at PCR. At the phylogenetic analysis all the sequences grouped in a monophyletic cluster inside the DENV-2 serotype, cosmopolitan genotype. The high prevalence of patients (41.6%) with warning signs including 3 patients with severe dengue could suggest the hypothesis of DENV secondary infections.

**Conclusions:** This study reports DENV-2 serotype, cosmopolitan genotype, as causative agent of the 2014 dengue outbreak in Dar es Salaam. The higher incidence of DENV infection among patients >15 years old may be related to the possible recent introduction of the DENV-2 serotype. The virus share high identity with strains isolated in China, India, East Timor and Singapore. These results indicate a possible epidemiological link with travel between Asia and Tanzania in recent years. This hypothesis could be supported by the reports of DENV-3 in the previous years in Zanzibar in contrast with the recently reported presence of DENV-2 in febrile patients in Kilosa.