

firmed in six of 16 samples. The peak of the epidemic period occurred on January 4, 2012. Drinking water from the Luangano river (OR 4.9, CI 1.7–13.9), eating at an event five days before contracting the disease (OR 8.9; CI 3.3–24.1), no use of latrine (OR 7.1, CI 3.2–15.5) were independent factors associated for contracting cholera in Lukapa.

**Conclusion:** The cholera outbreak was spread through a common source – the contaminated river – and propagated from person to person. Control measures carried out included health promotion campaigns, chlorination of drinking water, distribution of oral rehydration salts, and setting up of water tanks in the community.

<http://dx.doi.org/10.1016/j.ijid.2012.05.416>

#### Type: Poster Presentation

Final Abstract Number: 53.017

Session: *Epidemiology & Public Health*

Date: Saturday, June 16, 2012

Time: 12:45–14:15

Room: Poster & Exhibition Area

#### Incompleteness of death registration in Ghana: The role of mortuaries in death registration

C. Gyimah\*

*St Patrick's Hospital, Offinso, Ghana*

**Background:** Accurate worldwide information on the levels and patterns of mortality (deaths) is essential for planning and monitoring global public-health initiatives. The gold standard method for collecting such information is death registration. In high-income countries, death registration is effectively 100% complete, but the situation in many developing countries is very different. In most African countries, for example, less than one-quarter of deaths are officially recorded.

**Methods:** The study was done to find out how provision of mortuaries could help increase death registration coverage in Ghana from the current 25%. In a cross sectional survey of 20 districts (those with mortuaries and without), a structured questionnaire was administered to 204 relatives to seek their knowledge on deaths they registered in the year 2010; and 20 districts registrars of births and deaths to explore the problems associated with death registration.

**Results:** According to the relatives, 59.8% of the registered deaths expired at home compared to 33.3% deaths occurring in the hospitals and the remaining 6.9% were coroner's cases. Again, among the relatives, 46.1% were not aware of death registration and let alone knowing why they should register a death of a relative. In all the 20 districts studied, 95% had no computer. Eighty five percent of the registrars had only secondary education. Seventy percent of the districts had just one employed staff and 15% of the districts had no employed staff.

**Conclusion:** It was observed in the present study that, the districts with mortuaries registered more deaths as compared to the districts without mortuaries. It is therefore evident that death registration coverage will increase if mortuaries are provided in the districts. Public education should be intensified on the need to register deaths and the registry given the needed assistance to perform. A more holistic and durable programme should be put in place such as the keeping of community register for the entry of all deaths in every community (unit committee level).

<http://dx.doi.org/10.1016/j.ijid.2012.05.417>

Final Abstract Number: 53.018

Session: *Epidemiology & Public Health*

Date: Saturday, June 16, 2012

Time: 12:45–14:15

Room: Poster & Exhibition Area

#### Mapping genes & genomes: a molecular approach for epidemiological insight and targeted dengue control in Singapore

H.C. Hapuarachchi\*, S. Lo, S.S.Y. Tan, Y.L. Lai, H. Xu, C. Koo, C.R.R. Chua, S. Kaur, M. Punzalan, C.H. Tan, K.Y. Pok, S.G. Lam-Phua, L.K. Tan, K.S. Lee, L.C. Ng

*National Environment Agency, Singapore, Singapore*

**Background:** Dengue control rides solely on the suppression of vector populations as there is no alternative way to occlude Dengue virus (DENV) infection at present. In-depth understanding of virus-host interactions, vector biology and ecology facilitates such an indirect approach that targets to minimize the disease burden in endemic regions. Based on this fundamental, dengue control in Singapore utilizes an evidence-based decision support system inclusive of major elements of the disease cycle: host (case and entomological surveillance), pathogen (virus surveillance) and environment (ecological information).

**Methods:** *Aedes* breeding data is collected routinely as part of vector control operations by the National Environment Agency whereas case surveillance is spearheaded by the Ministry of Health. At the Environmental Health Institute, DENVs isolated from human sera obtained through an island wide network are routinely subjected to serotyping and genome sequencing. While circulating viruses are compared with a global pool for potential introductions, their spatial distribution is mapped in the local landscape of *Aedes* and dengue clusters to target enhanced vector control. In parallel, genetically diverse viruses are tested for fitness in mosquitoes and mammalian systems in order to determine their outbreak potential.

**Results:** From 2005–2011, 454 full length and 10 nearly complete envelope genes belonging to all 4 DENV serotypes (DENV-1 = 78, DENV-2 = 285, DENV-3 = 81, DENV-4 = 20) have been characterized. Data revealed a switch in the predominant serotype in two occasions in 2005 and 2007, both of which were associated with unprecedented outbreaks. Phylogenetic analyses revealed multiple introductions and alternating genotype/clade changes of all 4 DENV serotypes. One of the noteworthy was the clade change in DENV-2 cosmopolitan genotype in 2007. Post-2006 clade viruses showed higher transmission potential in *Ae. aegypti*, which may explain the outbreak in 2007 despite a low *Aedes* house index.

**Conclusion:** Utilizing the serotype switch combined with spatial analysis of cases and vector density as a major warning sign to alert control operations and monitoring virus evolution as a means of disease transmission have presumably contributed to avert a major dengue outbreak in Singapore since 2007.

<http://dx.doi.org/10.1016/j.ijid.2012.05.418>