

**Conclusion:** These results show increasing number of CDI in our hospital and emphasizing the importance of implementing better surveillance programs and improving infection control practice in order to prevent further spread CDI.

<http://dx.doi.org/10.1016/j.ijid.2014.03.717>

**Type: Poster Presentation**

Final Abstract Number: 43.011

Session: Infectious Disease Surveillance I

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

**Surveillance and response: Integrated indigenous health systems-based sentinel detection of human plague in a plague endemic West Nile region of Uganda (2008-2013)**



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**Background:** Bacterial plague, caused by *Yersinia pestis*, is a zoonotic disease predominantly rodent flea-borne. Approximately 2000 suspected cases of plague were reported from the plague endemic West Nile region of Uganda through the past decade. Case mortality rates were high due to delays in seeking appropriate medical treatment. Community health workers (CHWs), private for profit (PFP) clinics and drug-shops provide immediate alternative source of health care to those suffering from illness. Besides, an estimated 40-60% of the study population seeks the service of traditional healers (THs). This study piloted an innovative one health tailored community-based surveillance aimed at enabling the indigenous health care providers to recognize primary symptoms of plague among their clients and refer suspects to the nearest health center (HC); and to determine the number of patients referred by the participating THs, the proportion that actually arrive in the HCs, and the diagnostic outcome of referred patients.

**Methods & Materials:** Participating THs were provided with easy to use patient referral kits whilst the catchment HCs received rapid diagnostic tests (RDT) for on-spot detection of *Y. pestis* F1 antigen. Samples that tested positive by RDT at the HCs or negative but presented with clinical signs suggestive of *Y. pestis* infection were re-subjected to serial testing by RDTs direct fluorescent assay (DFA), bacterial culture and serology.

**Results:** Out of 562 patients referred to HCs by THs, 1 patient (0.18%) was confirmed with *Y. pestis* infection whilst a significant proportion tested positive to other febrile infections such as malaria (51.0%), pneumonia (18.9%), tuberculosis (4.3%) and others (25.8%). We summarized in table below human plague incidence and case mortality (2008-2012) in the study area.

Year	Confirmed	No. of deaths due to <i>Y. pestis</i>
2008	58	25
2009	2	1
2010	1	1
2011	2	2
2012	9	6

**Conclusion:** Although the proportion of referred patients confirmed with *Y. pestis* is minimal, it's clearly evident that the

involving THs has saved many lives from several illnesses. The integration of CHWs, clinics and drug-shops increased sensitivity of the surveillance system. Such community-based surveillance one health models that innovatively integrate indigenous health systems and scientific research are likely to have significant impact on mitigating public health crises in report settings.

<http://dx.doi.org/10.1016/j.ijid.2014.03.718>

**Type: Poster Presentation**

Final Abstract Number: 43.012

Session: Infectious Disease Surveillance I

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

**Seroprevalence of dengue amongst inhabitants of the semi-forested and forest fringe areas of peninsular Malaysia**



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**Background:** Dengue is an endemic disease in the urban areas of the tropics and subtropics regions of the world. Its significance in the semi-forested and forest fringe areas, however, has not been well described. The present study investigated the seroprevalence of dengue amongst the indigenous or Orang Asli communities of peninsular Malaysia and correlated it with the population, socio-economic and geographical attributes of the communities' surroundings.

**Methods & Materials:** Eight different Orang Asli communities consisting of 491 individuals were recruited. Their dengue antibody status was determined using the Dengue IgG capture ELISA. Land cover features surrounding these Orang Asli communities were visually measured using Google earth 5.2.1 and GE-Path 1.4.4. Remote sensing data were obtained from WorldClim, Moderate Resolution Imaging Spectroradiometer software and the Department of Survey and Mapping, Malaysian, respectively.

**Results:** Among the 491 volunteers, 17% were positive for the presence of dengue IgG indicating previous exposure to dengue virus (DENV) infection. Semai Perak community showed the highest prevalence of dengue (>50%) whilst the Orang Kuala community showed the lowest prevalence (<2%). From univariate analysis, high prevalence of dengue was significantly associated with females, those aged  $\geq 13$  years, lower education level, working individuals, and those earning less than RM500 (USD155) monthly. Multivariate analysis, however, showed that only those from low monthly household income of less than RM500 were significantly associated with high dengue seroprevalence. Dengue seroprevalence was also associated with the presence of industrial area ( $r=0.807$ ;  $p=0.015$ ) and the number of multilane roads nearby the community. Higher land surface temperature and lower land elevation were also significantly associated with dengue seroprevalence in the studied communities.

**Conclusion:** The present study suggests that prevalence of dengue amongst the Orang Asli in peninsular Malaysia is significantly associated with various socio-economic factors, the number

of multilane roads near the villages, industrial activities, and land surface temperature and altitude.

<http://dx.doi.org/10.1016/j.ijid.2014.03.719>

#### Type: Poster Presentation

Final Abstract Number: 43.013

Session: Infectious Disease Surveillance I

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

#### Malaria vector control

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**Background:** Since 2011, the NMCP of Benin has implemented a large IRS campaign using bendiocarb in the department of Atacora in Bénin. The aim of this study was to evaluate the susceptibility of *An. gambiae* mosquitoes to bendiocarb, before (2010) and after (2012) the implementation of IRS interventions and to report the evolution of *Ace-1<sup>R</sup>* mutation frequency in this region.

**Methods & Materials:** Mosquitoes resting in the house (indoor collection) were collected through Morning Spray Catch (MSC) from 7 a.m. to 9 a.m. in five treated districts (Kouandé, Natitingou, Matéri, Péhunco, Tanguiéta) and in the Control (Copargo, an untreated district) before and after IRS. Anopheles larvae were also reared in each district before and after IRS and emerging adults were exposed to WHO impregnated papers discriminating dosages with bendiocarb, 0.1%. PCR assays were run to determine the members of the *An. gambiae* complex, as well as phenotypes for insensitive acetylcholinesterase (AChE1) due to *Ace-1<sup>R</sup>* mutation.

**Results:** This study showed that the mean *Ace-1* mutation frequency have significantly increased from 2010 to 2012 after two years of IRS campaign. Mortality data indicated that mosquitoes were susceptible in 2010 to bendiocarb 0.1%. From 2010 to 2012, after two years of IRS campaign, there is a drastic decline in the *An. gambiae* susceptibility to bendiocarb in treated districts. The *Ace-1<sup>R</sup>* mutation was found in *An. gambiae* s.s. and *An. coluzzi* with frequency of 7.33% and 7.35%. The high proportion of homozygous susceptible specimens survived from the WHO bioassays may suggest the implication of the other mechanisms of resistance such as biochemical resistance mechanisms.

**Conclusion:** These results are of prime importance in the effort to document multiple impacts of operational control program on mosquito vectors. It showed a significant increase of *Ace-1* allele frequency and resistance to bendiocarb in *Anophele gambiae* population after IRS implementation that can be a threat for malaria vector control based on the IRS which is in progress in Benin.

<http://dx.doi.org/10.1016/j.ijid.2014.03.720>

#### Type: Poster Presentation

Final Abstract Number: 43.014

Session: Infectious Disease Surveillance I

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

#### Studies of reservoirs and vectors of plague in Northeastern, Tanzania



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**Background:** *Yersinia pestis*, the etiologic agent of plague, is transmitted to animals by infective flea-bites. Fleas associated with rodents, cats, dogs and other small mammals are considered important for the maintenance and transmission of bacterium. Therefore, a study was undertaken to investigate factors associated with flea infestation among rodents species, and to investigate the presence of *Y.pestis* in fleas of North-Eastern Tanzania during a quiescent period.

**Methods & Materials:** Fleas were collected from rodents and domestic animals by brushing the animal. House dwelling fleas were trapped with light traps. All collected fleas were identified to genus level and subjected to PCR test for *Y.pestis* DNA

**Results:** Among the captured rodents, *Rattus rattus* (26.5%), *Lophuromys flavopunctatus* (16.5%), *Praomys delectorum* (16.2%) and *Mastomys natalensis* (32.3%) were most abundant rodent species. Altogether, 805 fleas were collected from 61% of captured rodents. The most common fleas were *Xenopsylla spp*, *Dinopsyllus spp* and *Ctenophthalmus spp*. Fleas were found to be highly abundant in *M. natalensis*, *R.rattus*, *P.delectorum* and *L.flavopunctatus*. These flea species probably play an important role in the transmission of plague in these two districts. Fleas from domestic animals were mostly *Ctenocephalides spp* (>90%). *Pulex irritans* was dominant in human dwellings. Flea indices were high among rodents, house and other small animals indicating that there is high risk of plague outbreak. *Y.pestis* was not detected in all fleas, suggesting that during quiescent period fleas do not harbour the plague pathogens and also, rodent hosts may not have enough *Y.pestis* cells to infect the fleas.

**Conclusion:** We concluded that rodent species was the most important risk factor associated with flea infestation among the rodent population. Therefore, measures for control and prevention of plague in this area should particularly target rodents associated with high intensity of flea infestation. The findings of present study further suggest that fleas should be tested for *Y.pestis* DNA during the active phase of plague outbreaks for confirmation of infection and during inter-epidemic periods to confirm disease quiescence or detect infection activity.

<http://dx.doi.org/10.1016/j.ijid.2014.03.721>