Transmission intensity of *Wuchereria bancrofti* microfilariae in Okpochiri, Ebonyi state, Nigeria

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**Background:** Studies on the transmission intensity of *Wuchereria bancrofti* Microfilariae were carried out between September 2008- May 2009 to identify mosquito vectors of bancroftian filariasis in the study area, to ascertain the abundance and seasonal distribution of these species, as well to ascertain the infectivity rate in the study area in Okpochiri Local Government Area of Ebonyi State Nigeria. Okpochiri community is one of the communities in Ebonyi state where control measure (Ivermectin treatment and the distribution of treated bednets against Lymphatic filariasis has been ongoing since 2007.

**Methods & Materials:** Adults mosquitoes were caught using two methods, Pyrethrum Knock Down (PKD) and Mechanical Aspirator (MA), two days of every month, between 7.00am- 12 noon, with the aid of trained vilage volunteers. Each mosquito caught was identified and dissected to assess the parity.

**Results:** A total of 315 mosquitoes representing 3 genera, *Anopheles gambiae* (58.14%), *Culex quinquefasciatus* (41.26%) while *Aedes* (0.32%) were caught. The parity of the various mosquitoes species were: *An. gambiae* Nulliparous (13.65%), Parous gravid (44.65%), *Culex* Nulliparous (18.09%), Parous gravid (23.17%) while *Aedes* recorded (0.32%) Nulliparous. A sum total of (32.06%) Nulliparous mosquitoes and (67.93%) Parous gravid were observed respectively. The infectivity rate was found to be 0.01 (1%), because the study area has been treated with Albendazole and Ivermectin since 2007 and treated bednets have been distritributed. The seasonal distribution were evaluated based on dry and rainy seasons. However finding from the study has shown that mosquito abundance increases with increasing rainfall with peak in the rainiest month. Chi square analysis carried out to ascertain the abundance of mosquitoes on various months showed significant difference in the various months ($\chi^2 = 5.99$),$P < 0.05$). And Chi square analysis to assess the seasonal distribution showed significant difference in the two seasons ($P < 0.05$) as the rainy season favours the breeding habitats of mosquito vectors of Wuchereria bancrofti. Though mosquitoes were rather high, yet there were no much infectivity rate.

**Conclusion:** Preventive measures such as (treated bednets, residual sprays and repellants) and drugs such as Ivermectin and Albendazole given together yearly for 4-6 years should continue.

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Study on pathogenesis and genetic characterization of HPAI H5N1 isolated from a tiger in China

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**Background:** A zoo tiger in Shanghai, China, died after experiencing high fever and respiratory distress. An influenza A virus (A/Tig/SH/01/2005 (H5N1)) was isolated from the tiger’s lung. Complete genome sequence of isolate and its pathogenicity was studied to observe replication of virus in different organs.

**Methods & Materials:** Viral RNA was extracted and all gene fragments were amplified by using RT-PCR and cloned into pMD18-T vector. Complete genome sequence was determined using an automated sequencer. Isolated virus was inoculated intraperitoneally to mice. Immunohistochemical staining was done to locate the localization of antigen and Hematoxylin/Eosin (H/E) staining to observe histopathological changes.

**Results:** Genotyping results showed that viral segments belonged to genotype K,G,D,S,J,F,1J,F,1E. Phylogenetic analysis revealed it as clade 2.2 virus. Interestingly, slightly different sequence (SPQGERRRKKR) was observed at HA cleavage site. PB2 gene had Glu(E) at position 627 which indicated that this isolate could replicate efficiently in mammals. PB1 protein maintained pathogenic molecular determinants Met(M)171 and Lys(K)198.
Comparison of sequences of NP gene reflected Val(V)33Ile(1) substitution that have been identified as phylogenetically important position (PIP). M2 protein had human like amino acid Val(V)28. M1 protein showed presence of Ile(1) at position 15 which is a characteristic of HPAI. NS1 protein of tiger isolate and other viruses of 1E lineage showed deletion of 5 amino acids while viruses of 2A lineage had no deletion, Sequence ESEV at C terminus of NS1, characteristic of HPAI viruses, was conserved.

Microscopic examination revealed loss of epithelium from alveolar and bronchiolar walls (thickened by the presence of edema fluid, fibrin and RBCs). In the brain tissue, multiple randomly distributed foci of necrosis were observed. Immunohistochemistry results showed positive signals for antigen expression in both brain and lung tissues. In the lung, virus antigen expression was seen in pneumocytes, bronchiolar and bronchial epithelial cells. In the brain, virus antigen expression was seen in many neurons and glial cells.

**Conclusion:** Molecular characterization of all gene segments revealed characteristics of highly pathogenic influenza A viruses. These results may contribute to identify molecular determinants of virulence and highlight the necessity for continuous surveillance.

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**Influenza infections in live pig market, Nigeria**

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**Background:** The zoonotic and public health threat pose by emerging and pandemic swine influenza virus presents occupational risk for pig handlers. This is particularly important in live pig markets and trade points in Nigeria where people and pigs comes together in close proximity at weekly fair in a country with over 10 million pigs. This close range intermingling increases aerosol transmission of respiratory pathogens especially influenza at the human-animal interface.

**Methods & Materials:** A cross-section of pigs and pig fair attendants were sampled prospectively at weekly interval for four weeks in January 2013 during the cold dry season. The population include pig owners, pig buyers, pig restrainers and pork vendors who collectively spend between 6 to 10 hours with the animals at market days. Sera samples collected were screened with IDEXX commercial ELISA kit for the detection of influenza A antibody and positive samples were subtyped by haemagglutination Inhibition test using reference antigen and antiserum supplied in WHO/CDC Influenza surveillance kit.

**Results:** Eighteen out of 144 (12.5%) human sera collected were positive for influenza A antibody. 13 (9.2%) were subtype A/H1 while 5 (3.4%) were A/H3. Ninety four (35%) out of 268 swine sera collected were positive for influenza A antibody. 71 (75.5%) and 23 (6.3%) were positive for A/H1 and A/H3 subtypes respectively by haemagglutination Inhibition test.

Influenza A seroprevalence was higher in pigs than human contacts (p < 0.05) and lower than was previously observed in an intensive commercial piggery in southwest Nigeria. This may be due to lower influenza virus activity at live pig market than in husbandry settings.

**Conclusion:** This study however demonstrates the risk of zoonotic transmission of swine influenza virus in pig fair similar to reports from North America and that reassortment of swine and human influenza virus at this interface poses a significant public health risks requiring occupational health management programme including vaccination.

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**Bacteraemic Staphylococcus aureus at Charlotte Maxeke Johannesburg Academic Hospital**

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**Background:** S. aureus is a formidable pathogen, implicated in both community-acquired and nosocomial infections. CMJAH is a large tertiary hospital with both paediatric and adult units.

**Methods & Materials:** The case definition included all blood cultures positive for S. aureus (with repeat cultures within 21 days excluded). Patient clinical information was extracted from GERMS-SA enhanced surveillance data. Laboratory data for isolates was captured from Disa (laboratory information system).

**Results:** Over the 12-month period, September 2012- August 2013, 202 cases of bacteraemic S. aureus were identified. Forty two percent (84/202) of these were from paediatrics, with the remainder from adults. Half (101/202) of all the bacteraemias were methicillin-susceptible S. aureus (MSSA) in origin whilst the other half (101/202) were caused by methicillin-resistant S. aureus (MRSA). The proportion of MRSA infections in paediatrics was higher (67%), in comparison to that in adults (40%). In paediatrics, the majority of the MRSA infections were from neonatal and surgical units. Documented risk factors for MRSA in the paediatric patients, in order of decreasing frequency, included prematurity, surgery, burns and underlying cardiac conditions. For the adult patients, the trauma units had a high number of MRSA infections in comparison to the other units. Common MRSA risk factors in the adult patients included surgery, immunosuppressive therapy, metabolic disease and haematological abnormalities.

Bacteraemias without a focus, followed by pneumonia, were the most common clinical diagnoses documented. The overall inpatient mortality rate was 32%. The mortality rate for patients with MRSA infections (37%) was higher than that in patients with MSSA (27%).

The overall rates of resistance to erythromycin, cotrimoxazole, rifampicin and fucidic acid were, 51%, 46%, 16% and 6% respectively. For MRSA isolates, the vancomycin MIC50 and MIC90 was 1