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Animal-cell phone based surveillance and notification of infectious diseases in remote settings: A case study of plague in Uganda

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Background: This study aims to test effectiveness of animal-cellphone based disease surveillance and reporting model for Yersinia pestis, a primarily flea-borne bacteria that causes animal and human plague. In Uganda, Y. pestis is believed to be maintained in the wild rodents by Arvicanthis niloticus and Crocidura spp. These natural reservoirs do not develop clinical plague, unlike the domestic rat "Rattus rattus", which die in large numbers when infected. Upon deaths, rodent fleas go on rampage for alternative source of blood meals, putting humans at risk of Y. pestis infection.

Methods & Materials: This study utilizes Rattus rattus die offs "Rat Fall" to monitor transmission of Y. pestis in the rodent populations. Village Health Teams (VHTs) from 85 utmost risk villages were trained and equipped to safely collect and report carcasses. When village members report rodent die offs, the frontline VHTs collect and deliver to the carcass the plague laboratory. A toll free land line was installed in the laboratory for effective communication. Following a positive carcass, ecological investigation, health education and Indoor Residual Spraying (IRS) are undertaken in the case village. The study also tracks time lags between major events, right from time the rodent carcass was reported, to time when IRS or any other appropriate response is undertaken by the health authorities.

Results: Since inception in July 2013, 15 out of 435 rodent carcasses from 10 different villages; have tested positive for Y. pestis. The average time elapsed from VHT reporting rodent die off to VHT receiving laboratory results ranged from 1- 3 days, while days elapsed to IRS ranged from less than 5 to more than 30. Rattus rattus constituted over 76% of all reported carcasses, the others were Arvicanthis niloticus (14.5%), Crocidura Spp. (1.8%), Mastomys Spp. (1.8%), Mouse (1.4%), Zelotomys hildegardeae (0.9%), Lophuomys silkapusi (0.5%), and unidentified (3.4%). Human cases reduced drastically from 153 in 2008 to a low of 6 in 2014, and only 1 in 2015.

Conclusion: Partial results from this study suggest that animal-based disease surveillance and reporting models can be effective in reducing human plague in remote settings like the West Nile Uganda where the disease is endemic.

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Molecular characterization of human enteric adenovirus circulating among children below five years of age in Kolkata, India

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Background: Human enteric adenovirus belonging to subgenus F(HAdV) are one of the most common pathogens responsible for acute infantile gastroenteritis worldwide. Subgenus F adenoviruses comprises of two distinct serotypes, viz., AdV-40 and AdV-41. In this study we aimed at detecting and serotyping human enteric adenovirus subgenus F from fecal specimens based on one to three hypervariable region of the hexon gene and partial shaft region of fiber gene respectively.

Background on Adenovirus Infection

Methods & Materials: In a hospital based surveillance study, 3085 stool specimens from children below five years of age with mild to severe diarrhea were collected over a period of two years (January 2013-December 2014). Initial screening of adenovirus was done by Enzyme Immunoassay (EIA) from the fecal suspension. Further, viral genome (DNA) was extracted from the positive fecal specimens followed by amplification of hexon and fiber genes by Polymerase Chain Reaction (PCR) using specific primers. Nucleotide sequencing of purified PCR amplicons were carried out and enteric adenovirus-F serotypes 40 and 41 were determined using BLAST search. Phylogenetic dendrograms of hexon and fiber gene were constructed and genetic distances were analysed from the previously reported adenovirus-F 40 and 41 strains.

Materials and methods used in this study

Results: A total of 56(7.7%) and 131(14.9%) samples out of 3085 were positive for adenovirus-F(40/41) from hospitalized cases and outpatients respectively. No discrete seasonal variation of infection was observed and age distribution revealed a greater frequency in children between 6-24 months. Incidence of HAdVF-40 infection was found to be prevalent over HAdVF-41. Phylogenetic analysis of hexon genes from AdV-41 strains revealed co-circulation of both genome type cluster-1(GTC1) and GTC2 in Kolkata, reflecting accumulation of amino acid mutations in the HVR of the hexon gene. A recombination event was evident as hexon gene of five HAdV-41 strains belonged to GTC1, whereas fiber gene clustered with GTC2 strains. Sequence analysis of fiber genes of HAdV-41 strains revealed 15 amino acid deletion from 15th repeat motif of the shaft region which has been evolutionarily conserved among Kolkata strains.

Results of the study

Conclusion: Our findings revealed the prevalence of HAdV-F serotype 40 over 41 and co-circulation of both GTCs of HAdV-41 strains among children below five years of age in Kolkata.

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