57.022
Measles, neonatal tetanus (NNT), pertussis, cerebrospinal meningitis (CSM) and polio trends in Nigeria, 1994 to 2007
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Background: There has been concerted effort by the Nigerian public health system both at the National and State levels to tackle the problem of childhood vaccine-preventable diseases. This study was done to monitor the trend of these vaccine-preventable diseases and to assess the effects of the various interventions on these disease burden.

Methods: Data on some childhood vaccine-preventable diseases from 1994 to 2007 were obtained from the Federal Ministry of Health, Nigeria. Theses data were reviewed, summarized and graphically analyzed.

Results: Measles cases were highest (217,151) in 1999 and dropped steadily to 12,925 in 2007. CSM cases recorded their highest number (17,028) in 2003 and their lowest (3,547) in 2007. Pertussis cases dropped steadily from 50,175 in 1999 to 17,141 in 2006. NNT and polio cases maintained low values with peak values of 2,175 NNT cases in 2005 and 2,860 Polio cases in 2002. The case fatality rate (CFR) for NNT increased steadily from 3.5% in 1999 to 19.1% in 2007; CSM dropped from 18.8% in 1995 to 2.5% in 1997 and spiked again to 13.3% in 2003. Measles CFR dropped from 15.5% in 1997 to 1.8% in 2007. Pertussis had an annual steady CFR of 0.7% while Polio had a steady drop from 0.7% in 2001 to 0% in 2007.

Conclusion: The steady increase in the CFR of NNT, though it has low annual cases, calls for public health attention. Efforts should be intensified towards CSM control. The public health interventions for measles, polio and pertussis seem to be effective.

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57.023
A two year surveillance for influenza and RSV using Real-time PCR among children with acute respiratory infections in Kolkata reveals distinct seasonality of infection
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Background: Respiratory tract infections are one of the most common cause of morbidity and mortality in young children all over the world. Influenza and Respiratory Syncytial viruses (RSV) are the predominant etiology during seasonal epidemics and thus rapid and sensitive molecular tests for screening & timely identification of epidemics are required. In this study, we report comparison of real time PCR (Q-PCR) with conventional RT-PCR for parallel identification of Influenza A or -B and RSV.

Methods: Nasal and throat swabs were collected from 1091 children <5 years of age with fever and 2 or more symptoms of ARTI (cold/ cough, sore throat, myalagia, body-ache) from the B. C. Roy Memorial Hospital for children, Kolkata, India for 2 years (Jan 2007-Dec 2008). RNA was extracted from the clinical samples using RNeasy Mini Kit (Qiagen). Two one step multiplex Q-PCR assays were standardized. First assay was for matrix (M) genes of Inf- A and Inf-B {S. Lindstrom, CDC, USA}. Second assay was specific to the polymerase gene of RSV and the RNase P.

Results: Of 1091 samples, 275 (25.21%) were positive for either Influenza or RSV by Q-PCR compared to 262 (24%) positives by RT-PCR. Overall Inf-A, -B and RSV were detected in a total of 121 (11.075%), 59 (5.38%) and 95 (8.68%) samples respectively. Age distribution of virus infection in infants (< 1year), toddlers (1—2 years) or pre-school going children (2—5 years), the positive samples was analyzed. We observed increased prevalence of RSV in 0—1.0 (13.9%) and 1.0—2.0 years (12.1%) age group compared to only 3.8% positivity among 2—5 year old children. Influenza (A+B) was predominant in 1.0—2.0 and 2.0—5.0 yearr (19.6% and 17.2%) age group in Kolkata. In spite of overlapping clinical symptoms, RSV and Influenza showed distinct seasonal peaks. Inf-A positively and RSV, negatively correlated with rainfall and temperature (Fig. 1). No distinct seasonality was observed in Inf-B infections.

Correlation of meteorological variations with prevalence of Influenza-A, -B and RSV during 2007-08 in Kolkata.
Conclusion: This is the first report of a systemic surveillance of respiratory viruses with seasonal correlation and prevalence rate from Eastern India. The two year study confirmed feasibility of using Q-PCR in developing countries, which will not only improve scope for prevention of epidemics but also provide crucial epidemiological data from the tropical regions.

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57.024
Sampling considerations for Flavivirus arthropod vectors in Western Canada — Making sense at a data collection level

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Background: West Nile virus has displayed a remarkable geographical expansion in North America during the last ten years, with peaking numbers of diagnosed cases in 2003 and 2007, entailing numerous arthropod and vertebrate host monitoring programs throughout Canada. Culex tarsalis has been identified as the main vector for West Nile Virus transmission in Western Canada, however, other arthropod species are also discussed as potential vectors.

Methods: The presented work outlines factors that influence the spread of West Nile virus and epidemiological and ecological considerations to be taken into account to ensure appropriate data collection for the assessment of West Nile arthropod vector dynamics in the province of Alberta. The main factors that result in a change in vector composition and abundance are likely to be climate and habitat changes. The dynamics of successful viral transmission are subject to the suitable arthropod vector and vertebrate host communities, introduction of previously non-indigenous insect species, changes in mosquito habitats, genetic adaptations of the virus, and changes in insect biting behavior.

Results: Considering previously collected data in Canada, we propose weekly CO2 trap sampling for a minimum period from June to August in five of the six distinct geographic regions of Alberta (Boreal Forest, Canadian Shield, Foothills, Parkland and Grassland). The boundaries between Grassland and Parkland as well as Parkland and Boreal Forest are to be especially emphasized in the sampling. Vector speciation in conjunction with assessment of biting behavior of individual arthropod species on a molecular level is necessary for examination of variations in vector and vertebrate host interaction between these regions. Screening, characterization and phylogenetic analysis of variable regions (NS5 protein gene) of mosquito borne Flaviviruses from insects collected allows implementation of molecular epidemiologic relationships with preexisting data and assessment of possible routes of virus spread in relation to vector and host ecology and distribution.

Conclusion: Taking into account the complex ecology of West Nile virus spread, the importance of appropriate sampling is evident. The outlined experimental design covers virological, epidemiological ecological and entomological aspects in the context of the unique landscape of Alberta.

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