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Subacute sclerosing pan encephalitis in a tertiary care centre in North India

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Background: Subacute sclerosing pan encephalitis (SSPE) is caused by persistent, aberrant measles virus infection presenting as rapid neurocognitive decline, associated with myoclonus. Diagnosis is by distinctive clinical presentation, characteristic EEG changes and measles serology.

Methods and materials: Retrospective study from a tertiary care hospital SGPGI, Lucknow – a total of non-replicate 89 paired CSF and blood samples from patients presenting to OPD with clinical features suggestive of SSPE (i.e. dementia, myoclonic jerks and/or ataxia in a previously healthy individual) were analyzed from 2015 to 2018.

Total IgG and measles-specific IgG levels for CSF and value of relative CSF/serum quotient ≥ 1.5 was accepted indicative for intrathecal measles antibody synthesis. History of previous attack of measles, immunization status, EEG pattern were recorded.

Results: Presenting symptoms included myoclonus, behavioural changes, seizures, and cognitive, visual, and extrapyramidal disturbance. A total of 52.08% (47/89) patients had a high cerebrospinal fluid: serum anti-measles antibody ratio showing male preponderance. Age at onset of SSPE ranged from 6 years to 34 years, showing an increase in mean age at onset of SSPE. A sizable percentage of the patients were $\geq$18 years old and considered to have adult onset SSPE. A definitive history of measles could be elicited in 20% cases. Previous complete immunization history was present in about 40% and partial could be elicited in 35%. Characteristic EEG findings were present in about 80%. All patients received symptomatic therapy; 20% also received disease modifying agents with poor compliance. Demographic details showed more frequent clustering in some neighboring districts of UP.

Conclusion: WHO and Indian association of Pediatrics recommends two doses of vaccine. High SSPE cases could be attributed either to referral bias, decrease in the potency of the vaccine at the receiving end/inefficient cold chain system, improper vaccine coverage, poor quality of vaccine and possible circulation of atypical measles virus strain cannot be ruled out.

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Association of vitamin D receptor (VDR) gene polymorphism with disease severity among dengue patients

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Background: Vitamin D receptor (VDR) is coded by VDR gene located on chromosome 12. The present study was undertaken to decipher the effect of vitamin D receptor (VDR) gene polymorphism on dengue disease outcome, as there is a dearth of similar studies in the context of Indian population.

Methods and materials: The study was conducted in the Virology Laboratory, Department of Microbiology, Maulana Azad Medical College, New Delhi. We studied 100 cases (suspected dengue patients) and 100 healthy controls over a period of 1 year (January 2014 to December 2014). Revised WHO guidelines (2009) were followed to define and characterize a case of dengue. Peripheral venous samples were collected for diagnosis of dengue (NS1 antigen, IgM and IgG antibody). Genomic DNA was extracted from patients and healthy controls and Restriction Fragment Length Polymorphism was done for detection of VDRL gene polymorphism (start codon rs2228570 and 3′ UTR, rs7975232). Data was analysed using SPSS software (version 17.0). A p value < 0.05 was considered statistically significant.

Results: VDR gene polymorphism (rs 2228570 and rs 7975232) was screened in the samples. Genotype C/C, C/T and T/T (rs 2228570) was found in 11 (25.58%), 18 (41.9%) and 14 (32.6%) dengue positive cases and 59%, 25% and 16% healthy controls respectively ($p = 0.001$, significant). Significant association of the T allele of rs 2228570 polymorphism in a dominant mode of inheritance (C/T + T/T genotype) was seen with severe dengue cases [OR of 3.86 (1.59–9.35), $p = 0.002$ for C/T and 4.69 (1.79–12.3), $p = 0.001$ for T/T genotypes]. Genotypes A/A, A/C and C/C (rs 7975232) were found in 34.9%, 55.8%, 9.3% dengue positive cases and 31%, 40%, 29% healthy controls respectively. While comparing the A/A with A/C and C/C genotypes among dengue cases and healthy controls, the OR was estimated to be 1.24 (0.55–2.75, $p > 0.05$) and 0.28 (0.08–0.96, $p < 0.05$) respectively. This suggested that C/C genotype of rs7975232 was associated with reduced risk of developing symptomatic dengue ($p = 0.035$).

Conclusion: A significant association of T allele of rs 2228570 polymorphism was found in severe dengue cases in the study. The results also suggest that C/C genotype of rs 7975232 was associated with reduced risk of developing symptomatic dengue.

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Decade-long temporal analyses of circulating rotavirus genotypes during 2008–2017 in Eastern India: Phylodynamics during the pre-vaccination scenario

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Background: Group-A human rotaviruses (GARV) are among the leading etiological agents causing acute childhood gastroenteritis, worldwide. Despite the significant reduction in global infantile death toll due to rotaviral diarrhea, developing countries like India still contributes substantially to rotavirus-related hospitalization and mortality rates. In on-going hospital based diarrheal-disease surveillance in Kolkata, eastern India (2008–17), GARV was identified as the most common cause of infantile gastroenteritis. The circulating strains were genotyped and phylogenetically analysed to understand their dynamics and evolution prior to the vaccine introduction in eastern India.

Methods and materials: Stool samples were screened from children ($\leq$5 years) with diarrhea, seeking health care facilities at two hospitals in Kolkata. Preliminary screening for rotavirus VP6 antigen was done by ELISA. GARV positive samples were genotyped by multiplex semi-nested PCR. DNA sequencing of VP7 (G-type) and