ried out PCR analysis of ctx A, tcp genes. MAMA (Mismatched amplification mutation assay) PCR described by Lorita et al detects the ctxB sequence difference between classical and ElTor biotypes was used to confirm the hybrid vibrios. It detects the sequence difference on nucleotide at position 2003 of the ctxB gene.

Results: A total of 745 cases of cholera were admitted with an attack rate of 183 cases per thousand population. Number of cases varied from 15 to 400 in six clusters. Contamination of underground water supply (tubewell, wells and handpumps) was responsible. V. cholerae O1 Ogawa were isolated from stool cultures. Phenotypic characterization of 26 isolates revealed majority belonged to Eltor biotype. PCR showed tcp and ctxA of ElTor type in all strains. MAMA PCR results showed ctxB gene of both ElTor and Classical type in 66% of isolates.

Conclusion: Classical Vibrio cholerae has been extinct in Indian sub-continent since 1993 but the reservoir of its genes is present in the environment where genetic recombination is occurring. Hybrid vibrios may be more prevalent rather than being restricted to Bangladesh and Mozambique and may have pandemic potential.

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49.008

IgG Subclass and the FcG Receptor Iia Polymorphism Associate to Dengue Fever, Dengue Hemorrhagic Fever and Asymptomatic Dengue Infection in Cuba

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Background: FcG Receptors II (FcGRII) mediate a variety of biological response, including Antibodies Dependent Enhancement (ADE). The ADE theory shows that the presence of circulating dengue-specific IgG antibodies can enhance the viral entry trough FcGR and constitutes the largest risk factor for the individuals to develop of Dengue Hemorrhagic Fiver (DHF). An Arginine (R) to Histidine (H) substitution at position 131 of the FcGRIIa gene change the IgG binding affinity of the receptor with reduced opsonization of IgG2 associated with the arginine variant. The exceptional epidemiological circumstances in Cuba allow us to maintain a homogeneous sample with a similar history of natural dengue virus infections. In this work we investigate whether homozygosity for the arginine variant might be associated with a reduced risk of DHF caused by ADE and the subclass of IgG in the acute serum samples from individuals who suffered secondary infection to dengue 2 virus in the epidemic of Santiago de Cuba in 1997 with different clinical pictures.

Methods: The Subclass of IgG were detected using Dot Blot in the soluble fraction and the immunocomplex fraction phism associated to Fc gamma receptor IIa. The FcGRIIa genotypes (R/R131, H/H131 and R/H131) and allelic frequencies were compared.

Results: IgG1 are the predominant IgG subclass during the dengue acute infection even as a part of the immunocomplex or free in the serum. On the other hand IgG3 levels, only detected in the immunocomplex fraction, were observed in DF cases. The distribution of FcGRIIa genotype frequencies in Santiago de Cuba population showed the predominant RH genotype and the homozygocity for arginine variant did not found any protective effect associate to dengue infection in our population.

Conclusion: The IgG subclass involved in dengue infection are IgG1 and IgG3 and the ADE phenomenon probably take place by the FcGRIIIa and FcGRIIIb associate with these IgG.

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49.009

Higher Frequency of Detection of the New Human Polyomavirus, WU But not KI in HIV Exposed South African Children with Acute Lower Respiratory Tract Infections

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Two new polyomaviruses, WU- and KI, were identified in the last year in respiratory specimens from patients with respiratory tract infections in Australia, the USA and Europe. Limited information is so far available about their distribution or disease potential. Here we report the screening of nasopharyngeal aspirates (NPA) of patients with respiratory tract infections from hospitals in South Africa. WU virus was detected in 8% of cases which is significantly higher than previously reported and KI virus in <1%. Most cases were in children <3 years of age (95%). HIV exposure or infection was detected in 48% of WU virus positive cases which may account for the higher incidence in this group. Partial sequencing of the VP1 gene identified 4 distinct WU strains in South Africa, of which two were unique. KI viruses were identical to strains from Sweden. Further investigation is needed to determine the role of WU polyomaviruses in lower respiratory tract disease in HIV positive patients.

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