grow virus like hMPV. In this study the in-house cRT-PCR and Real Time RT-PCR were found to be equally sensitive.

doi:10.1016/j.ijid.2008.05.164

15.008

Adenovirus, Influenza Virus A, B and Respiratory Syncitial Virus Infection in Children

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Background: Acute respiratory infection is a major killer of children in developing countries. Viruses are common causes of it among children and Influenza, adenovirus and respiratory syncytial virus are some of them.

Method: A prospective cross sectional study was carried out in children from 3 month to 15 years old with upper respiratory infection who visited in OPD of Rasol-e-Acram hospital in one year (2006), Tehran, Iran.

Direct smear of patient's throat were evaluated by rapid chromatography test for adenovirus, RSV and influenza A and B virus infection.

Results: 160 children with upper respiratory tract infection with a mean age of 61.5 months were evaluated. 57.5% were boys. 77.4% had fever, 66% had sore throat, 37.4% had cough, 27% pharyngeal exudate, 16.4% had abdominal pain, 15.7% had vomiting, 13.8% had cevical lymphadenopathy, 10% had diarrhea, 5.7% had petechea in palate and 1.9% had conjectivitis. Influenza infection was detected in 7 cases (4.4%) with mean age of 82.3 month. They were detected 28.6% in spring, 14.3% in summer and 57.1% in winter. Adenovirus infection was detected in 10 (6.3%) cases with mean age of 83.7. they were detected 20% in spring, 30% in summer, 30% in fall and 20% in winter. RSV infection detected in 9(5.7%) cases, 7 (77.8%) boys and 2 (22.2%) girls with mean age of 54.7. They were detected 44.4% in spring, 44.4% in fall and 11.1% in winter.

Conclusion: Adenoviruses were more prevalent. Fevers were the most common clinical sign but in RSV sore throat and in Influenza cough, petechea and vomiting and in Adenovirus cervical lymphadenopathy were more prevalent than others. Influenza in winter and RSV in spring and fall were more prevalent but Adenovirus did not obey seasonal pattern.

doi:10.1016/j.ijid.2008.05.165

15.010

Prevalence of Skin infections in Nigerian Children- The University of Port Harcourt Teaching Hospital (UPTH) Experience

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Keywords: Prevalence; Skin; Infections; Children; Morbidity; Public health

Background: Skin infections are frequently encountered in the tropics; many are contagious and are a serious cause of morbidity, disfigurement and distress in all age groups. These infections are observed in children whose parents are of low socioeconomic background. The aim of this study is to determine prevalence and common dermatological infections encountered in UPTH.

Method: Children aged 0—16 years attending the dermatology clinic in UPTH from June 2005 to November 2007 were prospectively studied.

Results: A total of 1,226 skin infections were seen, 247 (20.1%) were children aged 0—16 years. Skin infection was commoner in females 139 (56.3%) than males 108 (43.7%). Papular urticaria 36 (14.6%), atopic dermatitis 34(13.8%) and tinea 31 (12.6%) were the most commonly observed childhood skin infections. Other skin infections included Human Immunodeficiency viral (HIV) skin lesions in about 30 (12.1%). The skin infections in the HIV infected patients included profuse oral candidiasis, herpes zoster (shingles), molluscum contagiosum and scabies.

Conclusion: It is obvious that skin diseases such as HIV skin lesions, papular urticaria and atopic dermatitis are important dermatological problems in our environment. HIV/AIDS is a major public health problem in our setting. Implementation of public health policies and improvement of the socioeconomic status of the people will bring about a fall in prevalence of skin infections in Nigerian children.

doi:10.1016/j.ijid.2008.05.166

15.011

Infection Factors Which Have a Role in the Aetiopathogenesis of Primary and Exacerbation Juvenile Idiopathic Arthritis and the Relationship of Infection Factors with Procalcitonin Levels

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The aetiopathogenesis of Juvenile idiopathic arthritis (JIA) is not fully understood; however, environmental factors including immunological tendency, infections stress and trauma in patients have been shown to play a role in the aetiopathogenesis of JIA. Although previous studies have shown that there was a clear relationship between adult arthritis and infections, this relationship was not fully demonstrated between juvenile arthritis and infections. Our work is the first international study in effort to show the relationship between juvenile group and infections by investigating extended bacterial and viral factors and monitoring procalcitonin (PCT) and C-reactive protein (CRP) levels in relevant infections.The study was performed between October 2004 and November 2005. Three groups were included in this study; a) 26 cases with primary JIA, b) 20 exacerbation JIA cases (EC) previously diagnosed with JIA and c) 24 healthy control (HC) individuals. Conventional culture and serological methods were used to detect microorganisms and also for aetiopathogenesis and/or exacerbation of

the cases. Immunoluminometric and immunonepholometric methods were used for PCT (Procalcitonin) and CRP (C reactive protein) detections, respectively.

Eighteen (39.13%) among the 46 primary JIA and EC groups had infections in different regions of their body whereas only two indivudials from the HC showed infections ($p < 0.05$). M. pneumoniae infections were found much higher in the groups with primary and EC when compared with the HC. Furthermore, C. jejuni IgG seropositivity was detected significantly higher in JIA group than that of the HC. While, in JIA cases with regard to bacterial and viral factors, PCT levels were not found significantly higher (0.02 ng/ml), the mean value for CRP levels in patients with JIA were found 7.62 mg/l. A statistically significant difference was detected between the primary JIA and EC groups and HC group for both PCT and CRP levels ($p < 0.05$).

In conclusion, the results of our study which is the first in this field and including such a large group organisms in the same serial for JIA pathogenesis gave the idea that some microorganisms could trigger or worsen the clinical appearence in subject level. In particular, M. pneumoniae ve C. jejuni draw attention especially in primary JIA and EC. We suppose that it is possible to prevent antigenic stimulation and as a result to obtain recovery in clinical presentation with early detection of microorganisms which were thought to be primary or interfering factors causing infections in the aetiopathogenesis of JIA and also adding specific antimicrobial therapy to the standard regimen of JIA therapy to eradicate these microorganisms. The relationship between JIA aetiopathogenesis and microorganisms has to be clarified for the above reasons. To reach this goal, we suppose that conducting larger, serial, especially molecular based serial studies which include samples from synovial regions which are very difficult sampling will be helpfull.

doi:10.1016/j.ijid.2008.05.167

15.012

Molecular Epidemiology of Diarrheagenic *Escherichia Coli* Isolated from Young Children with Diarrhea

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Background: Diarrheagenic *E. coli* (DEC) represents an important group of enteric pathogens that cause human diarrhea and has been of increasing public concerns recent years. Since it is not easily distinguished from normal non-pathogenic flora due to inappropriate diagnostic methods, modern molecular diagnostic assays are required. Several distinct groups of *E. coli* which include the enteropathogenic (EPEC), enteroinvasive (EIEC), enteroaggregative (EAEC), enterotoxigenic (ETEC) and Shiga toxin-producing (STEC) strains are important causes of diarrheal diseases in developing countries. The aim of this study was to evaluate the contribution of the different DEC categories to children's diarrhea.

Methods: Molecular techniques were used for studying the epidemiology of diarrheal infections due to DEC in Iran. In total, 750 *E. coli* strains isolated from stools of 200 patients with diarrhea were collected between JUN and SEP 2007. Polymerase chain reaction (PCR) was performed to determine the presence of the genes encoding DEC virulence factors including: *eaeA, bfpA, estA, eltB, inv, stx* and *pCVD432*, as virulence markers to distinguish EPEC, ETEC, EIEC, STEC and EAEC.

Results: ETEC strains were isolated from 13 children (6.5%). The distribution of these strains according to the type of enterotoxin synthesized was as follows: 10 strains (76.9%) produced the heat-stable toxin (ST), 2 strains (15.4%) synthesized the heat-labile toxin (LT), and 1 strain (7.7%) produced both toxins. EAEC strains were isolated from 16 (8%) children, and STEC was detected in 7 children (3.5%); no EIEC strains were isolated. two of these 16 EAEC strains also produced ST toxin. Finally, EPEC strains were isolated in 41 cases (20.5%). In this study, two PCR techniques, amplifying the *bfpA* gene, or the *eaeA* gene, were used to detect EPEC strains. Forty-one strains were found to have at least one of these genes; 29 of the 41 strains had only the *eaeA* gene, 3 strains had only the *bfpA* gene, 9 strains were both genes positive. Therefore, it seems that the presence of the *eaeA* gene is more highly linked to EPEC than is the presence of the *bfp* gene.

Conclusion: PCR was shown to be useful technique for the epidemiological study of DEC where this organism is a major cause of diarrhea. In this study, EPEC was found to be the category of DEC which most frequently causes diarrhea in children under 5 years of age, as has been reported for many developing countries.

doi:10.1016/j.ijid.2008.05.168

15.013

Multicenter Retrospective Evaluation of Tigecycline Tested Against Clinical Pathogens from Japan (2003—2004)

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Background: In preparation for therapeutic use of tigecycline (first in class glycylcycline) in Japan, a retrospective sample of clinical isolates (2003—2004) was tested by the SENTRY Antimicrobial Surveillance Program. All tests were by reference methods.

Methods: Three university hospitals collected 1,033 pathogens for central laboratory processing by the CLSI procedures (fresh MH broth media) with concurrent quality control. Tigecycline and 23 comparators were tested including minocycline and tetracycline. Most numerous organisms