Results

susceptibility test done by the Kirby Bauer method. Isolates were cultured using standard microbiological techniques. Biochemical groups in urinary tract infection were involved in Escherichia coli pathogenicity mechanisms were examined by PCR.

Background

Thirty two virulence factors including adhesions group, protectin related genes, common toxins related to UPEC, phylogenetic typing, Pathogenicity Island and miscellaneous genes which are involved in Escherichia coli pathogenicity mechanisms were analyzed by multiplex PCR.

Method

The PCR assay results identified vαt (96 vs. 4%), Pai IV386 (85 vs. 41%), Pai I UC703 (78 vs. 25%), kpsMTII (71 vs. 42%), ompT (68 vs. 53%), urs (52 vs. 3%), sat (47 vs. 3%), piuU (41 vs. 1%), Pai I UC703 (68 vs. 53%), Pai I UC703 (78 vs. 25%), Pai I UC703 (83 vs. 13%), Pai I UC703 (78 vs. 9%), fliC (70 vs. 4%), hlyD (22 vs. 2%), focG (21 vs. 3%), cft (21 vs. 0%), gasD (20 vs. 2%), cdtA (19 vs. 7%), bmaE (17 vs. 5%), Pai II J96 (11 vs. 3%), were more frequent virulence markers in urinary E.coli isolates than commensal E.coli, respectively. The frequency of afa (7 vs. 10%), fimH (92 vs. 97%), kpsMT (K1) (41 vs. 57%), kpsMTIII (11 vs. 5%), rfc (40 LPS) (9 vs. 2%), Pai I UC703 (20 vs. 24%), Pai I UC703 (3 vs. 0%), Pai I J96 (53 vs. 43%), iba (17 vs. 26%) markers was almost similar in both of them. cvaC (64 vs. 18%) was most frequent marker in commensal E.coli. PCR phylootyping revealed higher prevalence of commensal E. coli in groups A and D while uropathogenic strains were mainly found in subgroup B2.

Conclusion

Based on these results, the potential for Commensal E. coli to act as human UPEC or as a reservoir of virulence genes for UPEC should be considered.

923 MULTIPLEX PCR FOR DETECTION OF SHIGA-LIKE TOXIN AND PLASMID ANTIGEN H GENES OF DIARRHEAGENIC ESCHERICHIA COLI

Background and Aims

Despite the fact that Shiga-like toxin E. coli has been identified as a major etiologic agent of children with diarrhea worldwide, few studies have been performed to evaluate the etiology of Shiga-like toxin-producing Escherichia coli (STEC) in children with diarrhea, in Iran. The aim of this study was to evaluate the etiology of Shiga-like toxin-producing Escherichia coli (STEC) in children with diarrhea, in Iran.

Method

A total of 300 stool specimens from children of 300 children with diarrhea were tested for the detection of E. coli, according to standard methods. Out of 300 specimens, 39 were identified as diarrheagenic E. coli, and subjected to multiplex polymerase chain reaction (MPCR) for detection of stx1/stx2, eae and ipaH genes. We designed a single multiplex polymerase chain reaction (MPCR) for the detection of target genes in diarrheagenic Escherichia coli.

Results

EPEC was the dominated strain (55.6%) among the tested isolates, followed by HEPEC (25%) and IEIEC (19.4%) strains.

Conclusions

Shiga-like toxin E. coli has been identified as a major etiologic agent of children with diarrhea in Iran. Our method proved to be specific and rapid in detecting virulence genes from Shiga toxin-producing (stx1, stx2, and eae) enteropathogenic (eae), enteroinvasive (ipaH) Escherichia coli in stool samples, and able to simultaneously detect of diarrheagenic E. coli strains in a single reaction.

924 DIAGNOSIS AND PROGNOSIS OF CONGENITAL TOXOPLASMOSIS

Aims

Congenital toxoplasmosis can cause neurological impairment and ocular disease. To describe clinical profile of infants with suspected congenital toxoplasmosis.

Methods

Observational study of infants born to mothers with a suspected infection with Toxoplasma gondii during pregnancy between 2002 and 2011.

Serological tests were performed at birth: Toxoplasma specific antibodies IgA, IgM, IgG by Enzyme Immune Assay (EIA), Enzyme Linked Fluorescent Assay (ELFA), Western Blot (WB) tests and WB-IgG compared analysis for mother-infant pairs. Infants underwent cranial Ultrasound Scanning, fundoscopy examination, Auditory Brainstem Response, and periodic clinical evaluations.

Results

One hundred thirty-one infants Toxoplasma IgG-positive at birth were evaluated; 116/131 (90%) become IgG-negative at 12 months of life.

Congenital toxoplasmosis was confirmed in 13/131 infants (9.9%). Transmitters pregnant women seroconverted in the third trimester (mean 28±8 weeks).

IgM-ELFA test was positive in 9/13 infants; in 4/13 infants IgM positivity was detected by WB test (negative IgM-EIA/ELFA). Three of 6 infants had a different IgG-WB reactivity compared to their mothers.

Six of 13 infected infants (46%) were symptomatic at birth; 2/13 infants developed chorioretinitis; 4/13 had a pathological neuroimaging (4/4 cerebral calcifications, 1/4 ventriculomegaly). None had...
HAEMOPHILUS INFLUENZAE IN CHILDREN: RESISTANCE TO SIX OTHER BÊTA-LACTAMS AMONG AMPICILLIN-RESISTANT STRAINS

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Background and Aims Haemophilus influenzae (Hi) is a human pathogen responsible for various infections in both children and adults. We describe in this study the susceptibility patterns and β-lactam resistance mechanisms of 62 ampicillin-resistant H.i strains isolated from children at the children’s hospital of Tunis during 2009 and 2010.

Materials and Methods All strains were identified and serotyped using conventional methods. Antimicrobial susceptibility was determined by E-test. The antibiotics tested were amoxicillin, amoxicillin-clavulanate, cefixim, cefuroxim, cefotaxim, cefpodoxim and imipenem. The β-lactamase production was performed using the nitrocefin test. We determined the resistance genes (blaTEM-1, blaSHV-1, and bet) by PCR.

Results Isolates were identified as non capsulated and were classified into 3 groups according to their β-lactam resistance mechanisms: β-lactamase positive ampicillin-resistant (BLPAR: 50%); β-lactamase negative ampicillin-resistant (BLNAR: 40.52%) and β-lactamase positive amoxicillin-clavulanate-resistant (BLPCRA: 9.68%). All strains showed high amoxicillin, amoxicillin-clavulanate, cefuroxim and imipenem MICs. Among these, the less active one was imipenem with MIC exceeding 32 mg/l in all strains. The highest MICs of cefuroxim were in BLPCRA strains (2–4 mg/l). MICs ranges of clindamycin and MDR (multidrug resistance) were 22/27 (82%), respectively. Of the 39 (54%) Pnc serotyped the most common were: 19F (26%), 6B (18%), 14 (15%), 23F (15%) and 19A (8%). Penicillin highly resistant was found in 54.6% (11/20); 2–6 mg/l, 6–19 mg/l, 2–14 all included in the PCV 7-valent (PCV7), except for 2 isolates: 9A, 22F. Out of the 13 highly resistant serotypes 7 (53.84%) were multi drug resistant and all of them were 6B or 19F. 35/39 (90%) of all SP isolates are included in PCV-13.

Conclusions The proportion of penicillin resistance Pnc isolated from MEF was extremely high as well as resistance to other common antibiotics. Coverage of PCV7 and PCV10 vaccines was equal.

Abstracts

RHINOVIRUS INFECTIONS IN HIGH-RISK CHILDREN

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Background Human rhinoviruses (HRVs) are recognized as major cause of cold and flu-like illness.

Objectives To analyze the clinical features and disease burden for children with underlying medical disorders and documented HRVs infections.

Methods This is a retrospective study that include 48 children who were hospitalized for acute respiratory illnesses in KFSHRC between October 2007 and June 2010. HRVs in nasopharyngeal aspirates, swabs or Bronchoalveolar lavage were detected by nucleic acid detection tests in addition to 13 common respiratory viruses.

Results HRV was the most frequently detected virus 27% (48/181) in hospitalized children with acute respiratory disease. 65% of patients had chronic medical conditions and 37% of patients had immunocompromising conditions. The median age was 22 months, 58% were male. HRV showed broad seasonal activity. The peak incidence was in November, December and June. The most common symptoms were cough (58%), fever (56%), dyspnea 40% and running nose (25%). Crepitation and wheezes, were present in 25.9%, 20.8%, respectively. Twenty-two of 48 patients (46%) had chest radiographic abnormalities, most commonly atelectasis or loblar infiltrate. Seventeen (35%) patients needed intensive care unit (ICU) admission and thirteen (76%) required mechanical ventilation, there were two bacterial and one fungal co-infection documented in this patient. The mean duration of ICU stay was 17.9 days. Fifteen (88%) of the HRV-positive patients survived, while 2 (12%) patients died. Co-infection with other viral respiratory pathogens was common (17%).

Conclusion HRVs were associated with severe lower respiratory tract infection and hospitalization in children with chronic or immunocompromising conditions.