Background The present study is comparison of commensal and uropathogenic Escherichia coli (UPEC) pathotypes according to multiple virulence genes by multiplex PCR.

Methods Thirty two virulence factors including adhesions group, protectin related genes, common toxins related to UPEC, phylogenetic grouping, Pathogenicity Island and miscellaneous genes which are involved in Eschenichia coli pathogenicity mechanisms were examined by PCR.

Results The PCR assay results identified vat (96 vs. 4%), PAI IICFT073 (71 vs. 42%), ompT (53 vs. 52%), sat (47 vs. 3%), pscU (41 vs. 1%), PIJ356 (57 vs. 7%), flic (17 vs. 5%), hlyD (96 vs. 4%), focG (21 vs. 3%), cdf (41 vs. 1%), gadF (20 vs. 2%), cdtB (19 vs. 7%), bmaE (17 vs. 5%), PIJ196 (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(I) (41 vs. 57%), kpsMTIII (11 vs. 5%), rfc(O4 LPS) (9 vs. 2%), PAI IIS36 (20 vs. 24%), PAI IIS56 (3 vs. 0%), PIJ196 (53 vs. 43%), ivaC (17 vs. 26%) markers was almost similar in both of them. cvaC (64 vs. 18%) was most frequent marker in commensal E. coli. PCR phylotyping 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.

MULTIPEX PCR FOR DETECTION OF SHIGA-LIKE TOXIN AND PLASMID ANTIGEN H GENES OF DIARRHEAGEN E. 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 (SLTEC) in children with diarrhea, in Iran. The aim of this study was to evaluate the etiology of Shiga-like toxin-producing Escherichia coli (SLTEC) 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 EHEC (25%) and EIEC (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.
hearing loss. Infected infants received one-year therapy (pyrimethamine/sulfadiazine); 1/13 infant developed neutropenia as adverse therapy effect.

At a median age of 2 years all infected infants had a normal psychomotor development (range 1–10 years).

**Conclusions** It is advisable to perform IgM/IgG-WB on infant serum and the compared analysis for mother-infant pairs within the first month of life when high risk factors for Toxoplasmosis transmission are present.

**ANTIBIOTIC RESISTANCE AND PNEUMOCOCCAL CONJUGATED VACCINES COVERAGE OF STREPTOCOCCUS PNEUMONIA FROM MIDDLE EAR FLUID OF CHILDREN < 5 YEARS**

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**Aims** A prospective study was initiated in Brasov, Romania in 2009 to assess the antibiotic resistance pattern of Streptococcus pneumoniae (Pnc) isolated from middle ear fluid in children with acute otitis media (AOM) <5 years old.

**Methods** Patients diagnosed with AOM who underwent tympanocentesis or presented with purulent otorrhea of <24 hours duration were enrolled.

**Results** 206 patients were enrolled, 132 (64%) episodes occurred in children <2 years old; 105 (51%) were culture-positive. 108 isolates were recovered: Pnc - 75 (67%), H. influenzae - 26 (24%) and others - 7 (9%). Nonsusceptibility to penicillin was found in 25/27 (93%) [MIC >1.5 μg/mL]. Pnc resistance to TMP/SMX, erythromycin and clindamycin and MDR (multidrug resistance) were 22/27 (82%), 16/27 (59%), 13/27 (48%) and 15/27 (56%), 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 84.6% (11/13): 2–6B, 6–19F, 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 the PCV7-7valent.

**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. The PCV13 coverage was 90%. Most antibiotic resistant serotypes were included in the PCV13.

**HAEMOPHILUS INFLUENZAE IN CHILDREN: RESISTANCE TO SIX OTHER BETA-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 Hi 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-clavulenate, cefixim, cefuroxim, cefotaxim, cefpodoxim and imipenem. The β-lactamase production was performed using the nitrocefin test. We determined the resistance genes (blaTEM, blaSHV, blaOXY, and βlactamase) 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 (BLPACR: 9.68%). All strains showed high amoxicillin, amoxicillin-clavulanate, cefuroxim and imipenem MICs. Among these, the less active one was imipenem with MIC >=32 mg/l in all strains. The highest MICs of cefuroxim were in BLPACR strains (2–4 mg/l). MICs ranges of this antibiotic were 0.5–6 mg/l in BLNAR and 0.125–4 mg/l in BLPAR. Cefotaxim, cefixim and cefpodoxim were the most active agents tested against our strains.

**Conclusion** This study indicates that many β-lactams are ineffective among some Hi strains. So, it’s important to have an appropriate usage of antibiotics to stop these phenomena. We must make other investigations to know if these strains belonged to the same clone or if it’s a question of an outbreak in our hospital.

**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 HRV 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 15 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 lobar 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.