[1]M Navidinia, [1]S Najar Peerayeh, [2]F Fallah, [1]B Bakhshi, [2]S Adabian, [2]Z Gholinejad, [2]S Alimehr, [2]MA Malekan. *[1]Tarbiat Modares University; [2]Shahid Beheshti University of Medical Sciences, Mofid Children Hospital, PIRC, Tehran, Iran*

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, phylogenic typing, Pathogenicity Island and miscellaneous genes which are involved in Escherichia coli pathogenicity mechanisms were examined by PCR.
Results The PCR assay results identified *vat*(96 vs. 4%), PAI IV536(85 vs. 41%), PAI ICFT073(78 vs. 25%), *kpsMTII*(71 vs. 42%), *ompT*(68 vs. 53%),*usp*(52 vs. 3%), *sat*(47 vs. 3%), *picU* (41 vs. 1%), PAI IICFT073(38 vs. 13%), PAI I536(37 vs. 7%), *fliC (H7*(24 vs. 9%)), *hlyD*(22 vs. 2%), focG(21 vs. 3%), *cnf1*(21 vs.0%), gafD(20 vs. 2%), *cdtB* (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* (O4 LPS) (9 vs. 2%), PAI II536(20 vs. 24%), PAI III536(3 vs.0%), PAI I J96(53 vs. 43%), *ibeA*(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.

922 PHYLOGENIC TYPING OF URINARY *E.COLI* ISOLATES AND COMMENSAL *E.COLI IN PATIENTS WITH UTI* IN MOFID CHILDREN HOSPITAL IN IRAN

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[1]M Navidinia, [1]S Najar Peerayeh, [2]F Fallah, [1]B Bakhshi, [2]S Adabian, [2]S Alimehr, [2]Z Gholinejad, [2]MA Malekan. *[1]Tarbiat Modares University; [2]Shahid Beheshti University of Medical Sciences, Mofid Children Hospital, PIRC, Tehran, Iran*

Background The objectives of this study were to define the phylogenetic groups in urinary and commensal *E. coli* isolated from urine and stool samples of hospitalized children and to determine the pattern of resistance to antibiotics.
Method A total of 100 urine and stool samples were processed during the study period from September 2009 to August 2010. Samples were cultured using standard microbiological techniques. Biochemical testing was used to identify the organisms, *E. coli* isolates were tested for phylogenic grouping by using triplex PCR and antibiotic susceptibility test done by the Kirby Bauer method.
Results Phylogenic group B2 and D were predominant in urinary samples (54% and 34% respectively). Phylogenic group A, D and B2 were found in decreasing order of 41%, 26% and 16% respectively in the stool samples.

Following resistance patterns were observed in urinary *E. coli* isolates vs. commensal *E. coli*, respectively: nitrofurantoin(2% vs. 8%); imipenem (2% vs. 1%); amikacin (4% vs. 3%); ciprofloxacin(8% vs. 5%); nalidixic acid (8% vs. 27%); amoxicillin (16% vs. 20%); ceftazidime (12% vs.7%); amoxicillin-clavulanic acid (14% vs. 9%); gentamicin (22% vs. 12%); cefpodoxime (48% vs. 19%); cefotaxime (45% vs. 27%); co-trimoxazole (61% vs. 82%); and aztreonam (78% vs. 16%); Multi-drug resistance (MDR = resistance in>3 drugs) was most commonly associated with UPEC isolates.
Conclusion Although group B2 *E. coli* strains were uncommon in stool samples, as they are highly virulent they still represent a potential reservoir for urinary tract infection. Resistance to most antimicrobials is high both in UPEC and commensal strains.

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

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[1]MM Soltan Dallal, [1]Z Rajabi, [1]A Akbari, [1]S Heidarzadeh, [2]MK Sharifi Yazdi. *[1]Pathobiology, School of Public Health, Tehran University of Medical Sciences; [2]Laboratory, School of Paramedical Sciences, Tehran University of Medical Sciences, Tehran, Iran*

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 (*stx*1, *stx*2, 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

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[1]MG Capretti, [1]M De Angelis, [1]M Spinelli, [1]C Marsico, [1]E Tridapalli, [2]A Moroni, [2]A Marangoni, [1]L Corvaglia, [1]G Faldella. *[1]Department of Obstetrical, Gynaecological and Paediatric Sciences, Operative Unit of Neonatology; [2]Department of Haematology, Oncology and Laboratory Medicine, Operative Unit of Microbiology and Virology, St. Orsola-Malpighi University Hospital, University of Bologna, Bologna, Italy*

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; 118/131 (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±8weeks).

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

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.

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

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[1,2]O Falup-Pecurariu, [3]E Leibovitz, [2]A Mercas, [2]R Lixandru, [2]L Bleotu, [2]C Zavarache, [4]C Falup-Pecurariu, [3]N Porat, [3]R Dagan, [3]D Greenberg. *[1]Department of Pediatrics, Faculty of Medicine, Transilvania University; [2]Department of Pediatrics, University Children's Hospital, Brasov, Romania; [3]Pediatric Infectious Disease Unit, Soroka University Medical Center, Ben-Gurion University, Beer-Sheva, Israel; [4]Faculty of Medicine, Transilvania University, Brasov, Romania*

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) < 5years 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 < 2years 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 >1.5μg/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 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. The PCV13 coverage was 90%. Most antibiotic resistant serotypes were included in the PCV13.

926 *HAEMOPHILUS INFLUENZAE* IN CHILDREN: RESISTANCE TO SIX OTHER BÊTA-LACTAMS AMONG AMPICILLIN-RESISTANT STRAINS

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S Mzilem, H Smaoui, A Kechrid. *Children's Hospital of Tunis, Tunis, Tunisia*

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 (bla_{TEM-1}, bla_{ROB-1} and *fts*I) 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: 40.32%) 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_{50} >32mg/l in all strains. The highest MICs of cefuroxim were in BLPACR strains (2–4mg/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.

927 RHINOVIRUS INFECTIONS IN HIGH-RISK CHILDREN

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[1]S Al-Hajjar, [1]O Al-Ahmed, [2]S Al-Thawadi. *[1]Pediatrics; [2]Pathology and Laboratory Medicine, King Faisal Specialist Hospital & Research Centre, Riyadh, Saudi Arabia*

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. 63% 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 23.9%, 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.

928 NEUTROPHIL CD64 INDEX (CD64IN) IN CEREBROSPINAL FLUID IN DIAGNOSING BACTERIAL VENTRICULITIS IN CHILDREN WITH EXTERNAL VENTRICULAR DRAINAGE

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