Results 12 children (13.3%) were hospitalized during the first days, in the first 3 days — 32 children (35.5%). In 90 children (100%) was identificate the antigen of rotavirus. Most frequency of RI in the children was identificated in age 1–3 years. The syndrome of gastroenteritis developed in 1–3 day per acute period of disease Frequency of stool was 2–15 times per days. In the 20 children (22.2%) RI was associated with pathogenic flora: St. aureus (7.7%), Proteus(10%), Pseudomonas (4.4%). In the our contingent there were a decline of levels of copper of blood serum, zinc and iodine, at the insignificant increase of level of iron. Research of mineraluria in children gave the reference level of all investigated oligoelementss and phosphorus. In the patients with RI was identificated the disbalance of minerals of blood serum with association of their unchanged elimination.

Conclusions This dates presents the necessity of mineral ocorrection in the patients with RI.

918 GENETIC AND PHYLOGENETIC CHARACTERIZATION OF *STAPHYLOCOCCUS AUREUS* STRAINS ISOLATED FROM ATOPIC DERMATITIS PEDIATRIC PATIENTS AND THEIR COHABITANTS

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Atopic dermatitis (AD) is characterized by dysfunctional skin susceptible to *Staphylococcus aureus* colonization, which can exacerbate the symptoms. Recent studies indicate that the *S. aureus'*s great versatility is direct consequence of its genome's plasticity and adaptability.

The present study evaluated the prevalence of *S. aureus* in 175 pediatric AD patients and their 195 cohabitants in relation with the severity of the disease. Moreover, isolated strains were characterized for pathogenic and virulence factors (PCR analysis), for genome structure (PFGE analysis) and for phylogenetic relations (MLST analysis) to investigate the possible correlation between genetic characteristics and the different stages of disease and the effects of atopic environment on the genome structure of these strains.

Our data showed that both patients and their cohabitants had high prevalence of *S. aureus,* that was proportional to the severity of the disease. PFGE analysis showed the existence of clonal identity among isolates from different sites of the same patient and between isolates from patients and their cohabitants. MLST data showed that there was a significant phylogenetic distance among strains with identical PFGE profile.

Our results demonstrate that the family is a source of infection/reinfection for patients and a source of risk for cohabitants. Moreover, our data suggests that although bacterial strains from atopic skin show conserved genomic structures (identical PFGE profiles), they came from very different genetic backgrounds (different MLST profiles). We assume that the peculiar atopic tissue environment may induce the evolution of these strains, with changes in genomic structure and regulation of virulence factors.

919 HUMAN BOCAVIRUS IN HIGH-RISK CHILDREN

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From 1 October 2009 to 1 December 2010, we conducted a prospective hospital-based study at KFSHRC to evaluate the role of Bocavirus (HBoV) infections in hospitalized children with chronic medical or immunocompromising conditions. Clinical and epidemiological data were recorded and respiratory samples including nasopharyngeal aspirate or nasopharyngeal swabs were obtained from all children less than 14 years old with acute respiratory tract infections. HBoV was screened in all respiratory samples by real time PCR, in addition to 13 common respiratory viruses. During the study, HBoV was detected in respiratory samples from 25 (2%) of 1016 symptomatic patient. HBoV co-existence with other respiratory pathogens occurred in 72% (18/25) of respiratory samples from symptomatic patients. HBoV infections were detected in every month except June and July with peaks in the month of September, October, November, and December. The main diagnosis in 13 patients (52%) with HBoV was radiologically confirmed pneumonia. For the other 12 patients with HBoV infections the main diagnosis were gastroenteritis(4 cases), chest exacerbation (3 cases), upper respiratory tract infections (2 cases), persistent fever (1 case), seizure (1 case), otitis media (1 case). The main clinical signs and symptoms of HBoV positive patients included fever, cough tachypnea, dyspnea, crackles, wheezing, abdominal pain, vomiting and diarrhea. The present study suggest that HBoV may be a fairly common cause of pneumonia in high-risk children hospitalized with acute respiratory infections and associated with morbidity. However, further study is needed to clarify if HBoV plays a pathogenic role in community acquired pneumonia in high-risk children.

920 SIMILAR CLONE OF *SALMONELLA ENTERIC*A SEROVARES *ENTERITIDIS* ISOLATED FROM STOOL SAMPLES OF CHILDREN AND FOOD SOURCES

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Background *Salmonella enterica* subsp. *Enterica* serovar enteritidis is one of the major endemic causes of gastroenteritis worldwide. The objective of this study was to molecular analysis of *Salmonella enteritidis* (SE) isolates from children stools and food sources.

Methods During 6 months (2010), 1950 stool samples of children younger than 12 years in Tehran were collected. At the same time sampling from different food sources including chicken, beef, lamb and duck also, were done. The culture and susceptibility testing performed according to the standard methods. We also used rep-PCR with $(GTG)_5$ primers to study genetic relatedness of SE isolates from two sample sources.

Results A total of 30 SE isolates (15 of clinical and 15 of food samples) were identified. There were 14 different antibiotypes (AB) among stool and food sample isolates. AB1 (30%) and AB2 (24%) was the most prevalent antibiotic resistance patterns. The $(GTG)_5$-PCR banding pattern analysis reviled 3 different common types (CT1, CT2, CT3) and only one single type. CT1 and CT2 were shared between food and stool samples and CT2 was predominant clone. CT3 was limited only to the clinical samples.

Conclusion Antibiotic resistance of SE isolates from clinical and food sources did not differ significantly except for nitrofurantion and nalidixic acid. Food sources isolates were more susceptible than clinical ones. Using rep-PCR with $(GTG)_5$ primers, showed that some clones of SE are responsible for salmonellosis between human and food sources in Tehran and is of major public health concern.

921 VIRULENCE FACTORS OF UROPATHOGENIC AND COMMENSAL ESCHERICHIA *COLI* PATHOTYPES IN PATIENTS WITH URINARY TRACT INFECTION

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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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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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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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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