

Abstracts

enrolled patients simultaneously by the use of Reverse Transcription-Multiplex PCR technique (RT-m PCR). Viral pneumonia was detected in one third of enrolled patients (8/24), with predominance of respiratory syncytial virus A (4/8), followed by Influenza A virus (3/8) and Influenza B virus (1/8) while no cases of respiratory syncytial virus B were detected. The same results were identified in both blood and respiratory specimens.

Conclusion Reverse Transcription-Multiplex PCR technique Multiplex has a significant advantage in that it permits simultaneous amplification of several viruses in a single reaction making this well suited for use in epidemiological studies and to improve etiology-directed clinical management of viral pneumonia.

914 CLINICAL FEATURES OF MYCOPLASMAL PNEUMONIA AT EARLY AGE CHILDREN

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Background and Aims In recent years the problem of mycoplasma pneumoniae, especially in early age children attracted the attention of pediatricians around the world. Purpose - to study the peculiarities of clinical course of mycoplasma pneumoniae in early age children.

Methods From 2009 to 2011 among children with pneumonia analyzed for the presence of mycoplasma pneumoniae. The study involve 450 children aged 5 months to 3 years. Antibodies to Mycoplasma pneumoniae were detected by ELISA in 60 children. Raising antibodies indicated more than 4 times. Conducted clinical observations, X-ray methods, the method of ELISA for the detection of IgM antibodies to Mycoplasma pneumoniae, DNA display M. pneumoniae in sputum by PCR.

Results Mycoplasma pneumoniae began sharply at 80% of children with high fever, cough was dry and unproductive. Outpatient treatment starting antibiotics penicillin group did not give the effect. Pyrexia over 38°C was observed in 95% of children.

On radiographic studies, the bilateral homogeneous lobular infiltration revealed in the lungs at the majority of children (75%). Segmental nature of the infiltrative changes detected in 5% right-sided focal character pneumonic process occurred in 20%, left-side lung had 9.5% of children. In the analysis of peripheral blood revealed anemia in 25% of children, moderate leukocytosis in 89%, marked lymphocytosis (95%) and accelerated erythrocyte sedimentation rate (89%).

Conclusion For early age children with mycoplasma pneumoniae is characterized by severe intoxication, prolonged dry cough. On the radiograph indicated bilateral focal mainly infiltration. In the hemogram - a moderate leukocytosis, lymphocytosis, ESR acceleration.

915 FURAZOLIDONE AS AN ANTIBIOTIC FOR CHILDHOOD GASTROENTERITIS AND ITS COMPARISON WITH WHO GUIDELINE: IS IT USED STILL?

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Background Furazolidone is an anti-parasitic and anti-bacterial drug that used specifically for Giardia as a second-line choice. Some complications was reported that in 10% of children complication occur with diarrhea-vomiting, in children with lack of G6PD, and in children less than 1 years old this drug is not prescribed and is forbidden. This study was conducted to compare of the prescriptions of Furazolidone for treatment of diarrhea in children with the prevalence of Giardiasis.

Methods This is a cross-sectional study was done in North-west of Iran. As first step, we obtained the prevalence of acute gastroenteritis in this area for 2009 then all of related prescription that had inclusion criteria were evaluated in 2010. Related prescriptions adjusted by Furazolidone using frequencies.

Results In the primary study we found out that the total usage of drugs in first nine month of 2009 as below: 840425 Cotrimoxazole, 619044 Metronidazole, 174817 Furazolidone. There are total 1231 antibiotic syrup prescribed by physicians and pediatricians that 174 (14.1%) of them include the furazolidone. From this amount, 18.9% prescribed for children less than 1 years old, 23.6% prescribed for children 1–2 years old, 14.2% for 2–3 years old, 23.4% for 3–5 years old and 19.1% prescribed for children 5–7 years old. **Conclusion:** According to Giradia' prevalence (3.5%) and Furazolidone prescribing (174) for acute diarrhea, we can conclude that 75% of usage is more than prevalence of it's indication for acute diarrhea. Further studies and effective training programs are urgently needed to reverse current irrational treatment practices.

916 CLINICAL PARACLINICAL CHARACTERISTIC OF MEASLES IN THE CHILDREN IN THE ENDEMIC REGION

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Background and aims In this article we showed features of duration Measles in children from endemic region.

Methods We investigated 69 children with Measles in age from 3 to 15 months which used treatment in Uzhgorod Regional Clinical Infectious Hospital during 2012 years. All children were conducted by complex anamnestic and clinical paraclinical inspection.

Results 61 children (88.4%) had positive measles Ig M. Nobody of inspected in the past have't Measles and had routine measles vaccination. The first sign of measles were a high fever (55 children, 79.7%). A runny nose, a cough, red and watery eyes, and small white spots inside the cheeks developed in the initial stage. The first elements of rash appeared in patients were on face, which then spread on the neck, overhead part of breast, and on the second days were appeared on a trunk, hands, on the third days on legs. Rash in the prevalence cases was maculopapular, but in 19 children, 27.5% was generally slight; in 4 children, 5.7% patients-slightly hemorrhagic. Duration of rash was amount 4.7 days. Local pneumonia was confirmed in 7 patients (10.1%), in 5 (7.2%) - bronchiolitis, 5 (7.2%) - had obstructive bronchitis. Biochemistry investigation of blood serum identified decline of Albumin-2 (2.8%), Creatinine-22 (31.8%), Protein-23(33.3%), General Bilirubin-2(2.8%), ALT-3(4.3%), AST-31(44.9%), Alkaline Phosphatase-12(17.3%).

Conclusions Routine measles vaccination for children, combined with mass immunization campaigns in countries with high case and death rates, are key public health strategies to reduce global measles complication.

917 ROTAVIRUS DIARRHOEA IN THE CHILDREN FROM ENDEMIC REGION

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Background and aims: In Ukraine frequency of Rotavirus infection (RI) contain 35–75% of all cases of acute intestinal infections. Methods We investigated 90 children with rotavirus infection (age 1–5years), which used treatment in the infectious hospital during 2011 year. The group of children with RI distributed by gender signs: boys — 47 (52.2%), girls — 43 (47.8%). And by age: 1–3 years - 60 (66.6%), 3–4 years - 20 children (22.2%), after 4 years - 10 children 11.1%).

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 identified the antigen of rotavirus. Most frequency of RI in the children was identified 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 oligoelements and phosphorus. In the patients with RI was identified the disbalance of minerals of blood serum with association of their unchanged elimination.

Conclusions This dates presents the necessity of mineral correction 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 ENTERICA* SEROVARS *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 revealed 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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917 Rotavirus Diarrhoea in the Children from Endemic Region

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