Background and Aims: Transmission of immune competence from mothers to newborns is crucial for optimal development of neonate immune system. Maternal perinatal probiotics supplementation having been observed to be able to modulate this process, the goal of the present study was to investigate the importance of the time window of probiotics intervention (pregnancy/lactation) on early-life immune maturation and response to immunization.

Methods: Pregnant C57/B6J mice were supplemented with *Bifidobacterium lactis* CNCM I-3446, 2.5x10⁹ CFU/day, during either end of gestation and lactation, end of gestation only or lactation only. Maltodextrin was given during both periods (placebo) or in replacement of probiotics when not administered. Immune maturation was assessed by measuring natural mucosal IgA production (ELISPOTs) at weaning and 6 weeks later. Pups were mucosally immunized at weaning, and again four weeks later, with live attenuated *Salmonella typhimurium* ΔaceA. Two weeks after the second immunization, specific antibody responses in serum were analyzed.

Results: All probiotic regimens significantly enhanced natural IgA production in pups in comparison to placebo, an effect observed to the end of study, 6 weeks post-weaning. Supplementation during end of pregnancy and lactation, or lactation only provided significantly highest values. Specific antibody titers tended to be potentiated by all three regimens in pups responding to immunization with highest values being obtained after supplementation during both periods.

Conclusions: This study further supports the benefit of maternal perinatal intervention with probiotics on neonatal immune maturation, moreover emphasizing that supplementation during both pregnancy and lactation is needed to achieve overall optimal effects.

**269** SHIFTING SEROPOSITIVITY FOR HEPATITIS A IN CHILDREN IN ISTANBUL, TURKEY FROM 1996 TO 2011

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Background: Hepatitis A virus (HAV) is transmitted by the fecal-oral route, and the epidemiology of HAV is associated with hygiene and socioeconomic status. However, due to improvements in living conditions, there is an epidemiological shift in HAV infection.

Methods: In this study, we investigated the seropositivity for HAV in children aged between 2 and 18 years. In addition, we compared the results with previously reported seropositivity data from the same center in Uskudar, Istanbul, Turkey, from 1996.

Results: The mean age of the 400 children was 7 ± 3.7 years (range: 2–18). Of the 400 serum samples collected, all were tested for anti-HAV IgG, and 50 (12.5%) were positive. The rates of anti-HAV seropositivity within the age groups of 2–6, 6–10, and 10–18 years were determined. The seropositivity increased with increasing age: 11.5% in the 2- to 6-year-old group and 13.2% in the 10- to 18-year-old group.

Conclusions: There was a significant decline in the overall seropositivity for anti-HAV between 1996 and 2011 (p<0.001), and the pediatric age group has a high risk of HAV infection.

**268** SEROTYPE AND ANTIMICROBIAL SUSCEPTIBILITY DISTRIBUTION OF INVASIVE STREPTOCOCCUS PNEUMONIAE ISOLATED FROM CHILDREN IN TURKEY

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*Streptococcus pneumoniae* is a major cause of invasive infections. The aim of this study was to evaluate the serotype and antimicrobial susceptibility of invasive pneumococci isolated at 14 different centers in Turkey between January 2011–April 2012. Totally 79 clinical isolates from invasive infections were investigated, which were isolated from cerebrospinal fluid (CSF) (33, 42%), blood (31, 39%) and the other sterile body fluids (15, 19%). Susceptibility to penicillin, cefotaxime and erythromycin was determined by E-test (bioMerieux, France) according to CLSI standards. Latex agglutination method was used for determination of serogroups. Serotypes were determined by the capsular swelling (Quellung reaction) method (Denmark, Statens Serum Institute).

Abstract 269 Figure 1: Shifting seropositivity for Hepatitis A

In 1996, the overall seropositivity was 41.3%. In the 1996 study, the seropositivity was 35.2% in 2- to 6-year-old age group, 35.3% in the 6- to 10-year-old age group and 54.3% in children older than 10 years. Given the serological shift over time, greater susceptibility and a persistent risk of exposure to HAV suggest that outbreaks are possible.

**270** H1N1 PANDEMIC: COMPARISON OF THE CLINIC PRESENTATION BETWEEN CANADA AND FRANCE IN CRITICALLY ILL CHILDREN

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H1N1 influenza was first officially detected in early April in 2009. As of September 18th, 2009, there have been 87 reported cases in Canada. In addition, the first children with H1N1 influenza H1N1 has been identified in France. The purpose of this study is to compare the clinical presentation of critically ill children between Canada and France during the H1N1 pandemic.
Background and Aims The 2009 H1N1 pandemic (pH1N1) induced a large number of admissions of children in pediatric intensive care units (PICU). The objective of this study was to compare the severity of the 2nd wave of pH1N1 between France and Canada.

Methods All patients admitted to a pediatric intensive care unit (PICU) in Canada (PICU = 16) and France (PICU = 25) between October 1st 2009 and January 31st 2010, with a documented H1N1 infection were included.

Results 160 children in Canada (prevalence = 2.6/100,000 children) and 125 children in France (prevalence = 1.6/100,000) were hospitalized in SIP. pH1N1 incidence curve was different in the two countries (figure). pH1N1 acute respiratory failure was more severe in France, with a lower incidence, and a low vaccination rate (Table).

Abstract 270 Table 1 Comparison Canada-France: main Results

<table>
<thead>
<tr>
<th>Canada</th>
<th>France</th>
<th>p-value</th>
<th>Odds Ratio with 95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weight (median)</td>
<td>25.9 kg</td>
<td>20.1 kg</td>
<td>0.01</td>
</tr>
<tr>
<td>Vaccination H1N1 (%</td>
<td>34</td>
<td>2</td>
<td>&lt;0.0005</td>
</tr>
<tr>
<td>Infant heart disease (%)</td>
<td>21 (13.1%)</td>
<td>32 (25.6%)</td>
<td>0.007</td>
</tr>
<tr>
<td>Lung disease (%)</td>
<td>65 (40.6%)</td>
<td>29 (23.2%)</td>
<td>0.002</td>
</tr>
<tr>
<td>Asthma (%)</td>
<td>42 (26.3%)</td>
<td>16 (12.8%)</td>
<td>0.005</td>
</tr>
<tr>
<td>Congenital heart disease (%)</td>
<td>29 (18.1%)</td>
<td>3 (2.4%)</td>
<td>&lt;0.0005</td>
</tr>
<tr>
<td>Mechanical ventilation duration</td>
<td>6.3 days</td>
<td>10.2 days</td>
<td>0.016</td>
</tr>
<tr>
<td>Hospital length of stay</td>
<td>5.7 days</td>
<td>8.2 days</td>
<td>0.025</td>
</tr>
</tbody>
</table>

Conclusion pH1N1 2nd wave was different between Canada and France. The low vaccination rate in France is associated with an increase in severity but not in incidence.

271 DISTRIBUTION OF NSP4 GENOTYPES OF GROUP A ROTAVIRUS STRAINS CIRCULATING IN TUNISIAN CHILDREN FROM 2006 TO 2008

Background and Aims Non-structural protein 4 (NSP4), encoded by group A rotavirus (RVA) genome segment 10, is the first recognized virus-encoded enterotoxin. Recently, a new classification system for RVAs was proposed and a total of 14 NSP4 genotypes (E1 to E14) are currently described.

Methods A total of 1391 faecal specimens collected from children under 5 years old were screened by ELISA for the presence of RVA antigen. NSP4-encoding genes of RVA positive strains were analyzed using a semi-nested RT-PCR.

Results Genotypes E1 and E2 were identified in 183 (70.1%) and 78 (29.9%) samples, respectively. This report represents the first investigation on the genetic diversity of RVA NSP4 genes in Tunisia. Tunisian RVA strains analysed in the present study belonged to 2 different genotypes: E1 and E2. Such a result is concordant with literature data: indeed, although 14 RV NSP4 genotypes have been identified to date, previous molecular characterization has shown that most of the diversity in the NSP4-encoding gene lies in genotypes E1 and E2. Other studies, however, have detected unusual strains carrying genotypes E3 and E13. Moreover, a predominance of NSP4 genotype E1 was observed over the entire period of study, from 2006 to 2008. Such a result was also quite expected as previous investigations have also shown that NSP4 genotype E1 was largely predominant among children worldwide.

Conclusions These results underline the need for further investigations to assess the validity of NSP4 as a suitable target for epidemiologic surveillance of rotavirus infections and vaccine development.

272 IDENTIFICATION OF NON TUBERCULOUS MYCOBACTERIA ISOLATES USING PCR-RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS OF THE HSP65 GENE IN IRAN

Background Various molecular methods have been used for the rapid identification of mycobacterial species. In this survey, PCR-restriction fragment length polymorphism of the hsp65 gene was used to characterize the isolated mycobacteria from clinical specimens in comparison with classical biochemical method.

Methods Mycobacterial species of 4892 suspicious tuberculous patients were identified based on biochemical tests. Forty eight mycobacterial isolates were selected and followed by the conventional and PRA of hsp65 for species identification. A 459 bp PCR product of hsp65 in all selected isolates were amplified and digested with the BseEII and HaeIII restriction enzymes. The RFLP patterns were compared with Gelcomparrl software and revealed the species identification grouping.

Results According to the biochemical tests, a total of 229 mycobacterial isolates were identified as M. tuberculosis (163), M. bovis (14), and NTM (32). All of the 48 mycobacterial selected isolates including 16 M. tuberculosis, one M. bovis and all 32 isolates of NTM strains yielded detectable PCR product for hsp65 gene and the PCR-RFLP analysis, revealed 10 different species among NTM isolates.