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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/BL6 mice were supplemented with *Bifidobacterium lactis* CNCM I-3446, $2.5x10^8$ 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* ΔaroA. 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 observable up 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.

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). It was found that most common serotypes among 79 strains were 19 F (12, 15%), 6 A (7, 9%), 23 F (5, 6%), 6 B (4, 5%), 19 A (4, 5%) and 3 (4, 5%). For all invasive pneumococcal diseases, during the first 2 years of age, the potential coverage rates of PCV7, PCV10, and PCV13 were 47.8%, 56.5%, and 82.6%, respectively; meanwhile 40.5%, 44.3%, and 63.3% for the pediatrics age group (0–18). Serotypes 19F, 6A, 19A, 23F, 6B, 14 and 3 were predominate. All pneumococcal conjugate vaccine formulations cover these serotypes with the exception of serotype 19A which is covered only by PCV13. Serotype 19A has steadily increased in prevalence and become increasingly resistant to common antibiotic classes. Rational antibiotic use and vaccination of infants with pneumococcal conjugate vaccines should be considered as essential strategies for prevention of pediatric invasive infections in Turkey.

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

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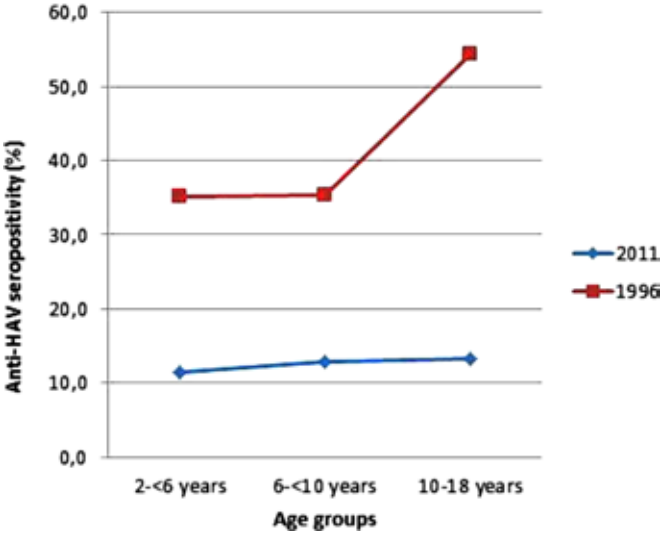
Background Hepatitis A virus (HAV) is transmitted by the fecal-oral route, and the epidemiology of HAV is associated with hygiene and socioeconomic status. However, due to improvements in living conditions, there is an epidemiological shift in HAV infection.
Methods In this study, we investigated the 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 7.9±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.



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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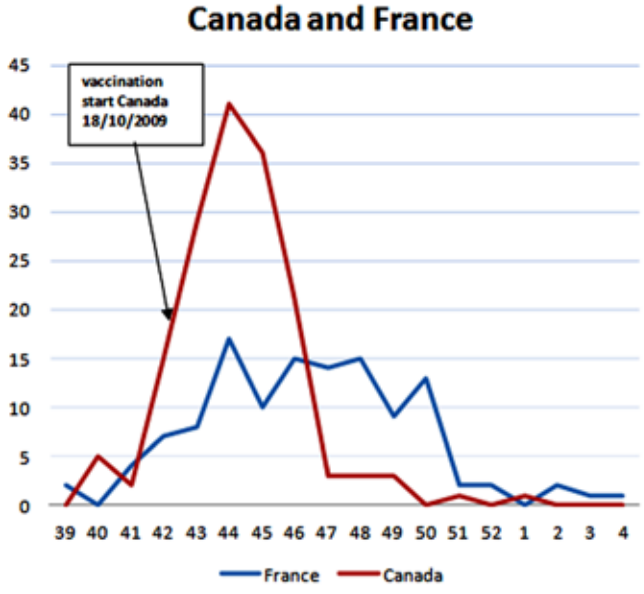
Background and Aims The 2009 H1N1 pandemic (pH1N1) induced a large number of admissions of children in pediatric intensive care units (PICU). The objective of this study was to compare the severity of the 2nd wave of pH1N1 between France and Canada.

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

	Canada	France	p-value	Odd Ratio with CI 95%
Weight (median)	25.9 kg	20.1 kg	0.01	
Vaccination H1N1 (n)	34	2	<0.0005	0.05 (0.01–0.2)
Infant<1an (n,%)	21 (13.1%)	32 (25.6%)	0.007	2.3 (1.2–4.2)
Lung disease (n,%)	65 (40.6%)	29 (23.2%)	0.002	0.4 (0.3–0.7)
Asthma (n,%)	42 (26.3%)	16 (12.8%)	0.005	0.4 (0.2–0.8)
Congenital heart disease (n,%)	29 (18.1%)	3 (2.4%)	<0.0005	0.1 (0.03–0.4)
Mecanical ventilation duration	6.3 days	10.2 days	0.016	
Hospital length of stay	5.7 days	8.2 days	0.025	



Abstract 270 Figure 1 Admission PICU per week

Conclusion pH1N1 2nd wave was different between Canada and France. The low vaccination rate in France is associated with an increase in severity but non in incidence.

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

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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

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Background Various molecular methods have been used for the rapid identification of mycobacterial species. In this survey, PCR-restriction fragment length polymorphism of the *hsp*65 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 *hsp*65 for species identification. A 439 bp PCR product of *hsp*65 in all selected isolates were amplified and digested with the *Bst*EII and *Hae*III restriction enzymes. The RFLP patterns were compared with GelcomparII software and revealed the species identification grouping.

Results According to the biochemical tests, a total of 229 mycobacterial isolates were identified as *M. tuberculosis* (183), *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 *hsp*65 gene and the PCR-RFLP analysis, revealed 10 different species among NTM isolates.