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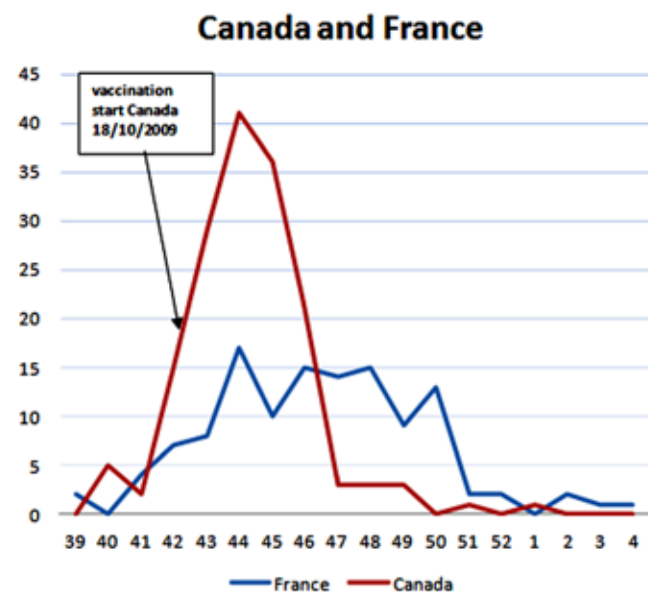
**Background and Aims** The 2009 H1N1 pandemic (pH1N1) induced a large number of admissions of children in pediatric intensive care units (PICU). The objective of this study was to compare the severity of the 2<sup>nd</sup> wave of pH1N1 between France and Canada.

**Methods** All patients admitted to a pediatric intensive care unit (PICU) in Canada (PICU=16) and France (PICU=25) between October 1<sup>st</sup> 2009 and January 31<sup>st</sup> 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 2<sup>nd</sup> 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 *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 439 bp PCR product of *hsp65* 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 *hsp65* gene and the PCR-RFLP analysis, revealed 10 different species among NTM isolates.

**Conclusion** In order to identify more rapidly a wide variety of mycobacteria, the PCR-restriction fragment length polymorphism analysis of *hsp65* procedure was applied. The PRA test among NTM isolates indicated that the most frequent mycobacterial strains were *M. kansasii*, *M. goodnae* III, *M. marinum*, *M. chelonae*, *M. scrofulaceum* and *M. gastri*. Our results showed that this method in comparison with classical methods is rapid and accurate enough for the identification of mycobacterial species from LJ culture isolates.

**273 MOLECULAR CHARACTERISTICS OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM CHINESE CHILDREN**

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**Objective** The present study aim to investigate the molecular characteristics of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates from Chinese children in seven city.

**Method** A total of 134 MRSA isolates were collected from eight hospitals. Multilocus sequence (MLST), staphylococcal chromosomal cassette mec (SCCmec) and spa typing were analyzed. The Panton-Valentine leukocidin (pvl) gene was also detected.

**Result** Overall, 16 sequence types (STs) were obtained, and CC59 (51.7%) was found to be the most prevalent, which including ST59 and ST338, followed by ST239 (16.4%). SCCmec type II, III, IV and V were identified in this study. SCCmec type IV was the most predominant type at 50.0%, followed by SCCmec type V at 23.9% and III at 23.9%. SCCmec subtypes IVa, IVc, and IVg were found among the SCCmec type IV strains, IVa was the main subtype at 77.6%. Twenty-six spa types were also identified, the predominant type was t437 (47.8%). The prevalence of pvl genes and the SCCmec type of the strain were relevant, the pvl gene positive rate was higher in SCCmecIV and V-type strains than in SCCmecII and III-type strains (58.6% vs. 14.3%,  $P < 0.05$ ); there was a significant difference between them. In the strains isolates from pneumonia and SSTIs, ST59-MRSA-Iva (t437) was the predominant clone.

**Conclusion** The result indicates that MRSA isolates in Chinese children are largely associated with the ST59-MRSA-IV (t437) and ST239-MRSA-III (t037) clone.

**274 COLONIZATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS WITH HIGH-LEVEL RESISTANCE TO MUPIROCIN IN KOREAN CHILDREN**

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Increased mupirocin use has been considered as a major cause to develop mupirocin resistance among MRSA isolates. High-level mupirocin resistance (HLMR) is associated with decolonization failure, but fortunately most MRSA have showed low-level mupirocin resistance (LLMR). Recently, we became aware of markedly high prevalence of clinical isolates with HLMR among Korean children. We investigated the proportion of HLMR isolates and mupirocin use between children (less than 18 years) and adult patients.

A total of 1134 MRSA (213 children and 921 adults) isolates were identified from two university hospitals in 2010–2011. Antimicrobial susceptibility testing was firstly performed by using the Vitek 2 instrument (bioMerieux, Marcy l'Etoile, France). The *mupA* genes were detected by polymerase chain reactions.

Overall, 38% of isolates collected from children showed HLMR, whereas 3.4% showed HLMR in adults. Children revealed only one LLMR isolate (0.4%), and adult patients had 80 LLMR isolates (8.6%). This tendency was also observed, when the patients were

divided into two groups under intensive care units or outpatient settings. A total of 4,009 mupirocin prescriptions were dispensed at our institutions during 2006. Afterward, there were 4,760, 5,250, 6,416, and 8,038 prescriptions from 2007 to 2010, respectively. But, prescription rates of mupirocin did not significantly differ between children and adults. In children with MRSA isolates, the presence of previous admission, prolonged hospitalization, and mupirocin use did not contribute to mupirocin resistance. In Korean children, the rate of HLMR in the MRSA isolates was very high and it was not associated with increased mupirocin use.

**275 EPIDEMIOLOGY OF POLIOMYELITIS AND MANAGEMENT OF ACUTE ASCENDING FLACCID PARALYSIS (AAFP) IN PAEDIATRIC INTENSIVE CARE UNIT (PICU) IN ALGERIA**

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**Background and Aims** As part of the implementation of National plan for the eradication of poliomyelitis, disease surveillance and management of cases of AAFP are key strategies of this program.

The aim is participation in the national program for poliomyelitis, eradication and to determine the efficacy of intravenous immunoglobulin (IG) for treatment of AAFP.

**Methods** From September 1994 to February 2012, 176 cases of AAFP were identified and supported in our PICU. Since January 2008, 25 children were treated by IG. The parameter studied were: age, gender, autonomic disorders, albuminocytologic dissociation of CSF after lumbar puncture, artificial ventilation, average time of stay, and mortality.

**Results** In this series, no case of poliomyelitis has been diagnosed by the Pasteur Institute of Algeria. Since 2008, use of IG seems to improve the mortality. 8% in the overall series ( $n = 176$ ) vs 4% in the group treated with immunoglobulins ( $n = 25$ ). All deaths are related to the existence of severe neurovegetative disorders. The need in ventilation and the duration of stay does not appear to be influenced by the use of the "IG".

**Conclusion** The eradication of poliomyelitis is a national goal to declare the Algeria zone free of polio by the WHO.

**276 INFANT MORTALITY FROM INFECTION OVER 2 DECADES: LESS GBS AND MENINGOCOCCUS, BUT DOUBLING OF DEATHS IN VERY PRETERM INFANTS**

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**Background** Infection is an important cause of neonatal/infant mortality. Antenatal care, neonatal intensive care and immunisation practices affect infectious mortality, but no good data show how these deaths have changed over time. Understanding this will help direct future medical priorities.

**Objective** To evaluate changes in neonatal/infant mortality from infection over 2 decades (1988–2008) in a geographical population.

**Design and Methods** We used a population database (Perinatal Mortality Survey, Northern region UK) and reviewed infant deaths coded as infection. Proportional contribution to deaths, pathogens identified and risk factors were analysed. To demonstrate changes over time, three 7-year epochs were created.

**Results** 625 deaths from infection were identified. Absolute numbers of deaths fell with time but the proportion from infection increased. Significantly preterm infants were increasingly represented in successive epochs.