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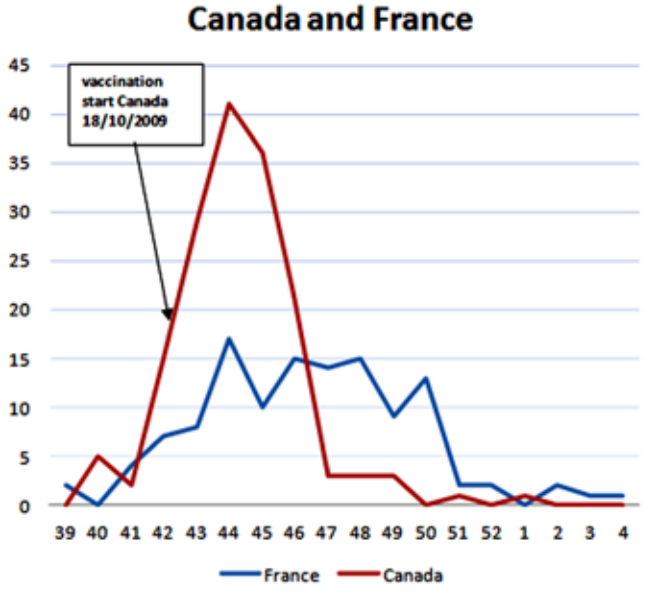
Background and Aims The 2009 H1N1 pandemic (pH1N1) induced a large number of admissions of children in pediatric intensive care units (PICU). The objective of this study was to compare the severity of the 2nd wave of pH1N1 between France and Canada.

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.