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Results: A total of 770 respiratory and alimentary specimens from 348 and 64 Chinese horseshoe bats were obtained in Hong Kong and in the Guangdong province in Southern China, respectively. RT-PCR for a 440-bp fragment in the RdRp genes of coronaviruses was positive in alimentary specimens from 58 (16.7%) of the 348 bats from Hong Kong, and from 8 (12.5%) of the 64 bats from Guandong. None of the respiratory specimens was positive. Sequencing results suggested the presence of two different coronaviruses among the 64 positive bats. Complete genome sequencing of four strains of bat-CoV revealed the smallest coronavirus genome (27164 nucleotides) and a unique spike protein evolutionarily distinct from the rest of the genome. This spike protein, sharing similar deletions with other group 2 coronaviruses in its C-terminus, also contained a 15-amino acid peptide homologous to a corresponding peptide within the RBM of spike protein of SARS-CoV, which was absent in other coronaviruses except bat-SARS-CoV. Further studies are required to determine if inter-group gene exchange was responsible for the origin of the spike of bat-CoV and its possible role in the evolution of the spike of SARS-CoV.
Conclusion: This is the first report that documents the presence of a spike evolutionarily distinct from the other parts of the coronavirus genome. It also suggests that the RBM of SARS-CoV and the corresponding region in bat-CoV and bat-SARS-CoV share different degrees of homologies, consistent with the hypothesis that the RBM of SARS-CoV may have originated from recombination events.

P1902 Toscana virus, a "Mediterranean" agent of aseptic meningitis: analysis of 42 consecutive cases

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Objectives: Aseptic meningitis (AM) is mostly caused by a number of viruses; among those, Toscana virus (Tosv) is an important arbovirus that is endemically present in our region as well as in both South-European and North-African shores of the Mediterranean basin. Here we describe the main features of 42 cases of Tosv-related AM observed in our unit during a seven-year period.
Methods: Between June 2000 and December 2006, a total of 94 patients with a diagnosis of AM were admitted to our unit. Of those, 42 cases (44.7%) resulted positive for IgM + IgG anti-Tosv as detected by an immune-capture test using monoclonal antibodies bound to the solid phase (IgM) and by an ELISA technique (IgG) (Chorus®, Diesse, Italy). Demographics, clinical picture, neuroimaging, and cerebrospinal fluid (CSF) findings of Tosv-related AM were reported.
Results: In our area, Tosv-related AM was prevalent during summer (73.7%) and by 30 years of age (52.4%) without differences per gender (male 54.8%, female 45.2%). Only 31.1% of patients habitually lived in the urban area of Florence, the remainder residing in flat and hilly surroundings. Clinical course was always self-limited, with a mean duration of the hospital stay of 6.2 days. Headache was present in all cases; it had an abrupt onset, and was mostly diffuse and moderate-to-severe. Clinical picture typically included nuchal/spinal rigidity (85.7%), moderate fever (78.6%), vomiting (64.3%), photophobia (35.7%), and nausea (33.3%). Systemic manifestations such as asthenia, joint and muscle pain, diarrhoea, abdominal discomfort, and pharyngodinia as well as impairment of consciousness were infrequent. Electroencephalography and CT scan showed brain abnormalities that were typical of encephalitis in four patients and in another one, respectively. Chemical analysis revealed clear CSF with increased levels of proteins and white blood cells (mostly mononuclear) and normal levels of glucose and chloride in all cases. No specific therapy was required.
Conclusion: As in other surveys, prevalently from Italy, our patients with Tosv-related AM generally showed clinical, radiological, and laboratory features of a self-limited disease. It is important that clinicians are universally familiar with this infection, that could be acquired during stay in endemic areas of the Mediterranean basin (Portugal, Spain, Southern France, Italy, Cyprus, North-African countries) and then clinically revealed in North America and North-Central Europe, where it is little or nothing known.

P1903 Molecular typing and epidemiology of Enterovirus in Belgium, 2005–2007

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Objectives: Non-Polio Enteroviruses (EVs) are the most common cause of aseptic meningitis. To evaluate the epidemiology of EVs in Belgium during the last 3 years, molecular typing of EV positive in cell cultures and in cerebrospinal fluid (CSF) samples was developed, based on RT-nested PCR and sequencing analysis.
Methods: From January 2005 to August 2007, typing of EV was carried out by immunofluorescence using monoclonal antibodies on viral cultures or genotyping. Eighty-seven cultures, grown on MRC5 or Vero cells, were identified as EV positive. During the same period, 121 CSF from patients suspected of aseptic meningitis were found to contain EV RNA using PCR or nested PCR assays targeting both 5′UTR and VP1 regions with combinations of PCR primers described previously (Oberste et al, J.Virol. 1999; Ishiko et al, JID 2002; Thoelen et al, JCM 2004). In addition, sequencing of 5′UTR or VP1 regions allowed the identification of EV type by comparison with the sequences available in Genbank and by alignments in the Bionumerics software (Applied Maths, Belgium).
Results: As expected, culture yield for EV isolation on CSF was poor (26%). All positive cultures, typable or not with monoclonal antibodies, were identified by sequence analysis. One hundred twenty-one CSF samples could be genotyped by our sequence analysis protocol. For 2005, the major genotyped EVs were Echovirus 9, Echovirus 13, Echovirus 6 and Echovirus 18 (24%, 22%, 14% and 14% respectively). For 2006, the predominant EVs were Echovirus 6, Coxsackie type B3 and B5 and Echovirus 18 (22%, 14%, 14% and 12% respectively). Finally, from January to august 2007, the principal types were Echovirus 30, echovirus 11 and echovirus 13 (with 40%, 16% and 12%, respectively).
Conclusion: In Belgium, during those 3 years, the data's showed that EVs were mostly belonging to group B but with a diversity of genotypes. However, three genotypes (Echovirus 6, 9 and 30) were involved in aseptic meningitis each year of this period, with a clear success of Echovirus 30 during 2007 (40% of cases). The genotyping protocol is rapid, sensitive and accurate for molecular typing of EVs directly on CSF samples and is very useful for epidemiological studies.

P1904 Epstein-Barr virus genotypes and LMP-1 gene variants in paediatric liver transplant recipients

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Objectives: The two Epstein-Barr virus (EBV) genotypes vary in their geographic distribution, tissue tropism and biological features. Latent Membrane Protein 1 (LMP1) is an oncogene and it is expressed in most EBV-positive post-transplant lymphoproliterative disorders (PTLD). Previous studies showed that 30- and 69 bp-deleted variants of LMP-1 have higher transforming capacity. The aim of this study was to determine the prevalence of A and B type and LMP-1 gene variants in blood and tissues of children after liver transplantation (LTx) including PTLD patients.
Methods: 115 children who had undergone LTx at Childrens' Memorial Health Institute between 1999 and 2007 were included in this study. The study involved 13 patients with histologically confirmed PTLD. Molecular assays were performed in blood samples of all children, and in 38 paraffin-embedded tissues from 24 patients. EBV genotype was determined by PCR by simultaneous analysis of two gene loci, EBNA-2 and EBNA-3C. LMP-1 variants were detected by PCR using primers flanking the site of characteristic 30- and 69-bp deletion.
Results: EBV genotype was determined in blood samples from 69 pts and in tissues from 16 pts (including 11 PTLD pts). Type A was detected in blood of 66 (95.6%) pts (including 11 PTLD pts) and in tissues of 15 pts (including 7 PTLD pts). Type B was detected in blood of 3 (4.4%) pts (including 1 PTLD pt) and in 2 tissue samples from one PTLD pt. Interestingly, coinfection with A and B EBV genotypes with different