prospectively monitored for active CMV infections using quantitative pp65-antigenaemia and viral isolation. Forty-three CMV seropositive patients with a prolonged ICU stay (<7 days) were included. Within two weeks fourteen patients (32.6%) developed an active CMV infection with low pp65-antigenaemia (median 3 positive per 500,000 WBCs). CMV reactivations occurred despite CMV specific Th1-cell functions. The active CMV infections turned negative without antiviral therapy after twenty days, on average. Following active CMV infection the frequency of CMV and of superantigen (SEB) reactive Th1-cells significantly increased which means that patients with septic shock were capable to mount an antiviral immune response and to repress active CMV infection. In patients without active CMV infection the frequencies of reactive Th1-cells remained low. In parallel active herpes simplex virus (HSV) infections were detected in sixteen patients using bronchial aspirates. The HSV and CMV reactivations were associated and occurred at the same time. ICU treatment and the need of mechanical ventilation was significantly prolonged in the group with active CMV infection and we suggest that viral reactivation could increase morbidity of patients with septic shock. Early antiviral therapy aimed at preventing viral associated morbidity of CMV seropositive patients with septic shock should be evaluated in future clinical as a new treatment option.

P1531 Persistence of the poliovirus genome in the cerebrospinal fluid of patients affected by post-polio syndrome

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Objectives: Polioviruses (PV; three types) are small, non-enveloped, positive-strand RNA viruses belonging to the Enterovirus genus of Picornaviridae. Twenty to thirty years after being hit by paralytic poliomyelitis, over 50% of patients develop the so called "post-polio syndrome" (PPS). PPS is characterised by slowly progressing muscular weakness, chronic pain, fatigue, and other symptoms. The cause of PPS is likely due to distal degeneration of enlarged post-poliomyelitis motor units. Virus persistence in the central nervous system (CNS) has long been investigated with controversial results.
Methods: PPS patients aged 50–65 years have been investigated. The PV genome has been searched for in cerebrospinal fluid (CSF) samples using RT-PCR with primers directed to different genomic regions. The utilised amplification methods were capable of detecting <10 genome equivalents per reaction tube. Direct sequencing of purified amplicons allowed identifying the persisting PV serotype. CSF samples from patients with non-infectious pathologies were used as controls.
Results: All investigated patients (11/11) were positive for the presence of PV genomic fragments. The 5′ untranslated sequence represented the most sensitive target for molecular detection. Sequencing of VP1 and 2A tracts revealed that the PV type-1 genome was present in most patients. Infectious virus was isolated in cell culture from a single patient undergoing orthopaedic surgery. Complete sequencing of the isolate is expected to shed light on molecular mechanisms of PV persistence. No PV amplicons were detected in CSF samples from control patients.
Conclusion: By gene amplification and genome sequencing, we have shown that PV genomes are able to persist for long periods of time (i.e., >30 years) in the CNS of PPS patients. Though the contribution of viral persistence to PPS pathogenesis is still undefined, our findings may contribute to introducing new molecular tools for PPS diagnosis. The finding of persistent PVs also indicates the need of exploring innovative therapeutic methods for PPS patients. PPS, in fact, represents the most prevalent motor neuron disease today.
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P1532 Serological evidence of hantavirus and arbovirus infections among acute febrile patients in Uzbekistan

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Objectives: Hantavirus and arbovirus infections are known to occur in Eastern Europe and Central Asia, particularly in Kazakhstan and Turkmenistan. These viral agents have not, however, been reported in neighbouring Uzbekistan.
Methods: We are currently conducting hospital based surveillance for undifferentiated fever in Tashkent and Samarqand, Uzbekistan. Following study enrollment, acute sera was collected from 817 patients presenting with acute febrile illness between October 2004 and May 2006. Convalescent sera were collected upon discharge or 2–3 weeks after the first specimen was drawn. Sera were screened at 1:100 dilutions for IgM antibodies to Hantavirus, West Nile (WN), Sindbis (SIN), Sandfly Naples (SFN) and Sandfly Sicilian (SFS) viruses using Focus® IgM-EIA kits (Cypress, California) for Hantavirus and an IgM capture-ELISA developed at the U.S. Naval Medical Research Unit-3, Cairo, Egypt. Samples testing positive by ELISA for arbovirus were confirmed by a plaque reduction neutralisation test (PRNT).
Results: A total of 127 (15.5%) patients were determined IgM positive to Hantavirus with rates of 6.1% (11/181) and 18.2% (116/636) in Tashkent and Samarqand, respectively. Six patients (0.7%) had anti-SFS IgM antibodies (titers ranged 1:400 to 1:6,400), all confirmed by PRNT. All specimens had no IgM titers against the other viruses tested. Clinical and epidemiological data of patients will be described.
Conclusions: Hantavirus infection may constitute a significant proportion of undiagnosed acute febrile illness particularly in Samarqand (rural area) in Uzbekistan. This is the first report of Hantavirus and SFS virus infections in Uzbekistan.

P1533 Crimean-Congo haemorrhagic fever and haemorrhagic fever with renal syndrome in Kazakhstan

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Objectives: We are undertaking a survey of the incidence of two endemic viral diseases in Kazakhstan. Both diseases are caused by bunyaviruses: CCHF is spread by ticks, while haemorrhagic fever with renal syndrome (HFRS), caused by hantaviruses, is contracted through contact with infected rodent host excreta. Our plan is to integrate studies of human disease with viral incidence in ticks and reservoir animals.
Methods: To achieve this, we are examining the strain characteristics of viruses (CCHFV and hantaviruses) that we identify through PCR, and are assessing incidence of antibody positivity by ELISA against viral antigens.
We have developed ELISA assays for six strains of both viruses using cloned, purified nucleocapsid protein, and PCR assays using detailed sequence analysis of strains that are likely to be circulating in this part of central Asia.
Results: We have collected field samples as follows: 350 human serum samples, 2,500 organ samples from over 1,000 rodents and 15,000 ticks (13,800 H. asiaticum and 1,200 other Ixoides spp.). In preliminary screening experiments, approximately 40% of ticks tested were positive for CCHF viral antigen by ELISA. Five percent of rodents were positive for hantavirus (Puumala) antigen by ELISA.
Conclusion: We anticipate that these numbers are substantial underestimates of the true incidence of viral infection in both ticks and rodents, and our current PCR and ELISA (for antibodies) studies are designed to be both more sensitive and specific than tests used in the past.