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Abstract No: 1641

Presentation at ESCV 2015: Poster 1

Viral load in serum of patients with VZV CNS infection

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Background: Varicella zoster virus (VZV) is recognized as one of the most common viral agents causing central nervous system (CNS) infections and comprises a wide spectrum of syndromes. Ameliorated diagnostic methods including real-time polymerase chain reaction (PCR) has facilitated the detection of virus in different body fluids and has also enabled quantification of the virus. Some data have been presented on viral load in the cerebrospinal fluid (CSF) of patients with VZV CNS infections, with diverging results, but so far no study has been published on the viral load in peripheral blood of these patients. Our aim was to investigate the viral load in peripheral blood in patients with acute neurological symptoms and detectable CSF VZV DNA by PCR and try to correlate the amount of VZV DNA to different clinical parameters.

Methods: Seventy-two patients with VZV DNA detected in the CSF by PCR and contemporary neurological symptoms were compared to a control group of 36 patients hospitalized for herpes zoster but without neurological symptoms. VZV CNS patients were compared to a control group of 36 patients hospitalized for herpes zoster but without neurological symptoms. VZV DNA concentrations in serum were measured by quantitative PCR and related to clinical manifestations and laboratory parameters.

Results: The VZV CNS patients showed lower concentrations of VZV DNA in serum compared with the control group (p ≤ 0.001). In the VZV CNS patients, 40 patients had no detectable VZV DNA in serum compared to eight of the controls. When the subgroups were compared, the group of encephalitis showed higher viral amount in serum compared to both the group of meningitis and Ramsay-Hunt syndrome or “other neurological symptoms”. The VZV CNS patients were compared to a control group of 36 patients hospitalized for herpes zoster but without neurological symptoms. VZV DNA concentrations in serum were measured by quantitative PCR and related to clinical manifestations and laboratory parameters.

Conclusions: The VZV viral load is lower in patients with VZV CNS infections compared to patients with herpes zoster and no neurological symptoms. The viremia in patients with VZV CNS infections seems associated with contemporary rash and possibly the degree of blood-brain barrier damage.

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Acute respiratory disease surveillance – Comparison of the two different seasons in the Czech Republic

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Background: A numerous group of taxonomically heterogeneous viruses can cause similar clinical symptoms to influenza. These are respiratory syncytial viruses (hRSV), human metapneumoviruses (hMPV), parainfluenza viruses (PIV), human adenoviruses (HAdV), coronaviruses (hCoV), rhinoviruses, and bocaviruses (HBoV). A comparison is presented of the virological spectrum of 2014/15, a typical influenza season, and the season 2013/14 with an unusually weak influenza epidemic.

Methods: The sentinel and non-sentinel specimens were screened for the presence of influenza A/B and if positive, the strains were identified to the subtype level. The sentinel samples were examined for other respiratory viruses (hRSV, hMPV, hADV, bocaviruses, CoV, PIV) which were assigned to groups, without further classification. The isolated strains of A/H3N2 and HAdV were sequenced. The genome segments (HA3/hexon) were compared at the nucleotide and amino acid levels and phylogenetic relations were identified (BigDye Terminator v 3.1 Cycle Sequencing Kit, 3500 Genetic Analyser, Life Technologies, the Mega 6, MAFFT, BioEdit software).

Results: In the season 2013/14, altogether 45.5% of 415 sentinel and 34 non-sentinel samples were positive for at least one respiratory virus. The most often detected viruses were adenoviruses (13%) while the less common ones were hRSVs (2%), A and B influenza viruses were identified only in 8% of 639 (415 sentinel, 224 non-sentinel) samples. In the season 2014/15, 1382 (sentinel and non-sentinel) samples were examined for influenza virus, with positivity rates of 37% for Influenza A virus (14% A/H1, 78% A/H3) and 16% for influenza B virus. The respiratory virus panel was only used to screen 462 sentinel samples of which 76% turned out to be positive for at least one respiratory virus. The most commonly detected was HAdV (7.5%) again and the rarest were hMPVs (0.01%). Phylogenetic analysis revealed the co-circulation of H3N2 viruses with at least three discernible H3 haemagglutinin molecules. The majority of H3 sequences belonged to sub-clades 3C.2a and 3C.3b while the 3C.3a viruses, which are relatives of the 2015/2016 vaccine strain A/Switzerland/9715293/2013 (H3N2), were remarkably underrepresented.

Conclusion: The unusually weak epidemic in the 2013/2014 season allowed the predominant manifestation of non-influenza respiratory viruses in comparison with the typical influenza season 2014/15, with the predominating A/H3 subtype followed by the second peak of B influenza. In spite of these virological findings, there was nearly no difference in the clinical manifestations, but much more non-sentinel samples were screened. We can assume, that much more patients required hospitalisation.

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