1170. CSF HSV PCR Testing in Adults and Children with Meningitis and Encephalitis

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Background. Herpes simplex virus (HSV) is a common treatable cause of meningitis and encephalitis. Delayed antiviral therapy is associated with worse clinical outcomes in HSV encephalitis.

Objectives. To determine the utilization of a cerebrospinal fluid (CSF) HSV polymerase chain reaction (PCR) and identify predictors for a positive HSV PCR result.

Methods. A retrospective review of 751 adults and children with meningitis and encephalitis at 9 hospitals in Houston TX from January 1 2005 to December 31 2010.

Results. Of 751 patients, 331 (44%) underwent CSF HSV PCR testing. Adults were more commonly tested than children (84% vs. 69%, P <0.001). Additionally, patients with more comorbidities and clinical findings of encephalitis (e.g., altered mental status, focal neurological findings, seizures) were more commonly tested for HSV (P <0.001). Patients tested for HSV were also more likely to be evaluated for West Nile Virus, receive empiric acyclovir and have worse outcomes (P <0.001). In total, 48 of 331 (14.5%) patients had a positive CSF HSV PCR. We measured the expression levels of hsp-miR-200b-3p and -200c-3p and TaqMan negative HCMV IHC test. We performed TaqMan real-time PCR for HCMV UL83 region to measure HCMV viral load in each FFPE. We selected among FFPEs with neither infection nor inflammation as well as (FFPEs) with cytopathic pathologic findings as well as positive immunohistochemical tissue had a lower expression level of hsp-miR-200b-3p and -200c-3p.

Conclusions. We confirmed that HCMV can be detected in CSF HCMV PCR in adults and children with meningitis and encephalitis. This study was aimed to evaluate whether HCMV-infected tissue had a lower expression level of hsp-miR-200b-3p and -200c-3p and regulate viral early (E) gene activation as well as propagate the subsequent steps of HCMV lytic replication. This study was aimed to evaluate whether HCMV-infected tissue had a lower expression level of hsp-miR-200b-3p and -200c-3p.

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1171. The Expression of hsp-miRNA-200b-3p and -200c-3p in Human Cytomegalovirus-infected Formalin-Fixed, Paraffin-Embedded Tissues

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Background. Human cytomegalovirus (HCMV), which exist as asymptomatic latent status, can cause the tissue invasive disease through reactivation in various immunocompromised conditions. Hsp-microRNA has a specific function of post transcriptional suppression through binding with 3' untranslated region (UTR) of mRNA. It is known that HCMV lytic replication. Immediate early protein 2 (IE2) protein. IE2 (pp86) plays an essential role to initiate transcriptional suppression through binding with 3'UTR of mRNA encoded by HCMV UL 122–123 region, which translate the immediate early protein 2 (IE2) protein. IE2 (pp86) plays an essential role to initiate regulation viral early (E) gene activation as well as propagate the subsequent steps of HCMV lytic replication. This study was aimed to evaluate whether HCMV-infected tissue had a lower expression level of hsp-miR-200b-3p and -200c-3p.

Methods. We collected the formalin-fixed, paraffin-embedded tissues (FFPEs) with 3'UTR of mRNA encoded by HCMV UL 122–123 region, which translate the immediate early protein 2 (IE2) protein. IE2 (pp86) plays an essential role to initiate regulation viral early (E) gene activation as well as propagate the subsequent steps of HCMV lytic replication.

Results. The expression levels of hsp-miR-200b-3p and -200c-3p were strongly correlated with 0.844 (P <0.001). The expression levels of hsp-miR-200b-3p and -200c-3p in HCMV-infected FFPEs (log, 3.50 ± 0.13 copies/µL) were significantly lower than normal tissues (log, 5.24 ± 0.12 copies/µL of input RNA, P <0.001). Also, HCMV-infected FFPEs showed lower levels of hsp-miR-200c-3p compared than normal tissues (log, 5.28 ± 0.18 vs. 7.81 ± 0.11 copies/µL of input RNA, P=0.025). The levels of miR-200b-3p and -200c-3p had the significant inverse correlation with HCMV VL (200-bp, spearman r=0.392, P <0.001 and 200-c-3p, spearman r=–0.355, P <0.001).

Conclusions. Expression of hsp-miR-200b-3p and -200c-3p could play a pathophysiologic role of development of HCMV tissue-invasive disease.

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1174. Molecular Investigation of an Ontario Mumps Outbreak using Whole Genome Sequencing

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Background. In early 2017 an outbreak of Mumps virus affected over 100 individuals in the province of Ontario, concurrent with multiple mumps virus outbreaks across North America. Traditional genotyping of mumps outbreaks relies on sequencing a portion of the small hydrophobic (SH) gene, but has limited capability to distinguish between strains of the same genotype. Most mumps cases in Ontario in recent years are of genotype G. We used a novel whole genome sequencing (WGS) protocol to perform a molecular epidemiological investigation of the outbreak.

Methods. Throat (n = 5) and buccal (n = 15) swabs positive by RT-PCR for SH or Fusion (F) gene targets were cultured in primary Rhesus monkey kidney cells. Cell viral extract underwent RT-PCR and subsequent PCR amplification using overlapping primer pairs to cover the entire 15 kilobase (kb) genome. The first 8 samples were amplified from viral extract underwent RT-PCR and subsequent PCR amplification using overlapping primer pairs to cover the entire 15 kb genome (kb) gene. We used a novel whole genome sequencing (WGS) protocol to perform a molecular epidemiological investigation of the outbreak.

Results. A total of 12 genomes were sequenced. The analysis identified 11 THV and 1 parainfluenza virus 3. Two distinct genotype G lineages comprised of 9 patients each and closely related to a 2009–2010 outbreak in Ontario and New York (Figure 1). Inter-lineage single nucleotide polymorphism (SNP) differences ranged from 25 to 31, whereas intra-lineage SNPs ranged from 0 to 8 SNPs. Two outlying sequences, of genotype C and G respectively, may represent sporadic introduction of virus from other areas. Time from virus isolation to SNP based analysis was approximately 4 days.

Conclusion. WGS of Mumps virus culture isolates using the PCR fragment method identified two distinct genotype G lineages in a large provincial outbreak. This method may aid public health authorities identify separate transmission chains in the case of large outbreaks.

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