

Turkey, ³Department of Infectious Diseases and Clinical Microbiology, Recep Tayyip Erdogan University, Rize, Turkey, ⁴Department of Infectious Diseases and Clinical Microbiology, Amasya University Sabuncuoglu Serefeddin Training and Research Hospital, Amasya, Turkey, ⁵Department of Medical Biochemistry, Karadeniz Technical University, Faculty of Medicine, Trabzon, Turkey

Session: 139. Adult Viral Infection
Friday, October 6, 2017: 12:30 PM

Background. Crimean-Congo hemorrhagic fever (CCHF) is a potentially fatal disease caused by a tick-borne virus from the Bunyaviridae family. Cytokines plays an important role in the pathogenesis of viral, bacterial, and immunologic diseases. This study aimed to investigate the role of TNF-alpha, IL-6, IL-10, and IFN-gamma levels in the severity of infection and clinical outcome of patients with CCHF.

Methods. Patients with confirmed CCHF were divided into two groups (severe cases: Patients who exhibited hemorrhage during their hospital stay, and mild/moderate cases: Patients who displayed no hemorrhage during their hospital stay). Demographic characteristics, laboratory tests on admission of all patients with CCHF were investigated, and serum TNF-alpha, IL-6, IL-10, and IFN-gamma levels were measured.

Results. A total of 154 patients with confirmed CCHF were investigated. Forty-six (29.9%) of these patients were in the severe group. In patients with severe CCHF, significantly higher serum levels of TNF-alpha (68.2 ± 23.5 ; $P = 0.008$) and IL-6 (73.1 ± 41.6 ; $P = 0.003$) were detected, compared with cytokine levels in patients who mild/moderate CCHF (Table 1). No differences in serum IL-10 and IFN-gamma levels between patients who severe CCHF and those who mild/moderate CCHF were detected ($P > 0.05$).

Table 1: Cytokine levels, demographic and laboratory characteristics in patients with severe and mild/moderate cases with CCHF.

Features	Severe cases <i>n</i> = 46	Mild/moderate cases <i>n</i> = 108	<i>P</i> -value
Age	50.6 ± 20.3	49.8 ± 21.0	0.682
Female gender, <i>n</i> (%)	31 (67.4)	63 (58.3)	0.291
TNF	68.2 ± 23.5	41.3 ± 17.4	0.008
IL-6	73.1 ± 41.6	38.0 ± 19.5	0.003
IL-10	6.32 ± 1.3	6.21 ± 1.4	0.753
IFN-gamma	145 ± 96	126 ± 92	0.664
WBC	3286 ± 5,602	2,275 ± 1,286	0.280
PLT	53,564 ± 36,520	98,065 ± 42,768	0.001
CRP	3.2 ± 2.6	1.1 ± 1.4	0.005
ALT	521 ± 482	208 ± 320	0.044
AST	869 ± 1.182	256 ± 215	0.016
CPK	1,138 ± 970	676 ± 835	0.007
LDH	1,800 ± 1,254	589 ± 271	0.002

Conclusion. Cytokines, chemokines, and other inflammatory mediators function in a manner, acting on many different cell types to regulate the host's immune response. When cytokines present in high concentrations, they might toxic or even lethal effects. In accordance with this view, we have detected increased serum TNF-alpha, IL-6 levels in the patients with severe CCHF.

Disclosures. All authors: No reported disclosures.

1034. Etiologic Involvement of Enterovirus and Human Bocavirus in Acute Flaccid Paralysis Cases in India

Manjari Baluni, Ph.D(Pursuing)¹; Dharamveer Singh, Ph.D(Pursuing)¹; Sneha Ghildiyal, PhD Pursuing²; Tanzeem Fatima, Ph.D (Pursuing)³; Amreen Zia, Ph.D(Pursuing)³ and Tapan Dhole, MD¹; ¹Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow, India, ²Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow, India, ³Microbiology, Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow, India

Session: 139. Adult Viral Infection
Friday, October 6, 2017: 12:30 PM

Background. Acute flaccid paralysis (AFP), characterized by the rapid onset of asymmetric paralysis, can be caused by a variety of viral infections or coinfections. Besides wild-type and revertant vaccine strains of polioviruses, several nonpolio enteroviruses, have also been associated with AFP. Enteroviruses (EVs) are RNA viruses in the family *Picornaviridae* comprising more than 100 serotypes that are divided into four species, human enteroviruses A to D. The clinical manifestations of EVs range from conjunctivitis, respiratory tract infection, myocarditis, meningitis, encephalitis, and neonatal sepsis, like illness. Human Bocavirus (HBoV), a newly classified member of the *Parvoviridae* family, has been detected frequently in feces of diarrhoeic children suggesting its possible etiological involvement in the disease.

Methods. Total 586 stool specimens were collected in 2016 from children suspected for AFP. Molecular method for targeting 5' untranslated region (UTR) and VP1 capsid region was used for detection of human enteroviruses (HEV), human boca viruses (HBoV) and scaffold viruses in direct clinical specimen.

Results. EV RNA was detected in 103 (17.6%) of 586 stool specimens by real-time RT-PCR targeting the highly conserved 5' UTR region. Out of them, 71 (12.11%) were NPEV, partially sequenced by VP1 which revealed the prevalence of echovirus (ECV) 19 (*n* = 6), ECV 11 (*n* = 7), ECV 18 (*n* = 4), ECV 33 (*n* = 5), ECV 29 (*n* = 1), ECV 25 (*n* = 2), ECV 24 (*n* = 3), ECV 3 (*n* = 3), ECV 14 (*n* = 2), ECV 13 (*n* = 1), ECV 2 (*n* = 1), ECV 20 (*n* = 2), ECV 27 (*n* = 4), ECV 6 (*n* = 2), CV A10 (*n* = 2), CV A9 (*n* = 1), CV A6 (*n* = 2), CV B4 (*n* = 1), CV B5 (*n* = 3), CV B6 (*n* = 3), EV 80 (*n* = 1), EV 83 (*n* = 1), EV 97 (*n* = 2).

Total 63 (10.75%) HBoVs were detected by real-time PCR which were further sequenced by VP1, consists of HBoV-1 (*n* = 8), HBoV-2 (*n* = 15), HBoV-3 (*n* = 9) and HBoV-4 (*n* = 5). Out of them 9 (1.5%) were detected as co infection with NPEVs. Phylogenetic analysis showed 0.9 - 5.6% divergence at nucleotide level among HBoVs.

Total 9 (1.5%) scaffold viruses was detected and characterized by VP1 sequencing. **Conclusion.** ECV and HBoV were found the main etiologic agent in children suspected with AFP. Molecular typing of these viruses is useful for characterizing emerging serotypes and their epidemiological investigation.

Disclosures. All authors: No reported disclosures.

1035. Frequency of Epstein-Barr Virus Genotypes in Pakistani Transgender SexWorkers

Sadia Salahud Din, Master; Biological Sciences, Gomal University, Dera Islamai Khan, Pakistan

Session: 139. Adult Viral Infection
Friday, October 6, 2017: 12:30 PM

Background. Transgender community large association with sex work has put them at a greater risk of contracting sexually transmitted infections (STIs).The aim of this study was to investigate the prevalence of Epstein-Barr Virus (EBV) genotypes in transgender sex workers (TSWs) of twin-cities of Pakistan. The high prevalence of EBV-2 genotype in sex workers has been previously reported. EBV genotypes were investigated in transgender sex workers to find out EBV-2 occurrence in Pakistani population.

Methods. A total of 86 transgender (Hijras) sex workers were randomly included in this study. Demographics, including age, the number of sex partners, sexual habits, and awareness about protective methods were obtained. Blood was collected from all subjects and The presence of Human Immunodeficiency Virus, Hepatitis B and C virus were determined by antibody strip testing. EBV detection and genotyping were performed by extracting genomic DNA from all whole blood samples. B-globin and EBNA-1 were amplified to assess the quality and presence of EBV DNA. Analysis of EBNA-2 genotyping was done by nested PCR.

Results. HIV was the most prevalent infection in 40 transgender sex workers (46.51%) followed by HCV in 15 (17.44%). Among HIV-seropositive TSWs, EBV genotype determination was only achievable in 60% of cases, where 62.5% were EBV-1, 29.16% of EBV-2 and co-infection was found in 8% samples. Among HIV-negative individuals, 78% were EBV-1, whereas EBV-2 genotype and co-infections were absent. All non-typable samples were amplifiable for the EBNA-1 gene in both populations, confirming EBV genome in the samples.

Conclusion. EBV-1 was the most common genotype of EBV in HIV seropositive and seronegative TSWs but the high occurrence of EBV-2 and co-infection of both types was observed only in HIV seropositive individuals. This is the first report of frequency of EBV infections in the HIV-positive transgender community of Pakistan.

Disclosures. All authors: No reported disclosures.

1036. Risk Factors for Herpes Zoster: a Systematic Review and Meta-Analysis

Kosuke Kawai, ScD¹ and Barbara P. Yawn, MD, MSc, MSPH, FAAFP²; ¹Boston Children's Hospital and Harvard Medical School, Boston, Massachusetts, ²Department of Research, Olmsted Medical Center, Rochester, Minnesota; University of Minnesota, Minneapolis, Minnesota

Session: 139. Adult Viral Infection
Friday, October 6, 2017: 12:30 PM

Background. Well-recognized risk factors for herpes zoster (HZ), commonly known as shingles, are age and immunosuppression. Numerous studies have investigated other various risk factors for HZ in recent years. The objective of our study is to systematically review studies examining risk factors for HZ and discuss implications based on the updated evidence.

Methods. We performed a literature search using PubMed, Embase, and Web of Science and included studies that examined risk factors for HZ. Random effects model was used to summarize the risk ratio (RR) or odds ratio (OR) and 95% confidence interval (CI).

Results. Of the 3450 studies screened, we included 84 studies in the systematic review and conducted meta-analysis in 62 studies. Women are at increased risk of HZ compared with men (pooled adjusted RR = 1.31; 95% CI: 1.27, 1.34). Black individuals have almost half the risk of HZ than White individuals (pooled RR = 0.54; 95% CI: 0.47, 0.63). Family history was found to be a risk factor for HZ (pooled OR = 3.59; 95% CI: 2.39, 5.40). Autoimmune diseases, including rheumatoid arthritis (pooled RR = 1.67; 95% CI: 1.41, 1.98) and systemic lupus erythematosus (RR = 2.10; 95% CI: 1.40, 3.15), were associated with an elevated risk of HZ. Other comorbidities were associated with an increased risk of HZ, with the pooled RRs ranging from 1.25 (95% CI: 1.13, 1.39) for asthma to 1.30 (1.17, 1.45) for diabetes mellitus, and 1.31 (95% CI: 1.22, 1.41) for chronic obstructive pulmonary disease. Statin use was also