Crimean–Congo hemorrhagic fever (CCHF) is a potentially fatal disease caused by a tick-borne virus from the Bunyaviridae family. Cytokines play 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 ± 23.3; P = 0.008) and IL-6 (73.1 ± 41.6; P = 0.003) were detected, compared with cytokine levels in patients who had mild/moderate CCHF (Table 1). No differences in serum IL-10 and IFN-gamma levels between patients who severe CCHF and those who had mild/moderate CCHF were detected (P = 0.05).

**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.

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

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**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 seizures, like illness. Human Bocavirus (HBoV), a newly classified member of the Parvoviridae family, has been detected frequently in feces of diarrheic 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 VPI capsid region was used for detection of human enteroviruses (HEV), human bocavirus (HBoV) and saffold 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 3' UTR region. 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 = 4), ECV 24 (n = 3), ECV 3 (n = 3), ECV 14 (n = 2), ECV 13 (n = 1), ECV 2 (n = 1), ECV 1 (n = 1), ECV 22 (n = 2), ECV 27 (n = 2), ECV 4 (n = 2), A6 (n = 2), A6 (n = 1), CV A6 (n = 1), 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 coinfection with NPEVs. Phylogenetic analysis showed 0.9 - 5.6% divergence at nucleotide level among HBoVs. Total 9 (1.5%) saffold viruses was detected and characterized by VPI sequencing. Coinfections of EV 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.

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### 103.5. Frequency of Epstein–Barr Virus Genotypes in Pakistani Transtraniger SexWorkers

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**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) in the city of Karachi, 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. The presence of Human Immunodeficiency Virus, Hepatitis B and C virus were detected by antibody strip testing. EBV detection and genotyping were performed by extracting genomic DNA from all available 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.** HSV was the most prevalent infection in 40 transgender sex workers (46.51%) followed by HCV in 15 (17.44%). Among HIV-seropositive TSWs, EBV genotyping 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.

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

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**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 ORs 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