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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 n = 46	Mild/moderate cases n = 108	P-value
Age	50.6 ± 20.3	49.8 ± 21.0	0.682
Female gender, n (%)	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.

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1034. 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 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.

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

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1036. 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 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

associated with a modest increased risk of HZ (pooled RR = 1.14; 95% CI: 1.11, 1.17). Recent physical trauma increased risk of HZ by almost two-fold (pooled RR = 2.56; 95% CI: 1.97, 3.33).

Conclusion. In addition to age and immunocompromised conditions, our review shows that female sex, race/ethnicity, family history, and comorbidities are risk factors for HZ. Efforts are needed to better understand risk factors and to increase the uptake of zoster vaccination.

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1037. Herpes-Zoster Infection in a Tertiary Hospital in Brazil

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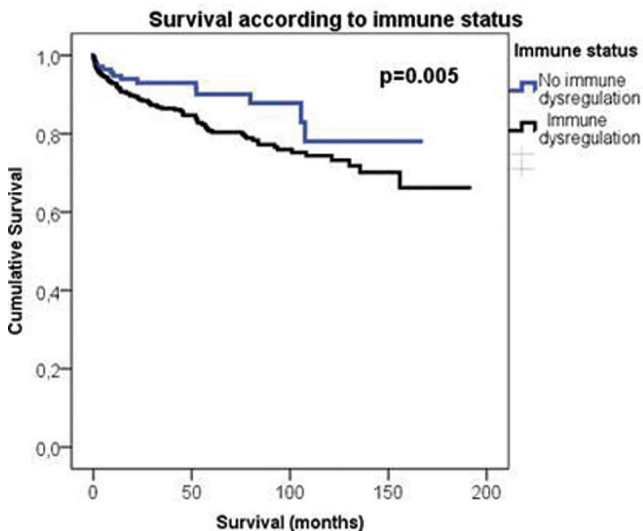
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Background. herpes zoster (HZ) is a common infection with potential complications requiring hospital care, especially for patients with multiple comorbidities. However, there is little information on HZ from hospital registries.

Methods. we searched for hospital-based records of B02 code (ICD-10) between March 2000 and January 2017 at Hospital de Clinicas de Porto Alegre, a tertiary, university hospital in south Brazil. To avoid misclassifications, we considered clinical evaluation for the diagnosis of cutaneous HZ and postherpetic neuralgia (PHN), ophthalmological evaluation for ophthalmic HZ and the combination of clinical, radiologic and cerebrospinal fluid analysis for HZ meningo-encephalitis (ME). We analyzed conditions associated with immune dysregulation, complications, length of hospital stay, and mortality. Chi-square test and Kaplan-Meier estimator were used for statistical analyses. $P < 0.05$ was considered statistically significant.

Results. there were 847 records for this period, of which 801 were confirmed according to our criteria and included in the analysis. Most patients were women ($n = 448$; 60%), with an average of 48.8 years, standard deviation of 22.2. There were more diagnoses in the inpatients group (74.4%), and fewer in the emergency room (22.4%) and outpatient (3.3%). The median length of hospital stay was 7 days (2-10, P25-P75) when HZ was the main reason for admission. Most patients presented cutaneous HZ ($n = 743$, 92.8%). There were fewer cases of PHN (6.1%), ophthalmic HZ (7.6%) and ME (4.1%). Seventy percent had some kind of immune dysregulation; more frequently AIDS (31%), use of immunosuppressive agents (18.7%) and malignant disease (16.2%). We followed the subjects for a median of 28.2 (2.8-77.5) months. During this period, there were 105 (13.1%) deaths. Five were related to HZ ME. The 30-day overall mortality rate was 1.5%. There was no statistical difference in cumulative survival (graph 1, $P = 0.05$) or incidence of complicated forms for patients with or without immune dysregulation.

Conclusion. our sample was characterized by a majority of inpatient diagnoses. The 30-day mortality rate was lower than reported in similar studies, but there was a relevant impact of complicated forms in mortality and sequelae.



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1038. Epidemiology of Influenza Viruses in Canada over the 2011–2012 to 2013–2014 Seasons: A Study from the Serious Outcomes Surveillance (SOS) Network of the Canadian Immunization Research Network (CIRN)

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Background. Influenza virus activity varies seasonally and within season. Epidemiology of serious influenza outcomes is contingent on the prevalent circulating strain/s and susceptible age group/s. Given the strain variability over the 2011–2012 through 2013–2014 seasons in Canada, this study examined the clinical and epidemiological profiles of different influenza strains causing adult hospitalizations.

Methods. During these three influenza seasons, the Serious Outcomes Surveillance (SOS) Network of the Canadian Immunization Research Network (CIRN) enrolled adults hospitalized with acute respiratory illness across Canada. Nasopharyngeal swabs (NPs) from influenza cases were tested for strain characterization using real-time reverse transcriptase polymerase chain reaction (rRT-PCR). A primary assay differentiated A and B influenza viruses. Subsequently, influenza A viruses were subtyped as H1N1 or H3N2, and influenza B lineages were differentiated as Victoria or Yamagata. Laboratory results were compared with patient demographic data and clinical outcomes.

Results. Over three consecutive influenza seasons, 3394 cases of hospitalized acute respiratory illness were laboratory-confirmed as influenza. At 72.4%, influenza A was predominant across all seasons, while influenza B caused 27.6%. Most of the influenza A cases were due to H3N2 (58.7%), while H1N1 accounted for 41.3%. For influenza B, the Yamagata lineage was predominant at 88.4% whereas the Victoria lineage accounted for 11.6%. Outcome analyses are presented for each influenza A subtype and influenza B lineage, overall and per season. Considering serious outcomes in patients ≥ 65 , higher proportions of patients hospitalized with the H1N1 strain experienced intensive care unit (ICU) admission and need for mechanical ventilation, while higher proportions of patients hospitalized with B/Yamagata and H3N2 died within 30 days of admission.

Conclusion. Comprehensive collection of surveillance data paired with NP specimens by the CIRN SOS Network was conducive to broader understanding of influenza strain activity and associated outcomes at the subtype and lineage level. This data is important to make informed recommendations for the use of multicomponent influenza vaccines.

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1039. Co-circulation of Influenza A and B During the 2016–2017 Influenza Season at Rush University Medical Center

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