Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

PS04.03 (285)

SARS-CoV-2 in pets of infected family groups in a severely affected region in Spain

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Purpose: The COVID-19 pandemic has caused an unprecedented health crisis with devastating effects. Current evidence suggests that SARS-CoV-2 could have an animal origin. Many uncertainties about the behaviour of the virus still persist, and understanding all the keys of this epidemic requires an interdisciplinary One Health approach spanning the human and animal health sectors. The closest coexistence between people and animals occurs in large cities. This study aims to identify the epidemiology (infection rate, risk habits, etc...) and evolution of the disease in pets that have coexisted during the confinement with family groups affected by the disease in areas of high population density and high disease incidence, i.e. Madrid.

Methods & Materials: A network of veterinary clinics was created to provide sampling points for the pets. The family groups included both health workers from the collaborating hospitals and affected pet owners informed through the network of clinics.

Results: Epidemiological and clinical data were collected from 60 family groups and their pets. An epidemiological questionnaire and sample collection (oral and nasal swabs, faeces and blood) were carried out on each pet. The samples were analyzed by RRT-PCR and ELISA. Of the 55 pets analysed (17 cats and 38 dogs), 5 cats presented antibodies. This seroprevalence is in agreement with that shown by Patterson et al, 2020 in cats in Italy in highly affected areas.

Conclusion: This study intends to extend the knowledge of the epidemiology and evolution of the disease in pets.

PS04.04 (485)

Prolonged shedding of SARS-CoV-2 at high viral load amongst hospitalised immunocompromised persons living with HIV in South Africa

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Purpose: There is limited information on SARS-CoV-2 shedding duration amongst persons living with HIV (PLWH). We hypothesised that PLWH shed SARS-CoV-2 for longer periods and at higher viral load than HIV-uninfected persons.

Methods & Materials: From May through December 2020, we conducted a prospective cohort study at 17 hospitals in South Africa. Patients aged >18 years hospitalised with symptomatic COVID-19 were enrolled and followed up every two days with nasopharyngeal/oropharyngeal (NP/OP) swabs until cessation of SARS-CoV-2 shedding (two consecutive negative NP/OP swabs). Real-time reverse transcription polymerase chain reaction (rRT-PCR) testing for SARS-CoV-2 was performed and Cycle-threshold (C_t) values <30 were considered a proxy for high SARS-CoV-2 viral load. Accelerated time-failure Weibull regression models were used to assess factors associated with prolonged shedding.

Results: Of 2,175 COVID-19 patients screened, 300 were enrolled and 258 individuals (156 HIV-uninfected and 102 PLWH) had >1 swabbing visit (median visits 5 (range 2-21)). Median time to cessation of shedding was 13 days (inter-quartile range (IQR) 6-25) and did not differ by HIV status. Among PLWH, when adjusting for CD4 count and obesity, those not currently taking antiretroviral therapy were more likely to have prolonged SARS-CoV-2 shedding (median 13 days (IQR 6-37) vs 10 days (IQR 4-22) on antiretroviral therapy, adjusted hazard ratio (aHR) 0.03, 95% confidence interval (CI) 0.002-0.38, p=0.007).

Amongst a subset of 94 patients with initial respiratory sample C_t values <30, median time of shedding at a high SARS-CoV-2 viral load was 8 days (IQR 4-17). Adjusting for age and glucocorticoid use, PLWH with a CD4 cell count<200 cells/µl shed at high SARS-CoV-2 viral loads for longer (median 27 days, IQR 8-43, aHR 0.14, 95% CI 0.07-0.28, p<0.001), whereas PLWH with CD4 cell count>200 cells/μl shed at high SARS-CoV-2 viral loads for a similar time period (median 7 days, IQR 4-10, aHR 1.14, 95% CI 0.56-2.31, p=0.713), compared to HIV-uninfected persons (median 7 days, IQR 4-13).

Conclusion: PLWH not on treatment or with CD4 cell count<200 shed SARS-CoV-2 for a longer duration and at a higher SARS-CoV-2 viral load than HIV-uninfected persons. Better HIV control may facilitate quicker clearance of SARS-CoV-2.

PS04.05 (610)

Population Mobility and Socioeconomic Indicators in California, USA and Ontario, Canada during the COVID-19 Pandemic

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Purpose: To explore the extent that socioeconomic indicators influenced mobility of populations during the COVID-19 pandemic in two jurisdictions.

Methods & Materials: We used anonymized, population-aggregated mobile-device location data to estimate dynamic

changes in population mobility patterns across the province of Ontario, Canada and the state of California, U.S.A. Data from the Ontario-Marginalization Index at the Census Subdivision (CSD) level, as well as the California Healthy Places Index (HPI) at the Census Tract (CT) level, were used to determine the census geographical units in the lowest and highest quantiles of socioeconomic indicators during the COVID-19 pandemic.

Ontario was under three province-wide stay-at-home orders between March 17, 2020 and June 2, 2021. California was under state-wide stay-at-home orders from March 19, 2020 to January 25, 2021. Weekly data from March 15, 2020 to June 19, 2021 were analyzed for Ontario, and weekly data were analyzed from March 15, 2020 to March 20, 2021 for California. We used the percentage of time spent away from home as the indicator for mobility and analyzed differences in mobility trends between the populations grouped by material deprivation score (Ontario) and HPI scores.

Results: In Ontario, populations with highest material deprivation spent an average of 25.7% of time away from home, while the populations with lowest material deprivation spent an average of 22.6% of their time away from home (difference: 3.1%, p <0.001) across the entire duration of the COVID-19 pandemic.

Similarly, in California, the least advantaged populations spent an average of 30.0% of time away from their home, while the most advantaged populations spent 24.3% of their time away from home (difference: 5.7%, p <0.001).

Conclusion: Across both geographical locations, the least advantaged populations observed highest mobility compared to the most advantaged populations throughout the pandemic. This indicates that populations in communities with the least advantage in Ontario and California may have less ability or inadequate resources to comply with stay-at-home orders, leading to increased risk of COVID-19 exposure among these more mobile populations. Strategies to protect those most at risk of exposure to COVID-19 are imperative for controlling spread within communities.

PS04.06 (673)

Characteristics and Early Predictors of Intensive Care Unit Admission among COVID-19 Patients in Qatar

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Purpose: This study aimed to explore the early predictors of intensive care unit (ICU) admission and in-hospital mortality among patients diagnosed with Coronavirus disease (COVID-19).

Methods & Materials: This was a case-control study of adult patients with confirmed COVID-19. Cases were defined as patients admitted to ICU during the period February 29 - May 29, 2020. For each case enrolled, one control was matched by age and gender. Univariate and multivariate logistic regression models were used to identify the predictors for ICU admission and in-hospital mortality among the COVID-19 patients.

Results: A total of 1560 patients with confirmed COVID-19 were included. Each group included 780 patients with a predominant male gender (89.7%) and a median age of 49 years

(interquartile range, IQR=18). Predictors independently associated with ICU admission included having cardiovascular disease (CVD) (adjusted odds ratio (aOR)=1.64, 95% confidence interval (CI): 1.16 - 2.32, p= 0.005), diabetes (aOR=1.52, 95% CI: 1.08 - 2.13, p= 0.016), body mass index $\geq$30 kg/m2 (aOR=1.46, 95% CI: 1.03-2.08, p= 0.034), lymphocytes $\leq 0.8 \times 10^3/\mu L$ (aOR=2.69, 95% CI: 1.80-4.02, p<0.001), aspartate aminotransferase (AST) >120 U/L (aOR= 2.59, 95% CI: 1.53-4.36, p<0.001), ferritin >600 $\mu g/L$ (aOR=1.96, 95% CI: 1.40-2.74, p<0.001), C-reactive protein (CRP) >100 mg/L (aOR=4.09, 95% CI: 2.81-5.96, p<0.001), and dyspnea (aOR=2.50, 95% CI: 1.77-3.54, p <0.001). Similarly, significant predictors of mortality included CVD (aOR=2.16, 95% CI: 1.32- 3.53, p=0.002), diabetes (aOR=1.77, 95% CI: 1.07-2.90, p=0.025), cancer (aOR=4.65, 95% CI: 1.50-14.42, p= 0.008), lymphocytes ≤ 0.8 x,$10^3/\mu L$ (aOR=2.34, 95% CI: 1.45-3.78, p= 0.001), and AST >120 U/L (aOR= 1.89, 95% CI: 1.04-3.43, p=0.036).

Conclusion: Having CVD, diabetes, lymphopenia, and increased AST were independent predictors for both ICU admission and in-hospital mortality in patients with COVID-19. In addition, obesity, high ferritin, and CRP levels were also associated with increased risk of ICU admission, while cancer was strongly associated with in-hospital mortality. Early identification and monitoring of patients at risk is essential in planning the level of care needed to prevent delay in medical intervention.

PS04.07 (935)

Early phase of COVID-19 epidemic in Albania

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Purpose: The index case of COVID-19 was diagnosed on March 8th with symptoms onset identified on March 6th, with a travel history within Italy. During the first month the number of identified imported cases was 25. The first 291 laboratory-confirmed cases of the COVID -19 outbreak are used to characterize the epidemiological pattern and estimate the epidemiological parameters such as serial interval, basic and effective reproduction numbers and to evaluate the effectiveness of first timely disease spread containment measures.

Methods & Materials: Epidemiological data were collected through case-based disease COVID -19 surveillance, outbreak investigation and contact tracing data for every confirmed case comprising information on demographics, travel history, date of symptom onset, clinical symptoms, laboratory results, hospitalization, and contacts details. Estimates of the reproduction number and serial interval were performed in R statistical software using R packages developed by the R Epidemics Consortium.

Results: Public health authorities were able to identify and trace an average of 10 close contacts per for every positive case. The number of transmission events reported per infector ranges from 1 to 16, with 30% having two secondary cases per infector. The median value of every positive case was with 2 secondary infected cases (mean 3.3, standard deviation 3.2). Based on 43 pairs of primary infectors and secondary cases the mean serial interval was estimated 4.8 days (standard deviation 3.9). The basic reproduction number has been estimated at 2.19 (95% CI 1.6 to 2.8), while effective reproduction number showed a decreasing trend by the second week and reaching a plateau around the critical value during the first month. The social distance measures such as were im-