PS04.03 (285)

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

A. Mendez[1], M.A. Jiménez-Clavero[2], C. Calvo[1], E. Pérez-Ramírez[2], J. Fernández-Pinero[2], F. Llorente[2], T. Sainz[1], P. Aguilera-Sepúlveda[2], S. Alcolea[1], L. Escolano[1], C. Cano[2], I. Novoa[3], A. De la Torre[3], I. Iglesias[3,*]

[1] *La Paz University Hospital, Madrid, Spain*
[2] *INIA: Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Emerging and Transboundary diseases, Madrid, Spain*
[3] *INIA: Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Epidemiology and environmental health, Madrid, Spain*

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

S. Meiring[1,2,*], S. Tempia[2,3,4], J. Bhiman[3,5], J. Kleynhans[2,3], A. Buys[3], M. Makhasi[3], M. Mcmorrow[4], J. Moyes[3], V. Quan[1], S. Walaza[3], M. Du Plessis[3,5], N. Wolter[3,5], A. Von Gottberg[3,5], C. Cohen[1,3]

[1] *National Institute for Communicable Diseases, a division of the National Health Laboratory Service, Division of Public Health Surveillance and Response, Johannesburg, South Africa*
[2] *University of the Witwatersrand, School of Public Health, Faculty of Health Sciences, Johannesburg, South Africa*
[3] *National Institute for Communicable Diseases, a division of the National Health Laboratory Service, Centre for Respiratory Diseases and Meningitis, Johannesburg, South Africa*
[4] *Centers for Disease Control and Prevention, Influenza Division, Atlanta, Georgia, United States*
[5] *University of the Witwatersrand, School of Pathology, Faculty of Health Sciences, Johannesburg, South Africa*

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

A. Marwah[1,*], J. Feldman[1], R. Moineddin[2], A. Thomas[1]

[1] *BlueDot Global, Toronto, Ontario, Canada*
[2] *University of Toronto, Toronto, Ontario, Canada*

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