

**PS03.03 (536)**

**Changing Geographic Distributions of *Coccidioides* spp. in the United States: A Narrative Review of Climate Change Implications**

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**Purpose:** Analysis of alterations in the United States prevalence of coccidiomycosis in geographic regions historically considered to not be endemic for the *Coccidioides* spp. pathogen taken with an evaluation of changing climate patterns within those areas.

**Methods & Materials:** The databases MEDLINE, Google Scholar, PubMed, and CINAHL were searched for English-language sources with combinations of the following keywords: climate change, *Coccidioides*, distribution, and United States with relevant synonyms. Preference was given within the inclusion criteria to sources published in the past 20 years. The bibliographies of the retrieved publications were also searched. Exclusion criteria included sources relative to areas outside the continental United States.

**Results:** Although *Coccidioides* species have classically been recognized as endemic to the southwestern United States, isolates have been found far outside this area and recent investigations have demonstrated a growing endemic zone. Ecological and outbreak data supports the conclusion that these findings result from a growing endemic range that is estimated to be as far east as Texas and as far north as Washington State. Investigations point to climate change as the underlying cause primarily via regional climate changes and large dust storms.

**Conclusion:** The geographic distribution of *Coccidioides* fungus is known to be larger than classically recognized or potentially considered in the formation of diagnostic differentials in the clinical setting. Timely diagnosis, appropriate treatment approaches, and accurate reporting for public health surveillance rely on a recognition of endemic range expansion. Physician education (via medical school curriculums and continuing education offerings), interprofessional team-based approach, and enhancement of surveillance in locations in potentially geographically novel areas are appropriate measures in improving the identification of coccidiomycosis cases.

Case studies from local outbreaks and natural disasters support adding coccidioidomycosis to a list of other infectious diseases (e.g., those that are vector borne) whose endemic areas are spreading due to climate change. Recognition of underlying climate change related mechanisms should also prompt steps to reduce environmental spread where mitigation is possible. Current climate model predictions support an expected increase in *Coccidioides* spp. infection; further research is recommended to clearly define the relationship between climate change and *Coccidioides* spp. geographic expansion.

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**PS03.04 (298)**

**Climate change, environmental factors and dengue in Africa**

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**Purpose:** The impact of climate change on the distribution of dengue rises controversy and debate; despite the existence of ev-

idence about the effect of changes in certain environmental variables have on its epidemiology. Africa, where data on dengue is limited, is one of the continents most affected by climate change. The objective is to evaluate the relationship between meteorological factors, climate change and dengue epidemiology in Africa through a systematic review.

**Methods & Materials:** We carried out a systematic review considering all the articles indexed in PubMed, Scopus, Embase and CENTRAL. The study area was Africa. The disease under study was dengue and its vector *Aedes*. Standard terms for climate change and/or environmental factors were included in the search.

**Results:** Nineteen studies met the inclusion and exclusion criteria, most of them using data on a global level (68%) and not just from Africa. 47% concluded that climate change is affecting the prevalence and/or incidence of dengue, compared to 42% that did not find such a relationship. According to 37%, the prevalence of dengue will increase in the coming decades, while it will decrease according to 11%. Sixty three percent showed an increase in the spread of dengue. Temperature and rainfall were the most frequently analyzed environmental factors. Most studies scored 11-12 (good-very good) in the quality assessment.

**Conclusion:** Half of the studies showed a positive relationship between observed or predicted results and climate change. We observed methodological heterogeneity and most studies had important limitations. We believe that it would be necessary to improve the surveillance of this disease and standardize the study approach to be able to contrast in the long term the effect of climate change and environmental variables in the epidemiology of dengue in Africa.

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**Topic 04: COVID-19 Big Data, Surveillance and Contact Tracing**

**OP04.01 (104)**

**COVID-19 Cluster among 2020 Matric Rage Festival Attendees, KwaZulu-Natal Province, South Africa, November–December 2020**

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**Purpose:** South Africa moved to lockdown alert Level-1 on 20 September 2020 midnight, lockdown regulations were relaxed, gatherings were permitted with the number of people not exceeding 50% of normal venue capacity. The National Institute for Communicable Diseases was alerted by a clinician of a number of COVID-19 cases amongst young people who reportedly have attended the 2020 Matric Rage Festival, KwaZulu-Natal Province. This prompted an investigation to ascertain the existence of a COVID-19 cluster related to attendance of Rage Festival (Rage) and provide epidemiological characteristics of the cluster.

**Methods & Materials:** We conducted a retrospective cohort investigation amongst 2 253 attendees. A cluster was defined as the identification/presence of  $\geq$ two laboratory confirmed COVID-19 cases amongst individuals who attended the Rage between 27 November to 4 December 2020. COVID-19 confirmed cases were identified using the organizers ticket purchaser and crew record list and the national COVID-19 laboratory confirmed cases line-list. A standardized questionnaire was circulated to 1814 attendees using Google Forms. A case was defined as any person within the cohort with SARS-CoV-2 RT-PCR positive results.

**Results:** Of the 2 253 attendees, 848 (37.6%) cases were identified, of which 846 (99.8%) were revelers and two were crew members (0.2%). Age ranged from 16 to 58 years (Median: 18, IQR: 18–18). The 15–19-year-old age group accounted for 802 (94.6%) of the cases, while 53.0% (425/802) were males. Most cases were from Gauteng (66.2%,561/848), followed by KwaZulu-Natal (30.0%, 254/848). Two of the attendees had positive SARS-CoV-2 results approximately 7–10 days before the festival. The questionnaire response rate was 1.0% (19/1814). Revelers attended other large events and private parties and mask wearing and social distancing was not always practiced.

**Conclusion:** Although organizers observed COVID-19 precautions and protocols; social distancing and mask wearing were compromised. Factors such as mass gathering without using appropriate personal protective equipment, crowded spaces, poor hygiene and ventilation may have produced a conducive environment for SARS-CoV-2 transmission. The study limitations included delayed questionnaire circulation, lack of contact tracing data to determine secondary attack rate, and lack of clinical information amongst cases. Non-pharmaceutical interventions are effective recommended prevention and control measures.

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**OP04.02 (797)**

**Excess Deaths during COVID-19 pandemic in Alberta, Canada**

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**Purpose:** To determine if there was excess mortality in Alberta, Canada during the pandemic. We sought to confirm if excess mortality affected all age groups equally and determine what proportion of excess deaths is directly related to COVID-19.

**Methods & Materials:** Excess mortality was calculated by comparing observed to expected number of deaths. Monthly Crude death rates (CDR) for 2015 to 2019 was calculated by dividing monthly deaths by the mid-year population. Expected deaths was calculated by multiplying mean monthly CDR by the mid-year population in 2020 and the projected mid-year population in 2021 to calculate expected deaths. Age-adjusted monthly mortality rates for January 2020 to March 2021 was compared to the previous 5 years.

**Results:** From January 2020 to May 2021 there was a 11% excess mortality corresponding to an average of 248 monthly excess deaths with a minimum of 49 deaths in January 2020 (no COVID-19-related deaths) and a maximum of 781 excess deaths in Decem-

ber 2020. COVID-19 related deaths (n=2266) account for 53.8 % of the total excess deaths (n=4214) that occurred in the 17 months.

Increase in all cause -excess deaths was proportionately higher, and in significantly greater numbers, in the younger age groups. Deaths directly linked to COVID-19 were: 8 (20–29 years), 12 (30–39 years), 32 (40–49 years), 74 (50–59 years), 225 (60–69 years), 409 (70–79 years), and 1274 (>80 years)

Statistically significant increases in monthly drug poisoning deaths from March 2020 to April 2021 with a total of 1819 deaths. Excess 731 drug poisoning deaths representing 18.2 % of total all-cause excess mortality affected mostly those age 25–60. 53.9 % of all excess deaths is directly related to COVID-19 and 18.2% are drug poisoning related excess deaths. The remaining 27.9 % of excess deaths are likely due other factors such as limited access to urgent medical care.

**Conclusion:** There was statistically significant increase in all-cause mortality. Although older adults are more likely to die of COVID-19, there was massive increase in non-COVID-19 related mortality among the youth. These should be factored in public policy decisions on epidemic/pandemic management.

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**OP04.03 (153)**

**Implementing a SARS-CoV-2 Early Warning System in Valencia (Spain) and its Correlation with Epidemiological Indicators**

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**Purpose:** To implement a SARS-CoV-2 wastewater surveillance system in Valencia and study the correlation between SARS-CoV-2 concentration levels and epidemiological indicators.

**Methods & Materials:** The working strategy developed in the municipality of Valencia consisted of monitoring wastewater effluents collected by 790,000 people. The city was divided into 24 different hydraulic sectors. 3,023 samples of untreated wastewater were collected and analysed between May 2020 and May 2021. RNA extraction from sewage material was carried out using the NucleoSpin RNA virus Kit. SARS-CoV-2 RNA detection was performed by RT-qPCR using One-Step PrimeScript™ RT-PCR Kit (Perfect Real Time), targeting the nucleoprotein (N), N1 and N2 fragments, and envelope protein (E) gene. Mengovirus RNA recovery rates were used as quality assurance parameters according to ISO 15216-1:2017.

**Results:** A total of 2,169 samples were positive for SARS-CoV-2 RNA material. SARS-CoV-2 variations were detected throughout the entire study evidencing trends during the first, second and third wave. As the National State of Emergency ended (June 2020), SARS-CoV-2 values began to increase reaching the first and most significant concentration spike of the study (20th–26th of July 2020), with a weekly average aggregate concentration of 34,5M GC/L (an increase of 2 units in the log scale). This translated in the worsening of epidemiological indicators (number of cases, hospitalizations, deaths and cumulative incidence (CI)), which maintained a stable increase until a second spike was detected during an important bank holiday in October (9th–12th), where the concentration changed from 28M GC/L to 345M GC/L in a 3-day period while the city was registering 1,100 new weekly cases and a CI of 200 cases/100,000 residents. Finally, a third wave placed Valencia with the worst historical epidemiological data (6,545 new cases; 1,000 new hospitalizations; CI= 1,318,04 cases/100,000 in-