

demological characteristics or trend of diseases qualitatively and to provide early warning of epidemics. In this study, we validated the use of Google queries of scarlet fever using routine surveillance data, and inferred disease trend of scarlet fever in other countries/regions where specific surveillance for scarlet fever is not available.

Methods & Materials: We collected scarlet fever surveillance data from Hong Kong, England, Germany and Taiwan from where surges in scarlet fever incidence have been reported. We obtained language-specific Google queries of scarlet fever corresponding to the time period where surveillance data was available in each country/region. We constructed Poisson regression models including trends and seasonality and tested for their significance using likelihood ratio tests, and also tested the presence of change point, separately for scarlet fever surveillance data and Google queries. Similar methods were applied to characterize Google query data for scarlet fever in other countries/regions.

Results: We identified change points in scarlet fever incidence resulting in long-term level changes from Hong Kong and England in 2011 and 2014, respectively. Although no change point was detected in Germany and Taiwan, both showed increasing trends. The overall characteristics identified from Google query data were consistent with those from existing surveillance data in each country/region, such as trend, seasonality and long-term change in disease incidence.

Among 63 countries/regions studied, we identified level changes in Argentina, China, Egypt, Ireland, South Korea, Philippines, Serbia, Singapore and United Arab Emirates. 38/63 (60.3%) of the countries/regions showed increasing trends. Seasonality was frequently observed across countries/regions.

Conclusion: We validated Google queries of scarlet fever using 4 countries/regions with existing surveillance data. Digital data suggested increased scarlet fever incidence globally especially in Europe and some parts of Asia. Our findings highlight the potential use of digital surveillance for detection of re-emerging and emerging diseases and may strengthen pandemic preparedness and response.

<https://doi.org/10.1016/j.ijid.2021.12.235>

PS21.06 (129)

Community Based Surveillance in Somaliland: Analysis of the Functionality and Effectiveness using the CBS Platform Nyss

J. Jung^{1,*}, A.H. Beledi², N. Riedel³, A.O. Ahmed⁴, T.M. Larsen³

¹Norwegian Red Cross, Nairobi, Kenya

²Somali Red Crescent Society, Hargeissa, Somalia

³Norwegian Red Cross, Oslo, Norway

⁴Norwegian Red Cross, Hargeissa, Somalia

Purpose: The Somali Red Crescent Society (SRCS) and the Norwegian Red Cross have implemented Community Based Surveillance (CBS) in Somaliland in 2018. This retrospective study analyses the functionality and effectiveness of the CBS programme using data from the innovative, custom created software platform Nyss. Nyss enables real-time CBS data collection and notifications, as well as management and analysis of reports submitted via SMS by community volunteers.

Methods & Materials: Aggregated and anonymous data from routine CBS activities between March and December 2020 of Togdheer region in Somaliland were the basis for the descriptive analyses. CBS indicators of completeness and accuracy of reporting, data quality, timeliness of verification, and effectiveness were evaluated. Analyses were done directly in Nyss or Excel.

Results: In average per month, 90% of the targeted villages were covered by a SRCS volunteers reporting on CBS at least once per month. Weekly completeness of reporting was at 47% in average. Most reports were sent in the correct format (95%). Health risk reports were accurately matching the community case definition with an average of 88%. Seventy eight percent of the alerts were notified to the public health authorities within 24 hours, the mean was at 2 days and 21 hours. Actions were taken in 91% of the escalated alerts.

Conclusion: The Nyss platform has been demonstrated to support rapid CBS programme monitoring, surveillance of the health situation in the community as well as early warning of potential health risks to SRCS and MoH staff. Though further efforts need to be taken to understand how Nyss is used in the field and to improve the reporting strategy and documentation to better support, monitor and analyse the programme implementation. The results are beneficial for CBS in Somaliland and other settings. Further development of M&E indicators and the CBS platform Nyss are required.

<https://doi.org/10.1016/j.ijid.2021.12.236>

PS21.07 (342)

Tracking SARS-CoV-2 in urban wastewater samples during the first wave of COVID-19 epidemic in Lombardy (Italy)

L. Pellegrinelli^{1,*}, S. Schiarea², V. Primache¹, C. Galli¹, L. Bubba¹, F. Mancinelli², D. Cereda³, E. Ammoni³, E. Pariani¹, S. Castiglioni², E. Zuccato², S. Binda¹

¹University of Milan, Department of Biomedical Sciences for Health, Milan, Italy

²Istituto di Ricerche Farmacologiche Mario Negri IRCCS, Department of Environmental Sciences, Department of Environmental Sciences, Milan, Italy

³DG Welfare, UO Prevenzione, Lombardy Region, Milan, Italy

Purpose: The value of SARS-CoV-2 monitoring in urban wastewater samples (WWS) for surveillance of virus spread at a population-wide level has been largely demonstrated. Aim of this study was to optimize an analytical workflow to detect SARS-CoV-2 RNA in WWS and to monitor SARS-CoV-2 spread during the first wave of COVID-19 epidemic (March–June 2020) in Lombardy, northern Italy.

Methods & Materials: The workflow consisted in WWS concentration by using PEG-8000 precipitation, a modified RNA extraction (QIAamp MinElute Virus Spin Kit; QIAGEN) and a one-step real-time RT-PCR detecting two portions of the N gene of SARS-CoV-2. Composite 24-hour WWS were collected once a week at the inlet of 8 wastewater treatment plants (WWTPs) with an overall catchment of 2,276,000 inhabitants, located in representative COVID-19 hotspots in Lombardy, from the end of March to mid-June 2020. 107 WWS were obtained and analysed. SARS-CoV-2 RNA copies/L/WWS were multiplied by the flow rate of each WWTP (m³/day) and the obtained load (copies/day/1,000 people) was normalized to the number of inhabitants served by WWTPs.

Results: The optimized workflow allowed to identify 1E+3 copies/mL of SARS-CoV-2 in concentrated WWS with a turnaround time of 8 hours. Overall, the presence of SARS-CoV-2 RNA was identified in 65/107 WWS (61%). The highest rate of positive WWS (78.7%; 26/33) was identified in the Bergamo province, that was the epicentre during the first wave of COVID-19 epidemic (March–June 2020) in Lombardy. The highest amount of SARS-CoV-2 RNA was identified in late March/early April, when the overall viral load