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demioleological 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.

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**PS21.06 (129)**

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

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**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 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.

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

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**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 WWWS 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 WWWS (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
reflecting the number of individuals shedding the virus ranged from 9.3E+10 copies/day/1,000 people to 8.2E+8 copies/day/1,000 people. Since the end of May, WWS tested negative to SARS-CoV-2 detection.

**Conclusion:** According to the epidemiological features of the first wave of SARS-CoV-2 epidemic in Lombardy, the highest amount of SARS-CoV-2 RNA was detected in WWS collected in the areas most affected by COVID-19 (i.e. Bergamo province). This optimized workflow of WWS surveillance can help assessing the real number of individuals – both symptomatic and asymptomatic – able to spread the virus and appraising the effect of preventive measures.

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**PS21.08 (523)**

**Examining the Relationship Between Novel Data from Electronic Health Records (EHRs) and Traditional Public Health Surveillance Data for Influenza-like Illness among 12 U.S. Jurisdictions, 2016-2019**

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**Purpose:** Timely, geographically representative, syndromic surveillance is important for early threat detection. In the United States, the ambulatory-based influenza-like illness (ILI) surveillance system, ILINet, relies on data reported to public health authorities up to 10 days after clinical care is sought, making it a lagging indicator. Intelligent Medical Objects (IMO) has a search and select (SS) tool that is deployed within electronic health records (EHRs) to facilitate clinician searches using highly specific, clinically friendly terminology. Data from this SS tool are available in near real-time, throughout the United States, and at the ZIP code level. We examined the correlation between the novel SS data and the data from the U.S. Centers for Disease Control and Prevention’s (CDC) ILINet, among 12 of the most populous U.S. jurisdictions.

**Methods & Materials:** We mapped IMO influenza-related terms to SNOMED CT and International Classification of Diseases Tenth Revision (ICD-10) codes. We then queried the SS data for the proportion of influenza-related IMO terms, among all searches, during each epidemiologic week (EW) of the study period (2016-2019) by state. For ILINet data, we utilized the proportion of ILI visits, among all visits, each EW (2016-2019), by state, which are publicly available from CDC. We calculated Pearson’s correlation coefficient between the two data streams overall as well as, a rolling average over 52 weeks.

**Results:** For the states of California, Georgia, Illinois, Massachusetts, Michigan, New Jersey, New York, North Carolina, Ohio, Pennsylvania, Texas, and Virginia, which represent ~53% of the U.S. population, the Pearson’s correlation coefficient between ILI from ILINet and influenza SS, was >0.83 for each state during the study period (0.90;0.96;0.86;0.90;0.87;0.92;0.84;0.93;0.94; 0.95;0.94, respectively). Among these 12 states, the correlation remained >0.70 for each EW during the study period.

**Conclusion:** We found high correlations between ILINet data and SS influenza data across 12 U.S. jurisdictions. Given the timeliness and geographic representativeness of the SS data, the SS data might be able to provide additional information to support real-time public health decision-making, beyond what is available today. Future analyses should examine the ability to predict current and future ILINet data using SS data.

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**PS21.09 (978)**

**DiFLUsion: A new spatiotemporal early warning system for HPAI**

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**Purpose:** Highly pathogenic avian influenza (HPAI) represents a global threat due to the devastating economic losses for the poultry industry and a recognized zoonotic potential. The migratory water birds play a critical role for the spread of HPAI between continents. A complex global One Health issue and capturing the disease at the livestock-wildlife-human interface is a major challenge. Addressing this major One Health gap and establishing an early-warning-system requires a multidisciplinary scientific approach combining computer, diverse data sources and decision-making in health sciences. Here we introduce DiFLUsion, a ground breaking early warning detection system for HPAI, that allows early detection of HPAI in free zones connected by movements of wild birds with HPAI affected zones.

**Methods & Materials:** DiFLUsion integrates several data sources and analytical tools using Python, MongoDB, neo4j and ArcGIS that allow modulating alerts according to the location of HPAI outbreaks in Europe, the seasonality of wild bird movements and the temperatures of virus survival. A primary objective was to be able to obtain user-friendly alerts for decision-making, including weekly reports and an interactive map viewer. DiFLUsion’s modular structure offers high flexibility and adaptability allowing adapted it to new geographical areas. To this end, DiFLUsion modules are being transferred to the University of Minnesota for application in a pilot disease surveillance project in the USA, in parallel to its use in Europe.

**Results:** DiFLUsion facilitates the decision-making capacity of livestock health managers in Spain where it is currently implemented, to prepare for and respond in advance to avian influenza epidemics. Here it is shown how cases of the disease originating in wild birds that have occurred recently or in past years are located in areas identified by the alert system as high risk. A validation tool for the system is currently being developed to evaluate its effectiveness in terms of specificity and sensitivity.

**Conclusion:** DiFLUsion represents a useful tool as an early-warning system for HPAI, once the effectiveness and use of the tool was tested in Europe and in the USA through the current studies, the method can be generalized to be used globally. Funding projects: CON20-171 (Spain); OMB-N°0925d-0001(USA).

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