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**PS02.03 (576)**

**Improved contact tracing using network analysis and spatial-temporal proximity**

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**Purpose:** Contact tracing is a crucial tool in infection prevention and control (IPC), which aims to identify outbreaks and prevent onward transmission. What constitutes a contact is typically based on strict binary criteria (i.e., being at a location at the same time). Missing data, indirect contacts and background sources can however substantially alter contact-tracing investigations. Here, we present StEP, a Spatial-temporal Epidemiological Proximity model that accounts for imperfect data by introducing a network-based notion of contact based on spatial-temporal proximity derived from background flows of patient movement.

**Methods & Materials:** We showcase StEP by analysing outbreaks of multidrug-resistant bacteria and COVID-19 within a large hospital Trust in London (UK). StEP utilises spatial-temporal patient trajectories and the background hospital movement flows to recover enhanced contact networks. Firstly, we study a well-characterised outbreak of carbapenemase-producing Enterobacteriaceae (CPE) involving 116 hospitalised patients where genetic sequencing is used to learn model parameters. Secondly, our trained model is deployed in an unsupervised manner on three unseen outbreaks involving 867 patients of related CPE-types. Thirdly, we test application to an altogether novel pathogen by analysing a hospital outbreak of COVID-19 among 90 hospital patients, and demonstrate the power of StEP when characterising newly emerging diseases, even when there is a lack of sequencing data.

**Results:** In addition to recovering core contact structures, StEP identifies missing contacts that link seemingly unconnected infection clusters, revealing a larger extent of transmission than conventional methods. Via genomic analyses we confirm that the additional contacts detected through StEP lead to improved alignment to the plasmid phylogeny (the major outbreak driving force). Hence the StEP contact network is most aligned to the transmission structure.

**Conclusion:** By considering spatial-temporal information in a continuous manner, StEP tackles several challenges associated with traditional contact-tracing. StEP allows both direct and indirect contacts as possible routes of disease transmission and is tunable to a pathogen's epidemiological characteristics. Such flexible use of heterogeneous data in uncertain situations can significantly enhance IPC.

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**PS02.04 (58)**

**Intra-genotypic Recombination and Polymorphisms of Hepatitis B Virus Genome Circulating in Bangladesh**

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**Purpose:** Severe liver diseases including cirrhosis are now frequently detected among the Hepatitis B virus (HBV) infected pa-

tients. Rapid genetic evolution of HBV with insertions, deletions or frameshift events promotes infection severity. Herein, the purpose of this study is to determine the alterations of the genomic pattern of HBV causing liver cirrhosis.

**Methods & Materials:** From 92 HBV-positive plasma samples, whole-genome of three samples, specifically one sample each for cirrhotic, chronic liver disease (CLD) and usual chronic (no detectable liver disease) patients confirmed by ultrasonography and fibroscan were sequenced and analyzed for potential mutations. Recombination analysis of the sequenced strain was performed using NCBI Genotyping tool and RDP4 software package.

**Results:** The whole-genomes of HBV from CLD, cirrhotic and normal chronic patients share a common potential substitution at 210 amino acid (AA) position in the surface (S) protein. Whole-genome of cirrhotic patient comprises mutations T118V, A128V, S207N, I208T and S210R in the S protein and N53D, Y54H, H126R, S219A in the polymerase (P) protein. However, mutations S53L, I126T, S210N and H9Y, N13H, I91L, I269L, V278I were observed in other two patients in the S and P proteins respectively. On the other hand, a vaccine escape mutation, A128V and a frame shift deletion of three amino acids in the S protein were observed in the strain isolated from the cirrhotic patient, which may have implications to cause liver cirrhosis. Moreover, recombination analysis of the sequences denotes that the HBV genome of cirrhotic patients composed of a recombination of three genotypes D, C and E. Of which, genotype E was not documented before in Bangladesh. This unusual tri-genotypic recombinant event is the first report in the world and might promote the severity of the liver abnormalities. Moreover, there is a stop codon at 28 position in the HBV Core protein in the recombinant strain.

**Conclusion:** The reports of this study emphasize that the genomic alterations of the HBV strains could be highly responsible for evolution of the strain that might boost the severity of the hepatitis B infection. Such evolved and recombinant HBV strains may cause dangerous public health problems in future.

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**Topic 03: Climate Change and Ecological Factors in Disease Emergence**

**OP03.01 (382)**

**Structural-Equation-Modelling (SEM) to analyze climatic factor's role on COVID-19 spreading**

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**Purpose:** Climate seems to influence the COVID-19 spreading, but the results of the published studies are conflicting. Aim of this study was to perform a world-wide investigation to analyze the role of all the main climatic factors (CF), trying to identify the causes that led to the discrepancy of the results.

**Methods & Materials:** 134,871 data (from 209 countries) were used for the analysis. These were extrapolated from an initial dataset of 1.200.000 data. To avoid biases present in most of the previously studies, a set of specific requirements was adopted: long observation period (16 weeks),

- the use of a relative time scale to synchronize the beginning of the outbreak among the countries,

- multiple data collection points (up to 4 cities/per country) to overcome the problem of climate variability within a country,
- the use of an appropriate technique to test the relationships among interdependent variables,
- the use of a lag-period to compensate the shift between the infection exposure and the diagnosis' confirmation.

Data's analysis was performed with SEM, a flexible statistical technique for modeling causal chain of effects simultaneously. Using hypothesis-testing, this technique examines the relationships between observed variables and latent variables, in turn linked to observed variables, their indicators. With this statistical model it was possible to consider the integrated effects of all the CF on COVID-19 and, at the same time, to investigate the effects of population density (PD) too.

**Results:** The results of the analysis showed that both climate and population density significantly influence the spread of COVID-19 ( $p < 0.001$ ;  $p < 0.01$ , respectively). Overall, climate outweighs population density (path coefficients: climate vs incidence=0.18, climate vs prevalence=0.11, PD vs incidence=0.04, PD vs prevalence=0.05). Among the climatic factors, irradiation plays the most relevant role, with a factor-loading of -0.77, followed by temperature (-0.56), humidity (0.52), precipitation (0.44), and pressure (0.073); for all  $p < 0.001$ . Fit indices demonstrated a good fit of the model (determination-coefficient=0.826, Root-Mean-Square-Error-of-Approximation=0.088, Standardized-Root-Mean-Square-Residual=0.078).

**Conclusion:** This study demonstrates that CF significantly influence the spread of SARS-CoV-2. However, demographic factors, together with other determinants, can affect the transmission, overcoming the protective effect of climate, where favourable.

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### PS03.01 (252)

#### Evaluation of the role of environmental factors on the transmission of West Nile Virus in the European Union and Mediterranean countries

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**Purpose:** West Nile virus (WNV) is one of the most widely distributed flaviviruses worldwide, and it is considered an endemic and emerging pathogen in different areas of Europe and the Mediterranean. Mosquitoes of the genus *Culex* spp. transmit it, and its main vertebrate hosts are birds, although it can occasionally infect mammals, including humans. Different environmental factors, mainly climatic, can influence the distribution and transmission of the virus, through its effects on vector and/or host populations. The objective of this study is to carry out a systematic review to determine the environmental factors associated with the distribution of vectors and the transmission of WNV in the European Union (EU) and Mediterranean countries.

**Methods & Materials:** Systematic peer review of indexed articles in PubMed, Scopus, Embase and CENTRAL published between 2000 and 2020. We selected studies on WNV and its vector *Culex* spp. carried out in the EU and Mediterranean countries in the last two decades. The search included terms referring to climatic factors such as temperature, precipitation, humidity, drought and flood events, as well as other environmental factors such as the altitude of the study area and changes in habitat or land use.

**Results:** We registered the protocol of the systematic review in PROSPERO. The search, selection and inclusion of studies, as well as data extraction, has been carried out. Preliminary results are as follows: 63 included studies, 32% conducted in Italy. *Culex* spp is studied in 43% of the studies, in 40% host animals (mainly birds and horses) and in 21% humans, among others. In 56% and 29% of the studies, a significant relationship was observed between changes in temperature and precipitation patterns and the epidemiology of WNV, respectively.

**Conclusion:** The epidemiology of WNV seems to be related to climatic factors; mainly temperature and precipitation are associated with changes in the transmission dynamics of WNV in the study area. To improve the surveillance and control of this emerging disease, it would be necessary to monitor these changes as well.

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### PS03.02 (226)

#### The parasitological investigation of soils in the southern Russia

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**Purpose:** In the biological cycle of geohelminthiasis, the crucial role belongs to the soil. The most important risk factor for infection is the soil of courtyards, child care facilities, sandpits, playgrounds, parks, waste bins and toilets. Sanitary and parasitological studies of these objects are relevant in determination of the risk of infection of the population with pathogens of geohelminthiasis.

The aim of the work is to assess the contamination of soil with pathogens of geohelminthiasis at epidemiologically significant objects on the basis of parasitological studies.

**Methods & Materials:** In the period from 2011 to 2019, was carried a study of 13 896 soil and sand samples from preschool institutions and recreational areas in the Republics of Adygea and Karachay-Cherkessia, Krasnodar Krai, Rostov and Astrakhan regions.

Flotation methods were used to identify parasitic pathogens. The rates of extensiveness and contamination intensity with helminth eggs of samples were determinate. Also the species composition of parasitic agents and their viability were analyzed.

**Results:** The extensive rate of contamination of soil with eggs of geohelminthiasis in the studied territories was: in the Republic of Adygea 23.3%; in the Astrakhan territory 17.0%; in the Rostov region 16.5%; in the Republic of Karachay-Cherkessia 12.9%; and in the Krasnodar Krai 5.3%. The share of positive soil samples in preschool institutions and courtyard playgrounds in the studied territories of southern Russia amounted to 18.9%.

The intensity of contamination of the soil with eggs and larvae of helminths in analyzed territories varied from 5 - 20 specimens/kg in the Republic of Adygea until more than 24 specimens/kg in the Republic of Karachay-Cherkessia. In the Rostov region, this indicator ranged 0 - 44 specimens/kg, in the Astrakhan region 2 - 22 specimens / kg. In the Krasnodar Krai - on average, the intensity of soil contamination was 16.3 specimens /kg. The share of viable eggs averaged 25.5%.

**Conclusion:** The results indicate high risks of geohelminths in the population, first of all children, in South of Russia.

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