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Editorial: Exploring the dynamics of emerging and re-emerging diseases: from origins to impact

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Editorial on the Research Topic
Exploring the dynamics of emerging and re-emerging diseases: from origins to impact

In this editorial, we summarize collections on the Research Topic "*Exploring the dynamics of emerging and re-emerging diseases: from origins to impact*". This Research Topic collected articles that cover the epidemiology, therapeutics, transmission dynamics, modelling, control, and prevention of infectious diseases including SARS-CoV-2/COVID-19, tuberculosis, anthrax, ticks, and tick-borne pathogens.

Ogunleye et al. undertook an intensive review of literature on *Bacillus anthracis*, the aetiologic agent of anthrax, with the aim of understanding the key drivers behind the spread of *B. anthracis* in different parts of the world, so that effective control and preventive measures including vaccines and therapeutics could be developed. The article presents a holistic description of the transmission pattern and epidemiology of the aetiologic agent as well as updates on the diagnostic techniques and approaches available for the detection of the pathogen. Furthermore, the study also highlights the importance of participatory epidemiology, hygienic measures, comprehensive surveillance systems, and collaboration as an effective critical step in controlling anthrax.

Chen et al., conducted a retrospective observational study in China analyzing data obtained from the National Influenza Center for a 12-year period (2011-2023) on the effects of nonpharmaceutical interventions (NPIs) on influenza virus transmission by comparing changes in influenza-positive patients before, during, and after the outbreak of the COVID-19 pandemic. The authors observed the suppression of influenza virus activity from 2019-2022 after the implementation of NPIs targeting COVID-19. The significant decrease in influenza-positive patients was 90.31% and 97.46% for northern and southern regions of China, respectively, by the 7th week after the implementation of NPIs. Sadly, by the winter and autumn of 2022-2023, when these policies were lifted, they prevalence of influenza cases increased by 206.41% in both regions of China.

Singh et al., carried out a systematic review of bovine and zoonotic tuberculosis in the Western Pacific (WPR) and the Southeast Asia region (SEAR) of the world. Following a review of 113 eligible articles, data obtained indicate the existence of several species of *Mycobacterium* in both humans and animals from both regions of the world. The predominant species in humans includes *M. tuberculosis, M. bovis, M. scrofulacium, M. kansasii, M. phlei, M. smegmatis*, and *M. orygis*. Species documented in animals were *M. africanum* subtype 1, *M. bovis, M. orygis, M. tuberculosis, M. fortuitum, M. phlei*, and *M. smegmatis*.

Ma et al., collected outbreak data on indigenous aggregated cases of COVID-19 caused by five SARS-CoV-2 strains in Nanjing, China and undertook a parametric analysis on the transmission dynamics from January 2020 to December 2022. The authors pointed out that transmission in the population was faster and the range of the population was wider compared with the original strain, with a significant reduction in the length of the incubation period. Specifically, their results indicate the gradual shortening of the incubation period from the original strain to the Delta variant, Omicron BA.2, Omicron BA.5.2, and Omicron BF.7 with 6d, 5d, 3d, 3d, and 2d respectively. A similar trend was observed for the serial intervals (SIs) which were 5.69 d, 4.79 d, 2.7 d, 2.12 d, and 2.43 d, respectively. On the other hand, there was a gradual increasing trend in the reproductive number (R0) of the five strains, from 2.39, 3.73, 5.28, 5.54, to 7.39 respectively.

Jamil et al., conducted a study in Kuwait during the peak of the COVID-19 pandemic to monitor the presence of SARS-CoV-2 on environmental surfaces using reverse transcriptase quantitative PCR. The results show the variable presence of SARS-CoV-2 and the authors strongly recommend the addition of surface environmental sampling as a pandemic preparedness strategy everywhere.

In the study by Khoza et al., a study on tick distribution in cattle and the associated bacterial pathogens was conducted. Consequently, 150 cattle were randomly selected across three sites in two provinces of South Africa. Collected ticks were identified to species level while bacterial community of the bovine blood was subjected to 16S rRNA gene microbiome sequencing using the PacBio sequencing platform. Results shows that eight tick species were identified, including *Rhipicephalus evertsi evertsi* as the most abundant, followed by *R. appendiculatus*; *R. microplus* was the least abundant. The other species were *R. afranicus*, *R. decoloratus*, *R. simus*, *Hyalomma rufipes*, and *H. truncatum*. Exactly 16 phyla and 30 classes of the bacterial microbiome were identified in the bovine blood, with Proteobacteria as the most dominant bacterial phyla. The results of this study add to the knowledge on the tick fauna and microbial communities in the three study sites.

The article by Shi et al. proposed the use of the Bayesian inference method by simulating stochastic and non-linear dynamics using state-space modeling to explore the transmission dynamics of emerging infectious diseases. The authors used the COVID-19 outbreak data in three different localities in China to validate the proposed method, They confirmed that this method is among the most accurate in estimating the onset time and key epidemiological parameters and is versatile and efficient, extending its utility beyond COVID-19. The findings obtained are consistent with empirical studies and with literature.

In the study carried out by Cai et al., the authors utilized novel high-resolution population mobility data before and during the COVID-19 pandemic to comprehend how mobility changes during the pandemic and seasonally and how these changes impact the spread of emerging diseases. By using a stochastic discrete time metapopulation model, they simulated the hypothetical spread of a directly transmitted disease obtained from Virginia (August 2019 – March 2023). Their results show that the urban areas of Virginia were at high risk of disease in the pre-pandemic era. However, rural areas became relatively high risk during the COVID-19 pandemic due to heterogeneous nature of the community response during the pandemic. Furthermore, counties with large student populations were particularly at risk during the months of September and January when students return to school.

In conclusion, the Research Topic has highlighted that, with the emergence and re-emergence of infectious diseases, healthcare systems, societies, and economies worldwide will be challenged, highlighting the need for a comprehensive understanding of the complex dynamics that underlie disease outbreaks. Also, it has highlighted the importance of surveillance for vectors and vector-borne pathogens so that effective prevention and control measures can be formulated for the control of disease.

Author contributions

AA-H: Resources, Writing – original draft, Writing – review & editing. TO: Writing – original draft, Writing – review & editing. WD: Writing – review & editing. SS: Writing – review & editing.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author(s) declared that they were an editorial board member of Frontiers, at the time of submission. This had no impact on the peer review process and the final decision.

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