

Abstract Book 2026

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Society of Clinical Microbiology
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ESCMID Global 2026 Abstract Programme –

Note from the Directors

This collection of abstracts from ESCMID Global 2026, held in Munich, Germany, from 17–21 April 2026, reflects the remarkable scientific contributions of the ESCMID community. The continued and growing engagement of researchers and clinicians from around the world further reinforces the role of ESCMID Global as a leading platform for the exchange of innovative research in clinical microbiology and infectious diseases.

This year's congress received a record number of 8,561 abstracts during the regular submission period and an additional 476 late-breaker submissions, reflecting the steady growth in scientific participation observed in recent years. The distribution of submissions across scientific categories remained consistent, with particularly strong representation in bacterial susceptibility and resistance, bacterial infections, and viral infections, accounting for 15%, 14%, and 11% of all submissions, respectively. Case reports and case series also represented a significant portion of contributions, comprising 14% of total submissions.

In total, 134 countries were represented among submitting authors, highlighting the truly international scope of the congress. Notably, 51% of submissions originated from outside Europe, including 17% from low- and middle-income countries, underscoring the expanding global engagement within the ESCMID community.

From the 9,037 abstracts submitted, 1,117 were accepted and selected for oral presentation in sessions held in halls and arenas, while 5,265 were accepted as poster presentations, resulting in an overall acceptance rate of 72%. The breadth, diversity, and quality of the research presented provide a strong foundation for scientific exchange and learning throughout the congress. The knowledge and discoveries shared at ESCMID Global 2026 will undoubtedly contribute to future advances in the prevention, diagnosis, and treatment of infectious diseases, ultimately benefiting patients and public health worldwide.

We would like to extend our sincere thanks to all authors who submitted abstracts and whose work forms the scientific backbone of the congress. We are equally grateful to the 1,141 dedicated reviewers, who contributed 42,602 individual reviews, ensuring a thorough and high-quality evaluation process. Finally, we acknowledge the invaluable commitment of the ESCMID Global 2026 Programme Committee, whose expertise and guidance helped shape a dynamic, diverse, and forward-looking scientific programme.

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Development of a multiplex lateral flow immunochromatographic strip test for rapid detection and serotyping of foot-and-mouth disease viruses in Pakistan

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Background

Foot and Mouth Disease (FMD) is one of the most contagious viral diseases of ruminants causing severe economic losses each year. In Pakistan, three of the seven serotypes (serotype A, O and Asia 1) are prevalent and rapid and precise diagnostic testing at the site of suspected outbreaks is critical for timely control measures. This study aimed to develop a rapid lateral flow immunochromatographic strip test (multiplex-LFI) for the detection and serotyping of FMD viruses prevalent in Pakistan.

Methods

The Monoclonal antibodies (mAbs) specific for serotypes O, A, and Asia 1 employed as capture mAbs, conjugated with fluorescein, rhodamine, or biotin, respectively. The detection mAbs included a serotype-independent mAb alongside a serotype A-specific mAb and an Asia 1-specific mAb, all colloidal gold-conjugated. The multiplex-LFI strips designed with one control line and three test lines corresponding to each targeted serotype.

Results

The multiplex-LFI strip test anticipated to specifically identify serotype O, A and Asia 1 from field isolates collected across diverse regions in Pakistan. The sensitivity of the strip test was expected to match that of the double antibody sandwich ELISA for serotypes O and A, while being slightly lower for Asia 1. The test aims to detect FMD viruses in tissue samples from experimentally inoculated animals, as well as in swab samples from infected livestock during outbreaks. The diagnostic sensitivity of the LFA for FMDV types O, A and Asia 1 was similar, at approximately 87.5%, to that of 87.1% obtained with antigen enzyme-linked immunosorbent assay (Ag-ELISA). The diagnostic specificity of the LFA was 98.2%, compared to 100% for the Ag-ELISA.

Conclusions

The multiplex-LFI strip test developed in this study promises to deliver rapid results with high specificity for multiple FMD serotypes, thereby enhancing disease surveillance and outbreak management efforts in Pakistan. By providing an efficient diagnostic tool, this research will aid veterinarians and public health officials in implementing effective control measures against FMD, ultimately reducing its economic burden on the livestock industry.

11g. Global health & health security (incl policy-making, climate change, biosafety/biosecurity)

Biogeography of diseases: dengue in people over 60 years of age

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Background

The transdisciplinary integration of data has enabled new perspectives on the origin and dissemination mechanisms of the main arboviral diseases affecting human populations. This includes the participation of biogeographic factors associated with the establishment and dispersal of vectors, such as climate and environmental stability, represented by the quality of vegetation cover. These factors are essential to understand, monitor, predict, and manage the dynamics of infectious diseases within the emerging transdisciplinary field of Disease Biogeography. The incidence of dengue arbovirolos among vulnerable populations in the Colombian Caribbean, a region characterized by high climatic seasonality that, in turn, drives changes in vegetation quality, constitutes a natural laboratory to investigate .

Methods

To comprehensively understand the eco-climatic scenarios (Environmental Health) associated with the prevalence of dengue arbovirolos (Animal Health) among individuals over 60 years of age (Human Health) under the holistic One Health framework, this study employed computational modeling tools combining Remote Sensing (RS) and Geographic Information Systems (GIS). These were optimized through programming procedures in the R environment to integrate and correlate climatic data on precipitation and temperature, obtained from the global WorldClim repository, with classified satellite imagery (Landsat-Copernicus) processed in ArcGIS 10.8. These images were used to calculate the Normalized Difference Vegetation Index (NDVI) and the Environmental Monitoring Index (EMI), which were then correlated with dengue incidence data among adults over 60 years of age.

Results

Our analyses demonstrated a positive and significant correlation between environmental variability, represented by the interaction between extreme mean temperature and precipitation levels, and vegetation quality indices (NDVI and EMI), with an increase in dengue incidence among adults over 60 years of age in Santa Rosa, Bolívar, in recent years (>2022) . In conjunction, these results highlight the importance of maintaining healthy vegetation cover in regulating hydroclimatic cycles and, consequently, the demographics of vector species

Conclusions

The technical integration of eco-climatic variables into the study of zoonotic events under the One Health approach emerges as a complementary tool to in situ environmental surveillance

Extreme flooding and the surge of *Salmonella* spp. infections: epidemiological shifts in Southern Brazil

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Background

Climate change has increased the frequency and severity of extreme weather events. Waterborne infections such as salmonellosis may rise after flooding due to compromised sanitation and contamination of drinking water systems. In April–May 2024, the state of Rio Grande do Sul in southern Brazil experienced the largest flood in its history, affecting more than 2.3 million people across 29 municipalities. This study assessed changes in the epidemiology, clinical characteristics and antimicrobial susceptibility patterns of *Salmonella* infections before and after this climatic event.

Methods

We conducted a retrospective cohort study across two major healthcare networks. The study was from January 2023 to October 2025. Patients were eligible if they had culture-confirmed *Salmonella* spp. Variables included demographics, epidemiology, antimicrobial susceptibility and 30-day all-cause mortality. Incidence and microbiological patterns were compared between the pre-flood and post-flood periods.

Results

A total of 207 infections were identified, with 27 cases (13.0%) before the floods and 180 (87.0%) afterwards — a 6.7-fold increase. Women accounted for 114 cases (55.1%). Median age was 64 years (IQR 42–75). A shift in the paediatric profile was noted: 14 cases (51.9%) pre-flood and 18 (10.0%) post-flood – $p < .05$. Most patients (155; 74.9%) resided in flood-affected municipalities. Species distribution showed *Salmonella enterica* in 23 cases (11.1%) and *Salmonella* spp. in 184 (88.9%). Isolation sites included stool cultures in 108 cases (52.2%), blood cultures in 79 (38.2%), urine in 16 (7.7%) and other sterile body fluids in 4 (1.9%). Overall, 68 infections (32.9%) were community-acquired, whereas 139 (67.1%) developed after at least one week of hospitalisation. Thirty-day mortality reached 54 cases (26.1%). Susceptibility remained high for amoxicillin–clavulanate (100%), ceftriaxone (100%), ciprofloxacin (99.5%) and trimethoprim–sulfamethoxazole (94.6%). A sharp rise in ampicillin susceptibility was observed, from 47.6% pre-flood to 94.6% post-flood ($p < .05$).

Conclusions

This study demonstrates a substantial increase in *Salmonella* infections following extreme flooding and suggests the persistence or amplification of a relevant waterborne pathogen. The findings raise concerns regarding contamination of municipal water systems and reinforce the need for public health strategies to ensure safe water during and after climate-related disasters.

The impact of COVID-19 non-pharmaceutical interventions on notifiable infectious diseases in Poland: a comprehensive analysis from 2014-2022

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Background

The COVID-19 pandemic prompted widespread non-pharmaceutical interventions (NPIs) like lockdowns and masking in Poland (2020-2022), significantly altering pathogen circulation. This created a unique opportunity to study the extended effects of these measures on other communicable diseases, moving beyond short-term observations. This study aimed to assess how the pandemic and associated NPIs affected the incidence of 17 notifiable infectious diseases in Poland over an extended period, from January 2014 to December 2022.

Methods

Using national surveillance data aggregated monthly, we compared incidence during pandemic years (2020-2022) against pre-pandemic (2014-2018) and baseline (2019) periods. Data were deseasonalized. A negative binomial generalized linear model calculated incidence rate ratios (IRRs) relative to 2019, controlling for confounders. Spearman correlation measured associations between disease incidence, COVID-19 cases, and nine NPIs.

Results

From 2020-2022, 13 of 17 diseases showed cumulative declines compared to 2014-2019, including whooping cough (peak reduction IRR 0.11 in 2021 vs. 2019), scarlet fever, chickenpox, and mumps. Invasive *Streptococcus pneumoniae* decreased initially but rebounded in 2022. Conversely, *Clostridioides difficile* incidence increased significantly (2021 IRR 1.84 vs. 2019). Norovirus, HIV, and syphilis surged later, coinciding with NPI relaxation. Higher NPI stringency generally correlated negatively with respiratory pathogens.

Conclusions

Long-term observation confirmed that widespread NPIs suppressed many communicable diseases, particularly respiratory infections, beyond SARS-CoV-2. The rebound of several infections upon NPI relaxation suggests potential shifts in population susceptibility. These findings can inform future public health strategies balancing disease control and societal needs, though further research on long-term dynamics is warranted.

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