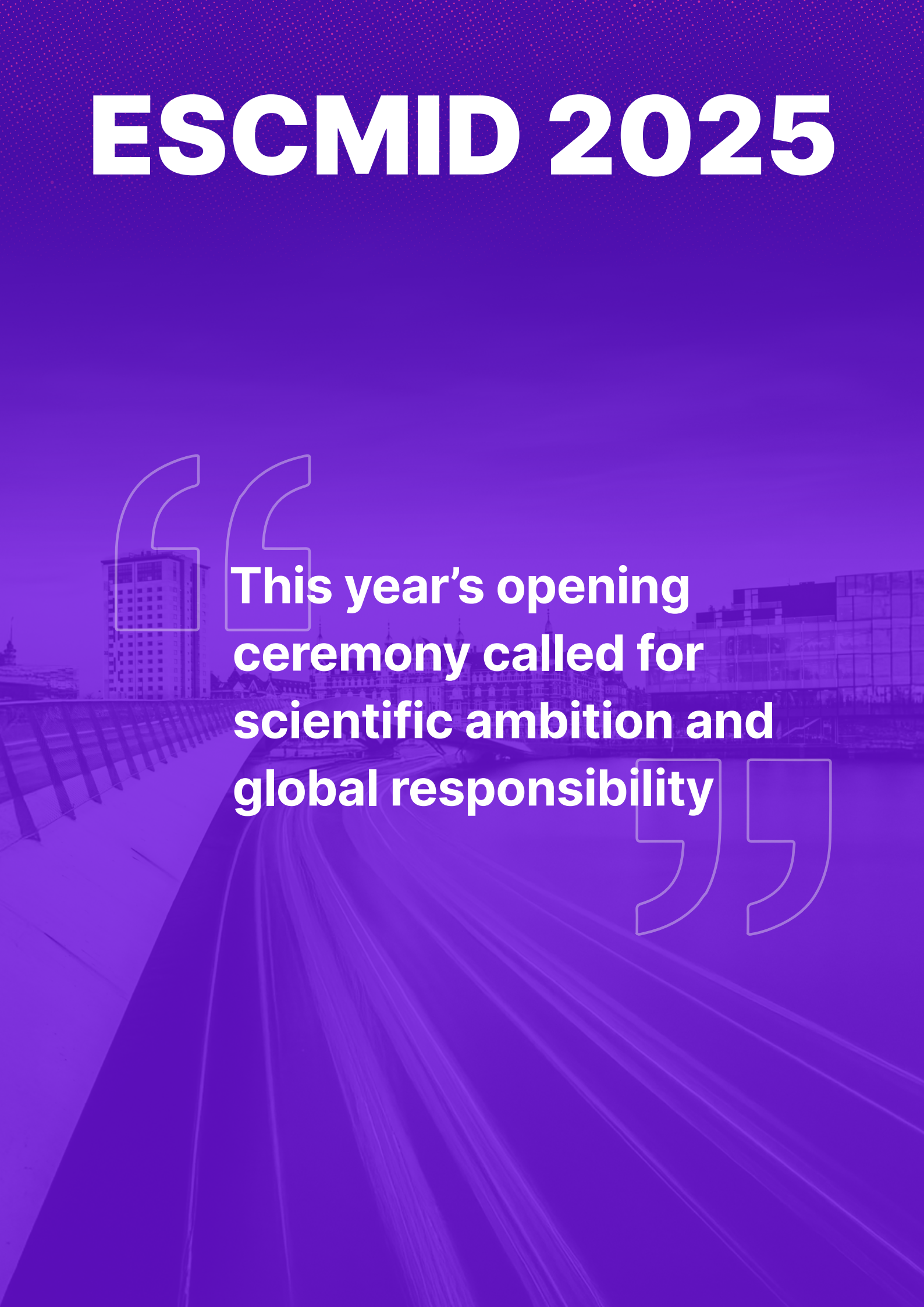
ESCMID 2025



This year’s opening ceremony called for scientific ambition and global responsibility

Congress Review

Review of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Global Congress 2025

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THIS SPRING, Vienna, Austria played host to a momentous gathering, welcoming over 15,000 attendees from across five continents for the 35th European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Global Congress.

This year's opening ceremony called for scientific ambition and global responsibility. With escalating misinformation, political interference, and declining public trust threatening progress in infection control, ESCMID President Robert Leo Skov, University of Copenhagen, Denmark, reminded the medical community of its essential role: to defend evidence, uphold truth, and champion global health equity.

> **ESCMID Global 2025 is deeply invested in capacity-building and high-level advocacy**

Reflecting on the congress's recent evolution from 'ECCMID' to 'ESCMID Global', Skov highlighted just how significant this change has proven to be. "Naming our congress ESCMID Global was a commitment then, and it is an even stronger commitment now," he declared, as he emphasised the urgency of international collaboration in the face of mounting global challenges, from vaccine hesitancy to antimicrobial resistance (AMR), and from funding cuts to the intimidation of scientists working with marginalised populations. Skov stressed that "this world needs our community now more than ever."

The 2025 programme mirrors this global, future-focused mission, introducing several new, exciting initiatives. Education Friday delivered hands-on workshops and small-group sessions using cutting-edge educational techniques, while the Mobile Lab, stationed just outside the congress venue, offered unique on-site parasitology training. Debuting this year was Pipeline Monday, a robust new track dedicated to research and development in AMR, diagnostics, and vaccines. ESCMID Global also served as a platform to spotlight upcoming landmark events: the relaunch of the ESCMID Vaccine Conference in Portugal, and the debut of the Global AMR Innovators Conference (GAMRIC) in Washington D.C., USA.

Crucially, the society's influence now extends well beyond the lecture halls. From a 1.2 million EUR research investment to the formation of the ESCMID Foundation for Education, and from launching a certificate programme on antimicrobial stewardship in Latin America to shaping AMR policy at the United Nations General Assembly, ESCMID

Global 2025 is deeply invested in capacity-building and high-level advocacy.

Next to take the stage was Jacob Moran-Gilad, Ben-Gurion University of the Negev, Beer Sheva, Israel, who returned for his 5th year as the ESCMID Global Programme Director. With pride and enthusiasm, he presented the scale, diversity, and innovation underpinning the 2025 ESCMID Global programme.

With over 7,500 abstracts submitted from 119 countries, and 20% of abstracts originating from underrepresented regions, the numbers reflect ESCMID's ongoing commitment to giving a voice to researchers from every corner of the world. This year also marked a major achievement: over 10% of the invited faculty also came from underrepresented regions, with over half of the faculty members being women. Looking ahead, Moran-Gilad announced plans to expand focus in areas such as paediatric infectious diseases and fundamental science in 2026. Efforts are also underway to integrate more stakeholder groups and societies into the congress ecosystem.

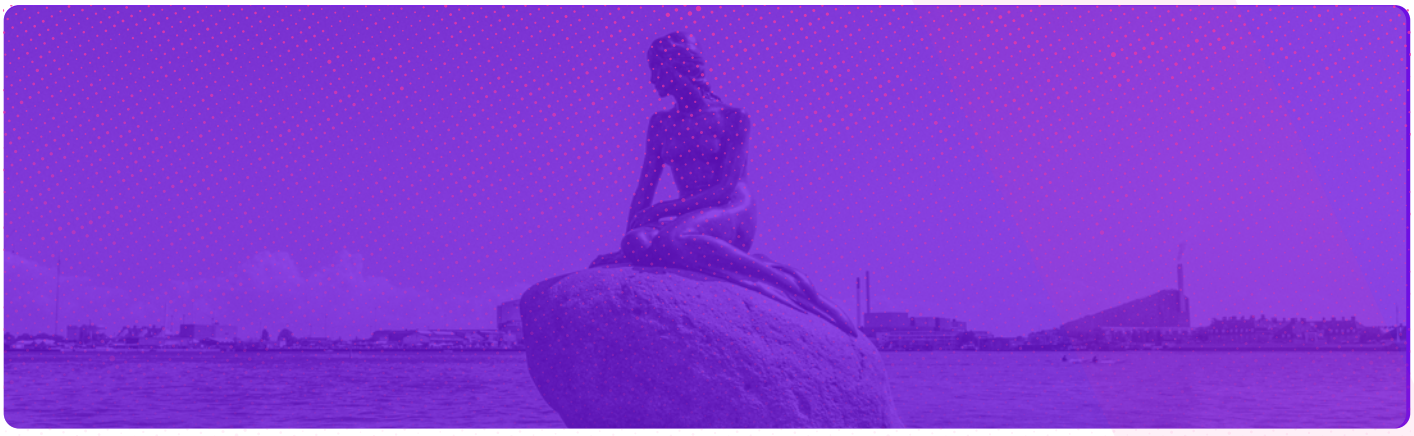
The opening ceremony came to a close with a celebration of excellence and legacy through the 2025 ESCMID Awards, which recognise members for their significant contributions to the field. Marion Koopmans, Erasmus Medical Centre, Rotterdam, the Netherlands, was awarded the 2025 ESCMID Award for Outstanding Contributions in the Field of Infection. Through her roles at the WHO Collaborating Centre, the Netherlands Centre for One Health, and the Pandemic and Disaster Preparedness Center, Koopmans has led global responses to COVID-19, Ebola, and influenza outbreaks.

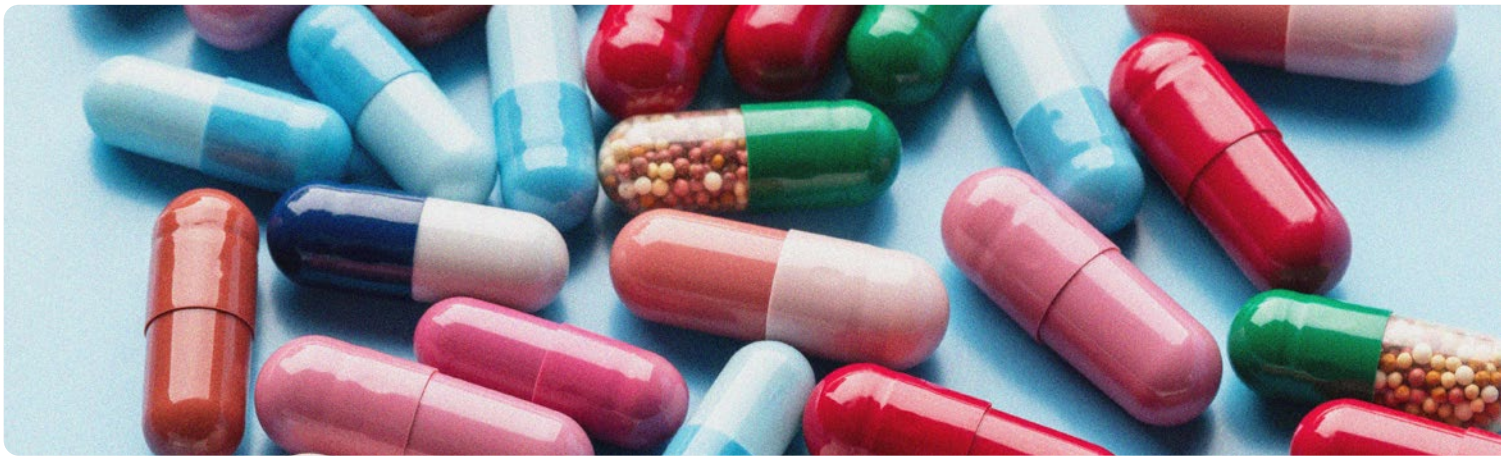
The 2025 ESCMID Award for Excellence in Science was presented to Arturo Casadevall, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA, who is widely respected for his work in fungal pathogenesis, antibody mechanisms, and the impact of climate change on fungal infections.

Finally, the evening concluded with a heartfelt tribute to one of ESCMID's founding members and the society's first ever president: Jan Verhoef, the Netherlands, who received the 2025 ESCMID Lifetime Achievement Award. Throughout his career, Verhoef mentored more than 100 PhD students and authored over 700 publications, with more than 30,000 citations to his name, and has remained an active voice in infectious diseases after retirement.

As the final applause echoed through the auditorium, the message was clear: ESCMID Global is not just a congress, it is a community. The future of infectious diseases hinges not only on innovation, but on open exchange, inclusivity, and relentless advocacy for science. As ESCMID enters its next chapter, its growing community of 30,000 members stands ready to meet the challenge.

Read on for key insights into this year's congress, and don't miss our coverage of ESCMID Global 2026, which will be held in Munich, Germany, from the 17th–21st April 2026.





Three Million Child Deaths Tied to Antimicrobial Resistance in 2022

MORE than three million children worldwide died from antimicrobial resistance (AMR)-related infections in 2022, according to a landmark study presented at ESCMID Global 2025, highlighting the urgent need for targeted action to curb AMR in paediatric populations.

Southeast Asia and Africa recorded the highest paediatric mortality, with **752,000** and **659,000** deaths, respectively

Researchers conducted a comprehensive global analysis of paediatric AMR data, examining regional usage patterns of antibiotics and associated mortality. The study evaluated antibiotic use categorised by WHO's Access, Watch, and Reserve classifications, and linked these trends to child mortality in various regions across the world. Special attention was given to Southeast Asia and Africa, where the burden of resistance-related deaths was highest, alongside analysis of healthcare infrastructure, antibiotic availability, and surveillance capacity.

The findings revealed that 2 million of the over 3 million paediatric AMR-related deaths were linked to Watch and Reserve antibiotics, classes of drugs intended for limited use due to their high resistance potential. Southeast Asia and Africa recorded the highest paediatric mortality, with 752,000 and 659,000 deaths, respectively. Between 2019 and 2021, Watch antibiotic use increased by 160% in Southeast Asia and 126% in Africa, while Reserve antibiotic use rose by 45% and 125% in the same regions, respectively. The African and Southeast Asian regions also showed the highest number of deaths linked to these high-risk antibiotics, surpassing all other WHO regions.

The authors warned that the expanding use of Watch and Reserve antibiotics, while sometimes necessary, poses significant risks without careful stewardship. Much of the AMR mortality burden is attributed to antibiotic overuse, poor sanitation, limited diagnostics, and underdeveloped antimicrobial surveillance systems in low- and middle-income countries. Hospitals in these settings often struggle with overcrowding and infection control, accelerating the spread of resistant pathogens.

Urgent, coordinated action is essential to prevent further escalation of AMR-related child mortality. Improved surveillance, stewardship, and paediatric-specific treatment protocols must be prioritised globally, particularly in high-burden regions.

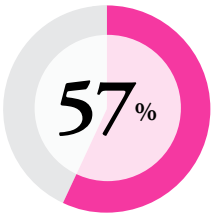
Reference

Hu Y et al. Global trends and impact of antimicrobial resistance in paediatric populations: an analysis using WHO AWaRe classification and priority pathogens. Poster E0503. ESCMID Global 2025, 11-15 April, 2025.

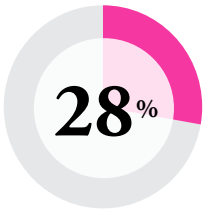
RSV-Linked Respiratory Illness Nearly Triples Adult Mortality

ADULTS diagnosed with respiratory syncytial virus-associated acute respiratory infection (RSV-ARI) face nearly triple the risk of death within 1 year compared to their peers, according to a large-scale Danish study presented at ESCMID Global 2025.

Hospitalisation rates were



in patients with RSV-ARI versus



in controls

Researchers conducted a nationwide cohort study involving 5,289 adults diagnosed with RSV-ARI between 2011 and 2022, matched against 15,867 controls from the general population. Participants were followed for 365 days, with analyses focusing on clinical outcomes, including hospitalisation and disease exacerbation, and economic impact. The study population included a significant proportion of patients with chronic respiratory conditions such as asthma and chronic obstructive pulmonary disease, allowing for subgroup evaluation of these at-risk groups.

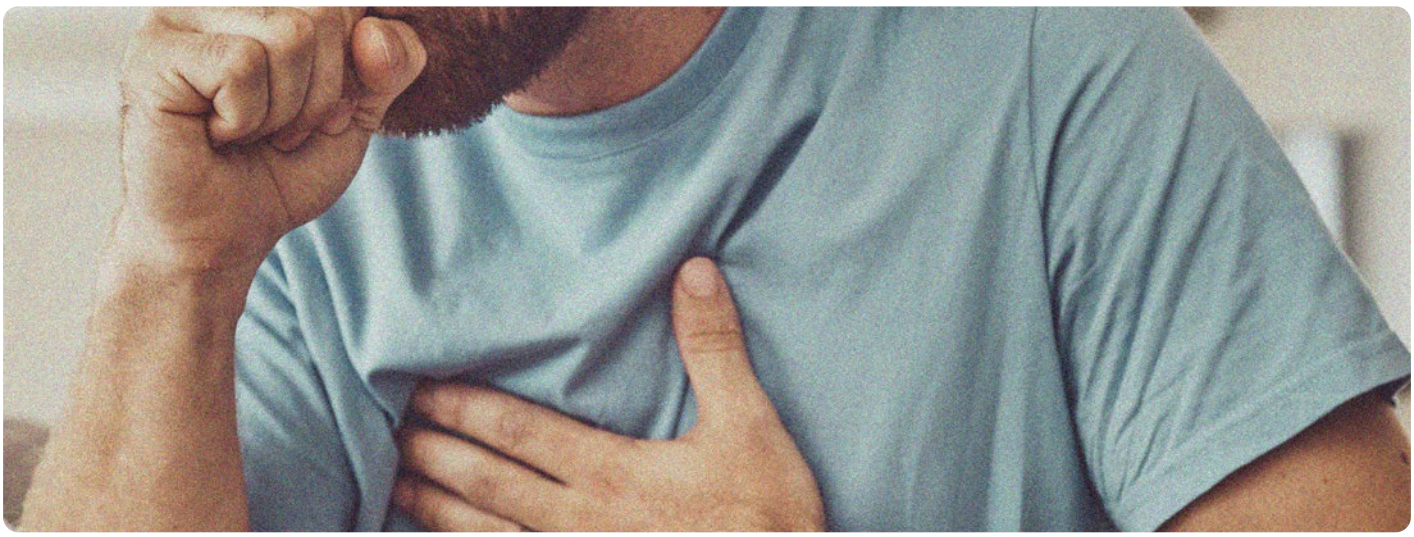
The results showed a 2.7-fold increased risk of death in patients with RSV-ARI within 1 year of diagnosis. These individuals also experienced significantly worse health outcomes compared to controls, with chronic obstructive pulmonary disease exacerbations occurring 3.1 times more frequently and asthma exacerbations 4.6 times more often. Hospitalisation rates were 57% in patients with RSV-ARI versus 28% in controls, while intensive care admissions were nearly quadrupled (5.3% versus 1.4%). The financial burden was equally substantial, with patients with RSV-ARI incurring average direct healthcare costs of 20,181 EUR over 1 year, more than double the 8,085 EUR spent on controls.

The authors highlighted the persistent nature of RSV-ARI's effects, noting that complications often extended well beyond the acute phase. They reinforced the importance of prioritising vaccination in vulnerable adults to reduce severe outcomes and mitigate associated healthcare costs.

This study adds significant evidence of RSV's under-recognised long-term burden in adults, particularly those with pre-existing respiratory conditions. With effective vaccines now available, targeted prevention strategies are more crucial than ever to protect high-risk populations and alleviate pressure on healthcare systems.

Reference

Fonseca MJ et al. Clinical and economic burden of respiratory syncytial virus in adults with acute respiratory infections – a Danish nationwide cohort study. Abstract O0228. ESCMID Global 2025, 11-15 April, 2025.



IL-6 Outperforms Traditional Tests for Early Sepsis Detection

A BREAKTHROUGH study presented at ESCMID Global 2025 highlights IL-6 as a highly accurate early biomarker for sepsis in neonates, children, and pregnant women, three of the most vulnerable patient groups.

The retrospective cohort study evaluated IL-6's diagnostic performance using serial blood samples from 252 patients with suspected sepsis, drawn from paediatric (n=111), maternity (n=72), and neonatal (n=69) populations. Patients were categorised by infection type (bacterial, viral, or no infection) and clinical response, ranging from systemic inflammatory response syndrome to septic shock. The researchers compared IL-6 against conventional biomarkers like C-reactive protein (CRP) and procalcitonin (PCT), with diagnostic accuracy assessed via Area Under the Receiver Operating Characteristic Curve (AUROC).

IL-6 consistently outperformed CRP and PCT in identifying bacterial infections and stratifying sepsis severity. AUROC values reached 0.94 in pregnant patients, 0.91 in children, and 0.86 in neonates, all indicating strong diagnostic utility. Sensitivity and specificity both exceeded 80% in paediatric and maternity patients, with IL-6 detecting bacterial infections with 91% sensitivity in children and 94% in pregnant women. While neonatal sensitivity was lower at 67.6%, specificity remained high at 97.1%, likely reflecting the diagnostic complexity of neonatal sepsis. In contrast to CRP and PCT, which peak later, IL-6 rises within 1–2 hours and peaks at 6 hours, providing a valuable early window for clinical intervention.

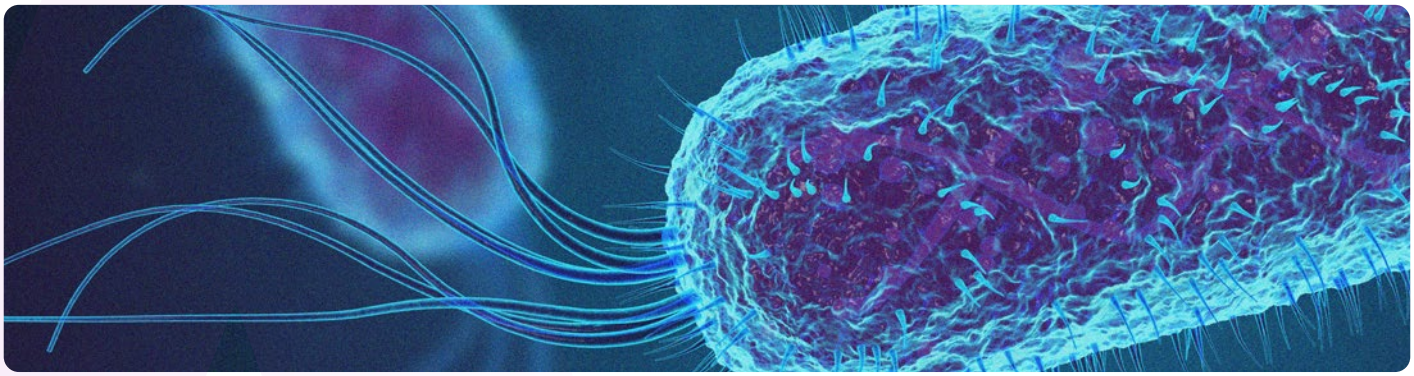
The study reinforces IL-6's value as a fast and reliable marker for sepsis detection and severity assessment, particularly in high-risk populations where early diagnosis is vital. With the availability of commercial assays and growing clinical familiarity following widespread use during the COVID-19 pandemic, IL-6 testing is increasingly feasible in real-world settings.

Reference

Whelan SO et al. Interleukin-6 as a diagnostic biomarker for sepsis in neonates, children and pregnant women – a real-world cohort study. Abstract O0177. ESCMID Global 2025, 11-15 April, 2025.

Sensitivity and specificity both exceeded **80%** in paediatric and maternity patients

Breath-Based Bacterial Test Shows Real-Time Diagnostic Promise



A NOVEL breath test that identifies bacterial infections by detecting unique metabolic signatures may offer clinicians a rapid, non-invasive diagnostic and monitoring tool, according to findings presented at ESCMID Global 2025.

Researchers from the University of California, San Francisco (UCSF), USA, and St. Jude Children's Research Hospital, Memphis, Tennessee, USA, evaluated the test using a laser-based platform known as integrated cavity output spectroscopy (ICOS) in preclinical models. The test involves administering ^{13}C-labelled sugar compounds, which are selectively metabolised by bacteria but not mammalian cells, leading to the production of [^{13}C]CO_2, which is detectable in exhaled breath. The team assessed five bacterial pathogens, including *Staphylococcus aureus* and *Escherichia coli*, and administered ^{13}C-maltose and ^{13}C-mannitol to infected mice, using various infection models such as pneumonia, osteomyelitis, and myositis.

> **The test involves administering ^{13}C-labelled sugar compounds, which are selectively metabolised by bacteria but not mammalian cells**

Results demonstrated that [^{13}C]CO_2 was reliably detected only in infected animals, with healthy mice producing no signal following administration of the tested tracers. ^{13}C-maltose and ^{13}C-mannitol showed high specificity for bacterial metabolism, unlike ^{13}C-glucose or ^{13}C-sorbitol, which were also metabolised by mammalian cells. In a further validation step, *E. coli*-infected mice treated with ceftriaxone exhibited a marked decline in [^{13}C]CO_2 levels after 24 hours, mirroring the drop in bacterial load.

These findings support the test's potential not only to diagnose infections but also to monitor treatment response in real time. Although this study did not quantify the test's sensitivity, previous research suggests that the ICOS platform offers practical advantages over traditional isotope ratio mass spectrometry, including portability and reduced cost (estimated at under 100,000 USD per unit).

The authors emphasised that confirming the test's specificity in healthy humans will be essential before clinical use, but they are optimistic about its broad future applications. If validated, this approach could significantly improve point-of-care diagnostics in emergency and intensive care settings.

Reference

Lopez-Alvarez M et al. [^{13}C]CO_2 breath testing for detecting and monitoring bacterial infection. Poster P-2293. ESCMID Global 2025, 11-15 April, 2025.

AI Lung Ultrasound Outperforms Experts in Tuberculosis Diagnosis

AN AI-powered lung ultrasound tool has outperformed human experts in diagnosing pulmonary tuberculosis (TB), offering a fast, accessible, and sputum-free solution that could transform TB triage in high-burden, resource-limited settings.

Presented at ESCMID Global 2025, the study evaluated the ULTR-AI suite, an integrated set of deep learning models developed to interpret lung ultrasound scans in real time using portable, smartphone-connected devices. Conducted in a tertiary centre in Benin, West Africa, the study included 504 patients after exclusions, 38% of whom had microbiologically confirmed pulmonary TB. Researchers applied a 14-point standardised lung ultrasound protocol and compared AI model performance against human expert readings. A single MTB Xpert Ultra test was used as the reference standard for diagnosis.

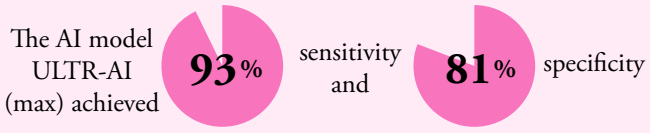
The AI model ULTR-AI (max) achieved 93% sensitivity and 81% specificity, with an Area Under the Receiver Operating Characteristic Curve (AUROC) of 0.93 (95% CI: 0.92–0.95), surpassing WHO's minimum target for non-sputum-based TB triage tools (90% sensitivity and 70% specificity).

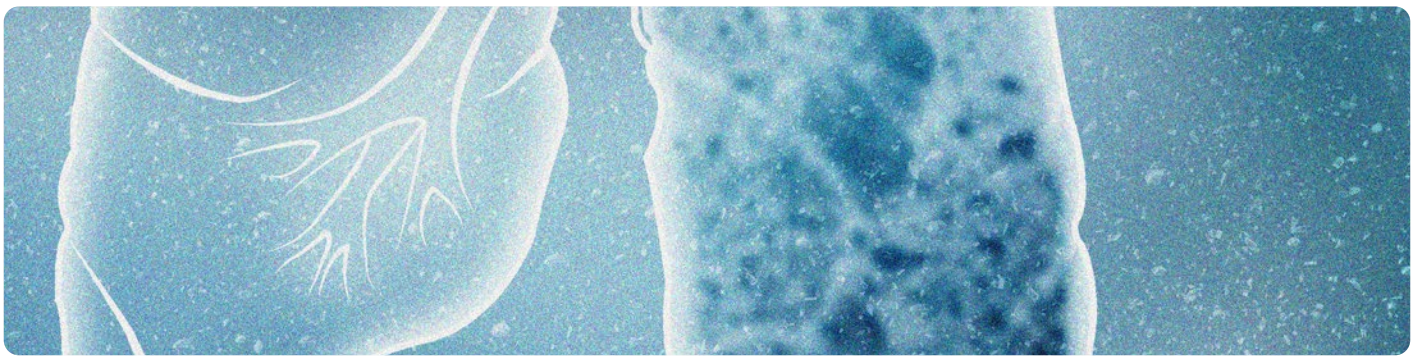
Compared to human experts, the AI system demonstrated a 9% improvement in diagnostic accuracy. The AI detected both human-recognisable features, such as consolidations and interstitial changes, and more subtle patterns that may be missed by trained clinicians. Importantly, the tool showed promise in identifying early, sub-centimetre pleural lesions associated with TB. The tool's performance was consistent even in patients with HIV co-infection and those with a prior history of TB. Once integrated into a mobile app, the AI model provided instant diagnostic results at the point of care.

This study highlights the potential of AI-enhanced ultrasound as a frontline diagnostic tool for TB, particularly in regions with limited access to radiological services. With real-time interpretation and minimal operator dependency, ULTR-AI could significantly improve early detection and reduce patient drop-out rates.

Reference

Suttels V et al. Lung ultrasound for the detection of pulmonary tuberculosis using expert and AI-guided interpretation. Abstract O0573. ESCMID Global 2025, 11-15 April, 2025.





AI Sleep Data Effectively Predicts Respiratory Hospitalisation Trends

A RECENT study, presented at ESCMID Global 2025, has highlighted the promise of using AI-powered sleep data for real-time public health monitoring, focusing on respiratory illnesses such as influenza and COVID-19.

The research evaluated data from the 'Cough Radar' system, developed by Sleep Cycle® (Gothenburg, Sweden), that anonymously analyses night-time audio from users of its app to detect coughing. Aggregated and anonymised, this data estimates regional cough rates across the USA, updating each morning and covering approximately 50 million hours of sleep per month.

To assess the system's accuracy, researchers compared Cough Radar data with state-level hospitalisation figures from the CDC, as well as Google (Mountain View, California, USA) search trends, between September 2023 and February 2025. The goal was to determine how well these sources could predict hospitalisation trends 14 days in advance. Two time periods were studied: 30th September 2023–1st April 2024, and 30th September 2024–1st February 2025.

Cough Radar showed a strong predictive correlation with hospitalisations, 0.62 and 0.74 for the two periods, respectively, outperforming Google Trends, which achieved 0.60 and 0.53. Notably, increases in cough rates preceded hospitalisation surges in up to 70% of cases, while search data predicted fewer peaks. However, search trends were better at signalling decline after peaks.

A neural network model trained using Cough Radar data outperformed one based on Google Trends, achieving an F1-score of 0.77 compared to 0.73, with higher recall and identical precision. This suggests Cough Radar may offer more timely warnings for incoming waves of respiratory illness.

The results indicate a compelling case for the use of AI-driven tools in public health surveillance. As respiratory illnesses remains a significant burden, especially during winter months, the integration of systems like Cough Radar into broader forecasting platforms could significantly enhance preparedness and response efforts.

Reference

Carlsson E, Kågebäck M. AI-driven live cough rate tracking for public health surveillance. Abstract L0009. ESCMID Global, 11-15 April, 2025.

Second UK Human Case of Avian Influenza Confirmed Amid Ongoing Outbreaks

PRESENTED at ESCMID Global 2025, the UK Health Security Agency (UKHSA) has confirmed a rare human case of avian influenza A(H5N1), following an outbreak at a poultry farm in January 2025.

The case was identified through UKHSA's Zoonotic Influenza Enhanced Surveillance Study, launched in 2023 to monitor individuals exposed to infected birds. A farm worker developed eye and upper respiratory symptoms after repeated exposure to sick poultry. Laboratory testing of nasopharyngeal and conjunctival swabs confirmed infection with A(H5N1), clade 2.3.4.4b.

The individual received antiviral treatment and was isolated at a High Consequence Infectious Disease unit. Full recovery was achieved within five days, with subsequent tests returning negative. Genomic sequencing revealed the virus matched strains found in UK birds, with no signs of mutations associated with human adaptation or antiviral resistance.

UKHSA, alongside the Animal and Plant Health Agency (APHA) and the Department for Environment, Food and Rural Affairs (Defra), is conducting joint risk assessments as part of the UK's annual avian influenza preparedness efforts. Active monitoring and post-exposure treatment were provided to high-risk contacts. No further transmission was detected.

The case highlights the need for continued vigilance as North America battles widespread A(H5N1) outbreaks in dairy cattle, poultry, and humans. Experts stress the importance of a coordinated One-Health approach to reduce the risks of future zoonotic transmission.

The case was identified through UKHSA's Zoonotic Influenza Enhanced Surveillance Study, launched in 2023 to monitor individuals exposed to infected birds

Reference

Hamzaoui N et al. Human infection in the United Kingdom: a One-Health approach. Abstract H5N1. ESCMID Global, 11-15 April, 2025.

ABCG1 Variants Linked to Tick-Borne Encephalitis Susceptibility

A NEW genetic study presented at ESCMID Global 2025 has identified suggestive associations between tick-borne encephalitis (TBE) and variants in the *ABCG1* gene, pointing to host genetic susceptibility as a factor in disease development and progression. The study, conducted by the European Genetics Study of Tick-borne Encephalitis (EU-TICK-BO) consortium, combined genome-wide association analysis with functional validation, offering new insights into how host factors may shape outcomes in TBE virus (TBEV) infection.

TBE is a potentially severe infection of the central nervous system caused by TBEV, presenting as meningitis, encephalitis, or myelitis. Despite vaccination efforts in endemic regions, many cases still occur each year, often leading to lasting neurological impairment. However, why some individuals develop severe diseases while others remain asymptomatic has remained poorly understood.

In this genome-wide association study, researchers analysed genetic data from 1,600 patients with confirmed TBE and 9,699 matched controls across Europe. They identified two independent intronic variants in the *ABCG1* gene on chromosome 21. Single-nucleotide polymorphism's rs35873421 and rs3787986 showed a genome-wide suggestive association with TBE susceptibility ($p=2.39\times10^{-7}$ and $p=3.2\times10^{-6}$, respectively). Although these findings did not reach genome-wide significance, they pointed to a consistent genetic signal within *ABCG1*, which encodes a transporter protein involved in lipid metabolism and immune cell regulation.

Further gene expression analyses demonstrated that these variants were linked to altered *ABCG1* expression in peripheral blood. To assess functional relevance, the researchers conducted *in vitro* experiments using neuronal cells and macrophages. Both pharmacological inhibition of *ABCG1* with benzamil and gene silencing with small interfering RNA led to significantly reduced TBEV replication in these cell types, suggesting a mechanistic role for *ABCG1* in viral propagation.

Importantly, *ABCG1* was the only gene reaching significance in gene-based analyses. While the study did not identify any variants meeting the threshold for genome-wide significance ($p<5\times10^{-8}$), the consistency of findings across statistical and experimental approaches underscores the gene's relevance in the host response to TBEV.

These results represent a significant step forward in understanding individual susceptibility to TBE, and could inform future studies focusing on predictive biomarkers, vaccine response, or antiviral targets. The EU-TICK-BO team emphasises the need for further validation in larger cohorts and additional mechanistic studies to fully delineate *ABCG1*'s role in TBE pathogenesis.

Reference

Gampawar P et al. Genome-wide association study identifies ABCG1 as a susceptibility locus for tick-borne encephalitis. Abstract L0026. ESCMID Global, 11-15 April, 2025.

> **"In this genome-wide association study, researchers analysed genetic data from 1,600 patients with confirmed TBE and 9,699 matched controls across Europe"**

Five-Day Antibiotic Course Is Non-inferior to Longer Treatment in Community-Acquired Pneumonia

SHORTENED antibiotic treatment for 5 days is non-inferior to longer courses in hospitalised patients with community-acquired pneumonia (CAP) who achieve clinical stability by 3–5 days, according to the results of a multicentre randomised controlled trial presented at ESCMID Global 2025.

Antimicrobial resistance remains a critical global health challenge, necessitating antibiotic stewardship strategies to optimise treatment efficacy while minimising unnecessary exposure. CAP, a leading cause of hospitalisation and mortality, presents a key opportunity to reduce antibiotic durations without compromising patient outcomes, though optimal treatment duration requires further investigation.

> **These results support implementing 5-day antibiotic courses for clinically stable hospitalised patients with CAP**

Therefore, this open-label trial randomised 395 adults, hospitalised with radiologically confirmed CAP, across six centres to 5-day (n=198) or ≥7-day (n=197) antibiotic regimens if clinical stability was achieved within 3–5 days. Exclusion criteria targeted immunosuppressed patients, those with extrapulmonary infections, complicated pneumonia, or intensive care needs. The primary outcome measured all-cause mortality at 90 days via absolute risk difference, with a 6% non-inferiority margin. Secondary outcomes included 90-day readmissions and adverse events.

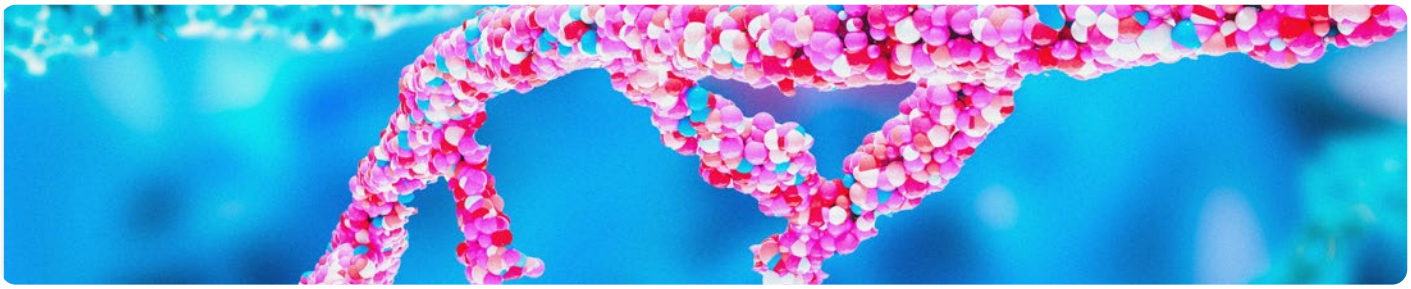
After exclusions, 393 patients comprised the intention-to-treat population (median age 75, 54% female), with 303 completing per-protocol treatment. Median antibiotic duration was 5.0 days (interquartile range: 4.7–5.5) in the intervention group, versus 7.1 days (interquartile range: 6.6–8.3) in controls. Mortality rates were 3.1% (5-day group) versus 2.0% (≥7-day group), demonstrating non-inferiority (risk difference: -1.1%; 95% CI: -4.1–2.0), with per-protocol results aligning closely (0.1%; 95% CI: -2.8–3.0). Readmission rates (18–23%) and adverse event frequencies showed no significant differences.

These results support implementing 5-day antibiotic courses for clinically stable hospitalised patients with CAP, as part of antimicrobial stewardship initiatives. The findings advocate for a shorter duration of antibiotic treatment based on stability criteria, reducing resistance risks without compromising recovery trajectories.

Reference

Bastrup Israelsen S et al. Shortened antibiotic treatment for 5 days in patients hospitalised with community-acquired pneumonia (CAP5): a multicentre randomised controlled noninferiority trial. AbstractL0024. ESCMID Global, 11-15 April, 2025.

New Understanding of Cervical Cancer Risk in Women with Schistosomiasis



NEW research presented at ESCMID Global 2025 has revealed a concerning link between the parasitic infection *Schistosoma haematobium,* a disease which is particularly prevalent in regions with limited access to sanitation and clean water, and the activation of cancer-related genes in the cervix.

Among women who cleared the infection, **23 genes** showed significant changes following treatment

While the parasite is already recognised as a cause of bladder cancer, understanding of its potential role in cervical cancer is limited. Crucially, the genetic changes appear to become even more pronounced following anti-parasitic treatment.

The researchers analysed cervical tissue samples from 39 Tanzanian women with *S. haematobium* infection (n=20) and without (n=19). Women with the infection were treated with praziquantel, and cervical samples were taken at baseline and 4–12 months post-treatment. Using RNA sequencing and gene expression analysis, the researchers investigated changes in cancer-related molecular pathways. Comparisons were made between infected, uninfected, and post-treatment samples to identify key genetic alterations.

Nine genes were found to be significantly altered between women with and without the infection, with four of these (*BLK proto-oncogene, Long Intergenic Non-Protein Coding RNA 2084, Trichohyalin,* and *TCL1 family AKT coactivator A*) having known associations with various cancers. Among women who cleared the infection, 23 genes showed significant changes following treatment. Additionally, 29 genes showed differences when comparing individuals who were post-treatment to those who had never been infected. Notably, cancer-related pathways associated with inflammation, tissue remodelling, and reduced apoptosis were more active after treatment, suggesting potential vulnerabilities to further cellular damage or oncogenic infections, such as human papillomavirus, due to treatment.

This study highlights a possible unintended consequence of anti-parasitic treatment, raising concerns about long-term risks for women previously infected with *S. haematobium*. While praziquantel remains essential for controlling schistosomiasis, these findings suggest treatment may not fully reverse parasite-induced changes and may even activate pathways that further heighten the risk of cervical cancer. Limitations of the study include the small sample size and the relatively short follow-up period. However, a larger ongoing study involving 180 women over 12 months aims to validate the results. Clinicians working in endemic areas should be aware of the potential link between schistosomiasis and cervical cancer, particularly when treating female patients. Enhanced post-treatment monitoring, combined with more widespread human papillomavirus vaccinations and potential adjunct therapies, could be key to reducing long-term cancer risk.

Reference

Mertelsmann AM et al. (2025). Schistosoma haematobium infection is associated with oncogenic gene expression in cervical mucosa, with enhanced effects following treatment. Abstract 00228. ESCMID Global, 11-15 April, 2025.