

individuals with healthy immune systems and in areas where the disease is uncommon. This condition is rarely reported in Morocco and the broader African continent

**Conclusion:** The lack of pleocytosis in the CSF should not rule out meningitis in a patient with signs of meningitis.

<https://doi.org/10.1016/j.ijid.2024.107751>

## Two decades of Lloviu virus in Europe: knowns and unknowns about the European filovirus

Dr Gábor Kemenesi<sup>1,2</sup>, Dr Zsófia Lanszki<sup>1,2</sup>, Ágota Ábrahám<sup>1</sup>, Dr Sándor A Boldogh<sup>3</sup>, Dr Simon Scott<sup>4</sup>, professor Nigel Temperton<sup>4</sup>, Dr Edward Wright<sup>5</sup>, Dr Pierre Nouvellet<sup>6</sup>, Dr Stefania Leopardi<sup>7</sup>, Dr Paola Di Benedictis<sup>7</sup>, Dr Adam Hume<sup>8</sup>, Dr Elke Mühlberger<sup>8</sup>, Levente Sipos-Szabó<sup>9</sup>, Dr Dávid Bajusz<sup>9</sup>, Dr Heliana Dundarova<sup>10</sup>, Dr Szilárd L Bücs<sup>11</sup>, Dr Branka Bajić<sup>12</sup>, Dr Ivana Budinski<sup>12</sup>, Dr Štefan Matis<sup>13</sup>, Dr Tamás Görfői<sup>1</sup>

<sup>1</sup> National Laboratory Of Virology, Szentágotthai Research Centre, University Of Pécs, Hungary

<sup>2</sup> Faculty of Sciences, Institute of Biology, University of Pécs

<sup>3</sup> Aggtelek National Park Directorate

<sup>4</sup> Viral Pseudotype Unit, Medway School of Pharmacy, Chatham Maritime, Universities of Kent & Greenwich

<sup>5</sup> Viral Pseudotype Unit, School of Life Sciences, University of Sussex

<sup>6</sup> School of Life Sciences

<sup>7</sup> OIE Collaborating Centre and National Reference Centre for Infectious Diseases at the Animal–Human Interface, Istituto Zooprofilattico Sperimentale delle Venezie

<sup>8</sup> Department of Virology, Immunology and Microbiology, Boston University Chobanian & Avedisian School of Medicine

<sup>9</sup> Medicinal Chemistry Research Group, HUN-REN Research Centre for Natural Sciences

<sup>10</sup> Institute of Biodiversity and Ecosystem Research

<sup>11</sup> Centre for Bat Research and Conservation

<sup>12</sup> Department of Genetic Research, Institute for Biological Research “Siniša Stanković” – National Institute of the Republic of Serbia, University of Belgrade

<sup>13</sup> National Park Slovak Karst Directorate

**Introduction:** The Lloviu cuevavirus (LLOV) was the first filovirus identified in Europe and at the temperate climate region. Its first discovery was associated with a massive die-off event of Schreibers's bats in Spain. Since its discovery this virus became the second filovirus ever isolated directly from bats. Initial in vitro experiments have suggested that this virus could be a potentially zoonotic filovirus and further experiments suggested an apathogenic nature in humans. During the last decades, several more die-off events in bats were associated with the virus, which therefore might be one of the few viruses pathogenic to bats under certain circumstances.

**Methods & Materials:** We initiated a complex monitoring program for Lloviu virus in 2013. During the last decade we collected and screened more than 2000 blood samples with PCR and serology from eight countries. In addition to blood samples, we screened urine, faeces, swab and ectoparasites from these animals. Using a mobile laboratory approach, we collected fresh blood samples from infected animals on-site to facilitate in vitro isolation ex-

periments. We used the SuBK12-08 cell line for the establishment of novel isolates. In parallel we analysed the ectoparasite samples with sequencing and histology to get a better understanding about their potential vector role.

**Results:** We detected the viral RNA in all sample types, except oral swabs. We generated more than 20 novel viral genomic sequences, covering the whole coding region of the virus. We established four in vitro isolates. Using the sequence data, we generated throughout the years we performed molecular modelling to understand the temporal variation regarding its receptor affinity to bats and found no evidence of adaptation to better receptor binding. Additionally, we were able to calculate the molecular evolution of the virus, describe its mutational landscape and phylogenetic tree.

**Discussion:** Over a decade of research activities, we now possess data that allow us to evaluate the hypothesis concerning the emerging versus enzootic nature of this virus in Europe. Based on the surveillance and sequence data we believe that this virus is endemic in the whole range of this bat species. We established a hypothesis about the potential connection of die-off events, Lloviu virus infection and hibernation of these animals.

**Conclusion:** Although we generated significant amount of data regarding the ecology and zoonotic nature of this virus, several key questions remained to be solved. These include the investigation of potential spillover hosts, other potential bat host species and the role of ectoparasites in the natural transmission cycle. In conclusion, our efforts may lead to a deeper understanding of temperate climate filoviruses and, as a model, provide insights into the ecology and spillover mechanisms of highly pathogenic African filoviruses.

<https://doi.org/10.1016/j.ijid.2024.107752>

## Understanding patient and community members views regarding antimicrobial use: A scoping review

Ms Nishana Ramdas<sup>1</sup>, Professor Johanna Meyer<sup>1</sup>, Professor Natalie Schellack<sup>2</sup>, Professor Brian Godman<sup>3</sup>, Ms Eunice Turawa<sup>4</sup>, Professor Stephen Campbell<sup>5</sup>

<sup>1</sup> Department of Public Health Pharmacy and Management, School of Pharmacy, Sefako Makgatho Health Sciences University

<sup>2</sup> Department of Pharmacology, Faculty of Health Sciences, University of Pretoria

<sup>3</sup> Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde

<sup>4</sup> Burden of Disease Research Unit, South African Medical Research Council

<sup>5</sup> School of Health Sciences, University of Manchester

**Introduction:** Antimicrobial resistance (AMR) poses a significant global threat. In 2019, AMR contributed to an estimated 4.95 million deaths with 1.27 million deaths attributed to AMR. It is influenced by factors including antibiotic usage and supply chain patterns, patient-provider dynamics, and community attitudes. Understanding patient views regarding the appropriate use of antibiotics for bacterial infections and inappropriately for viral infections, is crucial for addressing inappropriate antibiotic use and combating AMR. Africa experiences high death rates from AMR but there are little data or understanding of patient views especially in primary healthcare (PHC). This scoping review focused on PHC settings in low- and middle-income countries (LMICs) like South Africa. It aimed to identify key themes surrounding patient and community members views regarding antimicrobial use in PHC in LMICs.

**Methods:** The scoping review followed the Joanna Briggs Institute (JBI) methodology and PRISMA-ScR guidelines and included qualitative studies, close-ended questionnaires, and descriptive observational designs. The Covidence web-based platform was used for literature screening and data extraction including population characteristics, methods, tools and/or questionnaires used, and key findings and the Critical Appraisal Skills Programme (CASP) qualitative checklist was used for qualitative papers.

**Results:** The review identified several key themes related to: 1) patient factors including patient beliefs, expectations, knowledge and understanding, and perceptions of antibiotics, resistance and illness severity; satisfaction with and trust in healthcare providers and shared decision making and empowerment; community attitudes, perceptions and beliefs, and sociocultural factors; 2) provider factors including patient-provider relationship, healthcare utilisation and antibiotic prescribing provision and practices and healthcare delivery in PHC; 3) healthcare system factors including resource constraints and healthcare delivery, diagnostic tools and testing and technological advances and access to care, and 4) uptake, implementation, effectiveness and impact of educational interventions. Patients demonstrated varied levels of knowledge regarding infections and antibiotic resistance, influenced by factors such as migration, cultural background, and health literacy. Motivations for seeking antibiotics included cultural beliefs, family influences, and concerns about illness severity.

**Discussion:** Understanding patient and healthcare provider perspectives and understanding are crucial for designing effective interventions to combat AMR. This study emphasizes the need for enhancing antibiotic stewardship programs, addressing information needs, and considering population diversity and health literacy in educational interventions. Challenges related to resource scarcity and power dynamics within the healthcare system must also be considered.

**Conclusion:** Despite the growing awareness that a substantial portion of antibiotic consumption occurs within PHC settings, patients' roles in the use of antibiotics have often been overlooked. This review emphasizes the importance of understanding patient perspectives in LMICs regarding antibiotic use in PHC settings. The focus should be on implementing targeted interventions for both patients and providers to promote judicious antibiotic use and mitigate the global threat of AMR.

<https://doi.org/10.1016/j.ijid.2024.107753>

### Understanding the genomic landscape of *Klebsiella pneumoniae*: insights into bacteraemia across North-West London hospitals between April 2020-December 2021

Mr Jonah Rodgus<sup>1</sup>, Dr Maria Getino<sup>1</sup>, Dr Yu Wan<sup>1,2</sup>, Dr Frances Davies<sup>2</sup>, Professor Alison Holmes<sup>1</sup>, Dr Elita Jauneikaite<sup>1,2,3</sup>

<sup>1</sup>NIHR Health Protection Research Unit in Healthcare Associated Infections and Antimicrobial Resistance, Department of Infectious Disease, Imperial College London, Hammersmith Hospital

<sup>2</sup>Imperial College Healthcare NHS Trust

<sup>3</sup>Department of Infectious Disease Epidemiology, School of Public Health, Imperial College London

**Introduction:** *Klebsiella pneumoniae* is an opportunistic pathogen causing hospital-acquired antimicrobial-resistant (AMR) bacteraemia. The rise of multidrug-resistant strains of invasive *K. pneumoniae*, particularly those producing extended-spectrum  $\beta$ -lactamases or carbapenemases, necessitates comprehensive genomic investigation. Here, we characterise the genomes of *K.*

*pneumoniae* causing bacteraemia in North-West London to identify common AMR and virulence determinants.

**Methods:** We investigated 354 blood isolates collected at three tertiary hospitals across North-West London between April 2020 and December 2021. Genomic characterisation was completed using Kraken2, Bracken, MLST, PopPUNK, Kleborate, and ABRicate. Core-gene phylogenetic analysis was completed using ggCaller, SNP-sites, and IQ-TREE. Characterisation of plasmids was completed using MOB-suite.

**Results:** Genomic diversity was high, with 140 sequence types (STs) identified throughout 2020-2021 (2020, 50 STs [n=78]; 2021, 113 STs [n=276]). Just 32 STs comprised  $\geq 3$  isolates, with ST15 commonest (6.8%, 24/354), followed by ST37 (5.6%, 20/354), and ST307 (5.1%, 18/354). Critically, four distinct carbapenemase genes were identified (n=11), with two OXA-48-like genes (blaOXA-181 [n=2] and blaOXA-48 [n=6]) detected in eight isolates (two from ST15), consistent with national data to suggest a predominance of OXA-48-like genes among carbapenemase genes in England. blaCTX-M-15 (n=92), which confers cefotaxime resistance, was the most common  $\beta$ -lactamase gene, followed by variants of blaTEM-1-D (n=82), which confer resistance to penicillins/first-generation cephalosporins. Altogether, 24  $\beta$ -lactamase genes were carried by plasmids across 129 isolates from 123 distinct patients. 62.8% (91/145) of plasmids carrying such genes were positive for the replicon types, IncFIB or IncFII, which frequently co-occurred, underscoring the major role of IncF plasmids in disseminating AMR determinants among Enterobacteriaceae. 67.6% (98/145) of plasmids carrying  $\beta$ -lactamase genes were conjugative, with 49.7% (72/145) of these plasmids encoding MOBF-family relaxases, including a plasmid carrying blaNDM-5. However, all six blaOXA-48 genes were carried by an IncI/M MOBP conjugative plasmid, whilst other OXA-48-like genes (n=2) were carried on MOBP conjugative plasmids of two replicon types, and both blaNDM-1 genes carried on IncC MOBH conjugative plasmids. Carriage of carbapenemase genes on multiple conjugative plasmids is concerning, and, despite a maximum prevalence of 3.1% (11/354) here, underpins the importance of their surveillance nationally. 149 isolates (56 STs) carried 50 other AMR genes, including streptomycin-resistance gene, strA (n=76), and trimethoprim-resistance gene, dfrA14 (n=77). No isolates carried colistin-resistance genes. Three key virulence loci (ybt, clb, and iuc) were prevalent even among isolates carrying  $\beta$ -lactamase genes (ST23 [n=3]), highlighting the potential of AMR and virulence determinants to jointly increase patient morbidity. Notably, the ybt locus, which encodes the iron-scavenging siderophore yersiniabactin, was commonest at the population level, with gene ybtX found in 151 isolates.

**Conclusion:** All such insights may inform targeted interventions and the development of urgently needed therapeutics to combat the emergence and spread of multidrug-resistant *K. pneumoniae* in healthcare settings.

<https://doi.org/10.1016/j.ijid.2024.107754>

### Understanding the Infection Prevention and Control Landscape at a Tertiary Hospital in Blantyre, Malawi

Mrs Dorica Ng'ambi<sup>1,2</sup>, Dr Thomasena O'byrne<sup>1,2</sup>, Prof. Nicholas Feasey<sup>1,2,3</sup>, Dr. Tara Tancred<sup>2</sup>

<sup>1</sup>Malawi Liverpool Wellcome Research Programme, Kamuzu University of Health Sciences

<sup>2</sup>Liverpool School of Tropical Medicine

<sup>3</sup>University of St Andrews

**Introduction:** Surgical site infections (SSIs) can be prevented and reduced by following infection prevention and control (IPC)