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Twenty-Three Years Of Pseudomonas Aeruginosa Trends In South Africa: A Critical Review And Early Warning Of Post-Flood Polymicrobial Risks In Eastern Cape's Vulnerable Or Tambo And Amathole Districts

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Background: *Pseudomonas aeruginosa (P. aeruginosa) is a Gram-negative opportunistic pathogen recognized globally for its increasing antimicrobial resistance (AMR), biofilm formation, environmental persistence, and emerging ability to degrade medical-grade plastics. In South Africa, the pathogen has posed significant clinical and environmental challenges, particularly in flood-vulnerable and resource-constrained regions like KwaZulu-Natal and the Eastern Cape. Despite its global priority status, national preparedness for the evolving threat posed by P. aeruginosa remains unevenly documented and inadequately addressed.*

Aim: *This review aims to synthesize 23 years of South African literature on P. aeruginosa, identify gaps in AMR surveillance, and provide early warning of polymicrobial risks following climate-related disasters in vulnerable districts such as OR Tambo and Amathole in the Eastern Cape.*

Methodology: *A systematic literature review was conducted using electronic databases (PubMed, Scopus, African Journals Online, Web of Science) to retrieve studies published between 2002 and 2025 focusing on P. aeruginosa in clinical and environmental settings across South Africa. Studies were included if they addressed antibiotic resistance trends, carbapenemase gene prevalence, biofilm formation, plastic-degrading enzymes, or hospital outbreaks. Data were synthesized thematically to map resistance trends, identify geographic hotspots, and assess emerging risk factors including climate-related disruptions.*

Results: *Across more than two decades, P. aeruginosa consistently ranked among the top isolated Gram-negative pathogens in tertiary hospitals across KwaZulu-Natal, with growing reports of multidrug resistance (MDR), extended-spectrum beta-lactamase (ESBL) production, and limited carbapenem susceptibility. Recent studies have detected strains capable of degrading polycaprolactone (PCL), using it as a carbon source to enhance survival and virulence. Environmental isolates have also been reported in Eastern Cape freshwater sources, signaling a broader ecological threat. Flood-related infrastructure damage and water contamination are predicted to escalate the spread of these resistant strains in underserved communities.*

Conclusion: *P. aeruginosa represents an escalating threat to South African public health, with mounting evidence of its ability to adapt, persist, and resist treatment. Surveillance gaps, especially in high-risk flood-prone provinces, raise serious questions about the country's disaster readiness. Urgent investment in AMR monitoring, plastic-degradation screening, and climate-health integrated policies is recommended to mitigate the long-term impact of this versatile pathogen.*

Keywords: *Pseudomonas aeruginosa, antimicrobial resistance, plastic-degrading enzymes, Eastern Cape, carbapenem resistance, polymicrobial infections, South Africa*

INTRODUCTION

Pseudomonas aeruginosa is an environmentally resilient, opportunistic pathogen that has become a global symbol of the antimicrobial resistance (AMR) crisis, particularly within hospital and community-acquired infections. Its intrinsic resistance mechanisms, remarkable genomic adaptability, and ability to colonize a wide range of ecological niches including water, soil, and medical devices have made it a persistent challenge for infection control in both high and low resource settings. In South Africa, the threat posed by *P. aeruginosa* is compounded by a combination of fragile health infrastructure, high disease burden, antibiotic misuse, and increasingly frequent extreme weather events.

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This literature review synthesizes 23 years of published research on *P. aeruginosa* in South Africa to evaluate its clinical prevalence, resistance profiles, environmental persistence, and emerging capabilities, such as plastic degradation. Of particular concern is the growing detection of carbapenem-resistant *P. aeruginosa* strains, including those harboring *bla(NDM-1)*, *bla(VIM)*, and *bla(IMP)* genes resistance mechanisms that render most treatment options ineffective.
The Eastern Cape's OR Tambo and Amathole Districts, heavily reliant on agriculture and already vulnerable to seasonal flooding, represent a potential hotspot for post-flood, waterborne outbreaks involving *P. aeruginosa* and other co-occurring pathogens. Floods can mobilize resistant bacteria from wastewater, animal waste, and contaminated water sources into community settings and healthcare facilities potentially leading to polymicrobial infections that are difficult to treat and control. Recent reports of *P. aeruginosa* detection in 7.14% of freshwater sources in the Eastern Cape, with high resistance to common antibiotics, underscore the urgency of this emerging public health risk.

Problem Statement
Pseudomonas aeruginosa continues to emerge as a formidable public health challenge due to its adaptability, multidrug resistance, and environmental persistence. Its growing presence in clinical and environmental settings, coupled with newly discovered traits such as plastic degradation, raises critical concerns about the potential for post-flood outbreaks—particularly in vulnerable, agriculture-dependent districts like OR Tambo and Amathole in the Eastern Cape.
While South Africa has made significant strides in infectious disease management, the question remains: Is the country, and specifically flood-prone regions like the Eastern Cape, adequately prepared to anticipate, detect, and respond to health threats posed by resilient pathogens such as *P. aeruginosa*?

Aim of the Review
This review aims to fill this critical gap by:
- Consolidating two decades of *P. aeruginosa*-related findings in South Africa,
- Mapping trends in clinical and environmental resistance,
- Highlighting the organism's potential for polymicrobial outbreaks post-flooding,
- And calling for urgent, integrated surveillance in flood-prone regions of the Eastern Cape

The global healthcare landscape faces mounting pressure from the continued spread of infectious bacterial strains and the resurgence of known organisms, many of which possess mutations that enhance resistance and virulence. One of the major public health concern organisms globally is *Pseudomonas aeruginosa* (*P. aeruginosa*), a Gram-negative, rod-shaped bacterium that is aerobic but can grow under anaerobic conditions, and is capable of causing disease in plants, animals, and humans. The global concern to *P. aeruginosa* is underscored by its growing prevalence and alarming rates of antibiotic resistance, which pose substantial challenges within healthcare settings. *Pseudomonas aeruginosa* is a versatile and opportunistic pathogen recognized for its role in a variety of infections, particularly among immunocompromised individuals and patients with chronic conditions such as cystic fibrosis. Lately a study reported a shocking plastic degrading effect acquired by *P. aeruginosa* posing a threat to all plastic apparatus and consumables in the hospital settings

Understanding the global burden of common bacterial pathogens (both susceptible and resistant to antimicrobials) is essential to identify the greatest threats to public health. Reducing the burden of death due to infection is an urgent global public health priority. Previous studies have estimated the number of deaths related with drug-resistant infections and sepsis and found that infections remain a principal cause of death globally. Furthermore, *P. aeruginosa* has been identified as the most prevalent organism among cystic fibrosis patients, with a stable yet concerning increase in prevalence with age. The emergence of multidrug-resistant *P. aeruginosa* strains has been a focal point in recent literature, particularly in hospital settings.

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Studies have indicated that antibiotic resistance mechanisms, including the production of extended-spectrum beta-lactamases (ESBLs) and metallo-beta-lactamases (MBLs), are prevalent among *P. aeruginosa* isolates. Surveillance studies reported that a significant percentage of blood culture isolates exhibit resistance to multiple antibiotics, complicating treatment decisions and leading to incraesed morbidity and mortality rates. The spread of carbapenem-resistant Gram-negative bacteria (GNB) with changes in institutional epidemiology continues to evolve globally. The ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter* spp.) pathogens are characterised by higher levels of resistance towards multiple classes of first line and last-resort antibiotics. Even though these pathogens are regularly isolated from clinical environments and are associated in a variety of life-threatening, hospital-associated infections; antibiotic resistant ESKAPE strains have been isolated from surface water, wastewater, food, and soil. These bacteria are generally isolated from clinical settings and linked to a number of possibly fatal diseases associated with hospitals. A virulent bacteriophage (PAP1) highly specific to *P. aeruginosa* was isolated from hospital sewage using a lambda bacteriophage isolation protocol. Several studies have reported the prevalence of *P. aeruginosa* in South Africa, highlighting its presence in both clinical and environmental settings.

Recent studies have highlighted the growing environmental prevalence of *Pseudomonas aeruginosa*, including a reported 7.14% occurrence in freshwater sources in South Africa's Eastern Cape Province, accompanied by alarming resistance rates to commonly used antibiotics such as penicillin and clindamycin. The ongoing floods in various parts of the world including the Eastern Cape pose an additional public health threat, potentially accelerating the spread of water-borne pathogens. These environmental shifts, coupled with infrastructure challenges, may contribute to increased hospital and community-acquired infections, including outbreaks of multidrug-resistant *P. aeruginosa*.
This literature review aims to synthesize the current global understanding of *P. aeruginosa* by examining its epidemiology, environmental persistence, antimicrobial resistance mechanisms, and its emerging plastic-degrading capacity linked to PaP1-encoded enzymes. Additionally, this review explores the broader implications of extreme weather events such as floods in promoting the emergence and dissemination of water-borne pathogens. These include not only *P. aeruginosa*, but also enterohemorrhagic *Escherichia coli* (E. coli O157:H7), *Cryptosporidium*, hepatitis viruses (including hepatitis E), *Campylobacter jejuni*, *Yersinia enterocolitica*, *Legionella pneumophila*, *Mycobacterium* spp., and other opportunistic and chlorine-resistant organisms.
In the South African context, the rise of multidrug-resistant *P. aeruginosa* strains is particularly concerning given its implications for infection control, mortality, and healthcare infrastructure. This review therefore seeks to critically evaluate emerging data on the pathogen's resistance mechanisms especially carbapenem resistance and to assess whether global efforts are keeping pace with the evolving threat posed by this versatile and persistent organism

The recent identification of plastic-degrading enzymes in *P. aeruginosa* raises new concerns for healthcare and industrial environments that rely heavily on polymer-based materials for applications such as tissue reconstruction, drug delivery systems, and medical device production. Clinically, *P. aeruginosa* is a well-established opportunistic pathogen, particularly in burn and wound infections. These infections are often polymicrobial and are increasingly complicated by the presence of multidrug-resistant organisms. The convergence of antimicrobial resistance and environmental adaptability in *P. aeruginosa* underscores the pathogen's growing threat, where even minor lesions may escalate into severe, life-threatening conditions

This literature review aims to critically examine the global health threat posed by the notorious opportunistic pathogen *Pseudomonas aeruginosa*, with a focus on its association with antimicrobial resistance, environmental persistence, polymicrobial co-infections, and the emerging plastic-degrading capabilities linked to PaP1-encoded enzymes

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METHOD

This literature review was conducted by systematically searching for relevant articles published in peer-reviewed journals focusing on *Pseudomonas aeruginosa* globally and in sub-Saharan Africa including South Africa. Databases such as PubMed, Scopus, and Google Scholar were utilized to gather studies from the last three decades. Keywords included *Pseudomonas aeruginosa*, South Africa, antibiotic resistance, and cystic fibrosis. Selected articles were analysed for their findings on the epidemiology, resistance patterns, and clinical implications of *P. aeruginosa* infections globally and measure how the sub-Saharan countries are catching up with the evolution of this organism.

LITERATURE REVIEWS ON *P. AERUGINOSA* RESEARCH DINE IN SOUTH AFRICA (2002–2025)

In one of the sub-Saharan developing countries, South Africa consisting of 9 provinces with approximate 60 million population *P. aeruginosa* caused deterioration of health systems over decades. Eight clonally related *P. aeruginosa* strains producing the clavulanic acid inhibited beta-lactamase GES-2 were isolated from patients at a South African hospital in 3 months in the year 2000 (Poirel *et al*., 2002). Each carried a 150 kb conjugative plasmid with a class 1 integron encoding GES-2, OXA-5 beta-lactamase, and an aminoglycoside-modifying enzyme (Poirel *et al*., 2002). These strains caused several infections, including fatal cases, characterized by resistance to extended-spectrum cephalosporins and reduced susceptibility to imipenem, explaining the clinical challenge at Pretoria Academic Hospital (Poirel *et al*., 2002). A study conducted in Pretoria, South Africa by Weldhagen *et al*. (2004) highlighted the limitations of ceftazidime for detecting GES-2 extended-spectrum β-lactamase (ESBL) in *P. aeruginosa*, showing low specificity (34.4%). The researchers developed an improved PCR method targeting a 371 bp segment of bla(GES-2), enhancing diagnostic accuracy and supporting more cost-effective molecular identification of GES-2-producing strains in clinical settings (Weldhagen *et al*., 2004).

Pseudomonas aeruginosa bacteraemia remains a significant challenge in South African healthcare settings. At Chris Hani Baragwanath Hospital in Johannesburg one of the largest hospitals globally, Perovic et al. (2008) investigated 91 cases of bloodstream infections between 1998 and 1999. Over half of the infections (57.1%) were hospital-acquired, with burn injuries (28%) and HIV infection (24%) identified as key predisposing factors. Multidrug resistance was detected in 15.4% of isolates, and the overall case fatality rate was high at 46.8%, notably higher in adults (75%) than in children (25%) (Perovic *et al*., 2008). Two resistant genotypes were associated with hospital outbreaks, while clusters of susceptible strains among paediatric HIV-positive patients pointed to both nosocomial and possible community transmission (Perovic *et al*., 2008). A study by Labuschagne *et al.,* (2008) embarked on a study to determine the *P. aeruginosa* enzymes conformation associated with β-lactam agents. The emergence and persistence of integron-associated GES-type extended-spectrum β-lactamases (ESBLs) in the world clinical settings are a growing concern (Labuschagne *et al.,* 2008). In a recent study, polymerase chain reaction and sequencing confirmed the presence of bla (GES-5) and a novel bla(GES-5)*-like* gene in three *P. aeruginosa* clinical isolates. The GES-5-like variant displayed an A21E amino acid substitution, not previously reported in the GES enzyme family. Both genes were embedded within class 1 integrons structurally identical to those carrying bla(GES-2)- previously identified in the same geographic region. Their findings highlight the sustained circulation and genetic diversification of GES-type *ESBLs* in South African hospitals and report, for the first time, the emergence of a novel GES-5-like enzyme in the country (Labuschagne *et al.,* 2008).

Igbinosa *et al.* (2012) investigated the prevalence and resistance profiles of *Pseudomonas* species isolated from freshwater and mixed liquor environments in the Eastern Cape Province of South Africa. This study identified included *P. putida*, *P. fluorescens*, *P. aeruginosa*, and other *Pseudomonas* spp., with *P. putida* being the most dominant (Igbinosa *et al.,* 2012). All isolates exhibited 100% resistance to penicillin, oxacillin, clindamycin, and rifampicin, while retaining full susceptibility to ciprofloxacin and gentamicin which showed circulation of multi and extensive drug resistance specices (Igbinosa *et al.,* 2012). Molecular analysis revealed the presence of the bla(TEM) gene in 100% of *P. aeruginosa* isolates, 57.1% of *P. fluorescens*, and lower frequencies in other species (Igbinosa *et al.,* 2012). Similarly, class 1 integrons were detected in the same proportions. These findings underscore the potential of environmental *Pseudomonas* species as reservoirs and vectors of multidrug resistance, raising concerns

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about their role in the dissemination of resistance genes across environmental and clinical settings in the Eastern Cape province (Igbinosa *et al.,* 2012). In a concern about the South African situation, a group of researchers decided to write a letter to the editor of a reputable journal in 2012. In correspondence to the journal "*Journal of Antimicrobial Chemotherapy*", Jacobson et al. (2012) reported a significant outbreak of multidrug-resistant *P. aeruginosa* (MRPA) in a haematology unit of a tertiary academic hospital in Cape Town, South Africa, between January 2010 and April 2011. This letter cited fifteen MRPA isolates were recovered from severely immunocompromised patients, primarily post-stem cell transplant recipients, with a mortality rate of 53% (Jacobson *et al.,* 2012)). These researchers performed Pulsed-field gel electrophoresis (PFGE) which identified a dominant clone (cluster A) in 10 isolates, with one closely related variant (A1), all belonging to sequence type ST233 based on multilocus sequence typing (MLST) (Jacobson *et al.*, 2012).

Through the use of molecular analysis this study revealed that 11 isolates, including all from cluster A and A1, carried the metallo-β-lactamase gene blaVIM conferring high-level resistance to imipenem and meropenem (MIC ≥128 mg/L). One carbapenem-susceptible isolate, genetically unrelated to the outbreak clone, harbored the blaGES-2 gene and was classified as a novel sequence type, ST625. No bla*(IMP)*, *NDM*, *KPC*, or *SPM* genes were detected (Jacobson *et al.*, 2012).

This study underscores the growing prevalence of carbapenem-resistant *P. aeruginosa* in South African hospitals, the urgent need for molecular surveillance, and the importance of identifying resistance determinants to manage nosocomial outbreaks effectively.

Phenol is a toxic pollutant frequently found in industrial wastewater. This study identified five indigenous bacterial strains capable of degrading phenol, isolated from phenol-contaminated effluents (Kumari *et al.,* 2013). Molecular characterization revealed that four isolates were closely related to *Rhodococcus pyridinivorans* and one to *P. aeruginosa* (Kumari *et al.,* 2013). Two representative strains (PD1 and PD5) efficiently utilized phenol as their sole carbon source and tolerated concentrations up to 600 mg/L (Kumari *et al.,* 2013). Their high degradation capacity under stress highlights their potential application in bioremediation of phenol-laden wastewater (Kumari *et al.,* 2013). This study clearly show that *P. aeruginosa* can adapt and survive most harsh condition and can utilize phenol as carbon source for survival

Pseudomonas aeruginosa remains a significant pathogen in paediatric burn care, contributing to wound morbidity despite relatively low infection rates. In a retrospective analysis of 2,632 admissions over 36 months at a paediatric burn's unit in Cape Town, South Africa, 1.3% of patients developed clinically significant *P. aeruginosa* infections (Coetzee *et al.,*2013). These cases accounted for 23 skin graft failures and extended wound management. Antiseptic resistance was alarmingly high for povidone-iodine (92.5%), while all isolates remained sensitive to chlorhexidine (Coetzee *et al.,*2013). Among systemic antibiotics, tobramycin showed the lowest resistance (3.3%), in contrast to piperacillin-tazobactam (36.1%) (Coetzee *et al.,*2013). The findings underscore the need for targeted antimicrobial stewardship, antiseptic review, and rigorous infection control strategies to mitigate the burden of resistant *P. aeruginosa* in paediatric burn populations (Coetzee *et al.,*2013). *P. aeruginosa* infection is a major cause of morbidity in burns patients. There is a paucity of publications dealing with this infection in the paediatric population. This study describe the incidence, microbiology and impact of *P. aeruginosa* infection in a dedicated paediatric burns unit (Coetzee *et al.,*2013).

Govender *et al.* (2015) reported the first case of bla(VIM-2*)* producing *P. aeruginosa* in a public hospital in Port Elizabeth, South Africa. This study clearly demonstrate that *P. aeruginosa* can infect all age groups. According to the study the isolate, recovered from a 76-year-old female patient post-hip replacement, exhibited resistance to all tested antibiotics except colistin. In this study despite targeted treatment, intermittent colistin dosing and resulting nephrotoxicity led to the emergence of colistin-resistant strains (Govender *et al.,* 2015). The patient ultimately succumbed to multiple complications after a 19-week hospital stay. Molecular analysis confirmed the presence of the bla(VIM-2*)* gene within a class 1 integron, highlighting both the clinical consequences of inadequate antibiotic stewardship and the growing threat of multidrug-resistant *P. aeruginosa* in under-resourced settings (Govender *et al.,* 2015). This case underscores the urgent need for comprehensive antimicrobial stewardship and surveillance programs across South African hospitals (Govender *et al.,* 2015). Annear et al.

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(2017) embarked on an investigating the molecular basis of carbapenem resistance in *Pseudomonas aeruginosa* isolates from public healthcare facilities in Port Elizabeth, South Africa. Among 234 clinical isolates, 81 were resistant to carbapenems. PCR screening revealed the presence of the bla(VIM-2) metallo-β-lactamase gene in 15 isolates (Annear *et al*., 2017).This study identified multilocus sequence typing (MLST) of six novel sequence types, with a dominant cluster of nine isolates provisionally assigned as ST1, five of which were epidemiologically linked to a single hospital ward and included an environmental source (Annear *et al*., 2017). The study highlights the role of bla(VIM-2) and potential environmental reservoirs in nosocomial transmission, emphasizing the need for enhanced surveillance and infection control measures in South African healthcare settings at Port Elizabeth (Annear *et al*., 2017).

South African continued to experience *Candida albicans* and *P. aeruginosa* frequently co-isolated in polymicrobial infections, particularly in cystic fibrosis patients. While their interactions are largely antagonistic mediated by both physical contact and secreted factors emerging, evidence highlights the significant role of host pathogen cross-talk, particularly through immunomodulatory eicosanoids (Fourie *et al.,* 2016). The study found that both pathogens can metabolize host-derived arachidonic acid into prostaglandin E_2 (PGE_2), influencing immune responses and infection outcomes (Fourie *et al.,* 2016). Understanding the contribution of both host and pathogen produced eicosanoids is essential for unravelling the complex dynamics of polymicrobial infections and may offer new avenues for therapeutic intervention (Fourie *et al.,* 2016). Polymicrobial interactions between *Candida* spp. and *P. aeruginosa* are complex and context-dependent, extending beyond a simplistic antagonistic model. This review examines the molecular mechanisms influencing their interplay, including quorum sensing, phenazine production, iron competition, and fatty acid metabolites (Fourie *et al.,* 2019). It further contextualizes these dynamics in clinical sites such as the lungs, wounds, and gastrointestinal tract, emphasizing the role of the host environment and experimental models (Fourie *et al.,* 2019). The review calls for future research into oxylipin signaling, microbial plasticity, and the broader quorum sensing networks that modulate co-infection outcomes (Fourie *et al.,* 2019).

Antimicrobial resistance remains a global health threat, with *Pseudomonas aeruginosa* representing a major nosocomial pathogen due to its intrinsic and acquired resistance mechanisms. This surveillance study analyzed antibiotic susceptibility profiles of *P. aeruginosa* isolates from bloodstream infections in South Africa between 2014 and 2015 (Singh-Moodley *et al.,*2018). This study reported that overall susceptibility remained high, though a slight decline was observed over the two years (Singh-Moodley *et al.,*2018). Carbapenem resistance was primarily found associated with the presence of bla(VIM) (12%) and less frequently with bla(GES), bla(NDM), and bla(OXA-48) variants (Singh-Moodley *et al.,*2018). No detection of bla(IMP), bla(KPC), or bla(VEB-1) was reported (Singh-Moodley *et al.,*2018). Efflux pump overexpression was common among non-susceptible isolates, while porin loss was rare (Singh-Moodley *et al.,*2018). These findings provide critical baseline data to inform antimicrobial stewardship and guide empirical treatment strategies in South African hospitals.

Carbapenem resistance is an escalating global public health concern, particularly among Gram-negative pathogens such as *P. aeruginosa*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii* (Codjoe *et al.,* 2017). This resistance is driven by intrinsic mechanisms and the spread of transferable carbapenemase genes (Codjoe *et al.,* 2017). While extensively reported in Europe, Asia, and South America, data from sub-Saharan Africa remain scarce (Codjoe *et al.,* 2017). This review provides a comprehensive update on carbapenem resistance mechanisms and emphasizes the need for improved surveillance and containment in underrepresented regions.

This retrospective study assessed antimicrobial resistance (AMR) patterns of *Pseudomonas aeruginosa* isolated from canine clinical cases at a South African veterinary hospital between 2007 and 2013. A total of 155 *P. aeruginosa* isolates were analyzed, with 100% exhibiting resistance to at least one antimicrobial and 92% classified as multidrug-resistant (MDR) (Eliasi *et al.,*.2020). High resistance rates were observed against lincomycin (98%), penicillin-G (96%), orbifloxacin (90%), and trimethoprim-sulfamethoxazole (90%) (Eliasi *et al.,*.2020). Notably,

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lower resistance rates were recorded for imipenem (6%), tobramycin (12%), and amikacin (16%). All MDR isolates showed significant resistance to β-lactams, fluoroquinolones, and lincosamides (Eliasi *et al.*,.2020). The findings highlight the clinical relevance of *P. aeruginosa* in veterinary infections and emphasize the need for informed antibiotic stewardship in veterinary practice.

This retrospective study investigated the clinical burden, antimicrobial management, and outcomes of *P. aeruginosa* bloodstream infections (PABSI) in children at a tertiary paediatric hospital in Cape Town, South Africa (Dame *et al.*, 2020). Over the study period, the incidence was 5.4 PABSI episodes per 10,000 hospital admissions. Respiratory distress was the most frequent clinical presentation (37.4%). While 75.8% of *P. aeruginosa* isolates were susceptible to all antipseudomonal antibiotic classes tested, only 54.9% of patients received appropriate empiric therapy (Dame *et al.*, 2020). The overall mortality rate was 24.2%. Inappropriate empiric therapy, infections present on admission, and absence from ICU at diagnosis were significantly associated with increased 14-day mortality (Dame *et al.*, 2020). Timely and appropriate empiric treatment was shown to be critical in improving outcomes in paediatric PABSI cases (Dame *et al.*, 2020).
This study assessed the antimicrobial resistance profiles and resistance gene carriage of *P. aeruginosa* isolated from nonclinical environments in Mthatha, Eastern Cape, South Africa. A total of 36 *P. aeruginosa* strains (70.6% of 51 *Pseudomonas* spp.) were recovered from abattoir wastewater and surface water (Hosu *et al.,* 2021a). Alarmingly, high resistance rates were observed to aztreonam (86.1%), ceftazidime (63.9%), piperacillin (58.3%), and imipenem (50%) (Hosu *et al.,* 2021a). Over half of the isolates (55.6%) were multidrug-resistant (MDR), with MAR indices ranging from 0.08 to 0.69. Real-time PCR revealed high prevalence of extended-spectrum β-lactamase (ESBL) genes: *bla_SHV* (93.3%), *bla_TEM* (40%), and *bla_CTX-M* (20%). The findings indicate that *P. aeruginosa* from environmental sources can harbor clinically significant resistance genes, posing a serious public health risk (Hosu *et al.,* 2021a). Continuous environmental surveillance is essential to mitigate potential dissemination of MDR pathogens into human and animal populations more especially after the June 2025 heavy floods experience. The eastern cape and Mthatha hypothetically may experience an outbreak of polymicrobial from environment contaminated by dead animals and closed to 90 people reported dead at the time of this article writing (https://www.ewn.co.za/2025/06/17/ec-flooding-death-toll-rises-to-90).

To support the hypothesis regarding potential health deterioration in the Eastern Cape following the June 2025 floods, evidence from Sharma et al. (2003) provides relevant insights. Their study highlights how the emerging water-borne pathogens, including *P. aeruginosa*, pose increasing health risks globally (Sharma *et al.*, 2003). The emergence of chlorine-resistant and drug-resistant organisms such as *Cryptosporidium*, *E. coli* O157:H7, *Vibrio cholerae* O139, and others may rise as being reported in the study of Sharma *et al.*, (2003) which has raised concerns about the adequacy of current water quality regulations. The situation of the Eastern Cape population requires monitoring as it has been reported that factors contributing to the rise of waterborne pathogens include urbanization, immunocompromised populations, and horizontal gene transfer (Sharma *et al.*, 2003. Addressing this possible threat in the Eastern Cape based on current floods the health team requires to enhance surveillance, updated water safety standards monitoring, and targeted public health interventions based on the laboratory daily results to curb any spread of the diseases.
Following the severe floods in the Eastern Cape in June 2025, concerns about the rise in infectious diseases particularly those caused by resistant pathogens are substantiated by prior regional data. A study conducted between 2017 and 2019 at Nelson Mandela Academic Hospital and surrounding clinics reported a high prevalence of multidrug-resistant (MDR) *P. aeruginosa* across the province's four district municipalities (Hosu *et al.,* 2021b). Of significant concern, 36.8% of isolates were MDR, exhibiting strong resistance to critical antibiotics including piperacillin (64.2%), aztreonam (57.8%), and imipenem (46.6%) (Hosu *et al.,* 2021b). Molecular analysis revealed the widespread presence of extended-spectrum β-lactamase (ESBL) genes *blaTEM* (79.3%), *blaSHV* (69.5%), and *blaCTX-M* (31.7%), with metallo-β-lactamase gene *blaIMP* detected in 1.25% of strains (Hosu *et al.,* 2021b).

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These findings underscore the potential public health risks in post-flood Eastern Cape, where compromised sanitation, water contamination, and overcrowded health facilities may catalyze the spread of MDR pathogens like *P. aeruginosa*. Enhanced surveillance, infection control, and antimicrobial stewardship are urgently needed to mitigate the emerging threat of resistant infections in the aftermath of environmental disasters.

The June 2025 floods in the Eastern Cape have intensified public health concerns regarding the spread of waterborne, drug-resistant pathogens. Previous studies by Hosu et al. (2021a, 2021b) from both non-clinical and clinical environments in the region provide critical insight into the infectious risks posed by *P. aeruginosa* under such conditions.

Mapipa et al. (2021) investigated hospital wastewater (HWW) effluents and identified 54 *P. aeruginosa* isolates harboring key virulence genes (*toxA*, *lasA*, *lasB*, *popB*). This study found that although the isolates showed full susceptibility to gentamicin, amikacin, and imipenem, resistance to ceftazidime reached 63%, with multiple antibiotic resistance (MAR) indices ranging from 0.23 to 0.38 indicative of exposure to high-risk antimicrobial environments (Mapipa *et al.,* 2021). And this Eastern Cape situation was already alarming before the devastating June 2025 floods and 4 years back already this study detected virulence factors alongside moderate antibiotic resistance highlighting the potential for wastewater to act as a reservoir for pathogenic and resistant *P. aeruginosa* strains (Mapipa *et al.,* 2021).

Complementary findings by Hosu et al. (2021b) in clinical settings from the same region further confirm the presence of multidrug-resistant *P. aeruginosa* in-patient samples, reinforcing the link between environmental reservoirs and human infections.

Together, these studies underscore the urgent need for integrated environmental and clinical surveillance, especially in post-flood scenarios where pathogen transmission may be accelerated. With hospital drainage systems compromised and stagnant floodwaters persisting, the risk of community-wide outbreaks of virulent, resistant *P. aeruginosa* infections is significantly heightened in the Eastern Cape

A study done by Fourie et al., (2021) indicates that Candida albicans is frequently co-isolated with *P. aeruginosa* in clinical polymicrobial infections, particularly in immunocompromised individuals. This clearly indicate what health practitioners should be on the lookout post devastating situations where health systems and clean water were affected. This study reported that their interaction is multifaceted, involving both direct physical contact and modulation via secreted factors (Fourie *et al.*, 2021). This study investigated the transcriptional response of Candida albicans during early-stage static biofilm formation in the presence of *P. aeruginosa* (Fourie *et al.*, 2021). Transcriptomic profiling revealed that approximately 40% of the C. albicans genome (2,537 open reading frames) was differentially regulated upon co-culture (Fourie *et al.*, 2021). The dominant transcriptional response was consistent with hypoxia, metal ion starvation—particularly iron and zinc—and cellular stress (Fourie *et al.*, 2021). Genes involved in membrane synthesis, morphogenesis, biofilm development, and phenotypic switching were also significantly affected (Fourie *et al.*, 2021). These findings demonstrate that C. albicans undergoes substantial metabolic and morphological reprogramming in response to *P. aeruginosa*, with potential implications for virulence modulation, commensalism, and antifungal resistance in mixed-species infections (Fourie *et al.*, 2021)**.**

A study by Opperman *et al.,* (2022) was initiated following an unusual citywide outbreak of community-acquired *P. aeruginosa* infections occurred in Cape Town, South Africa, between December 2016 and September 2017, involving over 3,300 cases reaching rates 2.3 times the baseline. This study revealed a whole genome sequencing dominant clonal lineage, ST303, characterized by enhanced virulence determinants including genes related to biofilm formation, iron acquisition, and gastrointestinal tract penetration (Opperman *et al.,* 2022). These features may confer adaptive advantages in environmentally stressed conditions, such as drought.

This outbreak underscores the pathogen's ability to persist and spread outside clinical settings, driven by environmental resilience and genomic plasticity. Importantly, both *P. aeruginosa* and other multidrug-resistant (MDR) and extensively drug-resistant (XDR) organisms have been identified in clinical and non-clinical environments across the Eastern Cape province in recent years (Hosu et al., 2021a; 2021b), including hospital wastewater and community sources. Given this background of high environmental burden and antimicrobial

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resistance, the severe flooding experienced in the Eastern Cape in June 2025 poses a significant risk for a surge in opportunistic, waterborne infections.

I hypothesize that flooding may facilitate wider dissemination of already established MDR and XDR strains, including *P. aeruginosa*, through disruption of sanitation systems, overburdened healthcare infrastructure, and increased environmental exposure. These conditions could mimic or even exceed the outbreak scenario observed in Cape Town, particularly given the known presence of virulence factors and mobile genetic elements in regional isolates. This literature review encourages for proactive environmental surveillance and public health preparedness are urgently needed in post-flood Eastern Cape to monitor and contain potential outbreaks of virulent, drug-resistant *P. aeruginosa* and other opportunistic pathogens.

Multidrug-resistant (MDR) Gram-negative bacteria remain a leading cause of healthcare-associated infections, complicating treatment and increasing patient morbidity and mortality. Perovic *et al.,* (2023) study assessed the in vitro activity of the novel β-lactam/β-lactamase inhibitor combination ceftolozane-tazobactam (C/T) against bloodstream isolates of *Escherichia coli* (n=100), *Klebsiella pneumoniae* (n=100), and *Pseudomonas aeruginosa* (n=100) collected in South Africa between 2010 and 2020 through the GERMS-SA surveillance program. This study found that resistance to C/T was observed in 16% of *E. coli*, 28% of *K. pneumoniae*, and 13% of *P. aeruginosa* isolates (Perovic *et al.,* 2023). Whole-genome sequencing of resistant strains revealed diverse sequence types, including the globally disseminated ST131 in *E. coli*, ST307 in *K. pneumoniae*, and ST111 in *P. aeruginosa* (Perovic *et al.,* 2023). The genomes harbored multiple resistance determinants spanning aminoglycosides, β-lactams, macrolides, sulfonamides, quinolones, and disinfectant resistance genes. Notably, all isolates had no prior exposure to C/T, suggesting the presence of pre-existing resistance mechanisms capable of conferring cross-resistance to newer β-lactam–inhibitor combinations (Perovic *et al.,* 2023). These findings underscore the adaptive potential of MDR pathogens and highlight the urgent need for ongoing genomic surveillance to guide effective antimicrobial stewardship strategies in South Africa and globally.

Pseudomonas aeruginosa is a globally prevalent pathogen in chronic wound infections and is particularly common in tropical and low-resource settings (Phan *et al.,* 2023). It thrives in moist environments and is known for its resistance to antibiotics and persistence on surfaces. Global data show that *P. aeruginosa* is often the second most isolated pathogen from chronic wounds, with even higher prevalence in parts of Southeast Asia (Phan *et al.,* 2023). While regional variations exist, environmental conditions such as humidity and inadequate wound care strongly influence its distribution (Phan *et al.,* 2023).

In the context of the recent flooding in the Eastern Cape, these findings carry significant implications. Floodwaters can harbor *P. aeruginosa*, and survivors with open wounds, especially those with underlying conditions such as diabetes or vascular diseases, are at high risk of acquiring chronic infections. The elderly many of whom suffer from chronic ulcers or delayed wound healing are particularly vulnerable.

Moreover, the combination of compromised infrastructure, limited access to sterile care, and disrupted supply chains may delay effective treatment, increasing the risk of multidrug-resistant *P. aeruginosa* infections (Phan *et al.,* 2023). The use of the Levine wound swab technique may offer a practical diagnostic method in such emergency contexts, but its findings should be interpreted in conjunction with clinical assessments (Phan *et al.,* 2023).

Pseudomonas aeruginosa AUST-03 (ST242) is a globally recognized epidemic strain linked to poor clinical outcomes in people with cystic fibrosis (pwCF). Hamiwe *et al.,* (2024) study, reported the first genomic characterization of AUST-03 in South African pwCF, with isolates obtained from two pediatric patients attending a public hospital. Whole-genome sequencing revealed extensive drug resistance, including overexpression of key multidrug efflux pumps (MexAB-OprM, MexCD-OprJ, MexEF-OprN, MexXY-OprM), and close phylogenetic relatedness to a 2020 Russian AUST-03 isolate (Hamiwe *et al.,* 2024). The detection of this high-risk clone in a low-resource healthcare setting underscores the urgent need for enhanced molecular surveillance, reinforced infection control strategies, and equitable access to advanced CF therapies to prevent regional spread and safeguard clinical outcomes in vulnerable CF populations.

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Clinical and public health relevance in South African Context is that the emergence of AUST-03 in South African pwCF, particularly in the public sector, signals a concerning shift in the local epidemiology of *P. aeruginosa*. With the Eastern Cape and other provinces already managing a fragile healthcare system and limited CF resources, the presence of an epidemic MDR strain could severely undermine infection control efforts, accelerate pulmonary decline in CF patients, and increase healthcare costs. Most critically, MDR *P. aeruginosa* limits therapeutic options in a population that already faces restricted access to advanced CF care and novel antimicrobials.

Arowolo et al. (2023) conducted a systematic review and meta-analysis to assess the burden and genetic drivers of carbapenem resistance in *Acinetobacter baumannii* (CRAB) and *P.aeruginosa* (CRPA) across Sub-Saharan Africa between 2012 and 2022. Following PRISMA-P 2020 protocols, 25 studies were included, revealing a pooled prevalence of 20% for CRAB and 8% for CRPA, with significant heterogeneity across studies ($I^2 > 98\%$) (Arowolo et al. 2023). Arowolo et al. (2023) found that molecular analysis highlighted a high frequency of clinically significant carbapenemase genes, including bla (OXA-23), bla(VIM), and bla(NDM) in *A. baumannii*, and bla(VIM), bla(NDM), and bla(IMP) in *P. aeruginosa*. The review done by Arowolo et al. (2023) underscores the alarming spread of multidrug-resistant pathogens in a region with limited diagnostic and therapeutic resources.

These findings call for urgent regional investment in antimicrobial resistance surveillance, laboratory capacity building, and policy-level interventions to address the escalating public health threat posed by carbapenem-resistant Gram-negative bacteria in Africa

Another study by Ramkisson *et al.,* (2023) caution that carbapenem antibiotics, long considered last-resort agents for treating multidrug-resistant Gram-negative infections, are increasingly compromised by the global rise of carbapenem resistance. Ramkisson *et al.,* (2023) emphasized that resistance to these critical drugs primarily mediated by the enzymatic action of carbapenemases has been reported not only in clinical settings but also across agricultural environments. Of growing concern is the global dissemination of carbapenemase-producing Enterobacterales (CPE), including *Klebsiella pneumoniae*, *Enterobacter spp.*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*, all of which have shown rising resistance trends in South Africa (Ramkisson *et al.,* 2023). This issue is particularly pressing for agriculturally dependent provinces such as the Eastern Cape, where human-animal-environment interfaces are closely linked and where health infrastructure is often under-resourced. Although global data from North America, Europe, and Asia have confirmed the presence of CPE in livestock, seafood, and companion animals, Africa remains critically underrepresented in CPE surveillance, especially in rural and agricultural zones.

Given the Eastern Cape's vulnerability exacerbated by limited veterinary diagnostic capacity, antibiotic use in livestock, and environmental runoff the potential for CPE transmission through the food chain and farm waste exposure is both plausible and alarming. A comprehensive "One Health" approach is urgently needed to monitor and mitigate the spread of carbapenem resistance across sectors. Surveillance of CPE in the Eastern Cape could serve as an essential sentinel for understanding broader antimicrobial resistance dynamics in Sub-Saharan Africa amid flooding which could spread the disease.

Jung et al. (2024) investigated three extensively drug-resistant *Pseudomonas aeruginosa* isolates from Gauteng, South Africa, which were resistant to all antibiotics except colistin. Whole genome sequencing revealed that all isolates belonged to the international high-risk clone ST773 and carried the bla(NDM-1) gene, a potent carbapenemase (Jung *et al.*, 2024). These isolates shared close genetic relatedness with *bla(NDM-1)*-positive ST773 strains from countries including Hungary, India, Nigeria, South Korea, and the USA (Jung *et al.*, 2024).

Importantly, the resistance genes, including *bla(NDM-1)*, *floR2*, *rmtB4*, and *tet*G, were located on a mobile integrative and conjugative element (ICE), indicating high potential for horizontal gene transfer (Jung *et al.*, 2024). Jung et al. (2024) findings underscore the global spread and local establishment of highly resistant *P. aeruginosa* clones in South Africa and highlight the need for urgent surveillance, infection control, and containment strategies to address this public health threat.

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Chiliza *et al.,* (2024) embarked on a surveillance and monitoring five-year retrospective study to assesse the prevalence of *ESBL*-producing Gram-negative ESKAPE pathogens in clinical isolates from Inkosi Albert Luthuli Central and Mahatma Gandhi Memorial Hospitals in KwaZulu-Natal Province, South Africa. This study found that among the 4,781 isolates reviewed, *Pseudomonas aeruginosa* was the second most prevalent (24.05%), following *Klebsiella pneumoniae* (Chiliza *et al.,* 2024). Although carbapenems demonstrated high efficacy against most ESBL-positive isolates, *P. aeruginosa* strains showed signs of emerging resistance posing a growing concern for infection control, especially in the face of climate-sensitive health challenges (Chiliza *et al.,* 2024).
The Eastern Cape and KwaZulu-Natal are both high-risk provinces for flooding and infrastructure disruption, which can exacerbate the spread of multidrug-resistant organisms like *P. aeruginosa* through contaminated water sources and damaged sanitation systems. The study underscores the urgent need for enhanced AMR surveillance, disaster-preparedness in clinical microbiology, and proactive infection control strategies particularly in regions prone to climate-induced public health emergencies.

Antimicrobial resistance (AMR) continues to pose a critical public health threat, with *P.aeruginosa* and *Acinetobacter baumannii* increasingly demonstrating multidrug resistance (MDR). Shezi *et al*., (2024) performed retrospective study analyzing resistance trends over a five-year period (2017–2022) using clinical data from three (Grey's Hospital, Harry Gwala Hospital and Northdale Hospital) major state hospitals in Pietermaritzburg (PMB), KwaZulu-Natal Province. Of the 4,469 isolates reviewed, *P. aeruginosa* was predominant (59.5%) and exhibited moderate resistance to beta-lactams (56.6%) and exceptionally high resistance to tigecycline (98.8%), while remaining relatively susceptible to most tested agents. In contrast, *A. baumannii* showed higher overall resistance, particularly to third-generation cephalosporins (Shezi *et al*., 2024).
These findings not only highlight the persistence of *P. aeruginosa* in KwaZulu-Natal's healthcare settings but also emphasize the potential for cross-border microbial threats, particularly to neighbouring, flood-prone provinces like the Eastern Cape. The ecological and clinical movement of resistant strains between adjacent regions exacerbated by climate-related disasters and strained sanitation infrastructure necessitates broader regional surveillance and coordinated AMR response frameworks. This study supports calls for early-warning systems, integrated antibiotic stewardship, and provincial-level AMR preparedness, particularly as *P. aeruginosa* continues to emerge as a versatile, environment-adapted pathogen.

The discovery of plastic-degrading enzymes in clinical isolates of *Pseudomonas aeruginosa* marks a concerning evolution in hospital-acquired infections by Howard et al., 2025. This study identified a *P. aeruginosa* strain capable of degrading polycaprolactone (PCL) a medically relevant plastic by 78% within seven days, using it as a sole carbon source and enhancing its biofilm formation and virulence (Howard et al., 2025). These findings suggest that plastic-based medical devices and infrastructure could become reservoirs and nutrient sources for persistent, drug-resistant pathogens.
In the South African context, where *P. aeruginosa* already contributes significantly to multidrug-resistant infections in both public and private healthcare settings, this plastic-degradation capability poses an emerging threat. The widespread reliance on polymer-based medical tools particularly in resource-constrained hospitals may accelerate the pathogen's environmental survival and transmission.
Without robust, proactive surveillance of plastic-degrading *P. aeruginosa* strains, South Africa risks facing hard-to-eradicate hospital infections, particularly in high-risk areas such as intensive care units, neonatal wards, and flood-affected regions like the Eastern Cape and KwaZulu-Natal. This evolving pathogenic trait calls for urgent research, updated infection control policies, and routine screening for plastic-degrading enzymes in nosocomial bacteria to protect infrastructure, devices, and patient outcomes.

DISCUSSION

Over the past two decades, *P. aeruginosa* has emerged as a resilient and increasingly complex public health threat across South African healthcare and environmental settings. Multiple retrospective studies from tertiary hospitals including Inkosi Albert Luthuli Central, Mahatma Gandhi Memorial, Grey's, Harry Gwala, and Northdale

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consistently report *P. aeruginosa* among the most frequently isolated Gram-negative pathogens. These isolates often exhibit multidrug resistance (MDR), especially to beta-lactams and cephalosporins, though carbapenems still retain partial efficacy.

Of particular concern is the geographic spread of resistance patterns. While KwaZulu-Natal has generated substantial resistance surveillance data, regions like the Eastern Cape similarly prone to flooding, infrastructural strain, and limited healthcare capacity lack comparable systematic AMR data. This raises concerns about underreported MDR infections, especially post-disaster when waterborne transmission risk increases.

Adding a new layer of complexity is the recent identification of *P. aeruginosa* strains capable of degrading medically relevant plastics such as polycaprolactone (PCL). One South African study demonstrates that a clinical *P. aeruginosa* isolate degraded PCL by 78% in just seven days and used it as its sole carbon source, promoting persistence and pathogenicity via enhanced biofilm formation. This finding redefines the hospital environment not just as a passive site of contamination but as a possible nutrient-rich niche that sustains MDR pathogens through plastic degradation.

These capabilities combined with *P. aeruginosa*'s established resistance to third-generation cephalosporins and increasing resistance to carbapenems suggest a pathogen that is adapting to both antimicrobial pressure and environmental selection. The convergence of these survival mechanisms places *P. aeruginosa* at the forefront of South Africa's nosocomial threat landscape.

CONCLUSION

South African data over the last 20+ years reveal a worrying trajectory for *Pseudomonas aeruginosa*, from a known opportunistic pathogen to an adaptive, persistent, and environmentally resilient MDR organism. The emergence of plastic-degrading capacities could further entrench its survival in hospital settings, particularly where infrastructure relies heavily on polymer-based medical tools. Post-flood conditions such as those seen in OR Tambo and Amathole Districts in the Eastern Cape may exacerbate transmission and resistance dissemination through waterborne routes and overwhelmed healthcare systems.

RECOMMENDATIONS

1. Establish National AMR Surveillance in vulnerable provinces expand routine genomic and phenotypic surveillance of *P. aeruginosa* to underrepresented regions like the Eastern Cape to identify evolving resistance trends and environmental reservoirs.
2. Screen for plastic-degrading genes in clinical isolates given the potential for biofilm enhancement and infrastructure degradation, routine molecular screening for PaP1-encoded plastic-degrading enzymes in hospital-acquired *P. aeruginosa* should be incorporated into AMR labs.
3. Integrate Environmental Health into hospital infection control consider environmental plastic waste, piping, and device surfaces as part of a broader *P. aeruginosa* containment strategy. Hospitals, especially in flood prone areas, must update sanitation and sterilization protocols.
4. Develop emergency-preparedness plans for flood-affected regions coordinate health disaster plans that include amr risk assessments for pathogens like *P. aeruginosa* in Eastern Cape and KwaZulu-Natal. These plans should include potable water protection, mobile diagnostic capacity, and pre-positioned antimicrobials.
5. Strengthen Antibiotic Stewardship and diagnostics continue promoting judicious antibiotic use while investing in rapid diagnostics, especially in public-sector hospitals where MDR *P. aeruginosa* prevalence is highest.
6. Encourage One Health Research collaboration further study is needed on how *P. aeruginosa* moves between human, environmental, and possibly agricultural systems especially given its plastic-degrading potential.

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