Developing an Antimicrobial Strategy for Sepsis in Malawi

# Preface

Placeholder

# Introduction

## Chapter Overview

The syndrome of sepsis is an ancient one; from Hippocrates to Galen and Semmelweis, the potentially serious consequences of infection have long been recognized. Modern definitions of sepsis conceptualise it as a syndrome of life threatening organ dysfunction due to a deleterious and dysregulated host response to infection, but despite increased understanding of its pathogenesis, mortality from sepsis remains high. Progress has been made in improving sepsis mortality in high income settings through timely application of basic care: early appropriate antimicrobials, aggressive fluid resuscitation and organ support largely in a critical care environment. Limited data from low resource settings including sub-Saharan Africa (sSA) suggest that mortality remains high, and increasing evidence suggests that exporting high-income setting sepsis protocols to sSA has the potential to do harm. Data to guide sepsis management protocols for sSA are urgently needed.

Data on sepsis aetiology from sSA to guide antimicrobial strategies are lacking; currently, in Blantyre Malawi, for example, empirical management of sepsis is the norm and patients often receive prolonged empiric courses of broad spectrum antimicrobials – largely ceftriaxone, a third-generation cephalosporin antibiotic. The effects of this at an individual level are unknown, but on a population level invasive Escherichia coli and Klebsiella pneumoniae bacteria are showing an alarming increase in ceftriaxone resistance since the drug was introduced in Malawi in 2005. The majority of these resistant bacteria are so-called extended-spectrum beta lactamase producers (ESBL-producers) and are often untreatable with locally available antimicrobials. Novel antimicrobial strategies are needed to safely preserve ceftriaxone - a first and last line antibiotic - for those who need it.

It is the hypothesis of this thesis, then, that sepsis is Malawi is caused by a wide variety of infections that are currently unrecognised and untreated, and that this is contributing to high sepsis mortality. Conversely, prolonged ceftriaxone exposure in sepsis survivors is causing acquisition and carriage of resistant bacteria (principally ESBL Enterobacteriaceae, henceforth ESBL-E) and their transportation into the community. I will argue that sustainable antimicrobial strategies for sepsis in sSA can not only consider mortality; the unintended consequences in terms of antimicrobial resistance (AMR) acquisition in a setting where empiric management of infection is the norm must also be considered, and mitigated against where possible. In this chapter, I will review, firstly, the definitions, epidemiology, aetiology and management of sepsis, with a focus on aetiology and antimicrobial treatment; and secondly, the epidemiology and drivers of ESBL-E carriage, both with a focus on sSA.

## Sepsis in sub-Saharan Africa

### Search strategy

A review of the literature was undertaken to identify prospective cohort, case control studies or randomised controlled trials (RCTs) of sepsis in sub-Saharan Africa with the search terms sepsis *and* ((Angola *or* Benin *or* Botswana *or* Burkina Faso *or* Burundi *or* Cameroon *or* Cape Verde *or* Central African Republic *or* Chad *or* Comoros *or* Republic of the Congo *or* Congo Brazzaville *or* Democratic republic of the Congo *or* Cote d’Ivoire *or* Djibouti *or* Equatorial Guinea *or* Eritrea *or* Ethiopia *or* Gabon *or* The Gambia *or* Ghana *or* Guinea *or* Guinea-Bissau *or* Kenya *or* Lesotho *or* Liberia *or* Madagascar *or* Malawi *or* Mali *or* Mauritania *or* Mauritius *or* Mozambique *or* Namibia *or* Niger *or* Nigeria *or* Reunion *or* Rwanda *or* Sao Tome and Principe *or* Senegal *or* Seychelles *or* Sierra Leone *or* Somalia *or* South Africa *or* Sudan *or* Swaziland *or* Eswatini *or* Tanzania *or* Togo *or* Uganda *or* Western Sahara *or* Zambia *or* Zimbabwe) *or* Africa). Pubmed and scopus were searched, yielding 5460 unique studies on 17 July 2018. Inclusion criteria were any prospective cohort, RCT or case-control studies of sepsis in sSA (defined as taking place in the countries listed in search terms panel) recruiting patients using sepsis 1,2 or 3 definitions. Abstract review was undertaken resulting in inclusion of 91 studies for full text review. Eleven publications providing data on eight prospective cohorts[[1](#ref-Jacob2009)–[8](#ref-Amir2017)] and three intervention studies (two RCTs[[9](#ref-Andrews2014),[10](#ref-Andrews2017a)] and one before-after intervention[[11](#ref-Jacob2012)]) were identified. These data inform the following review, alongside non-systematically searched studies examining sepsis in high-resource settings.

In order to put sepsis aetiology data in context, systematic searches of the Pubmed and Scopus databases for leptospirosis, brucellosis, Q fever, Rickettsioses, arboviruses (dengue, or chikungunya) and histoplasmosis prevalence in unselected sepsis or fever cohorts in sSA were undertaken. Because a recent systematic review has examined these pathogens up to 2013 (see “sepsis aetiology” below), the date of these searches were restricted the 2014 to the present. Any studies examining disease prevalence in cohorts of febrile adults or children were included; outbreaks were excluded. Studies where the inclusion criteria were not clear (including those with, for example, “suspected leptospirosis” with no further details) were excluded. Finally, systematic searches of Pneumocystis Jiroveci pneumonia (PCP) were made using the search terms below; because a recent systematic review has examined the role of PCP up to 2015, the date on this search was restricted to 2015 or later. Table ?? shows the search terms, number of of hits and number of included studies after full text review: nine studies provided data on Leptospirosis[[12](#ref-Zida2018)–[20](#ref-Chipwaza2014)], seven on Brucellosis[[21](#ref-Cash-Goldwasser2018)–[27](#ref-Feleke2015)], seven on Q-fever[[19](#ref-Hercik2017),[23](#ref-Boone2017),[28](#ref-Amoako2018)–[31](#ref-Angelakis2014)] , six on Rickettsioses[[19](#ref-Hercik2017),[28](#ref-Amoako2018),[32](#ref-Maina2016)–[35](#ref-Mourembou2015)], eighteen on Dengue[[13](#ref-Guillebaud2018),[15](#ref-Gadia2017),[19](#ref-Hercik2017),[20](#ref-Chipwaza2014),[28](#ref-Amoako2018),[34](#ref-Elfving2016),[36](#ref-Vu2017)–[47](#ref-Mugabe2018)], thirteen on Chikingunya[[15](#ref-Gadia2017),[20](#ref-Chipwaza2014),[34](#ref-Elfving2016),[37](#ref-Waggoner2017),[40](#ref-Ngoi2016),[42](#ref-Kajeguka2016),[44](#ref-Kayiwa2018)–[50](#ref-Olajiga2017)], three on Zika [[43](#ref-Sow2016)–[45](#ref-Makiala-Mandanda2018)], two on Histoplasmosis[[51](#ref-Bahr2016),[52](#ref-Mandengue2015)] and none on PCP. Details of the included studies are provided below.

### Defining sepsis

Sepsis is a heterogenous syndrome, with no diagnostic gold standard. In 1991 the first modern sepsis diagnostic criteria were defined in a consensus conference of key opinion makers[[53](#ref-Bone1992)] (Table ??). Sepsis was defined as the presence of the systemic inflammatory response syndrome (SIRS) plus infection, with a gradient of severity increasing through severe sepsis (sepsis plus organ dysfunction) to septic shock. These definitions were widely adopted as entry points into clinical trials, but ongoing concerns that SIRS was both insensitive and nonspecific for the diagnosis of sepsis led to an expansion of the diagnostic criteria in 2001[[54](#ref-Levy2003)] again by expert consensus. Despite these revised guidelines the SIRS criteria largely continued to be preferred both as the entry point to clinical trials of sepsis and in clinical practice until the development of the current sepsis-3 definitions in 2016[[55](#ref-Singer2016)].

The sepsis-3 definitions redefined sepsis as “life threatening organ dysfunction triggered by infection”, a definition that rendered the sepsis-2 severe sepsis category obsolete. In contrast to the previous diagnostic criteria that had relied largely on expert opinion, the sepsis-3 criteria attempted to use a probabilistic approach to defining sepsis, by mandating that sepsis should be associated with excess mortality. The sequential organ dysfunction score (SOFA, Table ??, Appendix), an organ-dysfunction score already in use in high income settings, and shown to be associated with mortality[[56](#ref-Vincent1998)] was selected to operationalise the definition of sepsis. An acute change in SOFA of 2 or more points defines sepsis under sepsis-3.

Mindful that the SOFA score requires a large number of variables and is difficult to apply at the bedside, the consensus guideline group suggest the use of a simpler score, quick SOFA to identify patients who may have sepsis. Any two of: altered mental status, SBP < 100mmHg or respiratory rate > 22 defines a positive qSOFA score. qSOFA does not define sepsis; rather, under sepsis-3 patients with a qSOFA score of 2 or more are at increased risk of poor outcomes and should be screened for sepsis using a full SOFA score. The qSOFA was derived by identifying factors associated with mortality in large datasets of patients with infection from the United States and validated in further US and German datasets; in these datasets it showed good discriminant ability to predict mortality, equivalent to full SOFA score outside the intensive therapy unit (ITU)[[57](#ref-Seymour2016)].

Finally, sepsis-3 defines septic shock as persistent hypotension requiring vasopressors to maintain mean arterial blood pressure (MAP) above 65mmHg and serum lactate greater than 2mmol /L. This definition was arrived at by a combination of consensus and systematic review to identify potential defining variables and validation in large datasets from the United States, where it was found to be strongly associated with mortality[[58](#ref-Shankar-Hari2016)].

### Applicability of sepsis-3 definitions in sub-Saharan Africa

Application of the sepsis-3 definitions, both in terms of clinical use and as inclusion criteria for research studies in sub-Saharan African low resource settings, is problematic. Several of the domains of SOFA require the results of blood tests, which may not be available. In Blantyre, and elsewhere in sSA, intensive organ support with inotropes or mechanical ventilation (invasive or non-invasive) may not be available[[59](#ref-Jacob2011)] or be difficult to access[[60](#ref-Prin2016)], yet use of these treatment modalities form components of the SOFA score. Both lactate measurement and inotropic support may be unavailable in some settings and yet these define septic shock. Five studies have validated the qSOFA score in sub-Saharan African settings[[6](#ref-Moore2017a),[61](#ref-Huson2017b)–[64](#ref-Rudd2018)] and found variable discriminant ability for mortality but it is not clear how this score should be deployed in this setting; no studies have been undertaken to link qSOFA score to clinical action, and it is not intended to define sepsis under sepsis-3. The optimal sepsis definitions (both clinical and for research) for sSA are therefore not clear.

### Sepsis epidemiology in sub-Sahara Africa

#### Incidence

The changing case definition of sepsis over time hampers estimation of incidence even in high-income settings, furthermore sepsis is not included in global burden of disease estimates. Different methods of defining sepsis from disease registries can result in very different estimates[[65](#ref-Gaieski2013)], but a recent systematic review and meta-analysis of 27 studies from 9 high income countries found a recent population incidence rate of 437/100,000 person-years (95% CI 334-571) for sepsis and 270 (95% CI 176 – 412) for severe sepsis with an increasing incidence over time from 1979 to 2015[[66](#ref-Fleischmann2016)]. Crudely extrapolating these estimates to the worldwide population would result in 20.7 million sepsis and 10.7 million severe sepsis cases a year, largely in low resource settings. However, no data are available from low or middle income settings and these estimates must be treated with caution.

#### Risk factors: the sepsis population in sub-Saharan Africa

In high-income settings, risk factors for sepsis have been identified, though once again changing definitions as well as a lack of large scale community based studies make it difficult to draw definitive conclusions. However, chronic diseases (including HIV) and immunosuppressive agents have been associated with increased sepsis incidence, as well as older age[[67](#ref-Angus2001),[68](#ref-Tsertsvadze2016)]. In the United States, male sex and black ethnicity (vs white) and poverty are associated with increased sepsis incidence and severity[[69](#ref-Mayr2010)].

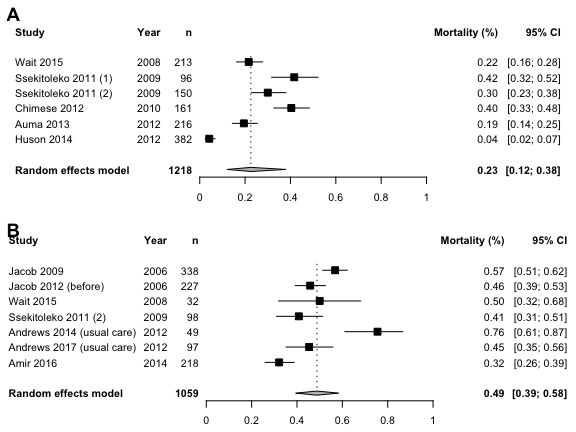
Though equivalent studies aiming to identify risk factors for sepsis in adults in sSA are lacking, it is clear from the available data that HIV-infection is the dominant risk factor there. Summary patient demographics from the 10 identified sepsis studies are shown in Table ??; of 2788 included patients with available HIV status, 69% (1809/2788) were HIV infected, and often with advanced disease; of 1278 HIV-infected patients from 5 studies the study median CD4 count ranges from 52-168 cells/L. In keeping with the epidemiology of the HIV epidemic in Africa, these patients are young, with average ages (variably reported as mean or median) ranging from 30-39 across the studies. These studies recruited an equal proportion of males and females (1444/2812 males, 51%), suggesting that sex is not a risk factor.

These data contrast sharply with the sepsis population in high income settings, from whom the majority of sepsis data have been generated, and who are older and mostly HIV uninfected[[67](#ref-Angus2001),[70](#ref-Seymour2017),[71](#ref-PRISMInvestigators2017)]. The need for data from sSA to guide sepsis treatment protocols, rather than extrapolating from the high-income setting sepsis population, is clear.

#### Outcomes

Summary outcomes for sepsis and severe sepsis in sSA from the identified studies are presented in Figure 1 below. Summary statistics of 28 or 30-day mortality were extracted from identified studies or, if 28- or 30-day data were not available, in-hospital mortality was used. For interventional studies, in order to reflect the “usual-care” mortality, only the usual care arms were included. Pooled mortality estimates were then generated using a random effect meta-analysis of proportions with a generalised linear mixed model (GLMM, the so called binomial-normal model) using the meta package in R. Exact binomial 95% mortality confidence intervals were used throughout.

It is clear that there is significant heterogeneity in outcomes of sepsis and severe sepsis in sSA, likely reflecting diverse patient and pathogen populations and variation in availability of available resources. This heterogeneity means that summary estimates should be interpreted with extreme caution but severe sepsis (49% [95% CI 39-58]), as expected, seems to carry a higher mortality hazard than sepsis (23% [95% CI 12-38]). Data of outcomes beyond 30 days are absent.

 How does this compare to high income settings? A recent meta-analysis of population level estimates in high income settings found that a pooled sepsis 30-day mortality estimate of 17% (95% CI 11-26%)[[66](#ref-Fleischmann2016)], though even older cohort studies as well as the more recent large sepsis-3 derivation cohorts have found considerably lower mortalities for sepsis (as defined by sepsis-2) ranging from 4-7%[[57](#ref-Seymour2016),[72](#ref-Rangel-Frausto1995),[73](#ref-Serafim2018)]. Most recent (largely post-2005) estimates of 30-day mortality from severe sepsis range from from 18-29%[[65](#ref-Gaieski2013),[66](#ref-Fleischmann2016),[71](#ref-PRISMInvestigators2017),[74](#ref-Kaukonen2014),[75](#ref-Stevenson2014)]. It seems likely therefore, that both sepsis and severe sepsis 30-day mortality is considerably higher in sSA than in high-income settings. The reasons for this are not clear, but are likely to be multifactorial; resource limitation is likely to play a part but the HIV epidemic in sSA, differing pathogen burden and lack of data and evidence based guidelines to inform optimal management in sSA may also play a role.

In the longer term, sepsis mortality continues to rise after the usual sepsis-study primary end point of 28 or 30 days, though data from sSA are absent. A systematic review in 2010 of long term sepsis mortality identified 26 studies (with none from low-resource settings) that reported long term sepsis mortality; 1 year mortality ranged from 22-72%, increasing to 45-75% at greater than 3 years[[76](#ref-Winters2010)]. Both short and long term morbidity is formidable also, though, once again, data from low income settings including sSA are absent. Cohort studies with no comparator group may not identify morbidity that is sepsis-specific (rather morbidity that is related to critical illness) but new, long-lasting reduction in physical and cognitive function with associated functional impairment have been identified in matched cohort studies in sepsis survivors[[77](#ref-Shah2013),[78](#ref-Iwashyna2010)]. Health-related quality of life in sepsis survivors in high-income settings have been found to be persistently below population norms[[76](#ref-Winters2010)]. Increased incidence of cardiovascular disease, renal failure and further episodes of infection are seen following a hospital discharge for sepsis[[79](#ref-Yende2014)–[81](#ref-Ou2016)]. Long term sepsis outcomes in sSA are unknown.

### Sepsis aetiology in sub-Saharan Africa

The 11 identified prospective sepsis studies in sSA carried out various combinations of diagnostic testing for malaria (either microscopy or rapid diagnostic test) and aerobic and mycobacterial blood culture; a summary is shown in Table ?? and ?? below. The commonest bloodstream infection (BSI) in all studies where mycobacterial blood cultures were carried out was tuberculosis – present in a higher proportion than of all BSI isolates from aerobic culture combined - though it is important to note that mycobacterial blood cultures in most studies were carried out in HIV infected people and bacteraemic tuberculosis is almost exclusively HIV-associated. The importance of bacteraemic tuberculosis as a cause of sepsis is further examined in an individual patient data meta analysis in chapter 3. With the exception of one study, malaria was less common than BSI, highlighting the importance of non-malarial fever in sSA as malaria control efforts reduce the burden of malaria.

#### Bacterial zoonoses, Rickettsioses and arboviruses

There are several reasons to suspect that aetiologic agents other than bacterial BSI and tuberculosis may be significant in sSA, though data in sepsis are sparse. Studies of febrile illness in sSA have implicated Rickettsioses, arboviruses and bacterial zoonoses as causes of fever, accounting for a third of fever in hospitalised adults in one study in Tanzania[[82](#ref-Crump2013)]. Historically, however, data on these pathogens have been lacking. A 2015 systematic review of fever aetiology in LMIC (considering studies from 1980-2013) found that small numbers of patients had been systematically screened for these pathogens: in sSA 40/453 (8.8%) of adults with fever fulfilled diagnostic criteria for Leptospirosis, 16/453 (3.5%) for Brucellosis, 36/450 (8.0%) for spotted fever group Rickettsiosis, 24/482 (5%) for Q-fever and 55/700 (7.9%) for Chikingunya[[83](#ref-Prasad2015)].

Increasing interest in non-malarial fever, however, has meant that data are accumulating from different settings in sSA, post-2013, as identified by the systematic review of the literature performed for this thesis. Details of the studies identified from this review are shown below in Table ?? in the chapter Appendix. These data highlight, firstly, the heterogeneity in diagnostics which are used for these pathogens – a combination of serology, PCR and antigen testing (often not using gold-standard case definitions), and secondly, the spatial and temporal heterogeneity across the continent.

These studies also demonstrate an increase, post-2013, in the use of molecular tests, particularly multiplex PCR assays (TaqMan array cards or PCR macroarrays) to detect multiple pathogens in fever aetiology studies. Despite the attractiveness of these assays – the ability to detect tens of pathogens in one assay on one body fluid sample – many infections will have only transiently detectable pathogen genetic material in blood and as such may have limited sensitivity. The post-2013 fever aetiology data strongly suggest paired sera will maximise the diagnostic yield of bacterial zoonoses and Rickettsioses: for example, in studies of leptospirosis using PCR only 23/2533 (0.9%) of samples were positive versus 75/1464 (5.1%) in studies using paired sera; for Q-fever 9/3811 (0.2%) of samples were positive in PCR only studies versus 25/370 (6.8%) for paired sera studies; for Brucellosis PCR only studies 15/1005 (1.5%) of samples were positive versus 39/562 (6.9%) for paired sera studies; and for Rickettsioses 55/1932 (2.8%) of samples were positive for PCR studies vs paired sera 63/364 (17%). Some care must be taken with this conclusion: there are no studies that aim to directly compare paired sera and PCR assays for diagnosis of febrile illness, so the possibility of confounding remains.

Available data therefore suggest that bacterial zoonoses, Rickettsioses and arboviruses are significant causes of febrile illness in sSA. Their role is sepsis however is unknown. Only two studies have directly addressed the question of sepsis aetiology beyond BSI, malaria and TB: the first[[84](#ref-Moore2018)] performed PCR for 43 pathogens (using a TaqMan array card) including viruses (including dengue, chikungunya, and causes of viral haemorrhagic fever), bacteria (including *S. pneumoniae*, *E. coli*, *Salmonella spp.*, *S. aureus* as well as *Coxiella burnetti*, *Rickettsia spp.*, *Brucella spp.* and *Leptrospira spp.*), Mycobacterial (including *M. tuberculosis* (MTB) and *M. avium* complex), fungal ( *Cryptococcus* and *Histoplasma spp.*) and parasitic (including malaria) on a convenience sample of 336 stored plasma samples from a Ugandan sepsis study. In keeping with the original study, MTB was frequently identified as was pneumococcus and malaria. Cytomegalovirus (CMV) was detected in 139/336 (41%) of patients, and was found to be independently associated with death, a finding which has been seen in sepsis studies in high-income settings[[85](#ref-Osawa2009)] and may be related to the immune paresis of sepsis and CMV viraemia rather than disease. This study had no pathologic specimens and could not address this question. Dengue was detected in 17/336 (5%) of patients; Rickettsia spp. in 6/336 (2%), Leptospira spp. in 2/366 (0.6%) and Coxiella burnetti and Brucella spp. in 1/336 (0.3%) each. The true burden of disease of these pathogens may be higher, given the potential for increased diagnostic yield fom serological assays.

The second study[[86](#ref-Rubach2015)] is a retrospective analysis of a fever aetiology cohort from Tanzania, in which paired serology for bacterial zoonoses and Rickettsioses was carried out, as well as arboviral PCR. Of 423 enrolled adults, 25 were retrospectively classified as having septic shock, 37 severe respiratory distress without shock and 109 severe pneumonia by WHO Integrated Management of Adolescent and Adult Illness (IMAI) District Clinician Manual criteria[[87](#ref-WorldHealthOrganisation2011)]. These patients would likely fulfil sepsis criteria under sepsis-2 or 3 guidelines, and were found to have a variety of diagnoses, though not all patients had all diagnostic tests: Chikungunya (6/154 [3%]),Leptospirosis (5/82 [6%]), Coxiella burnetti (7/83 [8%]) and spotted fever group Rickettsioses (6/83 [7%]).

#### HIV opportunistic infections: PCP, histoplasmosis and cryptococcal disease

The burden of HIV opportunistic infections in sepsis in sSA (including PCP, cryptococcal disease and including here Histoplasmosis as an opportunistic infection) is unclear. Beyond blood culture identification of *Cryptococcus neoformans* (present in 20/365 of positive blood cultures in the sepsis studies identified in this review) none of these pathogens have been systematically sought in sepsis cohorts in sSA, and their role as causative agents of sepsis is far from clear. Cryptococcal disease most commonly manifests as cryptococcal meningitis, is common in HIV infection and is thought to account globally for 15% of AIDS-related deaths[[88](#ref-Rajasingham2017)]. It is likely therefore to contribute significantly to aetiology of sepsis; of the 11 identified sSA sepsis cohorts, three[[4](#ref-Ssekitoleko2011a),[5](#ref-Chimese2012),[9](#ref-Andrews2014)] provide data on suspected site of infection, and CNS infection accounts for 14-31% of the total, of which cryptococcal disease is likely to be responsible for a large proportion. One study2 performed CSF examination on 41/213 patients for suspected meninigoencephalitis. Of these, 3/41 cultured *C. neoformans*.

No study has attempted to define the burden of PCP in sepsis in sSA, though a 2016 systematic review[[89](#ref-Wasserman2013)] addressed the prevalence and attributable mortality of PCP. Searches were limited to post-1995; 48 studies were identified comprising 6884 individuals from 18 countries, with a varying patient population including inpatients and outpatients with respiratory presentation or clinical or radiological community acquired pneumonia, often sputum smear negative for TB, and some autopsy studies. A number of diagnostic tests including bronchoscopy and bronchoalveolar lavage were carried out. Many of the inpatient cohorts would include patients with sepsis; the pooled prevalence of PCP in inpatients (n = 2593, 23 studies) was 22% (90% CI 17 – 27%) in random effect meta-analysis. Clearly there are significant difficulties with obtaining lower respiratory tract specimens in unwell hypoxic, shocked or obtruded patients; newer serologic tests (1,3, beta-d glucan) which have reasonable diagnostic characteristics for PCP in high-income settings[[90](#ref-Onishi2012)] and may have a role to play, but no study in sSA has attempted to use or validate this assay in any condition.

Data examining the role of Histoplasmosis as a cause of fever or sepsis in sSA are sparse. A 2015 systematic review[[83](#ref-Prasad2015)] identified only one study up to 2013 which Histoplasma urine antigen testing in 628 febrile adults and children in Tanzania and acute serum testing on a subset of 200, finding 9/628 (1%) probable cases, 6/9 of whom were HIV infected. Since then, two studies have addressed histoplasma prevalence in varying conditions: the first, in Uganda, enrolled HIV-infected patients with suspected meningitis[[51](#ref-Bahr2016)] and found 0/151 patients had detectable IgM to *Histoplasma capsulatum* and no Histoplasma antigen was detected in serum (n = 57), urine (n = 37) or CSF (n=63). The second study in Cameroon[[52](#ref-Mandengue2015)] recruited HIV infected patients with CD4 < 200 cells/L, chronic cough and Histoplasmosis like skin manifestations. Histopathologic examination and culture found Histoplasmosis in 7/56 (13%) of patients over 3 years.

### Sepsis management

The cornerstone of sepsis management is rapid administration of appropriate antimicrobial therapy, source control of any infectious focus and normalisation of tissue perfusion using intravenous fluids and, if necessary, inotropes, with other organ support as necessary (e.g. intubation and mechanical ventilation and renal replacement therapy). Several international guidelines for sepsis care are available; this section will examine these and specific guidance for sepsis in adults in sSA followed by a review of the evidence to inform these guidelines.

The surviving sepsis campaign has published four editions of comprehensive guidance on the management of sepsis in adults, which are endorsed by all the major critical care organisation in high income settings and form the basis of most sepsis care in high income settings; selected major recommendations of the latest guidance[[91](#ref-Rhodes2017)] are shown in Table ?? below.

Mindful that guidelines aimed at high-income settings may be impossible to implement in low-resource settings (including large areas of sSA) the Global Intensive Care Working Group of the European Society of Intensive Care Medicine (ESICM) published recommendations for sepsis management in resource-limited settings in 2012[[92](#ref-Dunser2012)], endorsed by a number of national and international sepsis organisations, and supplements in 2016-17 covering general supportive care[[93](#ref-Mer2017)], infection management[[94](#ref-Thwaites2016)], management of severe malaria and severe dengue[[92](#ref-Dunser2012)] and haemodynamic assessment and support[[95](#ref-Misango2017)] in sepsis in low-resource settings. The major recommendations of this guidance are consolidated in Table ?? below.

The World Health Organisation (WHO) in 2011 published the integrated management of adolescent and adult illness (IMAI) guidance[[87](#ref-WorldHealthOrganisation2011)], which includes guidance on the management of septic shock and is aimed at district-level clinicians in resource limited settings rather than critical care clinicians. This suggests defining shock as SBP < 90mmHg or pulse > 110/minute and suggest that, once shock is identified, oxygen should be given, a 1 litre bolus of fluid should be given immediately and pulse, SBP and signs of perfusion (urine output, mental status) should be rechecked. If shock persists, another litre should be given; if shock persists after the second litre then help should be sought. Antimicrobials should be administered: ceftriaxone IV or IM, and antimalarials if indicated. No evidence base is referenced for these recommendations.

#### Early goal directed therapy

In 2001 a pivotal single centre study in the United States of 263 patients with severe sepsis or septic shock[[96](#ref-Rivers2001)] found that protocolised aggressive early resuscitation (called Early Goal Directed Therapy, EGDT) significantly reduced mortality from 46.5% to 30.5%. EGDT called for early central venous catheterisation and protocolised resuscitation to central venous pressure (CVP), MAP and central venous oxygen saturation targets (ScvO2), and was widely adopted. However three large multicentre randomised controlled trials of EGDT – ProCESS in the United States[[97](#ref-Yealy2014)], ARISE in Australasia[[98](#ref-Peake2014)] and ProMISe[[99](#ref-Mouncey2015)] in the United Kingdom, reporting in 2014 and 2015 failed to show any difference in outcomes between the EGDT and usual-care arms. A pre-planned individual level meta-analysis of the 3723 patients included in these trials confirmed similar 90 day mortality in both arms (24.9% for EGDT vs 25.4% for usual care, aOR 0.97 [95% CI 0.82-1.14]) with no benefit found in pre-planned subgroup analysis for patients with worse shock or in hospitals with lower propensity for vasopressors or fluid administration[[71](#ref-PRISMInvestigators2017)]. It is likely therefore that the tenets of EGDT that improve outcomes (early antimicrobials and aggressive fluid resuscitation) have been absorbed into usual care in the fifteen years since the original EGDT study, as evidenced by the reduction is sepsis mortality over this time period, and so the specific package of protocolised care and EGDT targets does not in itself improve outcomes. Unanswered questions now remain regarding the most effective use of the individual components of EGDT (fluids, vasopressors etc). A number of attempts have been made to develop protocolised sepsis care packages in the style of EGDT for sSA; these are described below in relation to the individual components of sepsis care.

#### Evidence to guide antimicrobial therapy in sSA

There is evidence from high income settings that delay in appropriate antimicrobial administration is associated with worse outcomes in sepsis. The first study to investigate this relationship, published in 2006, found a very strong relationship between time to appropriate antimicrobial administration from onset of hypotension and mortality with an absolute increase in mortality of 7.6% for each hour delay over the first six hours[[100](#ref-Kumar2006)]. Subsequent data have been more nuanced: a 2015 meta-analysis addressing this question identified 11 studies of 16,178 patients and found no relationship between antimicrobial delay and mortality[[101](#ref-Sterling2015)], though many of the included studies are open to confounding by indication (sicker patients are given antimicrobials more quickly), timed antimicrobial administration to non-physiological events (e.g. arrival to hospital or time of blood culture draw rather than onset of hypotension) and did not assess the appropriateness of antimicrobial therapy, all of which could mask a relationship. Appropriate antimicrobial therapy has certainly been shown to be associated with improved survival: a 2010 meta-analysis quantified the pooled adjusted odds ratio to be 1.6 (95% CI 1.4-1.9) from 26 studies for appropriate versus inappropriate antimicrobial therapy[Paul2010]. A recent large retrospective study of 49,331 patients in New York hospitals[[70](#ref-Seymour2017)] confirmed the relationship between antimicrobial delay and mortality with an adjusted odds ratio of in-hospital death of 1.04 per hour delay (95% CI, 1.03 – 1.06), and rapid antimicrobial administration forms a key recommendation of current sepsis guidelines.

Data from sSA are lacking, however; neither of the meta analyses above (including between them 37 studies) included any data from sSA, but three of the sepsis studies identified in this systematic review attempt to address the question. The first[[1](#ref-Jacob2009)], in an observational study of 382 adults with severe sepsis in Uganda found no association between administration of antibiotics within 1 hour and mortality (OR 0.9 [95% CI 0.6-1.6]) but a total of 42 antibiotic regimens were used and there was a high proportion (22%) of bacteraemic tuberculosis; no assessment of appropriateness of antimicrobials was undertaken and it is possible that inappropriate antimicrobials could mask any association between time of administration and mortality, if one existed.

The second[[11](#ref-Jacob2012)], interventional, study in the same centres in Uganda used a before-after design with 661 patients to implement a clinical-officer delivered fluid resuscitation protocol (see below) and administration of antimicrobials. 426 patients were included in the intervention with 245 in the usual care group. The protocol resulted in more rapid administration of antibiotics (67% administered within 1hr versus 30%, p < 0.001) and less (though still very prevalent) inappropriate antimicrobial administration (81% versus 95%, p < 0.001). Antimicrobial administration was associated with a reduced hazard of death in a multivariable Cox proportional hazards model, but the comparator group used was patients who received no antimicrobials and the hazard ratio for rapid administration (< 1hr HR 0.44 [95% CI 0.21 – 0.89]) was not significantly different from delayed administration (> 6hr HR 0.39 [95% CI 0.19 – 0.81]). This type of study design is very prone to bias due to confounding as sepsis management changes over time, especially as the “before” arm was recruited two years before the “after” arm, so results from this study should be interpreted with caution.

A third observational study in a Ugandan teaching hospital[[102](#ref-Amir2016)] provides data on the effect of rapidity of administration of antimicrobials; this study enrolled 218 patients; 89% of them received any antibiotics within 6 hours, with a median time to antibiotic administration of 30mins. Antibiotic administration within 6hr (versus not) was not significantly associated with in hospital mortality in univariate analysis (OR 1.5 95% CI 0.6 – 3.8) though the confidence intervals are wide and could incorporate a clinically significant effect. Again, no assessment of appropriateness of antimicrobials was made.

Only one study provides limited evidence that appropriate antimicrobial therapy improves outcomes in infection in sSA[[103](#ref-Chalya2012)]: a combined retrospective-prospective analysis of 104 patients with typhoid perforation (defined by clinical and operative findings rather than culture) from a single Tanzanian teaching hospital found that adequate antimicrobial exposure (defined as at least 3 days of antimicrobial active against S. Typhi prior to hospital admission) was associated with improved in-hospital survival in multivariable analysis (aOR 2.9 [95% CI 2.1-4.5]), however it is doubtful that this very specific complication of typhoid fever is generalizable.

#### Evidence to guide intravenous fluid therapy in sub-Saharan Africa

The evidence base for rapid fluid administration – and the surviving sepsis recommendation of 30ml/kg within 3hrs following diagnosis - is less secure than for rapid antimicrobial administration. As with antimicrobial administration, adoption of guidelines in response to the EGDT study has meant that disentangling the independent effect of fluid administration is difficult. The data are contradictory. Several large retrospective observational analyses have found no impact on rapidity of fluid bolus administration following sepsis diagnosis: one multicentre study of 2796 adults with severe sepsis[[104](#ref-Ferrer2009)] found no propensity adjusted difference in in-hospital mortality for patients with shock or elevated lactate whether they received fluid bolus within the first 6hr following diagnosis (aOR 1.01 [95% CI 0.73 – 1.39]); the New York study of 49,331 septic adults described above[[70](#ref-Seymour2017)] found no association between time to completion of fluid bolus and mortality (aOR 1.01 per hour [95% CI 0.99 – 1.02]). Indeed, fluid clearly has the potential for harm; positive fluid balance for patients with sepsis in the ITU has been persistently linked with worse outcomes[@[[[70](#ref-Seymour2017)]; Boyd2011; Vincent2006].

In contrast, several studies contradict these findings; a retrospective single centre of 594 adults with severe sepsis or septic shock[[105](#ref-Lee2014)] found improved mortality in patients who had a higher proportion of 6-hour fluid administered in the first 3hr, when adjusted for total volume of fluid administered over 6hr (aOR 0.34 [95% CI 0.15 – 0.75]); a larger retrospective multicentre study of 11,182 patients with sepsis and hypotension[[106](#ref-Leisman2016)] found an independent mortality benefit for early intravenous crystalloid administration, with fluid administration within 30mins having the largest effect (aOR 0.74 [95% CI 0.62 – 0.87] versus > 120mins). A prospective study of 1866 patients from the same authors[[107](#ref-Leisman2017)] had similar findings (aOR 0.63 [95% CI 0.46-0.86]).

It may be that heterogeneity in response to fluids plays a role in these conflicting findings; a retrospective multicentre cohort analysis of 3686 patients[[108](#ref-Leisman2018)] found that 64% were “fluid responders” – that is, they had a sustained blood pressure response to initial fluid resuscitation without need for vasopressors. Heart failure, hypothermia, altered gas exchange, initial lactate > 4.0mmol/L, coagulopathy and immune compromise (including HIV/AIDS) were associated with fluid nonresponse, as was fluid initiation greater than 2 hours after sepsis diagnosis. Mortality was 15% greater (95% CI 10-18%) in fluid nonresponders.

In sSA, there is increasing evidence that liberal intravenous fluid administration to septic patients causes harm. The landmark FEAST trial[[109](#ref-Maitland2011)] randomised 3141 children with severe febrile illness in Kenya, Uganda and Tanzania to receive either albumin bolus or 0.9% saline bolus or usual care and found an increased risk of death by 48 hours in both bolus groups (RR 1.45 [95% CI 0.78-1.29] for any bolus compared to no bolus). In a secondary analysis[[110](#ref-Maitland2013)] this was thought to be due to cardiovascular collapse rather than pulmonary oedema; the mechanism of this is unclear.

Only three controlled studies have addressed the question of optimal intravenous fluid resuscitation for septic adults in sSA; the first is the before-after intervention study in septic shock patients carried out in Uganda and described above[[11](#ref-Jacob2012)]. 426 patients were included in the intervention with 245 in the usual care group; the intervention consisted of clinical-officer delivered protocolised care over the first 6 hours of hospital admission. The intervention increased fluid administration over 6 hours (3.0L vs 0.5L, p < 0.001) and 24 hours (3.5L vs 1.0L, p < 0.001), and more patients received fluid within 1 hour (97% vs 55%, p < 0.001). The study found a mortality benefit of > 1L fluid over the first 6hr compared to < 1L in multivariable Cox proportional hazard model (HR 0.54 [95% CI 0.35-0.82] for 1.0 – 2.5 L vs < 1.0L) though with the absence of any further dose-response effect above 1L. As stated above, the before-after study design means that this result should be interpreted with caution.

Two randomised controlled trials of protocolised early sepsis care in adults have been carried out at a single centre in Zambia, with a focus on fluid. The first[[9](#ref-Andrews2014)] recruited patients with severe sepsis with organ dysfunction criteria including respiratory rate > 40/min. Patients were randomised to usual care or an intervention protocol consisting of a 2L bolus of crystalloid (lactated Ringer’s or 0.9% saline) over 1 hour and then, if the jugular venous pressure (JVP) was below 3cm, a further 2L over 4 hours. Fluids were stopped if worsening respiratory signs or symptoms developed. If MAP was below 65mmHg after 2L of fluid, a dopamine infusion was started. Blood was transfused if Hb was < 7g/dL. This trial was stopped early (after recruitment of 109 patients) as it was felt that participants with baseline respiratory compromise (RR > 40 or oxygen saturation < 90%) might be at risk of harm; 7/10 (80%) of this subgroup died in the usual care group, compared to 8/8 (100%) in the intervention group (p = 0.09).

The same intervention was then used at the same centre in a similar trial[Andrews2017], this time recruiting patients with two SIRS criteria and hypotension (SBP < 90mmHg or MAP < 65mmHg), but excluding patients with baseline respiratory compromise( RR > 40/min or oxygen saturation < 90%) and randomising them 1:1 to the intervention protocol. 209 patients were recruited and patients in the intervention group (n = 106) at 6 hours received more fluid (median 3.5L vs 2.0L, p <0.001 ) with more vasopressor use (12% vs 2%, p = 0.01), but similar proportions of blood transfusion (16% vs 12%, p = 0.48). Lactate change by 6 hours was greater in the intervention group (median -1.2 vs -0.5 mmol/L, p = 0.02), but so too was in hospital mortality (48% vs 33%, p = 0.03). The reasons for this are not clear. More respiratory compromise (defined as increase in respiratory rate by 5 breaths/min or reduction in oxygen saturation of 3% or more) occurred in the intervention group (35% vs 22%, p =0.03) but persisted beyond 6 hours in similar numbers in both groups (17% vs 15%, p = 0.63).

## ESBL-E in sub-Saharan Africa

### Search strategy

A systematic review of the literature was undertaken to answer the following questions: firstly, what is the prevalence of ESBL-E amongst invasive isolates of *Klebsiella pneumoniae* and *Escherichia coli* infecting humans in sub-Saharan Africa? Secondly, what is the prevalence of gut mucosal carriage of ESBL-E amongst humans in sSA, and what risk factors for carriage have been identified? To this end a search of PubMed and Scopus was carried out using the search terms (((ESBL) OR Extended-spectrum beta-lactamase)) AND (((Angola OR Benin OR Botswana OR Burkina Faso OR Burundi OR Cameroon OR Cape Verde OR Central African Republic OR Chad OR Comoros OR Republic of the Congo OR Congo Brazzaville OR Democratic republic of the Congo OR Cote d’Ivoire OR Djibouti OR Equatorial Guinea OR Eritrea OR Ethiopia OR Gabon OR The Gambia OR Ghana OR Guinea OR Guinea-Bissau OR Kenya OR Lesotho OR Liberia OR Madagascar OR Malawi OR Mali OR Mauritania OR Mauritius OR Mozambique OR Namibia OR Niger OR Nigeria OR Reunion OR Rwanda OR Sao Tome and Principe OR Senegal OR Seychelles OR Sierra Leone OR Somalia OR South Africa OR Sudan OR Swaziland OR Eswatini OR Tanzania OR Togo OR Uganda OR Western Sahara OR Zambia OR Zimbabwe) OR Africa)).

Inclusion criteria were any study that took place in sSA and allowed the calculation of a prevalence of ESBL-E in *K. pneumoniae* or *E. coli* amongst invasive human isolates, or prevalence of human gut mucosal carriage of ESBL-E. Studies were excluded if no ESBL-E confirmatory testing was performed using phenotypic (double disc or combination disc or E-test) or molecular (PCR) methods. Invasive isolates were defined to be any blood or CSF sample other usually sterile fluid, or urine or wound swabs with clinical suspicion of infection. On 8th December 2018 this search identified 2975 unique studies; after abstract review 192 underwent full-text review, resulting in the inclusion of 86 studies, 54[[111](#ref-Guiral2018)–[163](#ref-Henson2017)] providing data on invasive infection and 32 [[164](#ref-Chirindze2018)–[196](#ref-Kurz2017)] 167–199 on carriage. Details of these studies are given below. A broad non-systematic review of the literature was also undertaken to place these studies in context and provide a background understanding of the classification and global epidemiology of ESBL-E, using the same literature databases.

### Introduction: definition and classification of ESBL-E

Beta-lactamases are enzymes that hydrolyse the active beta lactam ring in beta lactam antimicrobials. Though no standardised definition of ESBL exists, they are usually defined as enzymes which confer resistance via hydrolysis to penicillins, cephalosporins of the first, second or third generation (excluding cephamycins), aztreonam, but not carbapenems, and are inhibited by beta-lactamase inhibitors such as clavulanic acid[[197](#ref-Paterson2005)].

Two classification schemes are usually used for ESBL: the molecular (or structural) classification of Ambler[[198](#ref-Ambler1980)], or the Bush-Jacoby-Medeiros functional classification[[199](#ref-Bush2010)] (Table ??). Molecular classification is straightforward and depends on protein homology; class A, C and D enzymes are serine beta-lactamases and class B are metallo-beta lactamases, named for the composition of their active site. The functional classification is complex and clusters enzymes into four groups, with a number of subgroups, based on substrates and the effect of beta-lactamase inhibitors and EDTA: class 1 (corresponding to Ambler class C) are cephalosporinases that are not inhibited by clavulanic acid, and includes the AmpC enzymes of the Enterobacteriaceae; class 2 enzymes are beta lactamases that are largely inhibited by clavulanic acid and belong to Ambler class A or C; and class 3 are the metallo-beta-lactamases corresponding to Ambler class B. Class 4 enzymes are penicillinases which are not inhibited by clavulanic acid, though are of limited significance and not included in Table 14. The vast majority of clinically relevant ESBLs (and all of those defined as above) belong to Ambler class A, functional class 2be.

### Global molecular epidemiology of ESBL-E: an overview

The history of the global spread of ESBL-E is complex and an enormous number of unique ESBL amino acid sequences have been described; at the time of writing the NCBI beta-lactamase directory contains 1557 named beta-lactamase genes, many of them ESBL. However, there are 3 families which cause the majority of infections in humans: TEM, SHV, and CTX-M. They will be briefly described here in turn in the context of their putative origins and global dissemination in the latter half of the 20th century. A diverse range of other ESBL enzymes have been described, but are largely of less clinical significance than those described above, and are beyond the scope of this review: most notably the OXA type, which in contrast to TEM, SHV and CTX-M, are of the molecular class D and functional class 2d, and are characterised by a high rate of hydrolysis of cloxacillin[[200](#ref-Bradford2001)]; like TEM and SHV, OXA beta-lactamases are not always extended-spectrum.

#### 1980s-1990s: First identificatiom of ESBL in nosocomial pathogens

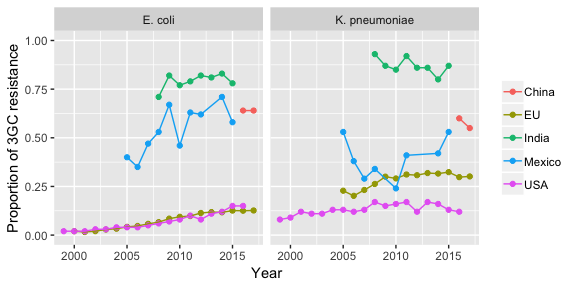
Beta-lactamases form an integral part of the natural armamentarium of many genera of bacteria – particularly gram negatives, including Enterobacteriaceae - and predate the antibiotic era; penicillinases were identified in E. coli, for example, prior to the widespread introduction of penicillin for treatment of human disease[[201](#ref-ABRAHAM1940)]. These beta-lactamases are often chromosomally located; the first plasmid-mediated narrow-spectrum beta-lactamase, TEM-1 -named for the patient, Temoneira, from whose blood it was first isolated – was found in Athens in the 1960s[[202](#ref-Datta1965)]. It rapidly disseminated globally and is thought to be responsible for a high proportion of ampicillin resistance in E. coli, for example[[200](#ref-Bradford2001)]. This worldwide spread spurred the development and use of beta-lactamase resistant extended-spectrum cephalosporin antimicrobials, which found wide use in the 1980s. Perhaps inevitably, an enzyme conferring resistance to extended-spectrum oxyimino-cephalosporins was subsequently identified in a German clinical *Klebsiella ozaenae* isolate in 1983, carried on a pBP60 plasmid and enzymes of this sort were named ESBLs[[203](#ref-Knothe1983),[204](#ref-Kliebe1985)].

This first ESBL enzyme was found to be similar to an existing plasmid-borne narrow spectrum beta lactamase, SHV-1, which had been described in the 1970s in E. coli, and was thought to itself be descended from a chromosomal *K. pnemoniae* narrow spectrum beta lactamase which was liberated onto a plasmid[[205](#ref-Liakopoulos2016)]. The point mutations in SHV-1 conferred the ESBL phenotype, and this enzyme was named SHV-2. This pattern - mutation of a narrow spectrum beta-lactamase to produce an ESBL phenotype - also occurred in TEM, and the first ESBL TEM was described in France in 1989[[206](#ref-Sougakoff1988)] and named TEM-3. Many TEM and SHV variants were subsequently described[[207](#ref-Gold1996)]. However, in this early stage of the epidemic, ESBL enzymes were largely nosocomial, and often associated with *Klebsiella spp.*[[208](#ref-Philippon1989)].

#### 1990s-2010s: Emergence and globalisation of CTX-M

From the late 1990s onwards, there were profound changes in the global epidemiology of ESBL-E, on three fronts, all intricately interrelated, and occurring simultaneously: first, the rapid emergence and globalisation of the successful CTX-M ESBL enzyme family[[209](#ref-Canton2006)], aided by mobile genetic elements; second, *E. coli* joining *Klebsiella spp.* as a major ESBL host[[210](#ref-Livermore2006)], and the emergence of so-called high risk bacterial clones; and third, the spread of ESBL-E into the community[[211](#ref-BenAmi2009)]. CTX-M-1 was first identified and named in Germany in 1989[[212](#ref-Bauernfeind1990)] and many variants were subsequently identified, largely in *E. coli* and *K. pneumoniae*, from isolates all over the world[[213](#ref-Bonnet2004)]. CTX-M genes are clustered by homology into 5 groups (CTX-M groups 1,2,8,9 and 25 ) and each group is thought to have descended from a chromosomal beta lactamase from *Kluyvera spp.*[[209](#ref-Canton2006)]

A year-on-year rise in incidence of invasive ESBL-E infection was seen in most high-income settings (Figure 2) throughout the 2000s and 2010s, the majority of which were CTX-M producers, though with varying proportions of different CTX-M enzymes in different locations[[[210](#ref-Livermore2006)]; Bevan2017]. Risk factors for ESBL-E infection in high income settings have persistently been shown to be hospital or long-term care facility exposure, antimicrobial exposure and chronic health conditions though it was recognised in the 2000s that a large proportion of patients with invasive ESBL-E lack any of these risk factors[[211](#ref-BenAmi2009)], suggesting acquisition in the community. Colonisation prior to infection is thought to be the norm; prior colonisation is a significant risk factor for infection and indeed when sought ESBL-E are found in the stool of healthy community members worldwide (see carriage, below).

Though less comprehensive, data from middle income countries suggests that prevalence of ESBL producers amongst invasive *E. coli* and *K. pneumoniae* are very high (Figure 2) and in countries such as India invasive *E. coli* and *K. pneumoniae* that are sensitive to third-generation cephalosporins are in the minority. The reasons for this are not clear but country and regional level associations (which are open to ecologic bias) have been shown with antimicrobial consumption[[[214](#ref-Goossens2005)]; Lai2011] and economic status; GDP per capita has been found to correlate inversely at a country level with third-generation cephalosporin resistance rates[[215](#ref-Alvarez-Uria2016)]. Data from sSA have historically been lacking and are systematically reviewed below. 

#### Epidemiology of gut mucosal carriage of ESBL-E: the first step towards invasive infection

Invasive infections with Enterobacteriaceae are thought to usually result from infection from an individual’s own gut microbiota, irrespective of resistance pattern[[216](#ref-Denis2015)], and whole genome sequencing has confirmed that invasive isolates are often closely related to prior gut carriage isolates[[217](#ref-Gorrie2018)]. Strategies to minimise carriage are therefore potentially attractive as interventions to reduce invasive infection and a number of studies have attempted to understand the dynamics of gut mucosal ESBL-E carriage in health and disease. A brief overview of ESBL-E community carriage is presented here, and ESBL-E carriage in sSA is systematically reviewed below.

ESBL-E community carriage in Spanish outpatients[[218](#ref-Mirelis2003)] and healthy children in Poland[[219](#ref-Franiczek2003)] was first described in 2001, and subsequently has been identified worldwide when sought[[220](#ref-Woerther2013)], though there are heterogeneities between and within countries which mirror the prevalence of invasive ESBL-E prevalence amongst *E. coli* and *K. pneumoniae*. In Europe, for example, community prevalence of ESBL-E carriage was estimated be 7.3% in the UK in 2014 in a large community study[[221](#ref-McNulty2018)], 4.5% in the Netherlands in 2012[[222](#ref-Wielders2017)] and 4.7% in Sweden in 2012/13[[223](#ref-Ny2017)] and 3.7% in Spain in 2003[[224](#ref-Valverde2004)], significantly lower than community carriage prevalence of 50.9% seen in China in 2009[[225](#ref-Li2011)] or 33.8% in India in 2011-2013[[226](#ref-Babu2016)].

Risk factors for colonisation have been identified in many studies and antimicrobial exposure[[227](#ref-Reuland2016),[228](#ref-Woerther2017)] and healthcare facility exposure[[[226](#ref-Babu2016)]; Luvsansharav2012] (including long term care facilities[[229](#ref-March2010)]) are consistently identified as such. Colonisation of a household member has also been identified as a risk factor[[[230](#ref-Valverde2008)]; Rodriguez-Bano2008], suggesting significant within-household spread. Antacid use has been associated with ESBL-E colonisation[[227](#ref-Reuland2016)] as has exposure to farming[@[[222](#ref-Wielders2017)]. In low prevalence areas, travel to high prevalence areas is a risk factor[[221](#ref-McNulty2018),[223](#ref-Ny2017),[227](#ref-Reuland2016),[228](#ref-Woerther2017),[231](#ref-VanDuijkeren2018)].

The majority of studies of ESBL-E carriage are cross sectional and only a handful have attempted to characterise longitudinal carriage of ESBL-E with a longitudinal sampling approach. Estimates of carriage duration vary, partly because of the difficulty in inferring them from interval-censored rectal swab or stool data, but it is clear that some patients remain colonised for many months. Following a Swedish ESBL-E outbreak, 12% of patients still carried ESBL-E at the final sampling visit, a median 58 months after the outbreak[[232](#ref-Alsterlund2009)]. French and German studies found a median duration of carriage of 4.3[[233](#ref-Zahar2010)] and 12.5[[234](#ref-Lohr2013)] months respectively following hospitalisation or outbreak. More transient carriage following international travel seems to be the norm with a median of 30 days in a large Dutch study[[235](#ref-Arcilla2017)]; the reasons for this are not clear.

The largest longitudinal community study of ESBL-E carriage took place in the Netherlands which recruited 76 ESBL-E colonised and 249 uncolonised community members and carried out longitudinal stool sampling at 5 time points over 8 months. 25/76 (32.9%) of initially-colonised participants remained persistently colonised after a median 242 days. Antimicrobial exposure in the past 6 months, proton-pump inhibitor use, colonisation with *E. coli* phylogroup B2 or D and presence of CTX-M-27 or CTX-M-14 was associated with persistent carriage, suggesting both host and bacterial factors may be important determinants of carriage duration. *K. pneumoniae* colonisation seemed to be less common in the persistent carriage group[[231](#ref-VanDuijkeren2018),[236](#ref-Teunis2018)]. This study also found significant heterogeneity of *E.coli* sequence type in longitudinal samples of persistent carriers but that ESBL genes and often detectable plasmid replicons remained unchanged, suggesting a significant role for mobile genetic elements.

#### Molecular mechanisms underlying success of CTX-M: mobile genetic elements and high-risk clones

The remarkable success of CTX-M has led to efforts to understand the molecular mechanisms by which this enzyme spread so rapidly. The system is complex, and poorly understood, but should be considered at multiple levels including that of the organism; the plasmid; the transposon, which may contain integrons or insertion sequences and, at the lowest level the ESBL gene. These will briefly be reviewed here.

The initial mobilisation event of CTX-M from *Kluyvera spp.* is thought to have been mediated by capture of transposable insertion sequences; the insertion sequence ISEcp1 has been experimentally demonstrated to mobilise the CTX-M precursor from *Kluyvera ascorbata*[[237](#ref-Lartigue2006)] and ISEcp1 is most consistently associated with CTX-M genes but IS26, ISCR1 and IS10 have also persistently been described upstream from CTX-M genes, suggesting multiple mobilisation events[[238](#ref-Bevan2017)]. There is also an association between particular pairs of CTX-M gene clusters and insertion sequences, consistent with a hypothesis of multiple mobilisation events[[239](#ref-Canton2012)]. These insertion sequences provide two roles: they encode a transposase enabling gene mobilisation but act as a strong promotor of CTX-M, without which phenotypic cephalosporin resistance is absent or reduced[[240](#ref-Zhao2013)].

After mobilisation from the *Kluyvera* genome, the CTX-M genes were integrated onto a plasmid backbone, a process which is likely ongoing as a substantial number of diverse CTX-M carrying plasmids have been described: there is, however, an association between CTX-M genotype and plasmid incompatibility group. The successful CTX-M 15 gene is very strongly associated with the narrow host-range IncF plasmid group, for example, which are restricted to Enterobacteriaceae[[[240](#ref-Zhao2013)]; Carattoli2009]. Identical CTX-M containing plasmids have been found across diverse geographical regions and have been termed “epidemic plasmids”[[238](#ref-Bevan2017)] though the mechanism of persistence of these plasmids within a bacterial population remains unclear.

In addition to frequently co-occurring CTX-M genes, transposable elements and plasmids, some clonal groups of *E. coli* and *K. pneumoniae* are both globally successful and associated with particular CTX-M genes and plasmids. These successful sequence types (STs) are known as “high risk clones.” The archetypal example is *E. Coli* ST131 which is often associated with an IncFII plasmid containing CTX-M-15[[241](#ref-Coque2008)]. First described in 2008, *E. coli* ST131 is thought to be responsible for around 80% of extra-intestinal ESBL E. coli infection[[242](#ref-Nicolas-Chanoine2014)]. Population genomics studies have demonstrated that a particular clade, ST131 clade C, is globally dominant and have shown a sequential acquisition of virulence determinants followed by mobile genetic elements conferring fluoroquinolone and ESBL resistance[[243](#ref-Stoesser2016),[244](#ref-Petty2014)]. These events may have contributed to the global success of ST131, but the precise mechanism of its apparent fitness advantage remains unknown.

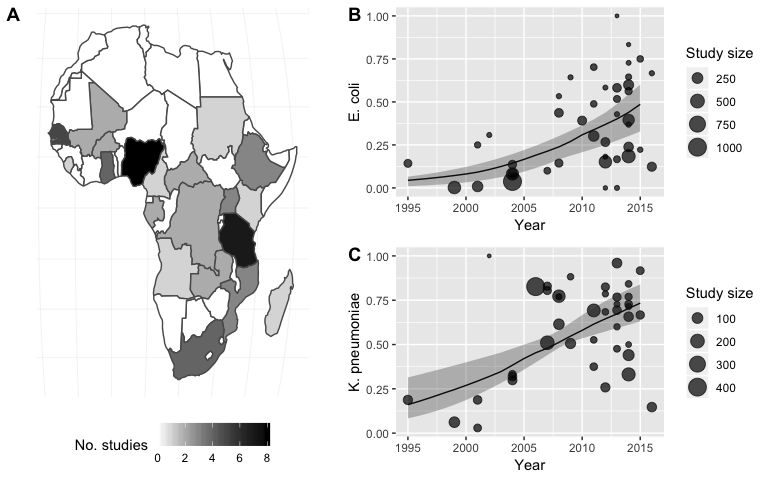
### Epidemiology of ESBL-E in sub-Saharan Africa

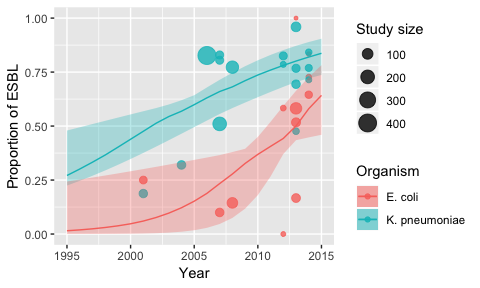
Of the 86 studies identified by the systematic literature review, 54 studies provided data on invasive ESBL-E and 32 provided data on human carriage is sSA. These are considered in turn below.

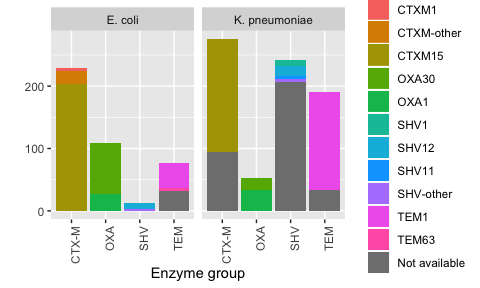
#### Invasive ESBL-E infection

Table xx in appendix xx shows the 54 included studies in this analysis, which provide data on 6067 *E. coli* and 2974 *K. pneumoniae* isolates. All studies were cross sectional in design. Of the 54, 18/54 were laboratory based (i.e. a survey of all samples received in the laboratory); 17/54 were truly invasive in that they included predominantly blood culture; a combination of urine, CSF, and wound swabs were included in the remaining studies. 36/54 studies provided data on adults and children; 6/54 on adults only; and 12/54 on children only. The majority of studies (42/54) include both community and nosocomial acquired infection. Of the remainder, 3/54 provided data on nosocomial infection only. Figure ??A shows a map of available data by country; data are available from across the continent though Nigeria (8 studies) and Tanzania (7 studies) are over represented and many countries provide no data.

The proportion of ESBL producers amongst invasive E. coli and K. pneumoniae in sSA is heterogeneous but many studies show extremely an extremely high prevalence (Figures ??B and ??C), comparable to that seen in the Indian subcontinent and other high-prevalence areas and highlighting the scale of the public health problem posed by ESBL-E in sSA. Meta regression shows clear temporal trends of an increase over time: addition of time as a fixed-effect covariate to the random effects model gives improved fit on likelihood ratio testing of nested models (p < 0.001 for both *E. coli* and *K. pneumoniae*). Though data are sparse pre-2000, those data that are available suggest that ESBL producing *E. coli* and *K. pneumoniae* were identified in West Africa even in the 1990s: a retrospective laboratory based study in Yaounde, Cameroon on isolates from a variety of clinical samples from 1995-1998 found that 13/91 *E coli.* and 12/64 *K. pneumoniae* were ESBL producers, with the SHV-12 enzyme predominant[[155](#ref-Gangoue-Pieboji2005)]; in Dakar, Senegal, 6/97 *K. pneumoniae* isolates from community acquired urinary tract infections in 1999-2000 were found to be ESBL producers[[158](#ref-Dromigny2003)].

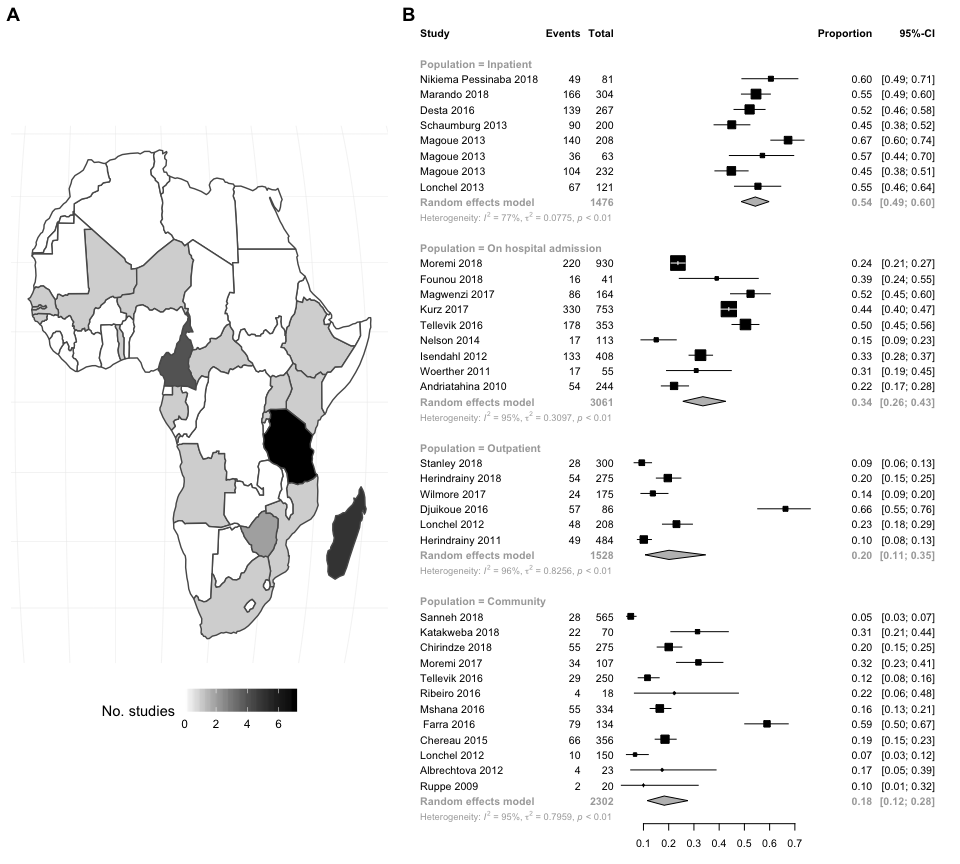
 Some of the heterogeneity in prevalence does however seem to be explained by sample type; a clearer picture appears when the analysis is restricted to the 16 studies including predominantly blood culture (Figure 4)[[115](#ref-Legese2017),[117](#ref-Sangare2017a)–[122](#ref-Eibach2016),[124](#ref-Kabwe2016),[127](#ref-Naas2016),[128](#ref-Ndir2016),[130](#ref-Sangare2016),[132](#ref-Dramowski2015),[137](#ref-Pons2015),[140](#ref-Irenge2014),[154](#ref-Blomberg2005),[163](#ref-Henson2017)]. In this analysis it seems clear that the worldwide epidemiology of ESBL-E was mirrored in sSA; ESBL initially spread amongst invasive K. pneumoniae post 2000 (particularly post 2005) before becoming established in E. coli after 2010. In 2014, the latest available data, the pooled population prevalence of ESBL from binomal-normal random effects meta analysis was 61% [95% CI 40-80%] amongst *E. coli* and 86% [95% CI 73-92%] amongst *K. pneumoniae* bloodstream infection isolates, suggesting endemicity of ESBL amongst these pathogens in sSA, and comparable to the highest prevalence areas in the world.

 ESBL genes were characterised in 10 studies by whole genome sequencing[[163](#ref-Henson2017)] (n=1) or by PCR[[116](#ref-Manyahi2017),[119](#ref-Agyekum2016),[120](#ref-Breurec2016),[122](#ref-Eibach2016),[129](#ref-Ouedraogo2016),[137](#ref-Pons2015),[138](#ref-Rafai2015),[154](#ref-Blomberg2005),[157](#ref-Ndugulile2005)] (n=9) for 821 *E. coli* and 791 *K. pneumoniae* isolates (Figure 5). CTX-M enzymes were the most commonly occurring ESBL genes, and the majority of these were CTX-M-15 in both organisms. OXA, TEM and SHV genes were also commonly found but were often not further characterised, presenting some problems of interpretation, as these enzymes can be narrow or broad-spectrum beta-lactamases. Certainly, SHV-1 and TEM-1 are narrow spectrum beta lactamase enzymes, which were commonly identified in these studies, though only a handful of isolates had characterisation of SHV enzymes beyond identification of the SHV group. All the identified OXA genes were narrow spectrum beta lactamases (OXA-1). These data suggest that the genomic landscape of invasive ESBL-E in sSA is dominated by CTX-M, and CTX-M-15 in particular, mirroring that seen worldwide.

 Though no data were identified from Malawi that fulfilled the inclusion criteria of the systematic review, there are three studies that suggest the epidemiology of invasive ESBL-E in Malawi is similar to that described above. A study from Blantyre in 2004-2005 found that ESBL-E were unusual in blood stream infection (BSI) isolates: of 1191 Enterobacteriaeciae BSI, only 8 unique isolates showed an ESBL phenotype (K. pneumoniae 4/8, K. oxytoca, 1/8, Enterobacter cloacae 2/8 and E. coli 1/8) though no denominators are provided to allow calculation of prevalence. CTX-M-15 (n = 1) was described, though in the minority: SHV-11 (n = 1), SHV-12 (n = 3), SHV-27 (n = 1) and TEM-63 (n = 2) were the other enzymes identified[[245](#ref-Gray2006)]. Longitudinal blood culture surveillance in Blantyre suggests that after 2005 – which coincided with the introduction of ceftriaxone in government hospitals – the prevalence of ceftriaxone resistance rapidly increased, to 90.5% in K. pneumoniae and 30.3% in E. coli BSI isolates by 2016[[246](#ref-Musicha2017b)], though this study did not carry out confirmatory ESBL testing. Finally, a retrospective whole-genome sequencing study which selected 94 diverse (largely invasive) clinical E. coli isolates from Blantyre from 1996-2014 found that 21/94 isolates carried an ESBL gene, with CTX-M predominating (20/21)[[247](#ref-Musicha2017a)].

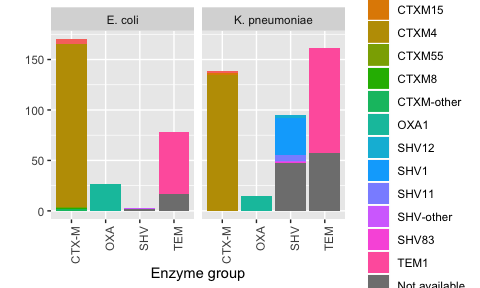
#### Gut mucosal carriage of ESBL-E in sub-Saharan Africa

Table xx in appendix xx shows the 32 identified studies that provide data on gut mucosal carriage in different populations in sSA. The populations recruited to the studies are heterogeneous but include community members, hospitalised patients, outpatients, orphanage residents, hospital workers and food handlers in schools. Adults and children are included. Data on 10,232 individuals from 19 countries are available in total (Figure A). The earliest samples were collected from staff and children in a Malian orphanage in 2003, when 49/68 participants were found to be colonised with ESBL-E[[190](#ref-Tande2009)]. There is significant heterogeneity in prevalence, some of which is explained by the study population (Figure ??); inpatients tend to have a higher ESBL-E carriage prevalence than community members. Outpatients have similar carriage prevalence to community members but inpatients even on hospital admission seem to have a higher carriage prevalence than community members.

 Significant heterogeneity in prevalence persists across all groups meaning that summary estimates should be interpreted with caution; community carriage if ESBL-E ranges from 5% in adults in The Gambia in 2015[[194](#ref-Sanneh2018)] to 59% in children in the Central African Republic in 2013[[169](#ref-Farra2016)], but a summary estimate from a random effect meta analysis is that 18% (95% CI 12-28%) of community members in sSA are colonised with ESBL-E, significantly higher than the prevalence in high-income settings.

Hospitalisation is clearly a driver of ESBL-E colonisation in the included studies - hospitalised cohorts have persistently higher prevalence of ESBL-E carriage – and prior antimicrobial exposure is consistently identified as a risk factor for carriage[[171](#ref-Djuikoue2016),[178](#ref-Nelson2014),[194](#ref-Sanneh2018)]. Consistent with a putative faecal-oral transmission route, boiling water and using a borehole as a source of water were identified as protective factors in studies in Rwanda[[193](#ref-NikiemaPessinaba2018)] and Togo[[196](#ref-Kurz2017)] respectively. Data to elucidate the role of within-household transmission are sparse, though one study in Rwanda found that a colonised family member was independently associated with ESBL-E carriage on admission to hospital[[196](#ref-Kurz2017)]. Lower socioeconomic status was found to both be protective against ESBL-E colonisation in the Central African Rebulblic[[169](#ref-Farra2016)] and be associated with ESBL-E colonisation in Madagascar[[185](#ref-Herindrainy2011)]; this relationship is likely to be complex and mediated by, for example, local availability and cost of antimicrobials. The role of HIV is not clear: in children in Dar-es-salaam, Tanzania, ESBL-E carriage was much more common amongst HIV infected children[[174](#ref-Tellevik2016)], and in Harare Zimbabwe, receipt of ART for less than a year was associated with carriage[[168](#ref-Wilmore2017)]. This relationship is very open to confounding and many studies have not found an association between ESBL-E carriage and HIV infection[[171](#ref-Djuikoue2016),[178](#ref-Nelson2014),[184](#ref-Lonchel2012),[192](#ref-Moremi2018),[194](#ref-Sanneh2018),[196](#ref-Kurz2017)].

Data on beta lactamase genes present in carriage isolates are available for 996 E. coli and 607 K. pneumoniae from 8 studies (Figure ??), showing a similar picture to invasive isolates; the landscape is dominated by CTX-M-15. One study used whole-genome sequencing [[191](#ref-Marando2018)], the remainder used a variety of PCR techniques[[167](#ref-Moremi2017),[179](#ref-Lonchel2013)–[181](#ref-Schaumburg2013),[184](#ref-Lonchel2012),[186](#ref-Woerther2011),[192](#ref-Moremi2018)].

Only 4 studies are longitudinal cohorts which could provide insight into temporal trends and determinants of carriage[[186](#ref-Woerther2011),[188](#ref-Andriatahina2010),[192](#ref-Moremi2018),[196](#ref-Kurz2017)]; all of these studies were health facility based and ascertained ESBL status on admission and discharge. Significant increases in ESBL-E carriage were seen in all studies: from 50 to 65% in Rwanda; from 30 to 95% in Niger; from 21.2 to 57% in Madagascar; and from 23% to 36% in Tanzania. No studies followed patients into the community, thus carriage duration of ESBL-E in sSA remains unknown and no interventional studies identified aiming to reduce ESBL-E carriage were identified.  ## Conclusions The aetiology of sepsis in sSA is poorly defined, hence optimal antimicrobial strategies are unknown; disseminated TB is likely to play a significant role, but data to guide tuberculosis therapy strategies in the critically unwell are lacking. The role of bacterial zoonoses, arboviruses and HIV opportunistic infections are not well defined, but may be significant. Diagnostic uncertainty and paucity of microbiologic support across sSA may be creating a permissive environment for the widespread broad spectrum antimicrobial use, often third-generation cephalosporins. It is likely that dose, duration and indication are frequently inappropriate, and thus could contribute both to increased mortality and to spread of ESBL-E.

Certainly, ESBL-E are endemic in sSA and are a problem of serious public health concern; sSA has rates of ESBL-E in invasive disease that are comparable to the highest in the world and ESBL-E gut mucosal carriage in healthy populations across the continent is common. Whilst it is clear that health care facilities are strongly associated with ESBL-E acquisition, a deeper understanding of the determinants and sources of acquisition, and carriage duration is lacking. In order to understand the role of health facilities in driving the ESBL-E pandemic, a high quality longitudinal ESBL-E carriage data from both healthy and sick (health facility exposed) populations are required.

It may be that optimising the treatment of severe febrile illness in hospitals is the best place to start to reduce over prescription of broad-spectrum antimicrobials and reduce selection pressure for ESBL-E whilst ensuring timely and appropriate access to the right treatments for those who need them. This is the central hypothesis of this thesis, and the following chapters present the data that can be used to define such a strategy.

### Specific aims

The specific aims of this thesis are: 1. To describe the presentation, aetiology, outcome, and determinants of mortality from sepsis in adults presenting to Queen Elizabeth Central Hospital, Blantyre Malawi; 2. To describe the acquisition and carriage of ESBL-E in sepsis survivors, with an analysis of determinants of carriage.

## Thesis overview

Chapter 2 (methods) presents the clinical study that forms the basis of the rest of this thesis; given the likely importance of disseminated TB in sepsis in sSA, chapter 3 presents a systematic review and individual patient data meta anlaysis of prevalence, diagnosis, and mortality hazard or TB bloodstream infection. Chapter 4 presents data on the clinical presentation, aetiology and outcomes of sepsis in Blantyre, Malawi; chapter 5 describes the determinants of long-term carriage of ESBL-E amongst sepsis survivors. Chapter 6 presents an overview of the genomic landscape of ESBL-E in Blantyre, Malawi whilst chapter 7 combines the genomic and epidemiologic data from chapters 5 and 6 to understand mechanisms and drivers of ESBL-E carriage in health and disease in Malawian adults. [microbiome stuff if available]. Finally, chapter 8 provides suggestions of further work.

## Appendix

## References

# Methods

Placeholder

## Chapter Overview

## Study site

### Malawi

### Queen Elizabeth Central Hospital

### Participating Laboratories

#### Malawi-Liverpool-Wellcome Clinical Research Programme

#### Malawi College of Medicine Tuberculosis Laboratory

#### Wellcome Trust Sanger Institute

## Clinical Study

### Entry Criteria

### Study Visits and Patient Sampling

#### Enrollment assessment and first six hours

#### Subsequent visits

#### Blood, urine, and stool, sputum and CSF collection

#### Imaging: chest x-ray and ultrasound scanning

### Outcomes and sample size calculations

## Diagnostic Laboratory Procedures

### Point of care diagnostics

### Laboratory diagnostics

#### Haematology and biochemistry

#### Aerobic blood and CSF culture

#### Mycobacterial blood culture

#### Sputum Xpert

#### Urinary LAM

#### Selective stool culture for ESBL-E

#### Acute and convalescent serologies

## Molecular methods

## Bioinformatics

## Statistical Analysis

## Study Team

## Data Collection and Storage

## Ethical Approval, Consent and Participant Remuneration

# *Mycobacterium tuberculosis* BSI: an IPD meta analysis

# Sepsis in Blantyre, Malawi

Placeholder

## Chapter overview

## Methods

## Study population

## Aetiology

## Treatment

## Outcome

# Early response to resusitation in sepsis

# Gut mucosal carriage of ESBL-E in Blantyre, Malawi

# Genomics of ESBL *E. coli*

Blah blah blah

# References

1 Jacob ST, Moore CC, Banura P *et al.* Severe sepsis in two Ugandan hospitals: a prospective observational study of management and outcomes in a predominantly HIV-1 infected population. *PLoS One* 2009;**4**:e7782. doi:[10.1371/journal.pone.0007782](https://doi.org/10.1371/journal.pone.0007782)

2 Waitt PI, Mukaka M, Goodson P *et al.* Sepsis carries a high mortality among hospitalised adults in Malawi in the era of antiretroviral therapy scale-up: a longitudinal cohort study. *The Journal of infection* 2015;**70**:11–9. doi:[10.1016/j.jinf.2014.07.004](https://doi.org/10.1016/j.jinf.2014.07.004)

3 Ssekitoleko R, Jacob ST, Banura P *et al.* Hypoglycemia at admission is associated with inhospital mortality in Ugandan patients with severe sepsis. *Crit Care Med* 2011;**39**:2271–6. doi:[10.1097/CCM.0b013e3182227bd2](https://doi.org/10.1097/CCM.0b013e3182227bd2)

4 Ssekitoleko R, Pinkerton R, Muhindo R *et al.* Aggregate evaluable organ dysfunction predicts in-hospital mortality from sepsis in Uganda. *Am J Trop Med Hyg* 2011;**85**:697–702. doi:[10.4269/ajtmh.2011.10-0692](https://doi.org/10.4269/ajtmh.2011.10-0692)

5 Chimese SM, Andrews B, Lakhi S. The Etiology And Outcome Of Adult Patients Presenting With Sepsis To The University Teaching Hospital, Lusaka, Zambia. *Med J Zambia* 2012;**39**:19–22.<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5663186/pdf/nihms524771.pdf>

6 Moore CC, Hazard R, Saulters KJ *et al.* Derivation and validation of a universal vital assessment (UVA) score: a tool for predicting mortality in adult hospitalised patients in sub-Saharan Africa. *BMJ Glob Health* 2017;**2**:e000344. doi:[10.1136/bmjgh-2017-000344](https://doi.org/10.1136/bmjgh-2017-000344)

7 Huson MAM, Kalkman R, Stolp SM *et al.* The impact of HIV on presentation and outcome of bacterial sepsis and other causes of acute febrile illness in Gabon. *Infection* 2015;**43**:443–51. doi:[10.1007/s15010-015-0753-2](https://doi.org/10.1007/s15010-015-0753-2)

8 Amir A, Saulters KJ, Muhindo R *et al.* Outcomes of patients with severe infection in Uganda according to adherence to the World Health Organization’s Integrated Management of Adolescent and Adult Illness fluid resuscitation guidelines. *J Crit Care* 2017;**41**:24–8. doi:[10.1016/j.jcrc.2017.04.042](https://doi.org/10.1016/j.jcrc.2017.04.042)

9 Andrews B, Muchemwa L, Kelly P *et al.* Simplified severe sepsis protocol: a randomized controlled trial of modified early goal-directed therapy in Zambia. *Crit Care Med* 2014;**42**:2315–24. doi:[10.1097/ccm.0000000000000541](https://doi.org/10.1097/ccm.0000000000000541)

10 Andrews B, Semler MW, Muchemwa L *et al.* Effect of an Early Resuscitation Protocol on In-hospital Mortality Among Adults With Sepsis and Hypotension. *JAMA* 2017;**318**:1233. doi:[10.1001/jama.2017.10913](https://doi.org/10.1001/jama.2017.10913)

11 Jacob ST, Banura P, Baeten JM *et al.* The impact of early monitored management on survival in hospitalized adult Ugandan patients with severe sepsis: a prospective intervention study\*. *Crit Care Med* 2012;**40**:2050–8. doi:[10.1097/CCM.0b013e31824e65d7](https://doi.org/10.1097/CCM.0b013e31824e65d7)

12 Zida S, Kania D, Sotto A *et al.* Leptospirosis as Cause of Febrile Icteric Illness, Burkina Faso. *Emerging Infectious Diseases* 2018;**24**:1569–72. doi:[10.3201/eid2408.170436](https://doi.org/10.3201/eid2408.170436)

13 Guillebaud J, Bernardson B, Randriambolamanantsoa TH *et al.* Study on causes of fever in primary healthcare center uncovers pathogens of public health concern in Madagascar. *PLOS Neglected Tropical Diseases* 2018;**12**:e0006642. doi:[10.1371/journal.pntd.0006642](https://doi.org/10.1371/journal.pntd.0006642)

14 Maze MJ, Cash-Goldwasser S, Rubach MP *et al.* Risk factors for human acute leptospirosis in northern Tanzania. *PLOS Neglected Tropical Diseases* 2018;**12**:e0006372. doi:[10.1371/journal.pntd.0006372](https://doi.org/10.1371/journal.pntd.0006372)

15 Gadia CLB, Manirakiza A, Tekpa G *et al.* Identification of pathogens for differential diagnosis of fever with jaundice in the Central African Republic: a retrospective assessment, 2008–2010. *BMC Infectious Diseases* 2017;**17**:735. doi:[10.1186/s12879-017-2840-8](https://doi.org/10.1186/s12879-017-2840-8)

16 Hagen RM, Frickmann H, Ehlers J *et al.* Presence of Borrelia spp. DNA in ticks, but absence of Borrelia spp. and of Leptospira spp. DNA in blood of fever patients in Madagascar. *Acta Tropica* 2018;**177**:127–34. doi:[10.1016/j.actatropica.2017.10.002](https://doi.org/10.1016/j.actatropica.2017.10.002)

17 Biscornet L, Dellagi K, Pagès F *et al.* Human leptospirosis in Seychelles: A prospective study confirms the heavy burden of the disease but suggests that rats are not the main reservoir. *PLOS Neglected Tropical Diseases* 2017;**11**:e0005831. doi:[10.1371/journal.pntd.0005831](https://doi.org/10.1371/journal.pntd.0005831)

18 Dreyfus A, Dyal JW, Pearson R *et al.* Leptospira Seroprevalence and Risk Factors in Health Centre Patients in Hoima District, Western Uganda. *PLOS Neglected Tropical Diseases* 2016;**10**:e0004858. doi:[10.1371/journal.pntd.0004858](https://doi.org/10.1371/journal.pntd.0004858)

19 Hercik C, Cosmas L, Mogeni OD *et al.* A diagnostic and epidemiologic investigation of acute febrile illness (AFI) in Kilombero, Tanzania. *PLOS ONE* 2017;**12**:e0189712. doi:[10.1371/journal.pone.0189712](https://doi.org/10.1371/journal.pone.0189712)

20 Chipwaza B, Mugasa JP, Selemani M *et al.* Dengue and Chikungunya Fever among Viral Diseases in Outpatient Febrile Children in Kilosa District Hospital, Tanzania. *PLoS Neglected Tropical Diseases* 2014;**8**:e3335. doi:[10.1371/journal.pntd.0003335](https://doi.org/10.1371/journal.pntd.0003335)

21 Cash-Goldwasser S, Crump JA, Halliday JEB *et al.* Risk Factors for Human Brucellosis in Northern Tanzania. *The American Journal of Tropical Medicine and Hygiene* 2018;**98**:598–606. doi:[10.4269/ajtmh.17-0125](https://doi.org/10.4269/ajtmh.17-0125)

22 Gafirita J, Njunwa KJ, Ruhirwa R *et al.* Seroprevalence of Brucellosis among Patients Attending a District Hospital in Rwanda. *The American Journal of Tropical Medicine and Hygiene* 2017;**97**:831–5. doi:[10.4269/ajtmh.16-0632](https://doi.org/10.4269/ajtmh.16-0632)

23 Boone I, Henning K, Hilbert A *et al.* Are brucellosis, Q fever and melioidosis potential causes of febrile illness in Madagascar? *Acta Tropica* 2017;**172**:255–62. doi:[10.1016/j.actatropica.2017.05.013](https://doi.org/10.1016/j.actatropica.2017.05.013)

24 Glanville WA de, Conde-Álvarez R, Moriyón I *et al.* Poor performance of the rapid test for human brucellosis in health facilities in Kenya. *PLOS Neglected Tropical Diseases* 2017;**11**:e0005508. doi:[10.1371/journal.pntd.0005508](https://doi.org/10.1371/journal.pntd.0005508)

25 Njeru J, Melzer F, Wareth G *et al.* Human Brucellosis in Febrile Patients Seeking Treatment at Remote Hospitals, Northeastern Kenya, 2014-2015. *Emerging infectious diseases* 2016;**22**:2160–4. doi:[10.3201/eid2212.160285](https://doi.org/10.3201/eid2212.160285)

26 Chipwaza B, Mhamphi GG, Ngatunga SD *et al.* Prevalence of Bacterial Febrile Illnesses in Children in Kilosa District, Tanzania. *PLOS Neglected Tropical Diseases* 2015;**9**:e0003750. doi:[10.1371/journal.pntd.0003750](https://doi.org/10.1371/journal.pntd.0003750)

27 Feleke SM, Animut A, Belay M. Prevalence of Malaria among Acute Febrile Patients Clinically Suspected of Having Malaria in the Zeway Health Center, Ethiopia. *Japanese Journal of Infectious Diseases* 2015;**68**:55–9. doi:[10.7883/yoken.JJID.2013.062](https://doi.org/10.7883/yoken.JJID.2013.062)

28 Amoako N, Duodu S, Dennis FE *et al.* Detection of Dengue Virus among Children with Suspected Malaria, Accra, Ghana. *Emerging Infectious Diseases* 2018;**24**:1544–7. doi:[10.3201/eid2408.180341](https://doi.org/10.3201/eid2408.180341)

29 Njeru J, Henning K, Pletz MW *et al.* Febrile patients admitted to remote hospitals in Northeastern Kenya: seroprevalence, risk factors and a clinical prediction tool for Q-Fever. *BMC Infectious Diseases* 2016;**16**:244. doi:[10.1186/s12879-016-1569-0](https://doi.org/10.1186/s12879-016-1569-0)

30 Mourembou G, Nzondo SM, Ndjoyi-Mbiguino A *et al.* Co-circulation of Plasmodium and Bacterial DNAs in Blood of Febrile and Afebrile Children from Urban and Rural Areas in Gabon. *The American Journal of Tropical Medicine and Hygiene* 2016;**95**:123–32. doi:[10.4269/ajtmh.15-0751](https://doi.org/10.4269/ajtmh.15-0751)

31 Angelakis E, Mediannikov O, Socolovschi C *et al.* Coxiella burnetii-positive PCR in febrile patients in rural and urban Africa. *International Journal of Infectious Diseases* 2014;**28**:107–10. doi:[10.1016/j.ijid.2014.05.029](https://doi.org/10.1016/j.ijid.2014.05.029)

32 Maina AN, Farris CM, Odhiambo A *et al.* Q Fever, Scrub Typhus, and Rickettsial Diseases in Children, Kenya, 2011–2012. *Emerging Infectious Diseases* 2016;**22**:883–6. doi:[10.3201/eid2205.150953](https://doi.org/10.3201/eid2205.150953)

33 Sothmann P, Keller C, Krumkamp R *et al.* <i>Rickettsia felis</i> Infection in Febrile Children, Ghana. *The American Journal of Tropical Medicine and Hygiene* 2017;**96**:16–0754. doi:[10.4269/ajtmh.16-0754](https://doi.org/10.4269/ajtmh.16-0754)

34 Elfving K, Shakely D, Andersson M *et al.* Acute Uncomplicated Febrile Illness in Children Aged 2-59 months in Zanzibar – Aetiologies, Antibiotic Treatment and Outcome. *PLOS ONE* 2016;**11**:e0146054. doi:[10.1371/journal.pone.0146054](https://doi.org/10.1371/journal.pone.0146054)

35 Mourembou G, Lekana-Douki JB, Mediannikov O *et al.* Possible Role of <i>Rickettsia felis</i> in Acute Febrile Illness among Children in Gabon. *Emerging Infectious Diseases* 2015;**21**:1808–15. doi:[10.3201/eid2110.141825](https://doi.org/10.3201/eid2110.141825)

36 Vu DM, Mutai N, Heath CJ *et al.* Unrecognized Dengue Virus Infections in Children, Western Kenya, 2014-2015. *Emerging infectious diseases* 2017;**23**:1915–7. doi:[10.3201/eid2311.170807](https://doi.org/10.3201/eid2311.170807)

37 Waggoner J, Brichard J, Mutuku F *et al.* Malaria and Chikungunya Detected Using Molecular Diagnostics Among Febrile Kenyan Children. *Open Forum Infectious Diseases* 2017;**4**:ofx110. doi:[10.1093/ofid/ofx110](https://doi.org/10.1093/ofid/ofx110)

38 Kolawole OM, Seriki AA, Irekeola AA *et al.* Dengue virus and malaria concurrent infection among febrile subjects within Ilorin metropolis, Nigeria. *Journal of Medical Virology* 2017;**89**:1347–53. doi:[10.1002/jmv.24788](https://doi.org/10.1002/jmv.24788)

39 Nasir IA, Agbede OO, Dangana A *et al.* Dengue virus non-structural Protein-1 expression and associated risk factors among febrile Patients attending University of Abuja Teaching Hospital, Nigeria. *Virus Research* 2017;**230**:7–12. doi:[10.1016/j.virusres.2016.12.011](https://doi.org/10.1016/j.virusres.2016.12.011)

40 Ngoi CN, Price MA, Fields B *et al.* Dengue and Chikungunya Virus Infections among Young Febrile Adults Evaluated for Acute HIV-1 Infection in Coastal Kenya. *PLOS ONE* 2016;**11**:e0167508. doi:[10.1371/journal.pone.0167508](https://doi.org/10.1371/journal.pone.0167508)

41 Onoja A, Adeniji J, Olaleye O. High rate of unrecognized dengue virus infection in parts of the rainforest region of Nigeria. *Acta Tropica* 2016;**160**:39–43. doi:[10.1016/j.actatropica.2016.04.007](https://doi.org/10.1016/j.actatropica.2016.04.007)

42 Kajeguka DC, Kaaya RD, Mwakalinga S *et al.* Prevalence of dengue and chikungunya virus infections in north-eastern Tanzania: a cross sectional study among participants presenting with malaria-like symptoms. *BMC Infectious Diseases* 2016;**16**:183. doi:[10.1186/s12879-016-1511-5](https://doi.org/10.1186/s12879-016-1511-5)

43 Sow A, Loucoubar C, Diallo D *et al.* Concurrent malaria and arbovirus infections in Kedougou, southeastern Senegal. *Malaria Journal* 2016;**15**:47. doi:[10.1186/s12936-016-1100-5](https://doi.org/10.1186/s12936-016-1100-5)

44 Kayiwa JT, Nankya AM, Ataliba IJ *et al.* Confirmation of Zika virus infection through hospital-based sentinel surveillance of acute febrile illness in Uganda, 2014–2017. *Journal of General Virology* Published Online First: July 2018. doi:[10.1099/jgv.0.001113](https://doi.org/10.1099/jgv.0.001113)

45 Makiala-Mandanda S, Ahuka-Mundeke S, Abbate JL *et al.* Identification of Dengue and Chikungunya Cases Among Suspected Cases of Yellow Fever in the Democratic Republic of the Congo. *Vector-Borne and Zoonotic Diseases* 2018;**18**:364–70. doi:[10.1089/vbz.2017.2176](https://doi.org/10.1089/vbz.2017.2176)

46 Muianga A, Pinto G, Massangaie M *et al.* Antibodies Against Chikungunya in Northern Mozambique During Dengue Outbreak, 2014. *Vector-Borne and Zoonotic Diseases* 2018;vbz.2017.2261. doi:[10.1089/vbz.2017.2261](https://doi.org/10.1089/vbz.2017.2261)

47 Mugabe VA, Ali S, Chelene I *et al.* Evidence for chikungunya and dengue transmission in Quelimane, Mozambique: Results from an investigation of a potential outbreak of chikungunya virus. *PloS one* 2018;**13**:e0192110. doi:[10.1371/journal.pone.0192110](https://doi.org/10.1371/journal.pone.0192110)

48 António VS, Muianga AF, Wieseler J *et al.* Seroepidemiology of Chikungunya Virus Among Febrile Patients in Eight Health Facilities in Central and Northern Mozambique, 2015–2016. *Vector-Borne and Zoonotic Diseases* 2018;**18**:311–6. doi:[10.1089/vbz.2017.2227](https://doi.org/10.1089/vbz.2017.2227)

49 Sow A, Faye O, Diallo M *et al.* Chikungunya Outbreak in Kedougou, Southeastern Senegal in 2009–2010. *Open Forum Infectious Diseases* 2018;**5**:ofx259. doi:[10.1093/ofid/ofx259](https://doi.org/10.1093/ofid/ofx259)

50 Olajiga OM, Adesoye OE, Emilolorun AP *et al.* Chikungunya Virus Seroprevalence and Associated Factors among Hospital Attendees in Two States of Southwest Nigeria: A Preliminary Assessment. *Immunological Investigations* 2017;**46**:552–65. doi:[10.1080/08820139.2017.1319383](https://doi.org/10.1080/08820139.2017.1319383)

51 Bahr NC, Sarosi GA, Meya DB *et al.* Seroprevalence of histoplasmosis in Kampala, Uganda. *Medical Mycology* 2016;**54**:295–300. doi:[10.1093/mmy/myv081](https://doi.org/10.1093/mmy/myv081)

52 Mandengue CE, Ngandjio A, Atangana PJ. Histoplasmosis in HIV-Infected Persons, Yaoundé, Cameroon. *Emerging Infectious Diseases* 2015;**21**:2094–6. doi:[10.3201/eid2111.150278](https://doi.org/10.3201/eid2111.150278)

53 Bone RC, Balk RA, Cerra FB *et al.* Definitions for sepsis and organ failure and guidelines for the use of innovative therapies in sepsis. The ACCP/SCCM Consensus Conference Committee. American College of Chest Physicians/Society of Critical Care Medicine. *Chest* 1992;**101**:1644–55.<http://www.ncbi.nlm.nih.gov/pubmed/1303622>

54 Levy MM, Fink MP, Marshall JC *et al.* 2001 SCCM/ESICM/ACCP/ATS/SIS International Sepsis Definitions Conference. *Critical Care Medicine* 2003;**31**:1250–6. doi:[10.1097/01.CCM.0000050454.01978.3B](https://doi.org/10.1097/01.CCM.0000050454.01978.3B)

55 Singer M, Deutschman CS, Seymour CW *et al.* The Third International Consensus Definitions for Sepsis and Septic Shock (Sepsis-3). *JAMA* 2016;**315**:801. doi:[10.1001/jama.2016.0287](https://doi.org/10.1001/jama.2016.0287)

56 Vincent JL, Mendonça A de, Cantraine F *et al.* Use of the SOFA score to assess the incidence of organ dysfunction/failure in intensive care units: results of a multicenter, prospective study. Working group on ‘sepsis-related problems’ of the European Society of Intensive Care Medicine. *Critical care medicine* 1998;**26**:1793–800.<http://www.ncbi.nlm.nih.gov/pubmed/9824069>

57 Seymour CW, Liu VX, Iwashyna TJ *et al.* Assessment of Clinical Criteria for Sepsis. *JAMA* 2016;**315**:762. doi:[10.1001/jama.2016.0288](https://doi.org/10.1001/jama.2016.0288)

58 Shankar-Hari M, Phillips GS, Levy ML *et al.* Developing a New Definition and Assessing New Clinical Criteria for Septic Shock. *JAMA* 2016;**315**:775. doi:[10.1001/jama.2016.0289](https://doi.org/10.1001/jama.2016.0289)

59 Jacob ST, West TE, Banura P. Fitting a square peg into a round hole: are the current Surviving Sepsis Campaign guidelines feasible for Africa? *Crit Care* 2011;**15**:117. doi:[10.1186/cc9981](https://doi.org/10.1186/cc9981)

60 Prin M, Itaye T, Clark S *et al.* Critical Care in a Tertiary Hospital in Malawi. *World J Surg* 2016;**40**:2635–42. doi:[10.1007/s00268-016-3578-y](https://doi.org/10.1007/s00268-016-3578-y)

61 Huson MA, Kalkman R, Grobusch MP *et al.* Predictive value of the qSOFA score in patients with suspected infection in a resource limited setting in Gabon. *Travel Med Infect Dis* 2017;**15**:76–7. doi:[10.1016/j.tmaid.2016.10.014](https://doi.org/10.1016/j.tmaid.2016.10.014)

62 Huson MAM, Katete C, Chunda L *et al.* Application of the qSOFA score to predict mortality in patients with suspected infection in a resource-limited setting in Malawi. *Infection* 2017;**45**:893–6. doi:[10.1007/s15010-017-1057-5](https://doi.org/10.1007/s15010-017-1057-5)

63 Aluisio AR, Garbern S, Wiskel T *et al.* Mortality outcomes based on ED qSOFA score and HIV status in a developing low income country. *The American Journal of Emergency Medicine* Published Online First: March 2018. doi:[10.1016/j.ajem.2018.03.014](https://doi.org/10.1016/j.ajem.2018.03.014)

64 Rudd KE, Seymour CW, Aluisio AR *et al.* Association of the Quick Sequential (Sepsis-Related) Organ Failure Assessment (qSOFA) Score With Excess Hospital Mortality in Adults With Suspected Infection in Low- and Middle-Income Countries. *JAMA* 2018;**319**:2202. doi:[10.1001/jama.2018.6229](https://doi.org/10.1001/jama.2018.6229)

65 Gaieski DF, Edwards JM, Kallan MJ *et al.* Benchmarking the Incidence and Mortality of Severe Sepsis in the United States\*. *Critical Care Medicine* 2013;**41**:1167–74. doi:[10.1097/CCM.0b013e31827c09f8](https://doi.org/10.1097/CCM.0b013e31827c09f8)

66 Fleischmann C, Scherag A, Adhikari NKJ *et al.* Assessment of Global Incidence and Mortality of Hospital-treated Sepsis. Current Estimates and Limitations. *American Journal of Respiratory and Critical Care Medicine* 2016;**193**:259–72. doi:[10.1164/rccm.201504-0781OC](https://doi.org/10.1164/rccm.201504-0781OC)

67 Angus DC, Linde-Zwirble WT, Lidicker J *et al.* Epidemiology of severe sepsis in the United States: analysis of incidence, outcome, and associated costs of care. *Critical care medicine* 2001;**29**:1303–10.<http://www.ncbi.nlm.nih.gov/pubmed/11445675>

68 Tsertsvadze A, Royle P, Seedat F *et al.* Community-onset sepsis and its public health burden: a systematic review. *Systematic reviews* 2016;**5**:81. doi:[10.1186/s13643-016-0243-3](https://doi.org/10.1186/s13643-016-0243-3)

69 Mayr FB, Yende S, Linde-Zwirble WT *et al.* Infection Rate and Acute Organ Dysfunction Risk as Explanations for Racial Differences in Severe Sepsis. *JAMA* 2010;**303**:2495. doi:[10.1001/jama.2010.851](https://doi.org/10.1001/jama.2010.851)

70 Seymour CW, Gesten F, Prescott HC *et al.* Time to Treatment and Mortality during Mandated Emergency Care for Sepsis. *New England Journal of Medicine* 2017;**376**:2235–44. doi:[10.1056/NEJMoa1703058](https://doi.org/10.1056/NEJMoa1703058)

71 PRISM Investigators, Rowan KM, Angus DC *et al.* Early, Goal-Directed Therapy for Septic Shock — A Patient-Level Meta-Analysis. *New England Journal of Medicine* 2017;**376**:2223–34. doi:[10.1056/NEJMoa1701380](https://doi.org/10.1056/NEJMoa1701380)

72 Rangel-Frausto MS, Pittet D, Costigan M *et al.* The Natural History of the Systemic Inflammatory Response Syndrome (SIRS). *JAMA* 1995;**273**:117. doi:[10.1001/jama.1995.03520260039030](https://doi.org/10.1001/jama.1995.03520260039030)

73 Serafim R, Gomes JA, Salluh J *et al.* A Comparison of the Quick-SOFA and Systemic Inflammatory Response Syndrome Criteria for the Diagnosis of Sepsis and Prediction of Mortality. *Chest* 2018;**153**:646–55. doi:[10.1016/j.chest.2017.12.015](https://doi.org/10.1016/j.chest.2017.12.015)

74 Kaukonen K-M, Bailey M, Suzuki S *et al.* Mortality related to severe sepsis and septic shock among critically ill patients in Australia and New Zealand, 2000-2012. *JAMA* 2014;**311**:1308–16. doi:[10.1001/jama.2014.2637](https://doi.org/10.1001/jama.2014.2637)

75 Stevenson EK, Rubenstein AR, Radin GT *et al.* Two Decades of Mortality Trends Among Patients With Severe Sepsis. *Critical Care Medicine* 2014;**42**:625–31. doi:[10.1097/CCM.0000000000000026](https://doi.org/10.1097/CCM.0000000000000026)

76 Winters BD, Eberlein M, Leung J *et al.* Long-term mortality and quality of life in sepsis: A systematic review\*. *Critical Care Medicine* 2010;**38**:1276–83. doi:[10.1097/CCM.0b013e3181d8cc1d](https://doi.org/10.1097/CCM.0b013e3181d8cc1d)

77 Shah FA, Pike F, Alvarez K *et al.* Bidirectional Relationship between Cognitive Function and Pneumonia. *American Journal of Respiratory and Critical Care Medicine* 2013;**188**:586–92. doi:[10.1164/rccm.201212-2154OC](https://doi.org/10.1164/rccm.201212-2154OC)

78 Iwashyna TJ, Ely EW, Smith DM *et al.* Long-term Cognitive Impairment and Functional Disability Among Survivors of Severe Sepsis. *JAMA* 2010;**304**:1787. doi:[10.1001/jama.2010.1553](https://doi.org/10.1001/jama.2010.1553)

79 Yende S, Linde-Zwirble W, Mayr F *et al.* Risk of cardiovascular events in survivors of severe sepsis. *American journal of respiratory and critical care medicine* 2014;**189**:1065–74. doi:[10.1164/rccm.201307-1321OC](https://doi.org/10.1164/rccm.201307-1321OC)

80 Bergh C, Fall K, Udumyan R *et al.* Severe infections and subsequent delayed cardiovascular disease. *European journal of preventive cardiology* 2017;**24**:1958–66. doi:[10.1177/2047487317724009](https://doi.org/10.1177/2047487317724009)

81 Ou S-M, Chu H, Chao P-W *et al.* Long-Term Mortality and Major Adverse Cardiovascular Events in Sepsis Survivors. A Nationwide Population-based Study. *American Journal of Respiratory and Critical Care Medicine* 2016;**194**:209–17. doi:[10.1164/rccm.201510-2023OC](https://doi.org/10.1164/rccm.201510-2023OC)

82 Crump JA, Morrissey AB, Nicholson WL *et al.* Etiology of Severe Non-malaria Febrile Illness in Northern Tanzania: A Prospective Cohort Study. *PLoS Neglected Tropical Diseases* 2013;**7**:e2324. doi:[10.1371/journal.pntd.0002324](https://doi.org/10.1371/journal.pntd.0002324)

83 Prasad N, Murdoch DR, Reyburn H *et al.* Etiology of Severe Febrile Illness in Low- and Middle-Income Countries: A Systematic Review. *PloS one* 2015;**10**:e0127962. doi:[10.1371/journal.pone.0127962](https://doi.org/10.1371/journal.pone.0127962)

84 Moore CC, Jacob ST, Banura P *et al.* Etiology of Sepsis in Uganda using a Quantitative PCR-based TaqMan Array Card. *Clin Infect Dis* 2019;**68**:266–72. doi:[10.1093/cid/ciy472](https://doi.org/10.1093/cid/ciy472)

85 Osawa R, Singh N. Cytomegalovirus infection in critically ill patients: a systematic review. *Critical Care* 2009;**13**:R68. doi:[10.1186/cc7875](https://doi.org/10.1186/cc7875)

86 Rubach MP, Maro VP, Bartlett JA *et al.* Etiologies of illness among patients meeting integrated management of adolescent and adult illness district clinician manual criteria for severe infections in northern Tanzania: implications for empiric antimicrobial therapy. *Am J Trop Med Hyg* 2015;**92**:454–62. doi:[10.4269/ajtmh.14-0496](https://doi.org/10.4269/ajtmh.14-0496)

87 World Health Organisation. IMAI district clinician manual: hospital care for adolescents and adults. 2011.

88 Rajasingham R, Smith RM, Park BJ *et al.* Global burden of disease of HIV-associated cryptococcal meningitis: an updated analysis. *The Lancet Infectious Diseases* 2017;**17**:873–81. doi:[10.1016/S1473-3099(17)30243-8](https://doi.org/10.1016/S1473-3099(17)30243-8)

89 Wasserman S, Engel ME, Mendelson M. Burden of pneumocystis pneumonia in HIV-infected adults in sub-Saharan Africa: protocol for a systematic review. *Syst Rev* 2013;**2**:112. doi:[10.1186/2046-4053-2-112](https://doi.org/10.1186/2046-4053-2-112)

90 Onishi A, Sugiyama D, Kogata Y *et al.* Diagnostic Accuracy of Serum 1,3--d-Glucan for Pneumocystis jiroveci Pneumonia, Invasive Candidiasis, and Invasive Aspergillosis: Systematic Review and Meta-Analysis. *Journal of Clinical Microbiology* 2012;**50**:7–15. doi:[10.1128/JCM.05267-11](https://doi.org/10.1128/JCM.05267-11)

91 Rhodes A, Evans LE, Alhazzani W *et al.* Surviving Sepsis Campaign. *Critical Care Medicine* 2017;**45**:486–552. doi:[10.1097/CCM.0000000000002255](https://doi.org/10.1097/CCM.0000000000002255)

92 Dünser MW, Festic E, Dondorp A *et al.* Recommendations for sepsis management in resource-limited settings. *Intensive Care Medicine* 2012;**38**:557–74. doi:[10.1007/s00134-012-2468-5](https://doi.org/10.1007/s00134-012-2468-5)

93 Mer M, Schultz MJ, Adhikari NK *et al.* Core elements of general supportive care for patients with sepsis and septic shock in resource-limited settings. *Intensive Care Medicine* 2017;**43**:1690–4. doi:[10.1007/s00134-017-4831-z](https://doi.org/10.1007/s00134-017-4831-z)

94 Thwaites CL, Lundeg G, Dondorp AM *et al.* Recommendations for infection management in patients with sepsis and septic shock in resource-limited settings. *Intensive Care Medicine* 2016;**42**:2040–2. doi:[10.1007/s00134-016-4415-3](https://doi.org/10.1007/s00134-016-4415-3)

95 Misango D, Pattnaik R, Baker T *et al.* Haemodynamic assessment and support in sepsis and septic shock in resource-limited settings. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 2017;**111**:483–9. doi:[10.1093/trstmh/try007](https://doi.org/10.1093/trstmh/try007)

96 Rivers E, Nguyen B, Havstad S *et al.* Early Goal-Directed Therapy in the Treatment of Severe Sepsis and Septic Shock. *New England Journal of Medicine* 2001;**345**:1368–77. doi:[10.1056/NEJMoa010307](https://doi.org/10.1056/NEJMoa010307)

97 Yealy DM, Kellum JA, Huang DT *et al.* A randomized trial of protocol-based care for early septic shock. *The New England journal of medicine* 2014;**370**:1683–93. doi:[10.1056/NEJMoa1401602](https://doi.org/10.1056/NEJMoa1401602)

98 Peake SL, Delaney A, Bailey M *et al.* Goal-Directed Resuscitation for Patients with Early Septic Shock. *New England Journal of Medicine* 2014;**371**:141001063014008. doi:[10.1056/NEJMoa1404380](https://doi.org/10.1056/NEJMoa1404380)

99 Mouncey PR, Osborn TM, Power GS *et al.* Trial of Early, Goal-Directed Resuscitation for Septic Shock. *New England Journal of Medicine* 2015;**372**:150317011022003. doi:[10.1056/NEJMoa1500896](https://doi.org/10.1056/NEJMoa1500896)

100 Kumar A, Roberts D, Wood KE *et al.* Duration of hypotension before initiation of effective antimicrobial therapy is the critical determinant of survival in human septic shock. *Critical care medicine* 2006;**34**:1589–96. doi:[10.1097/01.CCM.0000217961.75225.E9](https://doi.org/10.1097/01.CCM.0000217961.75225.E9)

101 Sterling SA, Miller WR, Pryor J *et al.* The Impact of Timing of Antibiotics on Outcomes in Severe Sepsis and Septic Shock. *Critical Care Medicine* 2015;**43**:1907–15. doi:[10.1097/CCM.0000000000001142](https://doi.org/10.1097/CCM.0000000000001142)

102 Amir A, Saulters KJ, Olum S *et al.* Outcomes of patients with severe sepsis after the first 6 hours of resuscitation at a regional referral hospital in Uganda. *J Crit Care* 2016;**33**:78–83. doi:[10.1016/j.jcrc.2016.01.023](https://doi.org/10.1016/j.jcrc.2016.01.023)

103 Chalya PL, Mabula JB, Koy M *et al.* Typhoid intestinal perforations at a University teaching hospital in Northwestern Tanzania: A surgical experience of 104 cases in a resource-limited setting. *World journal of emergency surgery : WJES* 2012;**7**:4. doi:[10.1186/1749-7922-7-4](https://doi.org/10.1186/1749-7922-7-4)

104 Ferrer R, Artigas A, Suarez D *et al.* Effectiveness of Treatments for Severe Sepsis. *American Journal of Respiratory and Critical Care Medicine* 2009;**180**:861–6. doi:[10.1164/rccm.200812-1912OC](https://doi.org/10.1164/rccm.200812-1912OC)

105 Lee SJ, Ramar K, Park JG *et al.* Increased fluid administration in the first three hours of sepsis resuscitation is associated with reduced mortality: a retrospective cohort study. *Chest* 2014;**146**:908–15. doi:[10.1378/chest.13-2702](https://doi.org/10.1378/chest.13-2702)

106 Leisman D, Wie B, Doerfler M *et al.* Association of Fluid Resuscitation Initiation Within 30 Minutes of Severe Sepsis and Septic Shock Recognition With Reduced Mortality and Length of Stay. *Annals of Emergency Medicine* 2016;**68**:298–311. doi:[10.1016/j.annemergmed.2016.02.044](https://doi.org/10.1016/j.annemergmed.2016.02.044)

107 Leisman DE, Goldman C, Doerfler ME *et al.* Patterns and Outcomes Associated With Timeliness of Initial Crystalloid Resuscitation in a Prospective Sepsis and Septic Shock Cohort\*. *Critical Care Medicine* 2017;**45**:1596–606. doi:[10.1097/CCM.0000000000002574](https://doi.org/10.1097/CCM.0000000000002574)

108 Leisman DE, Doerfler ME, Schneider SM *et al.* Predictors, Prevalence, and Outcomes of Early Crystalloid Responsiveness Among Initially Hypotensive Patients With Sepsis and Septic Shock\*. *Critical Care Medicine* 2018;**46**:189–98. doi:[10.1097/CCM.0000000000002834](https://doi.org/10.1097/CCM.0000000000002834)

109 Maitland K, Kiguli S, Opoka RO *et al.* Mortality after fluid bolus in African children with severe infection. *The New England journal of medicine* 2011;**364**:2483–95. doi:[10.1056/NEJMoa1101549](https://doi.org/10.1056/NEJMoa1101549)

110 Maitland K, George EC, Evans JA *et al.* Exploring mechanisms of excess mortality with early fluid resuscitation: insightsfrom the FEAST trial. *BMC Medicine* 2013;**11**:68. doi:[10.1186/1741-7015-11-68](https://doi.org/10.1186/1741-7015-11-68)

111 Guiral E, Pons MJ, Vubil D *et al.* Epidemiology and molecular characterization of multidrug-resistant Escherichia coli isolates harboring blaCTX-M group 1 extended-spectrum beta-lactamases causing bacteremia and urinary tract infection in Manhica, Mozambique. *Infect Drug Resist* 2018;**11**:927–36. doi:[10.2147/idr.s153601](https://doi.org/10.2147/idr.s153601)

112 Karppinen M, Bernardino L, Anjos ED *et al.* Etiology of Childhood Otorrhea in Luanda, Angola, and a Review of Otitis Media in African Children. *Pediatr Infect Dis J* Published Online First: 2018. doi:[10.1097/inf.0000000000002254](https://doi.org/10.1097/inf.0000000000002254)

113 Ibrahim Y, Sani Y, Saleh Q *et al.* Phenotypic Detection of Extended Spectrum Beta lactamase and Carbapenemase Co-producing Clinical Isolates from Two Tertiary Hospitals in Kano, North West Nigeria. *Ethiop J Health Sci* 2017;**27**:3–10.<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5390223/pdf/EJHS2701-0003.pdf>

114 Kassam NA, Damian DJ, Kajeguka D *et al.* Spectrum and antibiogram of bacteria isolated from patients presenting with infected wounds in a Tertiary Hospital, northern Tanzania. *BMC Res Notes* 2017;**10**:757. doi:[10.1186/s13104-017-3092-9](https://doi.org/10.1186/s13104-017-3092-9)

115 Legese MH, Weldearegay GM, Asrat D. Extended-spectrum beta-lactamase- and carbapenemase-producing Enterobacteriaceae among Ethiopian children. *Infect Drug Resist* 2017;**10**:27–34. doi:[10.2147/idr.s127177](https://doi.org/10.2147/idr.s127177)

116 Manyahi J, Moyo SJ, Tellevik MG *et al.* Detection of CTX-M-15 beta-lactamases in Enterobacteriaceae causing hospital- and community-acquired urinary tract infections as early as 2004, in Dar es Salaam, Tanzania. *BMC Infect Dis* 2017;**17**:282. doi:[10.1186/s12879-017-2395-8](https://doi.org/10.1186/s12879-017-2395-8)

117 Sangare SA, Rondinaud E, Maataoui N *et al.* Very high prevalence of extended-spectrum beta-lactamase-producing Enterobacteriaceae in bacteriemic patients hospitalized in teaching hospitals in Bamako, Mali. *PLoS One* 2017;**12**. doi:[10.1371/journal.pone.0172652](https://doi.org/10.1371/journal.pone.0172652)

118 Abera B, Kibret M, Mulu W. Extended-Spectrum beta (beta)-Lactamases and Antibiogram in Enterobacteriaceae from Clinical and Drinking Water Sources from Bahir Dar City, Ethiopia. *PLoS One* 2016;**11**:e0166519. doi:[10.1371/journal.pone.0166519](https://doi.org/10.1371/journal.pone.0166519)

119 Agyekum A, Fajardo-Lubian A, Ansong D *et al.* blaCTX-M-15 carried by IncF-type plasmids is the dominant ESBL gene in Escherichia coli and Klebsiella pneumoniae at a hospital in Ghana. *Diagn Microbiol Infect Dis* 2016;**84**:328–33. doi:[10.1016/j.diagmicrobio.2015.12.010](https://doi.org/10.1016/j.diagmicrobio.2015.12.010)

120 Breurec S, Bouchiat C, Sire JM *et al.* High third-generation cephalosporin resistant Enterobacteriaceae prevalence rate among neonatal infections in Dakar, Senegal. *BMC Infect Dis* 2016;**16**. doi:[10.1186/s12879-016-1935-y](https://doi.org/10.1186/s12879-016-1935-y)

121 Buys H, Muloiwa R, Bamford C *et al.* Klebsiella pneumoniae bloodstream infections at a South African children’s hospital 2006-2011, a cross-sectional study. *BMC Infect Dis* 2016;**16**:570. doi:[10.1186/s12879-016-1919-y](https://doi.org/10.1186/s12879-016-1919-y)

122 Eibach D, Belmar Campos C, Krumkamp R *et al.* Extended spectrum beta-lactamase producing Enterobacteriaceae causing bloodstream infections in rural Ghana, 2007-2012. *Int J Med Microbiol* 2016;**306**:249–54. doi:[10.1016/j.ijmm.2016.05.006](https://doi.org/10.1016/j.ijmm.2016.05.006)

123 Kpoda DS, Ajayi A, Somda M *et al.* Distribution of resistance genes encoding ESBLs in Enterobacteriaceae isolated from biological samples in health centers in Ouagadougou, Burkina Faso. *BMC Res Notes* 2018;**11**:471. doi:[10.1186/s13104-018-3581-5](https://doi.org/10.1186/s13104-018-3581-5)

124 Kabwe M, Tembo J, Chilukutu L *et al.* Etiology, antibiotic resistance and risk factors for neonatal sepsis in a large referral center in Zambia. *Pediatric Infectious Disease Journal* 2016;**35**:e191–8. doi:[10.1097/INF.0000000000001154](https://doi.org/10.1097/INF.0000000000001154)

125 Leski TA, Taitt CR, Bangura U *et al.* High prevalence of multidrug resistant Enterobacteriaceae isolated from outpatient urine samples but not the hospital environment in Bo, Sierra Leone. *BMC Infect Dis* 2016;**16**:167. doi:[10.1186/s12879-016-1495-1](https://doi.org/10.1186/s12879-016-1495-1)

126 Mohammed Y, Gadzama GB, Zailani SB *et al.* Characterization of Extended-Spectrum Beta-lactamase from Escherichia coli and Klebsiella Species from North Eastern Nigeria. *J Clin Diagn Res* 2016;**10**:Dc07–10. doi:[10.7860/jcdr/2016/16330.7254](https://doi.org/10.7860/jcdr/2016/16330.7254)

127 Naas T, Cuzon G, Robinson AL *et al.* Neonatal infections with multidrug-resistant ESBL-producing E. cloacae and K. pneumoniae in Neonatal Units of two different Hospitals in Antananarivo, Madagascar. *BMC Infect Dis* 2016;**16**:275. doi:[10.1186/s12879-016-1580-5](https://doi.org/10.1186/s12879-016-1580-5)

128 Ndir A, Diop A, Faye PM *et al.* Epidemiology and Burden of Bloodstream Infections Caused by Extended-Spectrum Beta-Lactamase Producing Enterobacteriaceae in a Pediatric Hospital in Senegal. *PLoS One* 2016;**11**:e0143729. doi:[10.1371/journal.pone.0143729](https://doi.org/10.1371/journal.pone.0143729)

129 Ouedraogo AS, Sanou M, Kissou A *et al.* High prevalence of extended-spectrum ss-lactamase producing enterobacteriaceae among clinical isolates in Burkina Faso. *BMC Infect Dis* 2016;**16**:326. doi:[10.1186/s12879-016-1655-3](https://doi.org/10.1186/s12879-016-1655-3)

130 Sangare SA, Maiga AI, Guindo I *et al.* Prevalence of ESBL-producing Enterobacteriaceae isolated from blood cultures in Mali. *J Infect Dev Ctries* 2016;**10**:1059–64. doi:[10.3855/jidc.7536](https://doi.org/10.3855/jidc.7536)

131 Seni J, Falgenhauer L, Simeo N *et al.* Multiple ESBL-Producing Escherichia coli Sequence Types Carrying Quinolone and Aminoglycoside Resistance Genes Circulating in Companion and Domestic Farm Animals in Mwanza, Tanzania, Harbor Commonly Occurring Plasmids. *Front Microbiol* 2016;**7**:142. doi:[10.3389/fmicb.2016.00142](https://doi.org/10.3389/fmicb.2016.00142)

132 Dramowski A, Cotton MF, Rabie H *et al.* Trends in paediatric bloodstream infections at a South African referral hospital. *BMC Pediatr* 2015;**15**:33. doi:[10.1186/s12887-015-0354-3](https://doi.org/10.1186/s12887-015-0354-3)

133 Irenge LM, Kabego L, Kinunu FB *et al.* Antimicrobial resistance of bacteria isolated from patients with bloodstream infections at a tertiary care hospital in the Democratic Republic of the Congo. *S Afr Med J* 2015;**105**:752–5. doi:[10.7196/SAMJnew.7937](https://doi.org/10.7196/SAMJnew.7937)

134 Onanuga A, Omeje MC, Eboh DD. CARRIAGE OF MULTI-DRUG RESISTANT UROBACTERIA BY ASYMPTOMATIC PREGNANT WOMEN IN YENAGOA, BAYELSA STATE, NIGERIA. *Afr J Infect Dis* 2018;**12**:14–20. doi:[10.21010/ajid.v12i2.3](https://doi.org/10.21010/ajid.v12i2.3)

135 Kateregga JN, Kantume R, Atuhaire C *et al.* Phenotypic expression and prevalence of ESBL-producing Enterobacteriaceae in samples collected from patients in various wards of Mulago Hospital, Uganda. *BMC Pharmacol Toxicol* 2015;**16**:14. doi:[10.1186/s40360-015-0013-1](https://doi.org/10.1186/s40360-015-0013-1)

136 Opintan JA, Newman MJ, Arhin RE *et al.* Laboratory-based nationwide surveillance of antimicrobial resistance in Ghana. *Infect Drug Resist* 2015;**8**:379–89. doi:[10.2147/idr.s88725](https://doi.org/10.2147/idr.s88725)

137 Pons MJ, Vubil D, Guiral E *et al.* Characterisation of extended-spectrum beta-lactamases among Klebsiella pneumoniae isolates causing bacteraemia and urinary tract infection in Mozambique. *J Glob Antimicrob Resist* 2015;**3**:19–25. doi:[10.1016/j.jgar.2015.01.004](https://doi.org/10.1016/j.jgar.2015.01.004)

138 Rafaï C, Frank T, Manirakiza A *et al.* Dissemination of IncF-type plasmids in multiresistant CTX-M-15-producing Enterobacteriaceae isolates from surgical-site infections in Bangui, Central African Republic. *BMC Microbiol* 2015;**15**. doi:[10.1186/s12866-015-0348-1](https://doi.org/10.1186/s12866-015-0348-1)

139 Adeyankinnu FA, Motayo BO, Akinduti A *et al.* A Multicenter Study of Beta-Lactamase Resistant Escherichia coli and Klebsiella pneumoniae Reveals High Level Chromosome Mediated Extended Spectrum beta Lactamase Resistance in Ogun State, Nigeria. *Interdiscip Perspect Infect Dis* 2014;**2014**:819896. doi:[10.1155/2014/819896](https://doi.org/10.1155/2014/819896)

140 Irenge LM, Kabego L, Vandenberg O *et al.* Antimicrobial resistance in urinary isolates from inpatients and outpatients at a tertiary care hospital in South-Kivu Province (Democratic Republic of Congo). *BMC Res Notes* 2014;**7**:374. doi:[10.1186/1756-0500-7-374](https://doi.org/10.1186/1756-0500-7-374)

141 Scherbaum M, Kosters K, Murbeth RE *et al.* Incidence, pathogens and resistance patterns of nosocomial infections at a rural hospital in Gabon. *BMC Infect Dis* 2014;**14**:124. doi:[10.1186/1471-2334-14-124](https://doi.org/10.1186/1471-2334-14-124)

142 Yusuf I, Arzai AH, Haruna M *et al.* Detection of multi drug resistant bacteria in major hospitals in Kano, North-West, Nigeria. *Braz J Microbiol* 2014;**45**:791–8.<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4204960/pdf/bjm-45-791.pdf>

143 Alabi AS, Frielinghaus L, Kaba H *et al.* Retrospective analysis of antimicrobial resistance and bacterial spectrum of infection in Gabon, Central Africa. *BMC Infect Dis* 2013;**13**:455. doi:[10.1186/1471-2334-13-455](https://doi.org/10.1186/1471-2334-13-455)

144 Ibrahim ME, Bilal NE, Magzoub MA *et al.* Prevalence of Extended-spectrum beta-Lactamases-producing Escherichia coli from Hospitals in Khartoum State, Sudan. *Oman Med J* 2013;**28**:116–20. doi:[10.5001/omj.2013.30](https://doi.org/10.5001/omj.2013.30)

145 Seni J, Peirano G, Okon KO *et al.* The population structure of clinical extra-intestinal Escherichia coli in a teaching hospital from Nigeria. *Diagn Microbiol Infect Dis* 2018;**92**:46–9. doi:[10.1016/j.diagmicrobio.2018.04.001](https://doi.org/10.1016/j.diagmicrobio.2018.04.001)

146 Obeng-Nkrumah N, Twum-Danso K, Krogfelt KA *et al.* High levels of extended-spectrum beta-lactamases in a major teaching hospital in Ghana: the need for regular monitoring and evaluation of antibiotic resistance. *Am J Trop Med Hyg* 2013;**89**:960–4. doi:[10.4269/ajtmh.12-0642](https://doi.org/10.4269/ajtmh.12-0642)

147 Raji MA, Jamal W, Ojemhen O *et al.* Point-surveillance of antibiotic resistance in Enterobacteriaceae isolates from patients in a Lagos Teaching Hospital, Nigeria. *J Infect Public Health* 2013;**6**:431–7. doi:[10.1016/j.jiph.2013.05.002](https://doi.org/10.1016/j.jiph.2013.05.002)

148 Meeren BT van der, Chhaganlal KD, Pfeiffer A *et al.* Extremely high prevalence of multi-resistance among uropathogens from hospitalised children in Beira, Mozambique. *S Afr Med J* 2013;**103**:382–6. doi:[10.7196/samj.5941](https://doi.org/10.7196/samj.5941)

149 Idowu OJ, Onipede AO, Orimolade AE *et al.* Extended-spectrum Beta-lactamase Orthopedic Wound Infections in Nigeria. *J Glob Infect Dis* 2011;**3**:211–5. doi:[10.4103/0974-777x.83524](https://doi.org/10.4103/0974-777x.83524)

150 Moyo SJ, Aboud S, Kasubi M *et al.* Antimicrobial resistance among producers and non-producers of extended spectrum beta-lactamases in urinary isolates at a tertiary Hospital in Tanzania. *BMC Res Notes* 2010;**3**:348. doi:[10.1186/1756-0500-3-348](https://doi.org/10.1186/1756-0500-3-348)

151 Bercion R, Mossoro-Kpinde D, Manirakiza A *et al.* Increasing prevalence of antimicrobial resistance among Enterobacteriaceae uropathogens in Bangui, Central African Republic. *J Infect Dev Ctries* 2009;**3**:187–90.<https://jidc.org/index.php/journal/article/download/19759473/21>

152 Mshana SE, Kamugisha E, Mirambo M *et al.* Prevalence of multiresistant gram-negative organisms in a tertiary hospital in Mwanza, Tanzania. *BMC Res Notes* 2009;**2**:49. doi:[10.1186/1756-0500-2-49](https://doi.org/10.1186/1756-0500-2-49)

153 Sire JM, Nabeth P, Perrier-Gros-Claude JD *et al.* Antimicrobial resistance in outpatient Escherichia coli urinary isolates in Dakar, Senegal. *J Infect Dev Ctries* 2007;**1**:263–8.<https://jidc.org/index.php/journal/article/download/19734603/210>

154 Blomberg B, Jureen R, Manji KP *et al.* High rate of fatal cases of pediatric septicemia caused by gram-negative bacteria with extended-spectrum beta-lactamases in Dar es Salaam, Tanzania. *J Clin Microbiol* 2005;**43**:745–9. doi:[10.1128/jcm.43.2.745-749.2005](https://doi.org/10.1128/jcm.43.2.745-749.2005)

155 Gangoue-Pieboji J, Bedenic B, Koulla-Shiro S *et al.* Extended-spectrum-beta-lactamase-producing Enterobacteriaceae in Yaounde, Cameroon. *J Clin Microbiol* 2005;**43**:3273–7. doi:[10.1128/jcm.43.7.3273-3277.2005](https://doi.org/10.1128/jcm.43.7.3273-3277.2005)

156 Zeynudin A, Pritsch M, Schubert S *et al.* Prevalence and antibiotic susceptibility pattern of CTX-M type extended-spectrum beta-lactamases among clinical isolates of gram-negative bacilli in Jimma, Ethiopia. *BMC Infect Dis* 2018;**18**:524. doi:[10.1186/s12879-018-3436-7](https://doi.org/10.1186/s12879-018-3436-7)

157 Ndugulile F, Jureen R, Harthug S *et al.* Extended spectrum beta-lactamases among Gram-negative bacteria of nosocomial origin from an intensive care unit of a tertiary health facility in Tanzania. *BMC Infect Dis* 2005;**5**:86. doi:[10.1186/1471-2334-5-86](https://doi.org/10.1186/1471-2334-5-86)

158 Dromigny JA, Ndoye B, Macondo EA *et al.* Increasing prevalence of antimicrobial resistance among Enterobacteriaceae uropathogens in Dakar, Senegal: A multicenter study. *Diagn Microbiol Infect Dis* 2003;**47**:595–600. doi:[10.1016/S0732-8893(03)00155-X](https://doi.org/10.1016/S0732-8893(03)00155-X)

159 Dromigny JA, Nabeth P, Perrier Gros Claude JD. Distribution and susceptibility of bacterial urinary tract infections in Dakar, Senegal. *Int J Antimicrob Agents* 2002;**20**:339–47.<https://www.ijaaonline.com/article/S0924-8579(02)00196-6/fulltext>

160 Ampaire L, Nduhura E, Wewedru I. Phenotypic prevalence of extended spectrum beta-lactamases among enterobacteriaceae isolated at Mulago National Referral Hospital: Uganda. *BMC Res Notes* 2017;**10**:448. doi:[10.1186/s13104-017-2786-3](https://doi.org/10.1186/s13104-017-2786-3)

161 Andrew B, Kagirita A, Bazira J. Prevalence of Extended-Spectrum Beta-Lactamases-Producing Microorganisms in Patients Admitted at KRRH, Southwestern Uganda. *Int J Microbiol* 2017;**2017**:3183076. doi:[10.1155/2017/3183076](https://doi.org/10.1155/2017/3183076)

162 Archary M, Adler H, La Russa P *et al.* Bacterial infections in HIV-infected children admitted with severe acute malnutrition in Durban, South Africa. *Paediatr Int Child Health* 2017;**37**:6–13. doi:[10.1080/20469047.2016.1198561](https://doi.org/10.1080/20469047.2016.1198561)

163 Henson SP, Boinett CJ, Ellington MJ *et al.* Molecular epidemiology of Klebsiella pneumoniae invasive infections over a decade at Kilifi County Hospital in Kenya. *Int J Med Microbiol* 2017;**307**:422–9. doi:[10.1016/j.ijmm.2017.07.006](https://doi.org/10.1016/j.ijmm.2017.07.006)

164 Chirindze LM, Zimba TF, Sekyere JO *et al.* Faecal colonization of E. coli and Klebsiella spp. producing extended-spectrum beta-lactamases and plasmid-mediated AmpC in Mozambican university students. *BMC Infect Dis* 2018;**18**:244. doi:[10.1186/s12879-018-3154-1](https://doi.org/10.1186/s12879-018-3154-1)

165 Founou RC, Founou LL, Essack SY. Extended spectrum beta-lactamase mediated resistance in carriage and clinical gram-negative ESKAPE bacteria: a comparative study between a district and tertiary hospital in South Africa. *Antimicrob Resist Infect Control* 2018;**7**:134. doi:[10.1186/s13756-018-0423-0](https://doi.org/10.1186/s13756-018-0423-0)

166 Magwenzi MT, Gudza-Mugabe M, Mujuru HA *et al.* Carriage of antibiotic-resistant Enterobacteriaceae in hospitalised children in tertiary hospitals in Harare, Zimbabwe. *Antimicrob Resist Infect Control* 2017;**6**:10. doi:[10.1186/s13756-016-0155-y](https://doi.org/10.1186/s13756-016-0155-y)

167 Moremi N, Claus H, Vogel U *et al.* Faecal carriage of CTX-M extended-spectrum beta-lactamase-producing Enterobacteriaceae among street children dwelling in Mwanza city, Tanzania. *PLoS One* 2017;**12**:e0184592. doi:[10.1371/journal.pone.0184592](https://doi.org/10.1371/journal.pone.0184592)

168 Wilmore SMS, Kranzer K, Williams A *et al.* Carriage of extended-spectrum beta-lactamase-producing Enterobacteriaceae in HIV-infected children in Zimbabwe. *J Med Microbiol* 2017;**66**:609–15. doi:[10.1099/jmm.0.000474](https://doi.org/10.1099/jmm.0.000474)

169 Farra A, Frank T, Tondeur L *et al.* High rate of faecal carriage of extended-spectrum beta-lactamase-producing Enterobacteriaceae in healthy children in Bangui, Central African Republic. *Clin Microbiol Infect* 2016;**22**:891.e1–4. doi:[10.1016/j.cmi.2016.07.001](https://doi.org/10.1016/j.cmi.2016.07.001)

170 Desta K, Woldeamanuel Y, Azazh A *et al.* High Gastrointestinal Colonization Rate with Extended-Spectrum beta-Lactamase-Producing Enterobacteriaceae in Hospitalized Patients: Emergence of Carbapenemase-Producing K. pneumoniae in Ethiopia. *PLoS One* 2016;**11**:e0161685. doi:[10.1371/journal.pone.0161685](https://doi.org/10.1371/journal.pone.0161685)

171 Djuikoue IC, Woerther PL, Toukam M *et al.* Intestinal carriage of Extended Spectrum Beta-Lactamase producing E. coli in women with urinary tract infections, Cameroon. *J Infect Dev Ctries* 2016;**10**:1135–9. doi:[10.3855/jidc.7616](https://doi.org/10.3855/jidc.7616)

172 Mshana SE, Falgenhauer L, Mirambo MM *et al.* Predictors of blaCTX-M-15 in varieties of Escherichia coli genotypes from humans in community settings in Mwanza, Tanzania. *BMC Infect Dis* 2016;**16**:187. doi:[10.1186/s12879-016-1527-x](https://doi.org/10.1186/s12879-016-1527-x)

173 Ribeiro TG, Novais Â, Peixe L *et al.* Atypical epidemiology of CTX-M-15 among Enterobacteriaceae from a high diversity of non-clinical niches in Angola. *Journal of Antimicrobial Chemotherapy* 2016;**71**:1169–73. doi:[10.1093/jac/dkv489](https://doi.org/10.1093/jac/dkv489)

174 Tellevik MG, Blomberg B, Kommedal O *et al.* High Prevalence of Faecal Carriage of ESBL-Producing Enterobacteriaceae among Children in Dar es Salaam, Tanzania. *PLoS One* 2016;**11**:e0168024. doi:[10.1371/journal.pone.0168024](https://doi.org/10.1371/journal.pone.0168024)

175 Chereau F, Herindrainy P, Garin B *et al.* Colonization of extended-spectrum-beta-lactamase- and NDM-1-producing Enterobacteriaceae among pregnant women in the community in a low-income country: a potential reservoir for transmission of multiresistant Enterobacteriaceae to neonates. *Antimicrob Agents Chemother* 2015;**59**:3652–5. doi:[10.1128/aac.00029-15](https://doi.org/10.1128/aac.00029-15)

176 Herindrainy P, Rabenandrasana MAN, Andrianirina ZZ *et al.* Acquisition of extended spectrum beta-lactamase-producing enterobacteriaceae in neonates: A community based cohort in Madagascar. *PLoS One* 2018;**13**:e0193325. doi:[10.1371/journal.pone.0193325](https://doi.org/10.1371/journal.pone.0193325)

177 Micheel V, Hogan B, Rakotoarivelo RA *et al.* Identification of nasal colonization with beta-lactamase-producing Enterobacteriaceae in patients, health care workers and students in Madagascar. *Eur J Microbiol Immunol (Bp)* 2015;**5**:116–25. doi:[10.1556/eujmi-d-15-00001](https://doi.org/10.1556/eujmi-d-15-00001)

178 Nelson E, Kayega J, Seni J *et al.* Evaluation of existence and transmission of extended spectrum beta lactamase producing bacteria from post-delivery women to neonates at Bugando Medical Center, Mwanza-Tanzania. *BMC Res Notes* 2014;**7**:279. doi:[10.1186/1756-0500-7-279](https://doi.org/10.1186/1756-0500-7-279)

179 Lonchel CM, Melin P, Gangoue-Pieboji J *et al.* Extended-spectrum beta-lactamase-producing Enterobacteriaceae in Cameroonian hospitals. *Eur J Clin Microbiol Infect Dis* 2013;**32**:79–87. doi:[10.1007/s10096-012-1717-4](https://doi.org/10.1007/s10096-012-1717-4)

180 Magoue CL, Melin P, Gangoue-Pieboji J *et al.* Prevalence and spread of extended-spectrum beta-lactamase-producing Enterobacteriaceae in Ngaoundere, Cameroon. *Clin Microbiol Infect* 2013;**19**:E416–20. doi:[10.1111/1469-0691.12239](https://doi.org/10.1111/1469-0691.12239)

181 Schaumburg F, Alabi A, Kokou C *et al.* High burden of extended-spectrum beta-lactamase-producing Enterobacteriaceae in Gabon. *J Antimicrob Chemother* 2013;**68**:2140–3. doi:[10.1093/jac/dkt164](https://doi.org/10.1093/jac/dkt164)

182 Albrechtova K, Dolejska M, Cizek A *et al.* Dogs of nomadic pastoralists in northern Kenya are reservoirs of plasmid-mediated cephalosporin- and quinolone-resistant Escherichia coli, including pandemic clone B2-O25-ST131. *Antimicrob Agents Chemother* 2012;**56**:4013–7. doi:[10.1128/aac.05859-11](https://doi.org/10.1128/aac.05859-11)

183 Isendahl J, Turlej-Rogacka A, Manjuba C *et al.* Fecal carriage of ESBL-producing E. coli and K. pneumoniae in children in Guinea-Bissau: a hospital-based cross-sectional study. *PLoS One* 2012;**7**:e51981. doi:[10.1371/journal.pone.0051981](https://doi.org/10.1371/journal.pone.0051981)

184 Lonchel CM, Meex C, Gangoué-Piéboji J *et al.* Proportion of extended-spectrum ß-lactamase-producing Enterobacteriaceae in community setting in Ngaoundere, Cameroon. *BMC Infect Dis* 2012;**12**. doi:[10.1186/1471-2334-12-53](https://doi.org/10.1186/1471-2334-12-53)

185 Herindrainy P, Randrianirina F, Ratovoson R *et al.* Rectal carriage of extended-spectrum beta-lactamase-producing gram-negative bacilli in community settings in Madagascar. *PLoS One* 2011;**6**:e22738. doi:[10.1371/journal.pone.0022738](https://doi.org/10.1371/journal.pone.0022738)

186 Woerther PL, Angebault C, Jacquier H *et al.* Massive increase, spread, and exchange of extended spectrum beta-lactamase-encoding genes among intestinal Enterobacteriaceae in hospitalized children with severe acute malnutrition in Niger. *Clin Infect Dis* 2011;**53**:677–85. doi:[10.1093/cid/cir522](https://doi.org/10.1093/cid/cir522)

187 Katakweba AAS, Muhairwa AP, Lupindu AM *et al.* First Report on a Randomized Investigation of Antimicrobial Resistance in Fecal Indicator Bacteria from Livestock, Poultry, and Humans in Tanzania. *Microbial Drug Resistance* 2018;**24**:260–8. doi:[10.1089/mdr.2016.0297](https://doi.org/10.1089/mdr.2016.0297)

188 Andriatahina T, Randrianirina F, Hariniana ER *et al.* High prevalence of fecal carriage of extended-spectrum beta-lactamase-producing Escherichia coli and Klebsiella pneumoniae in a pediatric unit in Madagascar. *BMC Infect Dis* 2010;**10**:204. doi:[10.1186/1471-2334-10-204](https://doi.org/10.1186/1471-2334-10-204)

189 Ruppe E, Woerther PL, Diop A *et al.* Carriage of CTX-M-15-producing Escherichia coli isolates among children living in a remote village in Senegal. *Antimicrob Agents Chemother* 2009;**53**:3135–7. doi:[10.1128/aac.00139-09](https://doi.org/10.1128/aac.00139-09)

190 Tande D, Jallot N, Bougoudogo F *et al.* Extended-spectrum beta-lactamase-producing Enterobacteriaceae in a Malian orphanage. *Emerg Infect Dis* 2009;**15**:472–4. doi:[10.3201/eid1503.071637](https://doi.org/10.3201/eid1503.071637)

191 Marando R, Seni J, Mirambo MM *et al.* Predictors of the extended-spectrum-beta lactamases producing Enterobacteriaceae neonatal sepsis at a tertiary hospital, Tanzania. *Int J Med Microbiol* 2018;**308**:803–11. doi:[10.1016/j.ijmm.2018.06.012](https://doi.org/10.1016/j.ijmm.2018.06.012)

192 Moremi N, Claus H, Rutta L *et al.* High carriage rate of extended-spectrum beta-lactamase-producing Enterobacteriaceae among patients admitted for surgery in Tanzanian hospitals with a low rate of endogenous surgical site infections. *J Hosp Infect* 2018;**100**:47–53. doi:[10.1016/j.jhin.2018.05.017](https://doi.org/10.1016/j.jhin.2018.05.017)

193 Nikiema Pessinaba C, Landoh DE, Dossim S *et al.* Screening for extended-spectrum beta-lactamase-producing Enterobacteriaceae intestinal carriage among children aged under five in Lome, Togo. *Med Mal Infect* 2018;**48**:551–4. doi:[10.1016/j.medmal.2018.07.004](https://doi.org/10.1016/j.medmal.2018.07.004)

194 Sanneh B, Kebbeh A, Jallow HS *et al.* Prevalence and risk factors for faecal carriage of Extended Spectrum beta-lactamase producing Enterobacteriaceae among food handlers in lower basic schools in West Coast Region of The Gambia. *PLoS One* 2018;**13**:e0200894. doi:[10.1371/journal.pone.0200894](https://doi.org/10.1371/journal.pone.0200894)

195 Stanley IJ, Kajumbula H, Bazira J *et al.* Multidrug resistance among Escherichia coli and Klebsiella pneumoniae carried in the gut of out-patients from pastoralist communities of Kasese district, Uganda. *PLoS One* 2018;**13**. doi:[10.1371/journal.pone.0200093](https://doi.org/10.1371/journal.pone.0200093)

196 Kurz MS, Bayingana C, Ndoli JM *et al.* Intense pre-admission carriage and further acquisition of ESBL-producing Enterobacteriaceae among patients and their caregivers in a tertiary hospital in Rwanda. *Trop Med Int Health* 2017;**22**:210–20. doi:[10.1111/tmi.12824](https://doi.org/10.1111/tmi.12824)

197 Paterson DL, Bonomo RA. Extended-spectrum beta-lactamases: a clinical update. *Clinical microbiology reviews* 2005;**18**:657–86. doi:[10.1128/CMR.18.4.657-686.2005](https://doi.org/10.1128/CMR.18.4.657-686.2005)

198 Ambler RP. The Structure of beta-lactamases. *Philosophical Transactions of the Royal Society B: Biological Sciences* 1980;**289**:321–31. doi:[10.1098/rstb.1980.0049](https://doi.org/10.1098/rstb.1980.0049)

199 Bush K, Jacoby GA. Updated functional classification of beta-lactamases. *Antimicrobial agents and chemotherapy* 2010;**54**:969–76. doi:[10.1128/AAC.01009-09](https://doi.org/10.1128/AAC.01009-09)

200 Bradford PA. Extended-Spectrum-Lactamases in the 21st Century: Characterization, Epidemiology, and Detection of This Important Resistance Threat. *Clinical Microbiology and Infection* 2001;**14**:933–51. doi:[10.1128/CMR.14.4.933-951.2001](https://doi.org/10.1128/CMR.14.4.933-951.2001)

201 ABRAHAM EP, CHAIN E. An Enzyme from Bacteria able to Destroy Penicillin. *Nature* 1940;**146**:837–7. doi:[10.1038/146837a0](https://doi.org/10.1038/146837a0)

202 Datta N, Kontomichalou P. Penicillinase synthesis controlled by infectious R factors in Enterobacteriaceae. *Nature* 1965;**208**:239–41.<http://www.ncbi.nlm.nih.gov/pubmed/5326330>

203 Knothe H, Shah P, Krcmery V *et al.* Transferable resistance to cefotaxime, cefoxitin, cefamandole and cefuroxime in clinical isolates of Klebsiella pneumoniae and Serratia marcescens. *Infection* 1983;**11**:315–7.<http://www.ncbi.nlm.nih.gov/pubmed/6321357>

204 Kliebe C, Nies BA, Meyer JF *et al.* Evolution of plasmid-coded resistance to broad-spectrum cephalosporins. *Antimicrobial agents and chemotherapy* 1985;**28**:302–7.<http://www.ncbi.nlm.nih.gov/pubmed/3879659 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC180236>

205 Liakopoulos A, Mevius D, Ceccarelli D. A Review of SHV Extended-Spectrum -Lactamases: Neglected Yet Ubiquitous. *Frontiers in microbiology* 2016;**7**:1374. doi:[10.3389/fmicb.2016.01374](https://doi.org/10.3389/fmicb.2016.01374)

206 Sougakoff W, Goussard S, Gerbaud G *et al.* Plasmid-mediated resistance to third-generation cephalosporins caused by point mutations in TEM-type penicillinase genes. *Reviews of infectious diseases* 1988;**10**:879–84.<http://www.ncbi.nlm.nih.gov/pubmed/3055179>

207 Gold HS, Moellering RC. Antimicrobial-Drug Resistance. *New England Journal of Medicine* 1996;**335**:1445–53. doi:[10.1056/NEJM199611073351907](https://doi.org/10.1056/NEJM199611073351907)

208 Philippon A, Labia R, Jacoby G. Extended-spectrum beta-lactamases. *Antimicrobial agents and chemotherapy* 1989;**33**:1131–6.<http://www.ncbi.nlm.nih.gov/pubmed/2679367 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC172613>

209 Cantón R, Coque TM. The CTX-M beta-lactamase pandemic. *Current opinion in microbiology* 2006;**9**:466–75. doi:[10.1016/j.mib.2006.08.011](https://doi.org/10.1016/j.mib.2006.08.011)

210 Livermore DM, Canton R, Gniadkowski M *et al.* CTX-M: changing the face of ESBLs in Europe. *Journal of Antimicrobial Chemotherapy* 2006;**59**:165–74. doi:[10.1093/jac/dkl483](https://doi.org/10.1093/jac/dkl483)

211 Ben‐Ami R, Rodríguez‐Baño J, Arslan H *et al.* A Multinational Survey of Risk Factors for Infection with Extended‐Spectrum ‐Lactamase–Producing Enterobacteriaceae in Nonhospitalized Patients. *Clinical Infectious Diseases* 2009;**49**:682–90. doi:[10.1086/604713](https://doi.org/10.1086/604713)

212 Bauernfeind A, Grimm H, Schweighart S. A new plasmidic cefotaximase in a clinical isolate of Escherichia coli. *Infection* 1990;**18**:294–8.<http://www.ncbi.nlm.nih.gov/pubmed/2276823>

213 Bonnet R. Growing group of extended-spectrum beta-lactamases: the CTX-M enzymes. *Antimicrobial agents and chemotherapy* 2004;**48**:1–14. doi:[10.1128/AAC.48.1.1-14.2004](https://doi.org/10.1128/AAC.48.1.1-14.2004)

214 Goossens H, Ferech M, Vander Stichele R *et al.* Outpatient antibiotic use in Europe and association with resistance: a cross-national database study. *The Lancet* 2005;**365**:579–87. doi:[10.1016/S0140-6736(05)17907-0](https://doi.org/10.1016/S0140-6736(05)17907-0)

215 Alvarez-Uria G, Gandra S, Laxminarayan R. Poverty and prevalence of antimicrobial resistance in invasive isolates. *International Journal of Infectious Diseases* 2016;**52**:59–61. doi:[10.1016/J.IJID.2016.09.026](https://doi.org/10.1016/J.IJID.2016.09.026)

216 Denis B, Lafaurie M, Donay J-L *et al.* Prevalence, risk factors, and impact on clinical outcome of extended-spectrum beta-lactamase-producing Escherichia coli bacteraemia: a five-year study. *International Journal of Infectious Diseases* 2015;**39**:1–6. doi:[10.1016/J.IJID.2015.07.010](https://doi.org/10.1016/J.IJID.2015.07.010)

217 Gorrie CL, Mirceta M, Wick RR *et al.* Antimicrobial-Resistant Klebsiella pneumoniae Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. *Clinical Infectious Diseases* 2018;**67**:161–70. doi:[10.1093/cid/ciy027](https://doi.org/10.1093/cid/ciy027)

218 Mirelis B, Navarro F, Miró E *et al.* Community Transmission of Extended-Spectrum ß-Lactamase. *Emerging Infectious Diseases* 2003;**9**:1024–5. doi:[10.3201/eid0908.030094](https://doi.org/10.3201/eid0908.030094)

219 Franiczek R, Sobieszczańska B, Grabowski M *et al.* Occurrence of extended-spectrum beta-lactamases among Escherichia coli isolates from hospitalized and healthy children. *Folia microbiologica* 2003;**48**:243–7.<http://www.ncbi.nlm.nih.gov/pubmed/12800510>

220 Woerther P-L, Burdet C, Chachaty E *et al.* Trends in human fecal carriage of extended-spectrum -lactamases in the community: toward the globalization of CTX-M. *Clinical microbiology reviews* 2013;**26**:744–58. doi:[10.1128/CMR.00023-13](https://doi.org/10.1128/CMR.00023-13)

221 McNulty CAM, Lecky DM, Xu-McCrae L *et al.* CTX-M ESBL-producing Enterobacteriaceae: estimated prevalence in adults in England in 2014. *The Journal of antimicrobial chemotherapy* 2018;**73**:1368–88. doi:[10.1093/jac/dky007](https://doi.org/10.1093/jac/dky007)

222 Wielders C, Hoek A van, Hengeveld P *et al.* Extended-spectrum -lactamase- and pAmpC-producing Enterobacteriaceae among the general population in a livestock-dense area. *Clinical Microbiology and Infection* 2017;**23**:120.e1–8. doi:[10.1016/J.CMI.2016.10.013](https://doi.org/10.1016/J.CMI.2016.10.013)

223 Ny S, Löfmark S, Börjesson S *et al.* Community carriage of ESBL-producing <i>Escherichia coli</i> is associated with strains of low pathogenicity: a Swedish nationwide study. *Journal of Antimicrobial Chemotherapy* 2017;**72**:582–8. doi:[10.1093/jac/dkw419](https://doi.org/10.1093/jac/dkw419)

224 Valverde A, Coque TM, Sanchez-Moreno MP *et al.* Dramatic Increase in Prevalence of Fecal Carriage of Extended-Spectrum  -Lactamase-Producing Enterobacteriaceae during Nonoutbreak Situations in Spain. *Journal of Clinical Microbiology* 2004;**42**:4769–75. doi:[10.1128/JCM.42.10.4769-4775.2004](https://doi.org/10.1128/JCM.42.10.4769-4775.2004)

225 Li B, Sun J-Y, Liu Q-Z *et al.* High prevalence of CTX-M -lactamases in faecal Escherichia coli strains from healthy humans in Fuzhou, China. *Scandinavian Journal of Infectious Diseases* 2011;**43**:170–4. doi:[10.3109/00365548.2010.538856](https://doi.org/10.3109/00365548.2010.538856)

226 Babu R, Kumar A, Karim S *et al.* Faecal carriage rate of extended-spectrum -lactamase-producing Enterobacteriaceae in hospitalised patients and healthy asymptomatic individuals coming for health check-up. *Journal of Global Antimicrobial Resistance* 2016;**6**:150–3. doi:[10.1016/j.jgar.2016.05.007](https://doi.org/10.1016/j.jgar.2016.05.007)

227 Reuland EA, Al Naiemi N, Kaiser AM *et al.* Prevalence and risk factors for carriage of ESBL-producing Enterobacteriaceae in Amsterdam. *The Journal of antimicrobial chemotherapy* 2016;**71**:1076–82. doi:[10.1093/jac/dkv441](https://doi.org/10.1093/jac/dkv441)

228 Woerther P-L, Andremont A, Kantele A. Travel-acquired ESBL-producing Enterobacteriaceae: impact of colonization at individual and community level. *Journal of travel medicine* 2017;**24**:S29–34. doi:[10.1093/jtm/taw101](https://doi.org/10.1093/jtm/taw101)

229 March A, Aschbacher R, Dhanji H *et al.* Colonization of residents and staff of a long-term-care facility and adjacent acute-care hospital geriatric unit by multiresistant bacteria. *Clinical Microbiology and Infection* 2010;**16**:934–44. doi:[10.1111/J.1469-0691.2009.03024.X](https://doi.org/10.1111/J.1469-0691.2009.03024.X)

230 Valverde A, Grill F, Coque TM *et al.* High rate of intestinal colonization with extended-spectrum-beta-lactamase-producing organisms in household contacts of infected community patients. *Journal of clinical microbiology* 2008;**46**:2796–9. doi:[10.1128/JCM.01008-08](https://doi.org/10.1128/JCM.01008-08)

231 Duijkeren E van, Wielders CCH, Dierikx CM *et al.* Long-term Carriage of Extended-Spectrum -Lactamase–Producing Escherichia coli and Klebsiella pneumoniae in the General Population in The Netherlands. *Clinical Infectious Diseases* 2018;**66**:1368–76. doi:[10.1093/cid/cix1015](https://doi.org/10.1093/cid/cix1015)

232 Alsterlund R, Carlsson B, Gezelius L *et al.* Multiresistant CTX-M-15 ESBL-producing Escherichia coli in southern Sweden: Description of an outbreak. *Scandinavian Journal of Infectious Diseases* 2009;**41**:410–5. doi:[10.1080/00365540902896079](https://doi.org/10.1080/00365540902896079)

233 Zahar J, Lanternier F, Mechai F *et al.* Duration of colonisation by Enterobacteriaceae producing extended-spectrum -lactamase and risk factors for persistent faecal carriage. *Journal of Hospital Infection* 2010;**75**:76–8. doi:[10.1016/j.jhin.2009.11.010](https://doi.org/10.1016/j.jhin.2009.11.010)

234 Lohr IH, Rettedal S, Natas OB *et al.* Long-term faecal carriage in infants and intra-household transmission of CTX-M-15-producing Klebsiella pneumoniae following a nosocomial outbreak. *Journal of Antimicrobial Chemotherapy* 2013;**68**:1043–8. doi:[10.1093/jac/dks502](https://doi.org/10.1093/jac/dks502)

235 Arcilla MS, Hattem JM van, Haverkate MR *et al.* Import and spread of extended-spectrum -lactamase-producing Enterobacteriaceae by international travellers (COMBAT study): a prospective, multicentre cohort study. *The Lancet Infectious Diseases* 2017;**17**:78–85. doi:[10.1016/S1473-3099(16)30319-X](https://doi.org/10.1016/S1473-3099(16)30319-X)

236 Teunis PFM, Evers EG, Hengeveld PD *et al.* Time to acquire and lose carriership of ESBL/pAmpC producing E. coli in humans in the Netherlands. *PLOS ONE* 2018;**13**:e0193834. doi:[10.1371/journal.pone.0193834](https://doi.org/10.1371/journal.pone.0193834)

237 Lartigue M-F, Poirel L, Aubert D *et al.* In vitro analysis of ISEcp1B-mediated mobilization of naturally occurring beta-lactamase gene blaCTX-M of Kluyvera ascorbata. *Antimicrobial agents and chemotherapy* 2006;**50**:1282–6. doi:[10.1128/AAC.50.4.1282-1286.2006](https://doi.org/10.1128/AAC.50.4.1282-1286.2006)

238 Bevan ER, Jones AM, Hawkey PM. Global epidemiology of CTX-M -lactamases: temporal and geographical shifts in genotype. *Journal of Antimicrobial Chemotherapy* 2017;**72**:2145–55. doi:[10.1093/jac/dkx146](https://doi.org/10.1093/jac/dkx146)

239 Cantón R, María González-Alba J, Galán JC *et al.* CTX-M enzymes: origin and diffusion. Published Online First: 2012. doi:[10.3389/fmicb.2012.00110](https://doi.org/10.3389/fmicb.2012.00110)

240 Zhao W-H, Hu Z-Q. Epidemiology and genetics of CTX-M extended-spectrum -lactamases in Gram-negative bacteria. *Critical reviews in microbiology* 2013;**39**:79–101. doi:[10.3109/1040841X.2012.691460](https://doi.org/10.3109/1040841X.2012.691460)

241 Coque TM, Novais Â, Carattoli A *et al.* Dissemination of Clonally Related Escherichia coli Strains Expressing Extended-Spectrum -Lactamase CTX-M-15. *Emerging Infectious Diseases* 2008;**14**:195–200. doi:[10.3201/eid1402.070350](https://doi.org/10.3201/eid1402.070350)

242 Nicolas-Chanoine M-H, Bertrand X, Madec J-Y. Escherichia coli ST131, an intriguing clonal group. *Clinical microbiology reviews* 2014;**27**:543–74. doi:[10.1128/CMR.00125-13](https://doi.org/10.1128/CMR.00125-13)

243 Stoesser N, Sheppard AE, Pankhurst L *et al.* Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. *mBio* 2016;**7**:e02162. doi:[10.1128/mBio.02162-15](https://doi.org/10.1128/mBio.02162-15)

244 Petty NK, Ben Zakour NL, Stanton-Cook M *et al.* Global dissemination of a multidrug resistant Escherichia coli clone. *Proceedings of the National Academy of Sciences* 2014;**111**:5694–9. doi:[10.1073/pnas.1322678111](https://doi.org/10.1073/pnas.1322678111)

245 Gray KJ, Wilson LK, Phiri A *et al.* Identification and characterization of ceftriaxone resistance and extended-spectrum -lactamases in Malawian bacteraemic Enterobacteriaceae. *Journal of Antimicrobial Chemotherapy* 2006;**57**:661–5. doi:[10.1093/jac/dkl037](https://doi.org/10.1093/jac/dkl037)

246 Musicha P, Cornick JE, Bar-Zeev N *et al.* Trends in antimicrobial resistance in bloodstream infection isolates at a large urban hospital in Malawi (1998–2016): a surveillance study. *The Lancet Infectious Diseases* 2017;**17**:1042–52. doi:[10.1016/S1473-3099(17)30394-8](https://doi.org/10.1016/S1473-3099(17)30394-8)

247 Musicha P, Feasey NA, Cain AK *et al.* Genomic landscape of extended-spectrum -lactamase resistance in Escherichia coli from an urban African setting. *Journal of Antimicrobial Chemotherapy* 2017;**72**:1602–9. doi:[10.1093/jac/dkx058](https://doi.org/10.1093/jac/dkx058)