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REVIEW ARTICLE

ESBL-producing *Enterobacteriaceae* in Africa – a non-systematic literature review of research published 2008–2012

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Introduction: *Enterobacteriaceae* producing extended-spectrum beta-lactamases (ESBL) has been found all over the world, and risk factors for acquiring these bacteria involve hospital care and antibiotic treatment. Surveillance studies are present in Europe, North America, and Asia, but there is no summarizing research published on the situation in Africa.
Aim: This review aims to describe the prevalence of ESBL-producing *Enterobacteriaceae* in hospital and community settings in Africa and the ESBL genes involved.
Method: A non-systematic literature search was performed in PubMed. All articles published between 2008 and 2012 were screened and read in full text. Relevant articles were assessed for quality of evidence and included in the review. Articles were divided into regional areas in Africa and tabulated.
Results: ESBL-producing *Enterobacteriaceae* in hospitalized patients and in communities varies largely between countries and specimens but is common in Africa. ESBLs (class A and D) and plasmid-encoded AmpC (pAmpC) were regularly found, but carbapenemases were also present.
Conclusion: ESBL-producing *Enterobacteriaceae* in hospital and community settings in Africa is common. Surveillance of antimicrobial resistance needs to be implemented in Africa to tailor interventions targeted at stopping the dissemination of ESBL-producing *Enterobacteriaceae*.

Keywords: *antibiotic resistance*; *Enterobacteriaceae*; *extended-spectrum beta-lactamases*; *Africa*; *hospital*; *community*

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Research has shown that there are several risk factors for acquiring an extended-spectrum beta-lactamase (ESBL)-producing bacterial infection. High use of antibiotics is one factor that has been shown to increase the risk of developing and acquiring ESBL for patients at hospitals and in the community (1–4). Nosocomial risk factors, such as the presence of intravascular catheters, undergoing surgery, staying at an intensive care unit, and international travel, have been shown to increase the risk of being colonized with ESBL-producing bacteria (1, 3, 5).

Introduction

ESBL has been found all over the world, and reviewing research has been done in Europe (6, 7), North America (8), and Asia (9) in recent years to understand the extent of ESBLs and other multiresistant bacteria; also, there are surveillance studies running in the same regions to guide the clinical treatment of infectious diseases. In Europe (during 1999–2008), there has been an increase in invasive infections caused by *Klebsiella pneumoniae* and *Escherichia coli* resistant to third-generation cephalosporins, and this is believed to be due to the dissemination of ESBLs in both hospitals and communities. An increase in carbapenemase production among isolates has also been seen and raises issues regarding future antimicrobial treatment (10). Urinary tract isolates collected in the SMART study between 2009 and 2010 concluded that in Europe, ESBL prevalence among *E. coli* and *K. pneumoniae* was 17.6 and 38.9%, respectively. In North America, the prevalence was 8.5 and 8.8%, respectively (11). In Asia, the prevalence of ESBL among *E. coli* and *K. pneumoniae* varied between 5 and 0%, respectively, in New Zealand and between 67 and 61%, respectively, in China (12). The class A ESBL gene CTX-M-15 was the most common gene in the European and American

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settings (found in >90% of *E. coli* isolates and in 35–65.5% of *K. pneumoniae*), but SHV- and TEM-type genes were also prevalent, between 1.7 and 42.9%, especially in *K. pneumoniae* (11). From the SENTRY Asia Pacific surveillance program, CTX-M genes were found in 38.2–55.5% of *K. pneumoniae* and *E. coli* isolates, and the prevalence of SHV- and TEM-type genes was higher (between 34.3 and 85.3%) (13).

In Africa, the prevalence of ESBL in *Enterobacteriaceae* has been researched at local levels in various countries, but there is no summarizing research on how prevalent ESBL is on the continent, what type of genes are involved, and where research is missing. This review aims to describe the prevalence of ESBL-producing *Enterobacteriaceae* in hospital and community settings in Africa and the ESBL genes involved.

Method

A literature search was conducted in PubMed in June 2013 with the keywords 'Africa', 'Enterobacteriaceae', and 'ESBL' or 'extended-spectrum beta-lactamases'. The search was limited to articles published in English, studying humans, and published from 2008/01/01 to 2012/12/31. From the 91 references found, seven articles could not be accessed in online databases or acquired in paper copy, and they were excluded; the remaining 84 articles were read in full text. 19 articles were excluded because they were not relevant for the aim of this study. The excluded articles did not research ESBL, studied countries outside of Africa, or looked at other colonized hosts than humans. 65 articles were finally included in the review.

The references were assessed in quality according to a value scale, modified from Hedin et al. (14), where the strength of evidence for different ESBL genes and prevalence in the selected references were graded low, middle, and high based on the method of analyses used in the studies. As many of the studies reported had used the same method, study size and what proportion of the sample was analyzed in detail were also taken into account to assess the strength of the scientific evidence (Table 1).

Results

This section is divided into regional areas of Africa, according to the UN regional composition (15). For detailed descriptions of sample sizes, organisms, settings and prevalence, sources of samples, and ESBL genes involved, see Tables 2–6.

Northern Africa

In Algerian hospitals, ESBLs existed in 16.4–31.4% of the samples. Class A ESBLs were most common, but plasmid-encoded AmpC (pAmpC) was also present (16–22).

In Egypt, ESBLs were found in 11–42.9% of samples in both hospitals and communities; the genes involved were class A ESBLs (23–25).

In Guinea-Bissau and Libya, class A and D ESBLs and a carbapenemase were found in 32.6 and 16%, respectively, in rectal or stool samples (26, 27).

In Morocco, class A and D ESBLs, pAmpC, and carbapenemases were found in hospital settings (28–30). In the community setting, class A and D ESBLs were found in between 1.3 and 7.5% of acquired urine samples (31–33).

In Tunisia, class A and D ESBLs, pAmpC, and carbapenemases were present, and the prevalence ranged from 11.7 to 77.8% in hospitals and was 0.7 and 7.3% in two communities (34–51).

Eastern Africa

In Ethiopia and Kenya, 62.8 and 37.4%, respectively, of hospital and community samples were ESBLs (52, 53). Class A ESBLs and pAmpC were present in the Kenyan sample (53). In samples taken from Kenya and Malawi, class A and D ESBLs were found (54).

In Rwanda, ESBLs were found in 38.3% of hospital urine samples and in 5.9% of community urine samples (55).

In Tanzania, class A ESBLs were found in various samples from hospital settings (56, 57).

Table 1. Value scale used for assessing strength of evidence

Grade		Criteria
High	Method	Polymerase chain reaction (PCR)
		Plasmid transfer assays (PTA)
		Pulsed field gel electrophoresis (PFGE)
	Sample size	>15
		Data set completely analyzed
Middle		Combination of criteria from high and low grade (e.g., sample <15 but using PCR analyses)
Low	Method	Synergy tests
	Sample size	<15
		Data set partly analyzed

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Table 2. Northern Africa

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Algeria (1982–2005)	12	*S. Enterica* serotype Senftenberg	Hospital (n/r)	Not specified	Exemplary 1 isolate: TEM-1 (100) CTX-M-3 (100)	Low	(20)
Algeria (2003–2007)	141	*E. cloacae*	Hospital (17.7)	Urine (52) Blood (24) Pus (24)	CTX-M-15 (44) CTX-M-3 (36) SHV-12 (16) VEB (4)	High	(17)
Algeria (2003–2007)	505	*Enterobacteriaceae*	Hospital (16.4)	Urine (63.6) Blood (18.2) Pus (18.2)	CTX-M group I (84.3) TEM (15.7) SHV (15.7) CMY-2 (9.6) DHA-1 (3.6)	Middle	(16)
Algeria (2005)	3	*K. pneumoniae*	Hospital (n/r)	Pus (33.3) Cerebrospinal fluid (33.3) Urine (33.3)	CTX-M-15 (66.6) CTX-M-3 (33.4) TEM-1 (100) SHV-98 (33.3) SHV-99 (33.3) SHV-100 (33.4)	Middle	(22)
Algeria (2008–2009)	200	*S. Enterica* serotype Infantis	Hospital (99)	Stool (88.2) Blood (5.9) Gastric fluid (5.9)	Exemplary 16 isolates: CTX-M-15 (100) TEM-1 (100)	High	(19)
Algeria (2009)	207	*Klebsiella* *Enterobacter* *Serratia*	Hospital (31.4)	Urine (53.7) Pus (19.5) Distal sampling (14.6) Valve (2.4) Pleural fluid (2.4) Ear (2.4) Nasal fossae (2.4) Tumoral fluid (2.4)	Exemplary 41 isolates: CTX-M group I (88) TEM (41.4) SHV (31.1) DHA-1 (9.7)	High	(12)
Algeria (not specified)	196	*K. pneumoniae*	Hospital (19.9)	Urine (38.9) Blood (22.2) Bronchial (13.6) Pus (13.6) Ascites fluid (5.9)	Exemplary 18 isolates: TEM (100) CTX-M-3 (66.7) CTX-M-15 (33.3)	High	(18)

Table 2 (*Continued*)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Egypt (2007)	70	*E. coli*	Hospital and community (42.9)	Stool (not specified) Urine (not specified)	Exemplary 8 isolates: CTX-M-1 (75) CTX-M-9 (87.5)	Middle	(24)
Egypt (2007–2008)	520	*Enterobacteriaceae*	Hospital (19) Community (11)	Urine (78.7) Wound (10.6) Ascites fluid (4.3) Sputum (6.4)	Exemplary 74 isolates: CTX-M-15 (100) SHV-12 (1.4)	Middle	(23)
Egypt (not specified)	5	*K. pneumoniae* *E. coli* *E. cloacae*	Hospital (n/r)	Wound (80) Catheter (20)	CTX-M-14 (40) CTX-M-15 (20) TEM (20) SHV (20)	Middle	(25)
Guinea-Bissau (2010)	408	*K. pneumoniae* *E. coli*	Hospital (32.6)	Stool (100)	CTX-M group I (94.8) CTX-M group 9 (4) CTX-M group 8/25 (0.8) CTX-M group 2 (0.8) SHV (2.3)	High	(26)
Libya (2011)	25	*Enterobacteriaceae*	Hospital (16)	Rectal (100)	Exemplary 1 isolate OXA-48 (100)	Middle	(27)
Morocco (2004–2007)	535	*E. coli*	Community (1.3)	Urine (100)	CTX-M-15 (100) TEM-1 (28.6) SHV-5 (14.3)	High	(33)
Morocco (2004–2009)	803	*K. pneumoniae* *E. coli*	Community (1.5)	Urine (100)	CTX-M-15 (91.7) TEM-1b (33.3) SHV-1 (16.7) SHV-5 (8.3) OXA-1 (91.7)	High	(31)
Morocco (2006–2007)	39	*Enterobacteriaceae*	Hospital (n/r)	Urine (66.7) Pus (10.3) Bronchial (2.6) Blood (7.7)	Exemplary 14 isolates: TEM-1 (85.7) CTX-M-28 (35.7) CTX-M-15 (25) SHV-12 (35.7) SHV-1 (25) DHA-1 (58.3)	Middle	(28)

Table 2 (*Continued*)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Morocco (2010)	453	*K. pneumoniae*	Community (7.5)	Urine (100)	CTX-M-15 (94.1) CTX-M-1 (2.9) TEM-1 (52.9) TEM-1b (29.4) SHV-1 (35.3) SHV-11 (11.8) SHV-12 (8.8) SHV-26 (5.9) SHV-28 (8.8) SHV-32 (2.9) SHV-36 (2.9) SHV-76 (5.9) SHV-110 (2.9) OXA-1 (64.7) ACT-2 (2.9) DHA-1 (2.9)	High	(32)
Morocco (not specified)	3	*K. pneumoniae*	Hospital (n/r)	Urine (33.3) Blood (33.3) Abscess (33.4)	NDM-1 (100) CTX-M-15 (100) TEM-1 (100) SHV-1 (100) SHV-5 (100) OXA-1 (100) OXA-9 (100)	Middle	(29)
Morocco (not specified)	3	*K. pneumoniae*	Hospital (n/r)	Not specified	NDM-1 (100) CTX-M-15 (100) OXA-1 (100)	Low	(30)
Tunisia (1999–2005)	1280	*K. pneumoniae*	Hospital (11.7) Community (0.7)	Urine (41.2) Lung (11.8) Catheter (7.8) Cerebrospinal fluid (3.9) Blood (25.5) Pus (3.9) Nasal (3.9) Rectal (2)	51 exemplary isolates (hospital): CTX-M-15 (37.3) CTX-M-27 (3.9) SHV-12 (62.8) SHV-2a (5.9) TEM-1 (19.6)	High	(42)

Table 2 (*Continued*)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Tunisia (2003–2007)	11	*K. pneumoniae* *E. coli*	Hospital (n/r)	Urine (27.3) Sputum (18.2) Blood (36.4) Pus (9.1) Catheter (9.1)	CTX-M-15 (100) SHV-1 (54.6) SHV-11 (9.1) SHV-27 (9.1) SHV-103 (9.1) TEM-1a (54.6) TEM-1b (36.4) OXA-1 (72.7)	High	(34)
Tunisia (2004)	1	*K. pneumoniae*	Hospital (n/r)	Not specified	CTX-M-28 (100)	Low	(36)
Tunisia (2004)	1	*P. mirabilis*	Hospital (n/r)	Not specified	VEB-1 (100)	Low	(48)
Tunisia (2004)	1	*K. pneumoniae*	Hospital (n/r)	Not specified	TEM-164 (100)	Low	(35)
Tunisia (2005–2006)	856	*Enterobacteriaceae*	Hospital (19.9)	Urine (58) Blood (42)	100 exemplary isolates: CTX-M-15 (93) TEM-1 (82) SHV-12 (9) SHV-2a (7) OXA-1 (92)	High	(40)
Tunisia (2005–2007)	281	*Enterobacteriaceae*	Hospital (n/r)	Urine (63.9) Blood (36.1)	36 exemplary isolates: CTX-M-15 (69.4) SHV-28 (13.9) SHV-12 (5.6) SHV-2a (2.8) TEM-1 (77.8) LAP-2 (5.6)	Middle	(41)
Tunisia (2005–2009)	20	*P. stuartii*	Hospital (n/r)	Blood (53.5) Trachea (33.3) Pus (6.7) Chest drainage (6.7)	VEB-1a (100)	Middle	(47)
Tunisia (2006)	47	*E. coli*	Hospital (68.1)	Urine (34.4) Stool (31.3)	CTX-M-15 (96.9) TEM-1b (81.3)	High	(51)

Table 2 (*Continued*)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
				Intra-abdominal peritonitis (9.4) Trachea (6.3) Blood (6.3) Pus (6.3) Wound (3.1) Lung (3.1)	TEM-34 (9.4) SHV-12 (6.3)		
Tunisia (2007)	14	*E. coli*	Hospital (n/r)	Urine (64.3) Blood (7.1) Wound (28.6)	CTX-M-15 (85.7) CTX-M-14a (7.1) CTX-M-14b (7.1) OXA-1 (85.7) TEM-1 (35.7)	Middle	(38)
Tunisia (2008)	1	*M. morganii*	Hospital (n/r)	Pus (100)	CTX-M-15 (100) TEM-24 (100) DHA-1 (100)	Low	(49)
Tunisia (2009)	44	*E. cloacae*	Hospital (n/r)	Urine (59.9) Pus (20.5) Blood (9.1) Broncho-pulmonary (4.6) Gastric (4.6) Catheter (2.3)	CTX-M-15 (88.6) TEM-1 (77.3) SHV-12 (13.6) SHV-27 (2.3)	High	(34)
Tunisia (2009)	1	*P. stuartii*	Hospital (n/r)	Rectal (100)	TEM-116 (100)	Low	(45)
Tunisia (2009–2010)	9	*E. cloacae*	Hospital (n/r)	Urine (57.1) Placenta (28.6) Blood (14.3)	SHV-12 (100)	Low	(44)
Tunisia (2009–2010)	150	*E. coli*	Community (7.3)	Stool (100)	CTX-M-1 (90.9) TEM-1b (9.1) TEM-52c (9.1)	High	(37)
Tunisia (2010)	2	*K. pneumoniae*	Hospital (77.8)	Urine (100)	CTX-M-15 (100) TEM-1 (100) SHV-1 (100) OXA-48 (100)	Low	(46)
Tunisia (2010)	10	*E. coli*	Hospital	Urine (100)	CTX-M-15 (100)	High	(39)

Table 2 (Continued)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
			(n/r)		TEM-52 (100)		
Tunisia (2011)	11	*P. stuartii*	Hospital (n/r)	Nose (45.5) Rectal (27.3) Axilla (27.2)	OXA-48 (100) CMY-4 (100) PER-1 (100)	Middle	(50)

n/r: not relevant.

Central Africa

In Cameroon, class A and D ESBLs were found in 55.3 and 82.8% of hospital stool samples and in 17.2% of community stool samples (58, 59).

In the Central African Republic, ESBLs were found in 11.3% of community urine samples (60).

Western Africa

In Ghana and Mali, class A ESBLs were found in 49.4 and 63.4–96%, respectively, in hospital and community samples (61–64).

In Niger, 40% of hospital samples carried class A ESBLs or pAmpC (65).

In Nigeria, class A and D ESBLs and pAmpC were found in hospital settings, and the prevalence ranged from 10.3 to 27.5% (66–71). In a mixed sample from a hospital and a community, the prevalence was 11.7% (72).

In Senegal, class A and D ESBLs were found in 10% of community stool samples (73).

Southern Africa

In South Africa, class A and D ESBLs and pAmpC were present, and the prevalence ranged from 8.8 to 13.1% in hospitals and was 0.3 and 4.7% in two communities (74–80).

Discussion

This review indicates that ESBL-producing *Enterobacteriaceae* are a large problem in African healthcare institutions and communities.

In patients treated in African hospitals, the prevalence of ESBL-producing *Enterobacteriaceae* has been shown to vary between countries and the type of specimen studied. There is a trend of higher prevalence of ESBL in stool samples than in other specimens. There is also a trend of increasing prevalence over time. This is noticeable in the Tunisian setting, where a large amount of studies are available. In two hospitals studied (study periods: 1999–2005 and 2010), ESBLs have increased from 11.7 to 77.8% among *K. pneumoniae* (42, 49). In other settings, the trend is not noticeable among the few studies available. In the studied countries in Africa, the prevalence is widely different: in Algeria, it was between 16.4 and 31.4% in mainly urine samples (16–18, 21) and even 99% among *Salmonella enterica* in stool samples (19); 19 and 42.9%, respectively, in urine and stool samples in Egypt (23, 24); 32.6% among stool samples in Guinea-Bissau (26); 11.7–77.8% in mainly urine, blood, and stool samples from Tunisia (40, 42, 46, 51); 62.8% in stool and blood samples from Ethiopia (52); 38.3% in urine samples from Rwanda (55); 55.3 and 82.8% in stool samples from Cameroon (58, 59); 10.3–27.5% in mainly urine and stool samples from Nigeria (66, 69–72); and

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Table 3. Eastern Africa

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Ethiopia (2004–2006)	113	*Salmonella*	Hospital (62.8)	Stool (68) Blood (32)	Not analyzed	Middle	(52)
Kenya (1992–2010)	912	*E. coli*	Hospital and community (37.4)	ESBL: Urine (53) Stool (26) Blood (21) pAmpC: Urine (72) Stool (14) Blood (14)	140 exemplary isolates ESBL: CTX-M-14 (29) CTX-M-15 (24) CTX-M-1 (6) CTX-M-3 (11) CTX-M-9 (2) CTX-M-8 (4) TEM-52 (16) SHV-5 (3) SHV-12 (5) 94 exemplary isolates pAmpC: OXA-12 (66) CMY-1 (18) CMY-2 (82)	High	(53)
Kenya and Malawi (not specified)	18	*S. typhimurium*	Hospital (n/r)	Blood (100)	OXA-1 (100) TEM-1 (100)	High	(54)
Rwanda (2009)	196	*Enterobacteriaceae*	Hospital (38.3) Community (5.9)	Urine (100)	Not analyzed	Middle	(55)
Tanzania (2009–2010)	17	*Enterobacteriaceae*	Hospital (n/r)	Blood (100)	CTX-M-15 (100)	Medium	(56)
Tanzania (not specified)	32	*E. coli*	Hospital (n/r)	Wound (34.3) Urine (25) Pus (21.9) Blood (18.8)	CTX-M-15 (100) TEM-1 (25)	High	(57)

n/r: not relevant.

Table 4. Central Africa

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Cameroon (2009)	121	*Enterobacteriaceae*	Hospital (55.3)	Stool (100)	CTX-M-15 (96) SHV-12 (4) SHV-1 (25) TEM-1 (79) OXA-1 (65)	High	(59)
Cameroon (2009)	358	*Enterobacteriaceae*	Hospital (82.8) Community (17.2)	Stool (100)	CTX-M-15 (98) CTX-M-1 (2) TEM-1 (67) SHV-1 (4) SHV-12 (3) OXA-1 (58)	High	(58)
Central African Republic (2004–2006)	443	*Enterobacteriaceae*	Community (11.3)	Urine (100)	Not analyzed	Middle	(60)

n/r: not relevant.

8.8–13.1% in urine, nasopharyngeal, and wound samples from South Africa (74, 75, 77).

The most common type of genes involved in the African hospital strains of ESBL is class A ESBLs. CTX-M-15 is the most prevalent gene in a high proportion of the samples, disregarding country. It is usually combined with other types of CTX-M, TEM, and SHV genes (17–19, 22, 25, 28, 29, 34, 38, 40–43, 46, 51, 53, 56–59, 65–67, 69, 70, 78). There is a high proportion of class D ESBLs existent, mainly OXA-1, and it has been found in between 3.3 and 93.3% of the studied isolates (34, 38, 40, 53, 54, 58, 59, 67, 69, 78, 80). pAmpC genes exist in some isolates, mainly DHA-1 and CMY-2 (16, 18, 21, 28, 29, 32, 49, 50, 53, 65, 69, 79), but because of the different classifications of ESBLs, these are not always included in the analyses performed in the studies. Disturbing results are the existence of carbapenemase genes. The NDM-1 gene was found in three samples taken from urine, blood, and an abscess from two patients in Morocco (29, 30), and the OXA-48 gene was found in a rectal swab sample from a patient originating from Libya (27). The presence of carbapenemase genes is a risk for future use of antimicrobial treatment in the region.

In the community setting, ESBL-producing *Enterobacteriaceae* have a lower prevalence than in the hospital: 6.7% of healthy students in Cameroon (58), 1.3% in a Moroccan community (33), 5.9% in Rwandan outpatients (55), 2.7% in a healthy community in Nigeria (72), 11.3% of outpatients in Central African Republic (60), 10% of healthy children in a remote village in Senegal (73), and 4.7% in a referral site in South Africa (77). The genes involved in the community were the same as in the hospital setting.

To solve the problem of ESBL-producing *Enterobacteriaceae* and other types of resistant bacteria, prevention is crucial and surveillance of antimicrobial resistance is needed to guide prevention interventions. Because of globalization, including international travel, it is important to have a global approach to antibiotic resistance. The majority of the studies in this review are performed in northern or southern Africa, leaving a large gap in the areas in between. Future research should focus on areas where research is scarce, describing the current situation in healthcare services and increasing the consistent surveillance to follow the changes in prevalence and incidence, making relevant interventions possible on both local and global levels.

Conclusion

ESBLs (class A and D) are common in Africa, with the gene CTX-M-15 being most prevalent, but other types, such as pAmpC and carbapenemases, also exist. Surveillance of antimicrobial resistance needs to be implemented in Africa to tailor interventions targeted at stopping the dissemination of ESBL-producing *Enterobacteriaceae*.

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Table 5. Western Africa

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
Ghana (2008–2009)	156	*E. coli*	Hospital and community (49.4)	Urine (not specified) Blood (not specified) Sputum (not specified) Wound (not specified) Aspirates (not specified)	CTX-M (not specified) TEM (not specified) SHV (not specified)	Middle	(61)
Mali (2001–2008)	41	*Salmonella*	Community (63.4)	Stool (100)	CTX-M-15 (19.2) TEM-1 (96.2) SHV-12 (80.8)	High	(62)
Mali (2002–2005)	25	*Enterobacteriaceae*	Community (96)	Stool (100)	Exemplary 52 isolates: CTX-M-15 (80.8) SHV-12 (7.7) SHV-2 (1.9) TEM-1 (78.8)	High	(63)
Mali (2003)	68	*Enterobacteriaceae*	Community (83.3)	Stool (100)	Not analyzed	Middle	(64)
Niger (2007–2008)	55	*Enterobacteriaceae*	Hospital (40)	Stool (100)	CTX-M-15 (90.1) SHV-2a (9.1) SHV-12 (9.1) SHV-44 (4.6) CMY-2 (4.6) CMY-30 (4.6)	High	(65)
Nigeria (1999)	1	*E. aerogenes*	Hospital (n/r)	Blood (100)	AmpC (100) TEM-1 (100) SHV-12 (100)	Low	(68)
Nigeria (2005–2007)	134	*Enterobacteriaceae*	Hospital (20.9)	Sputum (not specified) Ear (not specified) Wound (not specified) Throat (not specified) Vaginal (not specified) Eye (not specified) Aspirates (not specified) Urine (not specified) Blood (not specified) Catheter (not specified)	TEM (81.3) SHV (24.6) OXA (11.2) CTX-M-15 (17.9) CTX-M-3 (0.8) Exemplary 6 isolates: DHA-1 (66.7) ACT-1 (16.7) CMY-2 (16.6)	High	(69)

Table 5 (*Continued*)

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
				Cerebrospinal fluid (not specified)			
Nigeria (2006–2007)	116	*E. coli*	Hospital (10.3)	Urine (66.7) Stool (25) Blood (8.3)	Exemplary 9 isolates: CTX-M-15 (100)	High	(70)
Nigeria (2006–2007)	44	*E. coli*	Hospital (n/r)	Urine (77.2) Vaginal (13.6) Wound (9.0)	CTX-M group I (100) 3 exemplary isolates CTX-M-15 (100) TEM (93.1) OXA-1 (93.1)	Middle	(67)
Nigeria (2006–2007)	145	*Enterobacteriaceae*	Community and hospital (11.7)	Urine (82.4) Vaginal (11.8) Wound (5.9)	Not analyzed	Middle	(72)
Nigeria (2007–2008)	153	*Salmonella* *Shigella*	Hospital (27.5)	Stool (100)	Not analyzed	Middle	(71)
Nigeria (2008–2009)	109	*E. coli*	Hospital (12.8)	Urine (35.7) Stool (21.4) Wound (21.4) Semen (7.1) Blood (7.1) Catheter (7.1)	CTX-M-15 (100)	High	(66)
Senegal (not specified)	20	*E. coli*	Community (10)	Stool (100)	CTX-M-15 (100) TEM-1 (100) OXA-1 (100)	High	(73)

n/r: not relevant.

Table 6. Southern Africa

Country (study period)	Sample size	Organism	Setting and prevalence of ESBL (%)	Source of ESBL isolate (%)	Genes (%)	Evidence	Reference
South Africa (2001)	59	*Salmonella*	Hospital (n/r)	Stool (100)	TEM-1 (50.9) TEM-63 (20.3) TEM-116 (13.3) TEM-131 (3.3) SHV-12 (50) CTX-M-15 (6.7) CTX-M-34 (3.3) CTX-M-3 (3.3) CTX-M-37 (16.7) OXA-1 (3.3) CMY-2 (10)	High	(80)
South Africa (2002–2003)	181	*Enterobacteriaceae*	Hospital (8.8)	Nasopharyngeal (100)	Not analyzed	Middle	(75)
South Africa (2003–2009)	6,833	*Shigella*	Community (0.3)	Stool (80) Blood (20)	CTX-M-15 (90) CTX-M-14 (5) TEM-1 (80) SHV-2 (5) CMY-2 (30)	High	(79)
South Africa (2004–2009)	1,019	*Enterobacteriaceae*	Hospital (10.8)	Wound (100)	Not analyzed	Middle	(74)
South Africa (2005–2006)	1,125	*Enterobacteriaceae*	Hospital (13.1) Community (4.7)	Urine (100)	Not analyzed	Middle	(77)
South Africa (2007)	46	*Enterobacteriaceae*	Hospital (n/r)	Not specified	TEM (95.7) SHV (58.7) CTX-M (54.4) Exemplary 10 isolates of CTX-M: CTX-M-15 (100).	Middle	(76)
South Africa (2008–2009)	22	*E. coli*	Hospital (n/r)	Urine (77.3) Pus (22.7)	CTX-M-15 (59.1) CTX-M-14 (31.8) CTX-M-3 (4.6) SHV-2 (4.6) TEM-1 (54.6) TEM-2 (4.6) OXA-1 (40.9)	High	(78)

n/r: not relevant.

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