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Prevalence of methicillin-resistant coagulase-negative staphylococci in Africa: a systematic review and meta-analysis

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Abstract

Coagulase-negative staphylococci (CoNS) represent a diverse group of opportunistic pathogens associated with human and animal infections. The burden of infectious diseases attributed to antibiotic-resistant CoNS, particularly methicillin-resistant CoNS (MR-CoNS), is a global public health concern. However, there is limited data on the epidemiology of MR-CoNS in Africa. This systematic review provides insights on MR-CoNS from human and non-human sources in Africa, the methicillin-resistance gene determinants and the associated mobile genetic elements. The review retrieved articles from four electronic databases: PubMed, Scopus, Web of Science, and Google Scholar, using specific keywords. This study was carried out until 20 November 2024. Articles were screened and data was extracted and analyzed following the PRISMA guidelines. The meta-analysis used the binary random effects model with a 95% confidence interval. Overall, 65 articles from 16 African countries were included in the study. The pooled prevalence rates for CoNS and MR-CoNS in Africa were 27% and 36%, respectively. The review identified 36 species of CoNS from human and non-human sources. In addition, 20 (31%) studies each reported CoNS and MR-CoNS from human and animal infections. The most prevalent species of MR-CoNS included *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, and *Mammaliicoccus sciuri*. The African MR-CoNS harboured different staphylococcal chromosome cassette *mec* (SCC*mec*) elements (types I, II, III, IV, V, VI, VIII, and a SCC*mec-mecC* (hybrid), and the most common SCC*mec* element was the SCC*mec* type IV. The findings highlight the paucity of data on the epidemiology of MR-CoNS in Africa. The identification of MR-CoNS from human and animal infections indicates the need for a detailed characterization using molecular methods. This strategy will provide data to healthcare practitioners and policymakers to develop effective measures to combat antimicrobial resistance in Africa.

Keywords Coagulase-negative staphylococci, Methicillin resistance, SCC*mec*, Meta-analysis

Background

Coagulase-negative staphylococci (CoNS) are a diverse group of staphylococci that lack the coagulase enzyme responsible for clotting fibrinogen [1]. This group currently consists of 81 species, including coagulase-variable ones such as *Staphylococcus agnetis* and *Staphylococcus hyicus* (lpsn.dsmz.de, accessed 15 December 2024). CoNS are categorized into several species groups based on phylogenetic analysis using four housekeeping genes: 16S rRNA, *dnaJ*, *rpoB*, and *tuf* [1, 2]. The species groups

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are auricularis, hyicus-intermedius, epidermidis-aureus, saprophyticus, simulans, and sciuri. In 2020, the sciuri group, i.e., *S. sciuri*, *S. fleurettii*, *S. lentus*, *S. vitulinus*, and *S. stepanovicii*, was reclassified into a new genus called *Mammaliicoccus* [3]. This investigation was based on the whole-genome phylogeny complemented with genome-based indices such as the average nucleotide identity and digital DNA-DNA hybridization. Hence, the members of this group are designated as *M. sciuri*, *M. fleurettii*, *M. lentus*, *M. vitulinus*, and *M. stepanovicii*.

CoNS are commensals of the skin and the mucous membrane of humans and animals [1]. However, they are opportunistic pathogens of humans causing infections including skin and soft tissue infection [4, 5] bacteremia [6, 7], eye infection [8], urinary tract infections [9, 10] and implant-associated nosocomial infections, especially among immunocompromised individuals [11]. The global reports of CoNS infections are rising due to the increasing use of prosthetic devices in many clinical procedures [11, 12]. They are also associated with clinical and sub-clinical mastitis in animals [13–15], resulting in economic losses. The burden of infections caused by CoNS is exacerbated by the development of resistance to various antibiotics, especially the β-lactam antibiotics [11]. Moreover, antibiotic-resistant CoNS is increasing in human and non-human settings due to antibiotic selective pressure linked to healthcare facilities, antibiotic use in animal production (as a growth factor, prophylaxis and therapeutic) and the environment [16]. Resistance to the classical β-lactam antibiotics, especially methicillin, is a major concern. This characteristic confers resistance to all members of the antibiotic class except two anti-methicillin-resistant *Staphylococcus aureus* (MRSA) cephalosporins [11, 17]. Methicillin resistance is associated with an alternate penicillin-binding protein (PBP2a) with low affinity for the antibiotic and encoded by the *mec* genes, i.e., *mecA*, *mecB* and *mecC* [1, 17–20]. These genes are carried on the staphylococcal cassette chromosome *mec* (SCC*mec*) element—a 20-70 kb mobile genetic element (MGE) in staphylococci. So far, fifteen SCC*mec* types have been described in the staphylococci [17, 21]. This MGE has been postulated to have originated from *M. sciuri* [1, 21], and there is evidence of the exchange of this gene determinant and other resistance genes [22, 23] among staphylococci, including *S. aureus* in the natural environment [24, 25]. This scenario poses a risk to treating infections caused by *S. aureus* and CoNS.

High rates of resistance to methicillin (70 to 90%) have been reported among CoNS from Europe and North America [11, 26]. In Africa, the prevalence of MR-CoNS from human infections in Egypt is between 26 and 95% [27–30]. Also, the rate of MR-CoNS from animal samples has been reported to be 12.5% in Libya [31], 21.6% in Ethiopia [32] and between 20 and 96% in Egypt [14, 33]. However, there is currently no data on the pooled prevalence of CoNS and MR-CoNS from human and non-human sources in Africa. Furthermore, there is a paucity of data on the SCC*mec* types in MR-CoNS on the continent. This systematic review aims to determine the diversity of CoNS from human and non-human samples in Africa, the pooled prevalence of CoNS and MR-CoNS in Africa, and the SCC*mec* types among the MR-CoNS in Africa.

Methods

This systematic review and meta-analysis were conducted following the PRISMA guidelines. The literature search was conducted using four databases to retrieve eligible articles using specific search terms with Boolean operators (supplementary data) until 20 November 2024. These databases included PubMed, Scopus, Web of Science and Google Scholar (Publish or Perish 8). All articles retrieved from the search were screened by removing duplicates and categorized using the Rayyan AI (https://new.rayyan.ai/). The screening and extraction of data was carried out by two independent reviewers and consensus decisions were made on discrepancies.

Inclusion criteria

The inclusion criteria were articles that investigated and identified MR-CoNS and at least one methicillin resistance (*mecA*, *mecB* and *mecC*) gene from various African samples. Furthermore, this study included articles from the recently reclassified members of the *M. sciuri* group.

Exclusion criteria

Articles published in languages other than English were excluded. Review articles, conference proceedings, abstract posters, letters, editorials and original articles from non-African countries were also excluded.

Data extraction

The relevant data from all the eligible articles were extracted and organized into a Microsoft Excel spreadsheet. Data including country, sample source, sample type, clinical significance, prevalence, species identification (including methods) of isolates, methicillin resistance gene (s) identified and detection of the SCC*mec* element (including the techniques) were extracted from the articles. The data obtained were used for descriptive statistics and meta-analysis. The pooled prevalence of CoNS and MR-CoNS was calculated from articles that provided information on the total number of samples, CoNS or MR-CoNS. For the meta-analysis, the forest and funnel plots were generated using the comprehensive meta-analysis software

(version 3; Biostat, USA). The data were analyzed using the binary random effect model with a 95% confidence interval based on the DerSimonian-Laird method. The test for heterogeneity across the studies was determined using the inverse variance index (I^2) and estimated using the random-effects model. The I^2 values at 25%, 50%, and 75% represented low, moderate, and high heterogeneity, respectively [34]. Egger's test was used to validate the asymmetry of the funnel plot.

The prevalence of CoNS and MR-CoNS were calculated in eligible studies using the formulae:

(i)Prevalence of CoNS = Number of CoNS obtained/Total Number of samples collected.

(ii)Prevalence of MR-CoNS = Number of MR-CoNS/Number of CoNS obtained.

Results

Study description

The database search yielded 10,152 articles. After removing duplicates, 6,718 articles were screened based on their titles and abstracts. Overall, 65 articles were eligible for inclusion (Fig. 1). The articles were published between 2006 and 2024, with the majority (61/65; 94%) published in the last decade (2014 to 2024) (Fig. 2). These eligible studies were derived from only 16 of 54 (30%) African countries. Based on the African Union classification, 30 (46%) of the articles were from North Africa, 18 (28%) from the West African sub-region, and 16 (24%) were evenly distributed between East and Southern Africa, with only one study from Central Africa (Fig. 3). Specifically, most of the articles were from Egypt ($n=17$), Nigeria ($n=15$), South Africa ($n=7$), Tunisia ($n=7$), and Algeria ($n=4$).

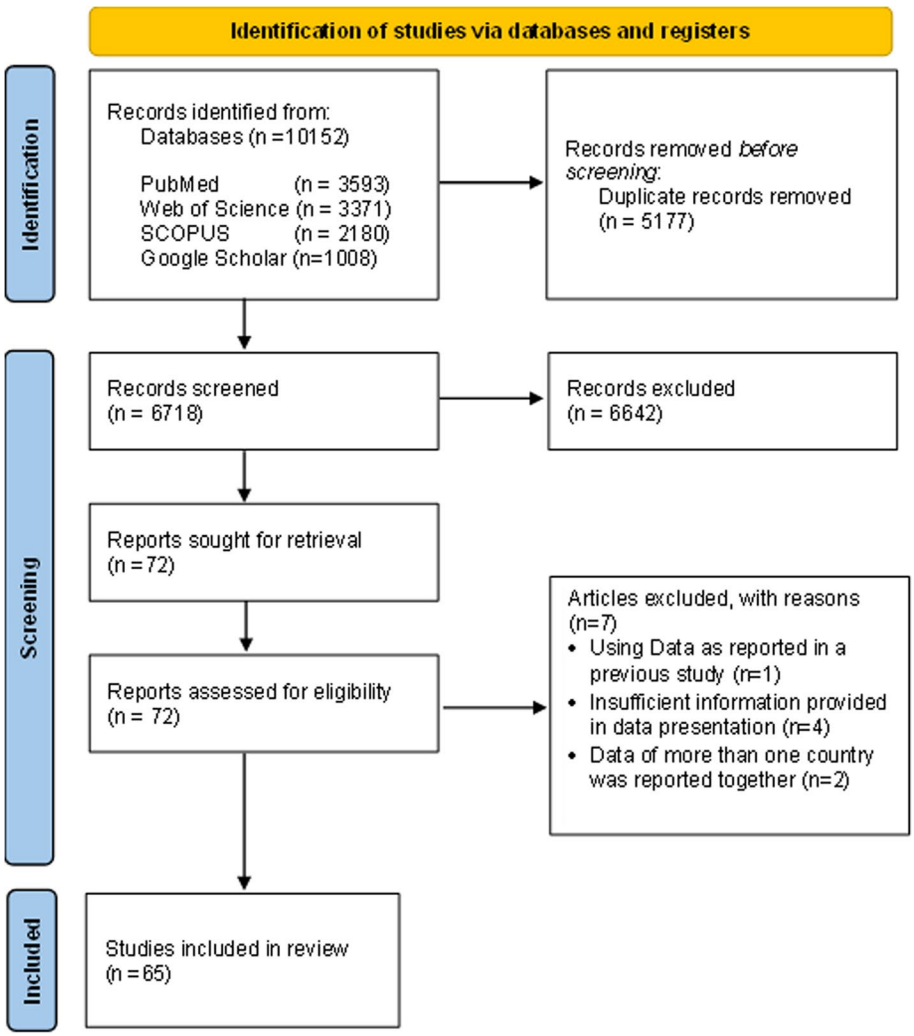

Fig. 1 PRISMA flowchart of the systematic literature search

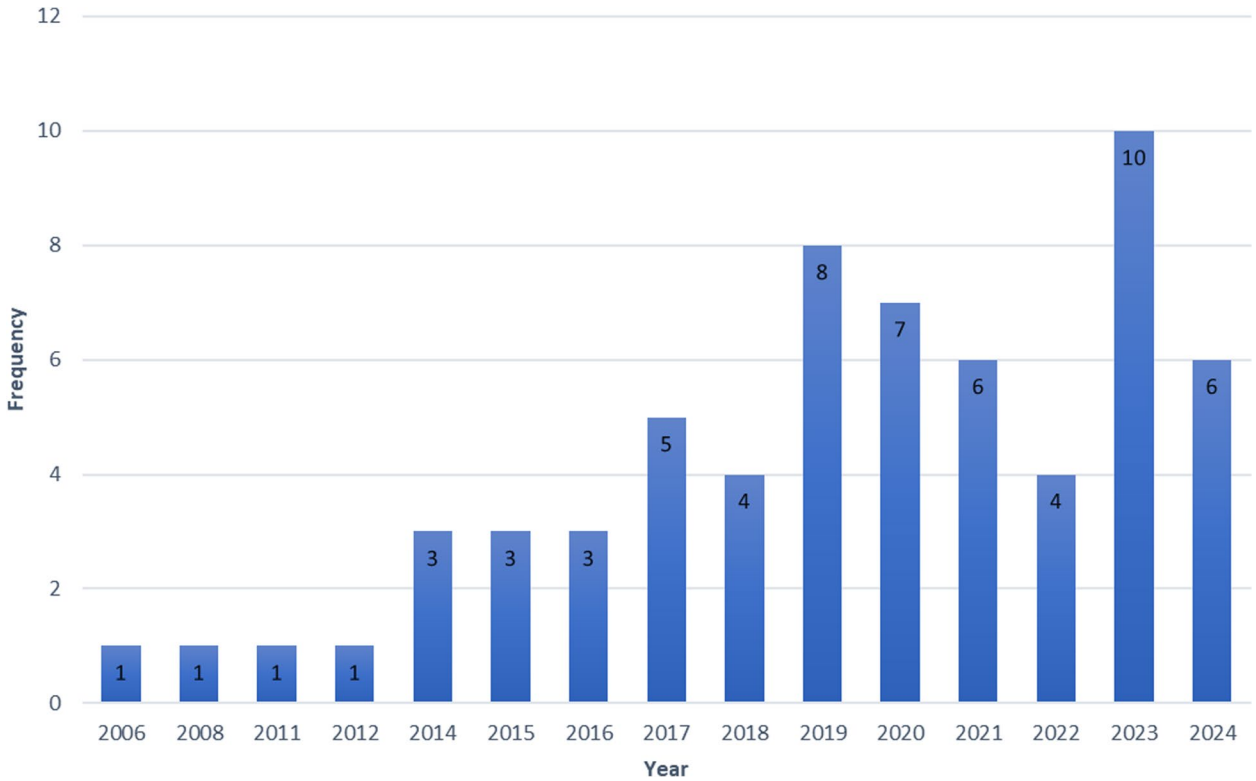

Fig. 2 Summary of number of articles recovered by year

Of the 65 eligible articles, 23 (35%), 22 (34%), and 2 (3%) reports identified CoNS from animal, human and environmental samples, respectively. Other studies reported CoNS from other sources, including food samples ($n=3$, 5%), fomites ($n=1$, 2%) and a combination of different sources, i.e., human and animal ($n=4$, 6%), human and food samples ($n=3$, 5%). Other sample sources include human and the environment ($n=2$, 3%), animal and environment ($n=1$, 2%), human, food and the environment ($n=1$, 2%), and human, animal and the environment ($n=2$, 3%) (Table 1). The pooled prevalence of CoNS was calculated from 54 articles. However, two articles were not included in the pooled prevalence calculation as more isolates were reported than the samples collected. The pooled prevalence of MR-CoNS was calculated from 61 articles.

Species identification and diversity of coagulase-negative staphylococci

The majority ($n=56$; 86%) of the studies identified CoNS to species level, of which 49 (87.5%) used only one method, while 7 (12.5%) used a combination of techniques. Of the 49 studies, the most common techniques were the matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) in 13 (27%) studies, 16S rRNA gene sequencing in 10 (20%), biochemical tests in 7 (%) and Analytical profile index (API) Staph kit in 6 (12%) reports (Supplementary file).

From the 65 eligible studies, 3,468 isolates and 36 species of CoNS were identified. The most frequently isolated species of CoNS were *S. epidermidis* ($n=905$, 26%), *S. haemolyticus* ($n=561$, 16%), *M. sciuri* ($n=485$, 14%), *S. xylosus* ($n=299$, 9%), *S. chromogenes* ($n=175$, 5%), and *S. saprophyticus* ($n=171$, 4.9%). The CoNS with lower isolation frequencies included *S. muscae* and *S. devriesei* (0.06% each with two isolates), as well as *S. lutrae*, *S. piscifermentans*, and *S. saccharolyticus* (0.03%, one isolate each) (Fig. 4). Overall, 17% ($n=687$) of all CoNS ($n=4,155$) in the studies were not identified at species level.

Among the CoNS species of human origin in the eligible studies, the most prevalent species include *S. epidermidis* ($n=466$), *S. haemolyticus* ($n=341$), *S. hominis* ($n=161$), *M. sciuri* ($n=45$) and *S. saprophyticus* ($n=44$). However, the CoNS obtained from animal samples consisted of *M. sciuri* ($n=175$), *S. xylosus* ($n=160$), *S. epidermidis* ($n=120$), *S. haemolyticus* ($n=85$) and *S. chromogenes* ($n=76$) as the most prevalent species (supplementary file).

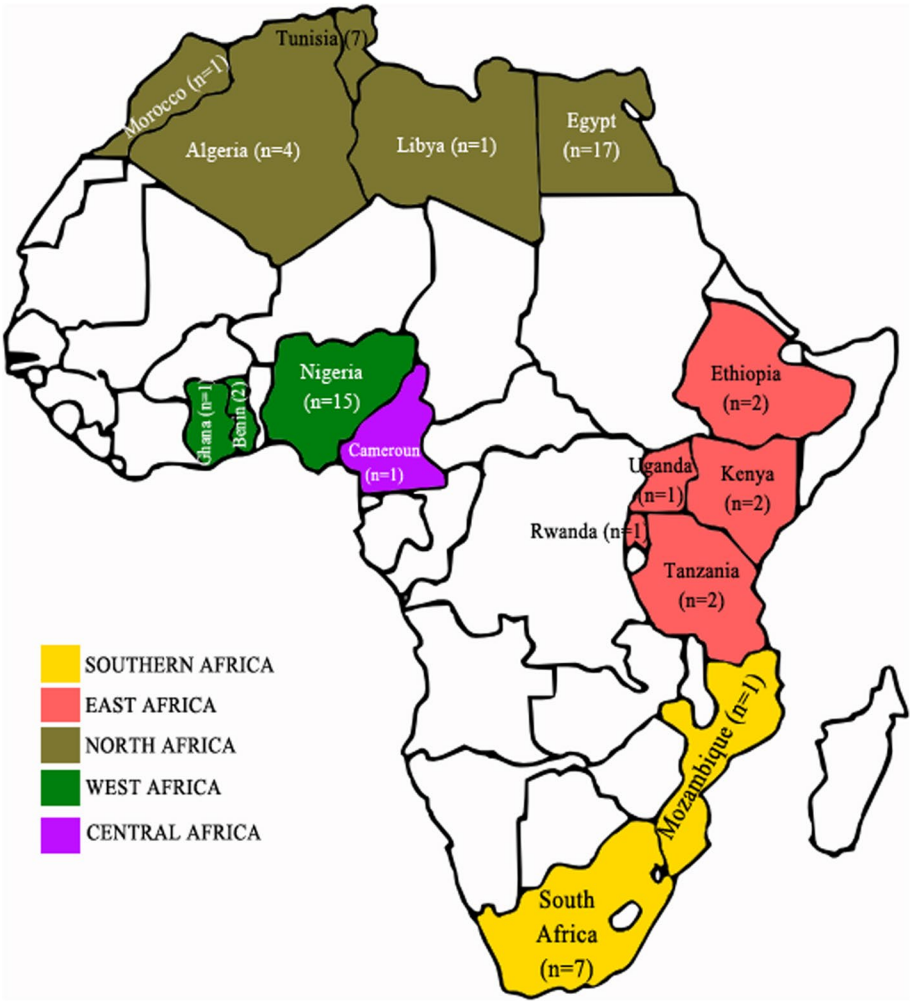

Fig. 3 Map of Africa showing countries from which eligible studies were conducted and the number of studies

Methicillin resistance genes and SCC*mec* typing

Polymerase chain reaction (PCR) detection of the methicillin resistance genes was carried out in > 80% ($n=53$) of the studies. Furthermore, whole-genome sequencing (WGS) was employed for gene detection in 10 studies. One study utilized both PCR and WGS. The *mecA* was the most frequently reported gene ($n=64$, 98%). Moreover, the combination of *mecA*/*mecA1* and *mecA*/*mecC* was observed in four studies each. The *mecB*-positive MR-CoNS was not detected in Africa, though one study screened for the gene (Table 1). Nineteen studies did not specify the species from which the methicillin resistance gene was identified. Overall, 812 MR-CoNS from 26 species carried the methicillin resistance gene determinants. The most common species of MR-CoNS included *S. epidermidis* ($n=202$, 25%) and *S. haemolyticus* ($n=191$, 24%) reported in 23 studies each, and *M. sciuri* ($n=183$, 23%) in 24 studies (Fig. 5). From the human studies, the most prevalent MR-CoNS was *S. haemolyticus* ($n=131$), *S. epidermidis* ($n=121$), *S. hominis* ($n=31$) and *M. sciuri* ($n=23$). However, the common MR-CoNS observed among animal studies include *S. epidermidis* ($n=60$), *M. sciuri* ($n=51$), *S. haemolyticus* ($n=23$) and *S. saprophyticus* ($n=22$). Only one of the studies ($n=2$) that investigated MR-CoNS among the environmental samples alone reported the species, i.e., *S. epidermidis* and *S. saprophyticus*.

SCC*mec* elements comprising types I, II, III, IV, V, VI, VIII, and the SCC*mec-mecC* hybrid were identified in MR-CoNS in Africa. These studies were reported mainly in Tunisia ($n=5$), Nigeria ($n=3$), and two each from Algeria, Egypt, and South Africa. The SCC*mec* type IV was commonly reported ($n=43$), followed by types III ($n=20$), II ($n=18$), and VIII ($n=15$). The SCC*mec* element with *mecA* and *mecC* (the SCC*mec-mecC* hybrid) was identified in eleven MR-CoNS isolates (Table 2). Among the MR-CoNS identified from human origin, the SCC*mec* types I, II, III, IV, V, VI and VIII were reported.

Table 1 Study characteristics

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
North Africa	Human											
Algeria	Human	Wound and skin swabs	Colonization and Infection	26/94	*S. epidermidis* (9), *S. haemolyticus* (8), *S. hominis* (1), *M. sciuri* (1)	WGS	√ mecA1	-	-	III (1)	WGS	[35]
Egypt	Human	Blood	Infection	31/56	CoNS	API Staph	√	NC	NC	NC	PCR	[30]
	Human	Blood, CSF, Urine, wound and sputum	Infection	43/500	*S. epidermidis* (16), *S. haemolyticus* (15), *S. hominis* (5), *S. saprophyticus* (5)	VITEK 2	√	NC	-	NC	PCR	[29]
	Human	Skin swab	Infection	85/140	*S. epidermidis* (3)	MALDI-TOF	√	-	-	II (1), V (2)	WGS	[5]
	Human	Nasal swab	Colonization	50/340	CoNS (41)	API Staph	√	NC	NC	N	PCR	[36]
	Human	Eye Swab	Infection	44/200	CoNS (26)	ND	√	NC	NC	NC	PCR	[8]
	Human	Blood	Infection	38/150	*S. epidermidis* (7), CoNS (3)	Biochemical Tests	√	NC	NC	NC	PCR	[27]
	Human	Blood	Infection	58/743	CoNS (44)	API Staph	√	NC	NC	NC	PCR	[28]
Tunisia	Human	Blood	Infection	45/NR	*S. epidermidis* (34), *S. haemolyticus* (10), *S. hominis* (1)	Biochemical Tests	√	NC	NC	II (2), III (11), IV (14), V (1)	PCR	[37]
	Human	Blood	Infection	54/246	CoNS (20)	API Staph	√	NC	NC	I (1), II (7), III (4), IV (13), VI (1), VIII (1)	PCR	[38]
East Africa												
Ethiopia	Human	Wound swabs and aspirate	Infection	NR/752	*M. sciuri* (5), *S. warneri* (1), *S. haemolyticus* (1)	MALDI-TOF	√	NC	NC	NC	PCR	[39]
Kenya	Human	Nasal swab	Colonization	16/NR	*S. sciuri**(8), *S. lentus**(4), *S. vitulinus**(3)	VITEK 2	√	NC	√	NC	PCR	[40]
Tanzania	Human	Urine	Infection	65/NR	*S. haemolyticus* (21), *S. hominis* (2), *S. saprophyticus* (1), *S. warneri* (1), *S. epidermidis* (1)	WGS	√	-	-	-	WGS	[10]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
Uganda	Human	Nasal swabs	Colonization	319/664	*S. epidermidis* (31), *S. haemolyticus* (8), *S. pasteuri* (3), *S. lugdunensis* (2), *S. xylosus* (2), *S. kloosii* (2), *S. lentus** (1), *S. sciuri** (1), *S. caprae* (1), CoNS (16)	BD Phoenix	√	NC	NC	NC	PCR	[41]
West Africa												
Benin	Human	Urine	Infection	7/170	CoNS (7)	ND	√	NC	NC	NC	PCR	[9]
Nigeria	Human	Swabs, blood, Urine, Seminal fluid, aspirate	Infection	41/84	CoNS (17)	ND	√	NC	NC	NC	PCR	[6]
	Human	Nasal swabs	Colonization	15/240	*S. haemolyticus* (5)	ITS-PCR	√	NC	NC	NC	PCR	[42]
	Human	Wound swabs, GTI, Aspirate, Blood	Infection	40/NR	*S. haemolyticus* (17), *S. sciuri** (9), *S. epidermidis* (1), *S. warneri* (1)	VITEK 2	√	NC	NC	NC	PCR	[43]
	Human	Feacal samples	Colonization	149/293	CoNS (45)	Biochemical Tests	√	NC	NC	NC	PCR	[44]
	Human	Feacal Sample	Colonization	53/117	*S. epidermidis* (9), *S. warneri* (2), *S. xylosus* (2), *S. saprophyticus* (1), *S. capitis* (1)	VITEK 2	√	NC	NC	I (4), IV (9)	PCR	[45]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
Southern Africa												
South Africa	Human	Blood	Infection	89/NR	*S. haemolyticus* (14), *S. epidermidis* (10), *S. hominis* (12), *S. lentus** (6), *S. sciuri** (5), *S. xylosus* (4), *S. saprophyticus* (3), *S. succinus* (3), *S. gallinarum* (2), *S. capitis* (1), *S. warneri* (1), *S. arlettae* (1), *S. auricularis* (1)	VITEK 2	√	NC	NC	NC	PCR	[7]
	Human	Feacal Samples	Colonization	238/150	*S. haemolyticus* (32), *S. borealis* (20), *S. hominis* (2), *M. sciuri* (2)	VITEK MS, MALDI-TOF and WGS	√	-	-	III (2), VI (5), VIII (2)	WGS	[46]
North Africa	Animal											
Algeria	Animal	Milk	Colonization	35/82	*S. hominis* (1), *S. sciuri** (1), *S. cohnii* (1)	MALDI-TOF	√	NC	NC	NC	PCR	[47]
	Animal	Nasal swab	Colonization	61/46	*M. lentus* (6), *S. epidermidis* (6), *S. hominis* (1)	MALDI-TOF	√	-	√	SCC*mec*-*MecC* (5), II (5), IV (1), V (1), VIII (1)	WGS	[20]
Egypt	Animal	Milk	Infection	181/488	CoNS (4)	API Staph	√	NC	NC	NC	PCR	[13]
	Animal (Cattle and Buffalo)	Milk	Infection	30/50	CoNS (29)	MALDI-TOF	√	NC	-	NC	PCR	[14]
	Animal (Cattle and Buffalo)	Milk	Infection	75/140	*S. haemolyticus* (2), *S. warneri* (1)	MALDI-TOF	√	NC	NC	V (1)	Microarray	[48]
	Animal (Turkeys)	Cloacal swabs	Colonization	39/250	*S. sciuri** (3), *S. lentus** (2), *S. saprophyticus* (1), *S. simulans* (1), *S. epidermidis* (1)	MALDI-TOF	√	NC	NC	NC	PCR	[33]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
	Animal	Chicken (meat)	Contamination	36/100	*S. lugdunensis* (4), *S. epidermidis* (4), *S. hominis* (2), *S. haemolyticus* (1), *S. schleiferi* (1), *S. lentus** (1)	16S rRNA sequencing	√	NC	NC	NC	PCR	[49]
	Animal	Meat	Contamination	11/100	*S. lugdunensis* (1)	16S rRNA sequencing	√	NC	NC	NC	PCR	[50]
	Animal (Cattle and Buffalo)	Milk	Colonization	30/240	*S. carnosus* (2), *S. capitis* (3), *S. xylosus* (1), *S. saccharolyticus* (1), *S. auricularis* (1)	Biochemical Tests	√	NC	NC	NC	PCR	[51]
	Animal	Chicken carcass	Colonization	25/250	*S. warneri* (3), *S. chromogenes* (3), *S. hominis* (2), *S. saprophyticus* (2), *S. gallinarum* (2), *S. epidermidis* (1), *S. caprae* (1)	Biochemical Tests	√	NC	NC	NC	PCR	[52]
Libya	Animal (Cat and Dog)	Nasal swabs	Colonization	24/151	*S. capitis* (1), *S. cohnii* (1), *S. sciuri** (1)	BD Phoenix	√	NC	NC	NC	PCR	[31]
Tunisia	Animal	Milk	Infection	68/300	*S. epidermidis* (4), *S. pasteuri* (4), *S. haemolyticus* (2), *S. sciuri** (1), *S. warneri* (1), *S. chromogenes* (1), *S. cohnii* (1)	*sodA* sequencing	√	NC	NC	IV (4)	PCR	[15]
East Africa												
Ethiopia	Animal	Milk	Infection	83/290	*S. epidermidis* (7), *S. warneri* (5), *S. simulans* (2), *S. capitis* (2), *S. chromogenes* (1), *S. cohnii* (1)	Biochemical Tests	√	NC	NC	NC	PCR	[32]
Kenya	Animal	Nasal swab	Colonization	24/167	*M. sciuri* (15), *M. lentus* (1)	MALDI-TOF	√ MecA1	-	-	-	WGS	[53]
Rwanda	Animal	Milk	Infection	118/303	*S. hominis* (1), *S. sciuri** (1)	MALDI-TOF and *rpoB* sequencing	√	NC	-	NC	PCR	[54]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
Tanzania	Animal	Milk	Colonization	42/117	CoNS (1)	ND	√	NC	NC	NC	PCR	[55]
West Africa												
Nigeria	Animal	Nasal swabs and Milk	Colonization	64/283	*S. epidermidis* (17), *S. haemolyticus* (15), *S. saprophyticus* (13), *S. chromogenes* (8), *S. simulans* (7), *S. xylosus* (4)	16S rRNA sequencing	√	NC	NC	NC	PCR	[56]
	Animal	Meat	Contamination	20/126	*S. epidermidis* (16), *S. saprophyticus* (2), *S. xylosus* (1)	16S rRNA sequencing	√	NC	NC	NC	PCR	[57]
	Animal	Meat	Contamination	24/255	*S. sciuri** (5), *S. saprophyticus* (1)	*sodA* and 16S rRNA sequencing	√	NC	NC	NC	PCR	[58]
	Animal	Anal Swab	Colonization	6/23	*M. sciuri* (4), *S. gallinarum* (1)	MALDI-TOF and WGS	√	-	-	-	WGS	[59]
	Animal	Groin swab	Colonization	16/109	*S. sciuri**(10), *S. lentus**(3), *S. haemolyticus* (2), *S. simulans* (1)	*sodA* sequencing	√	NC	NC	V(1)	PCR	[60]
	Animal	Nasal and Ear swabs	Colonization	NR/291	*S. sciuri** (10), *S. lentus** (6), *S. cohnii* (3), *S. haemolyticus* (1)	*sodA* and 16S rRNA sequencing	√	NC	NC	NC	PCR	[61]
Central Africa												
Cameroun	Animal	Whole shrimp	Colonization	9/NR	CoNS (9)	ND	√	NC	NC	NC	PCR	[62]
	Environment											
Nigeria	Environment	Wastewater	Contamination	31/56	*S. epidermidis* (4), *S. saprophyticus* (3)	Biochemical Tests	√	-	-	NC	PCR	[63]
South Africa	Environment	Wastewater	Contamination	23/192	CoNS (16)	16S rRNA sequencing	√	NC	NC	NC	PCR	[64]
	Others											
North Africa												
Algeria	Food and Humans	Milk, Meat, Cake, Pizza, Sausage	Contamination and Colonization	24/112	CoNS	ND	√	NC	NC	NC	PCR	[65]
Egypt	Food	Milk, Yogurt, Burger, Meat	Contamination	3/140	*S. epidermidis* (1), *S. sciuri** (1)	API Staph	√	NC	NC	NC	PCR	[66]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
	Food and Humans	Cheese, yogurt, Hand and nasal swabs	Colonization and Contamination	79/210	CoNS (52)	ND	√	NC	NC	NC	PCR	[67]
Morocco	Human, Food and the Environment	Whole food, nasal, hand environmental swabs	Contamination and Colonization	205/608	CoNS (12)	ND	√	NC	NC	NC	PCR	[68]
Tunisia	Human, Animal and the Environment	Nasal swab, milk and manure	Colonization and Infection	49/156	*S. sciuri** (9), *S. xylosus* (2), *S. haemolyticus* (1), *S. cohnii* (1)	16S rRNA sequencing	√	NC	√	I (1), II (3), IV (2), V/VII (2)	PCR	[69]
	Human and Animal	Nasal Swab	Colonization and Infection	77/152	*M. sciuri* (19)	*tuf* sequencing	√	-	√	III (3), SCC*mec*-*mecC* (6)	PCR and WGS	[70]
	Human and Environment	Fomite and Hand swabs	Colonization	83/200	*S. haemolyticus* (18), *S. epidermidis* (1), *S. saprophyticus* (1)	16S rRNA sequencing	√	NC	NC	NC	PCR	[71]
	Fomite	Mobile Phones	Colonization	5/100	*S. warneri* (1), *S. haemolyticus* (1)	MALDI-TOF	√	NC	NC	NC	PCR	[72]
West Africa												
Benin	Animal and Environment	Fish and Water	Colonization and Contamination	21/43	CoNS (7)	ND	√	NC	NC	NC	PCR	[73]
Ghana	Humans and Animals	Nasal swabs	Colonization	149/320	*S. sciuri** (27), *S. epidermidis* (1), *S. haemolyticus* (1)	MALDI-TOF	√ mecA1	-	-	-	WGS	[74]
Nigeria	Food	Kindirmo, Nono, Iru, wara, Ogi and Kunu	Contamination	255/255		16S rRNA sequencing	-	NC	NC	NC	PCR	[75]
	Human and Animals	Urine, Nasal and wound swab, Fecal samples	Colonization and Infection	37/350	*S. haemolyticus* (10), *M. sciuri* (8)	MALDI-TOF	√ mecA1	-	-	III (2), V (4)	WGS	[76]
	Human and Environment	Urine, Wound and skin swabs, Wastewater	Infection and contamination	43/NR	*S. sciuri** (6), *S. cohnii* (6), *S. arlettae* (5), *S. epidermidis* (5), *S. saprophyticus* (1)	16S rRNA sequencing	√	NC	NC	NC	PCR	[77]
Southern Africa												
Mozambique	Food	Whole food	Contamination	51/81	CoNS (22)	16S rRNA sequencing	√	NC	NC	NC	PCR	[78]
South Africa	Animal and Environment	Nasal and ear swabs, cow dung	Colonization	92/150	CoNS (31)	API Staph and PCR	√	NC	NC	NC	PCR	[79]

Table 1 (continued)

Country	Sample source	Sample type	Clinical Significance	No of CoNS isolates/No of samples	MR-CoNS Species (N)	Identification method	Methicillin resistance gene detected			SCC*mec* element (N)	Methicillin gene detection method	References
							mecA	*mecB*	*mecC*			
	Food and Humans	Mushroom and Hand swab	Contamination and Colonization	55/582	*S. haemolyticus* (1), *S. succinus* (1), *S. equorum* (1)	MALDI-TOF	√	NC	NC	NC	PCR	[80]
	Human, Animal and the Environment	Nasal and Environmental swabs	Colonization	150/208	*M. sciuri* (31), *S. epidermidis* (1)	VITEK MS and MALDI-TOF	√	-	-	III, V, VIII	WGS	[81]
	Humans and Animals	Nasal Swab and Milk	Colonization and Infection	196/3466	*S. epidermidis* (12), *S. haemolyticus* (5)	MALDI-TOF	√	NC	NC	NC	PCR	[82]

*S. sciuri**: renamed *M. sciuri*; *S. lentus**: renamed *M. lentus*; *S. vitulinus**: renamed *M. vitulinus*; *NC* Not checked, *ND* Not done, *NR* Not reported

PCR Polymerase chain reaction, *WGS* Whole-genome sequencing, *MALDI-TOF* Matrix-assisted laser desorption ionization-time of flight mass spectroscopy

CoNS Coagulase-negative staphylococci, √present, - Absent

N (Number in parenthesis) No: Number

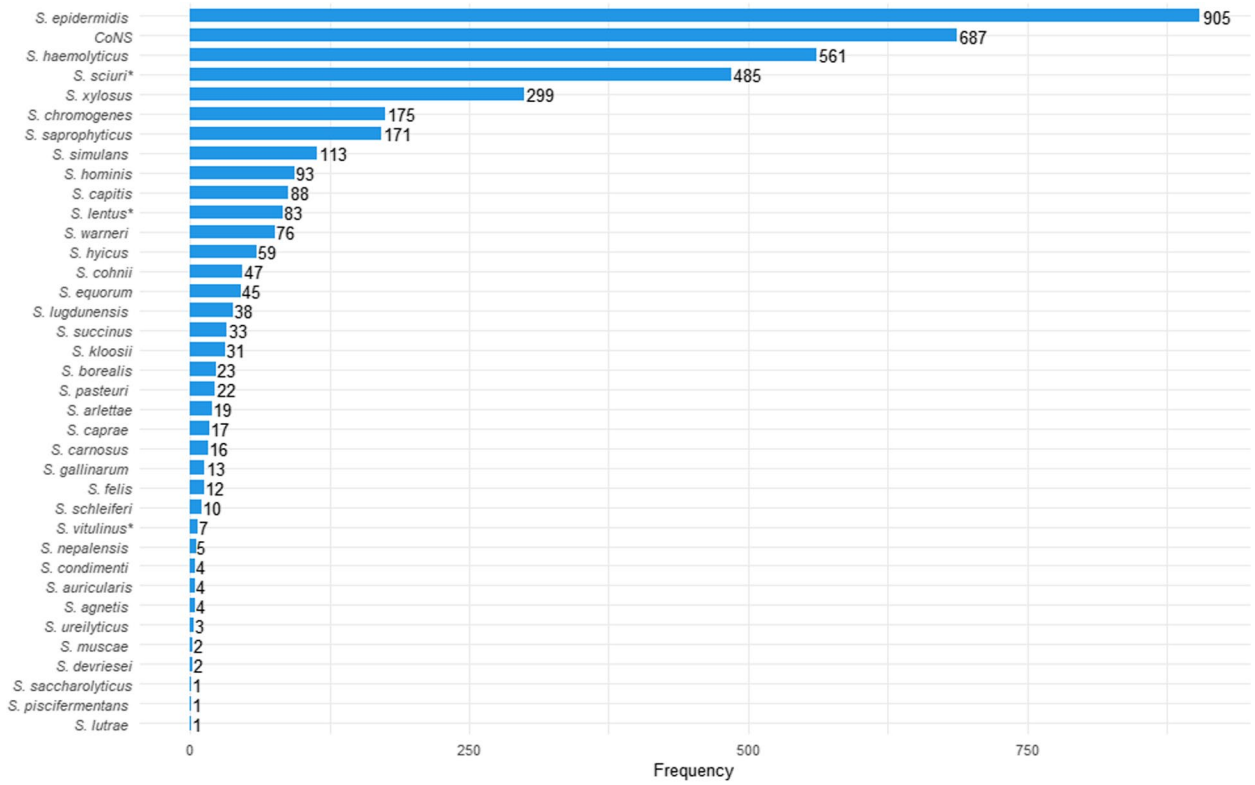

Fig. 4 The prevalence of CoNS recovered from various sources in Africa. Legend: *S. sciuri**: renamed *M. sciuri*; *S. lentus**: renamed *M. lentus*; *S. vitulinus**: renamed *M. vitulinus*

The most prevalent SCC*mec* types were type IV ($n=36$), followed by III ($n=18$) and II ($n=10$). However, only SCC*mec* types II, III, IV, V, VIII and SCC*mec-mecC* hybrid were identified among MR-CoNS obtained from animal origin. Five isolates each possessed the SCC*mec* types II, IV and the SCC*mec-mecC* hybrid.

Prevalence of coagulase-negative and methicillin-resistant coagulase-negative staphylococci

The pooled prevalence of CoNS among isolates of human origin was 26% ($n=14$; 95% CI = 16.5 – 38.2; $I^2=97.7\%$; $p<0.0001$), and the pooled prevalence of CoNS in isolates of animal origin was 24% ($n=20$; 95% CI = 18.6 – 30.0; $I^2=93.6\%$; $p<0.0001$). However, the pooled prevalence of CoNS in the environment was 29% ($n=2$; 95% CI = 4.5 – 78.1; $I^2=97.5\%$; $p=0.418$). Overall, the pooled prevalence of CoNS in Africa was 27% (95% CI: 22.8 – 32.3; $I^2=97.7\%$; $p<0.0001$). Moreover, the pooled prevalence of CoNS in East Africa was 39% ($n=5$; 95% CI = 36.7 – 41.7; $I^2=94.5\%$; $p<0.0001$), 32% ($n=14$; 95% CI = 29.8 – 34.2; $I^2=96.5\%$; $p=0.003$) in West Africa, 28% ($n=27$; 95% CI = 26.3 – 28.8; $I^2=95.9\%$; $p>0.0001$) in North Africa and 15% ($n=6$; 95% CI = 13.8 – 16.5; $I^2=99.4\%$; $p=0.255$) in Southern Africa (Fig. 6A).

The existence of publication bias was statistically confirmed with the random-effect model and represented by an asymmetrical funnel plot. The heterogeneity of the included articles was observed to be high, as indicated by the $I^2=97.7\%$ and the Cochrane Q test value ($Q=2199.94$, $p<0.0001$). The intercept of the Eggers regression model was 0.092 (95% CI: -4.44856 – 4.63251 with a statistical *t*-value of 0.04 ($p=0.38$) (Fig. 6B).

The pooled prevalence of MR-CoNS in isolates from human samples was estimated as 53% ($n=20$; 95% CI = 40.5 – 65.0; I2 = 92.6%; $p=0.645$), and MR-CoNS in isolates from animal studies was 32% ($n=22$; 95% CI = 19.5 – 46.8; $I^2=88.3\%$; $p=0.468$). The overall pooled prevalence of MR-CoNS was estimated as 36% (95% CI: 29.6 – 43.8; $I^2=91\%$; $p>0.0001$) in Africa. The pooled prevalence in the African regions are as follows: 45% ($n=17$; 95% CI: 32.5 – 57.9; $I^2=85\%$; $p=0.44$) in West Africa, 35% ($n=28$; 95% CI: 23.7 – 47.5; $I^2=92.5\%$; $p=0.02$) in North Africa, 28% ($n=8$; 95% CI: 15.9 – 43.7; $I^2=94.1\%$; $p=0.008$) in Southern Africa, and 26% ($n=7$; 95% CI: 13.0 – 45.8; $I^2=90.8\%$; $p=0.019$) in East Africa. Also, the prevalence of MR-CoNS in Cameroun, Central Africa, was 95% ($n=1$; 95% CI: 52.5 – 99.7; $p=0.042$) (Fig. 7A) in CoNS from

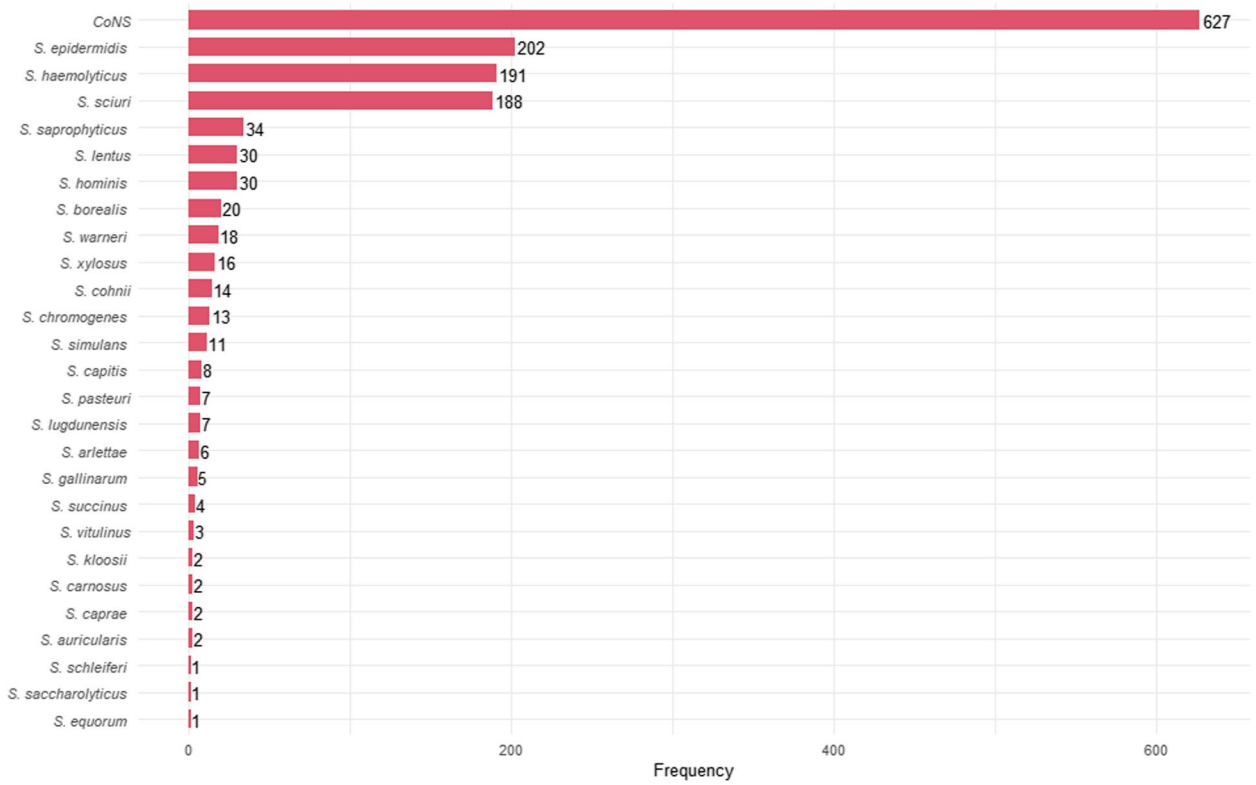

Fig. 5 The prevalence of MR-CoNS recovered from various sources in Africa. Legend: *S. sciuri*: renamed *M. sciuri*; *S. lentus*: renamed *M. lentus*; *S. vitulinus*: renamed *M. vitulinus*

Table 2 Staphylococcal chromosome cassette *mec* (SCC*mec*) types detected among MR-CoNS isolates in Africa

SCC*mec* Types	Frequency	Species (Number)
I	6	*S. epidermidis* (4), *S. cohnii* (1), *S. warneri* (1)
II	18	*S. epidermidis* (10), *S. haemolyticus* (4), *M. sciuri* (2), *M. lentus* (1), *S. xylosus* (1)
III	20	*S. epidermidis* (11), *M. sciuri* (8), CoNS (1)
IV	43	*S. epidermidis* (34), *M. sciuri* (2), *S. xylosus* (2), *S. haemolyticus* (2), *S. warneri* (1), *S. saprophyticus* (1), *S. capitis* (1)
V	12	*S. haemolyticus* (5), *S. epidermidis* (4), *S. xylosus* (1), CoNS (2)
VI	6	*S. borealis* (4), *S. haemolyticus* (1), CoNS (1)
VIII	15	*S. haemolyticus* (11), *S. hominis* (3), CoNS (1)
SCC*mec-mecC*	11	*M. sciuri* (6), *M. lentus* (5)

water shrimp. The likelihood of publication bias was confirmed using the random effect model and presented in a funnel plot. The visual inspection of the plot showed the distribution was slightly asymmetrical (Fig. 7B).

The heterogeneity of the articles was observed to be high, as indicated by the $I^2 = 91.1\%$ and the Cochrane Q test value ($Q = 677.1$, $p < 0.0001$). The intercept of the Eggers regression model was 1.26248 (95% CI: -0.51030 – 3.03526) with a statistical t-value of 1.425 ($p = 0.07$). This data suggests that there is an unlikely potential publication bias in the eligible studies.

Discussion

The clinical significance of CoNS and MR-CoNS is rising globally with huge economic costs and severe healthcare consequences [11, 12]. In this systematic review, 65 studies from 16 of 54 African countries were eligible for inclusion, providing evidence of the paucity of data on the epidemiology of CoNS and MR-CoNS in Africa. Most

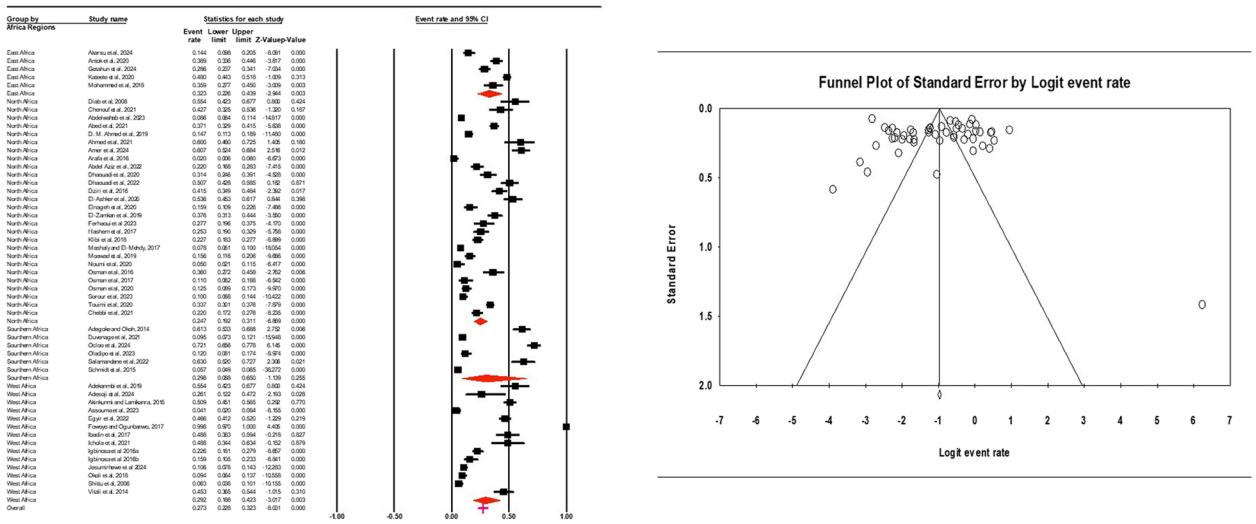

Fig. 6 **A** Forest plot with the adjusted average prevalence of CoNS from various samples in Africa (**B**) Funnel plot of CoNS from various samples in Africa. Legend: Random effects mode (95% CI: -4.44856 – 4.632513; $I^2 = 97.7\%$; $p < 0.0001$). X-axis is the proportion of CoNS reported in individual studies as listed along the Y-axis, with the range of proportion in the 95% confidence interval (CI). I^2 = heterogenicity, $p = p$-value. The estimate of prevalence was calculated by pooling 52 studies

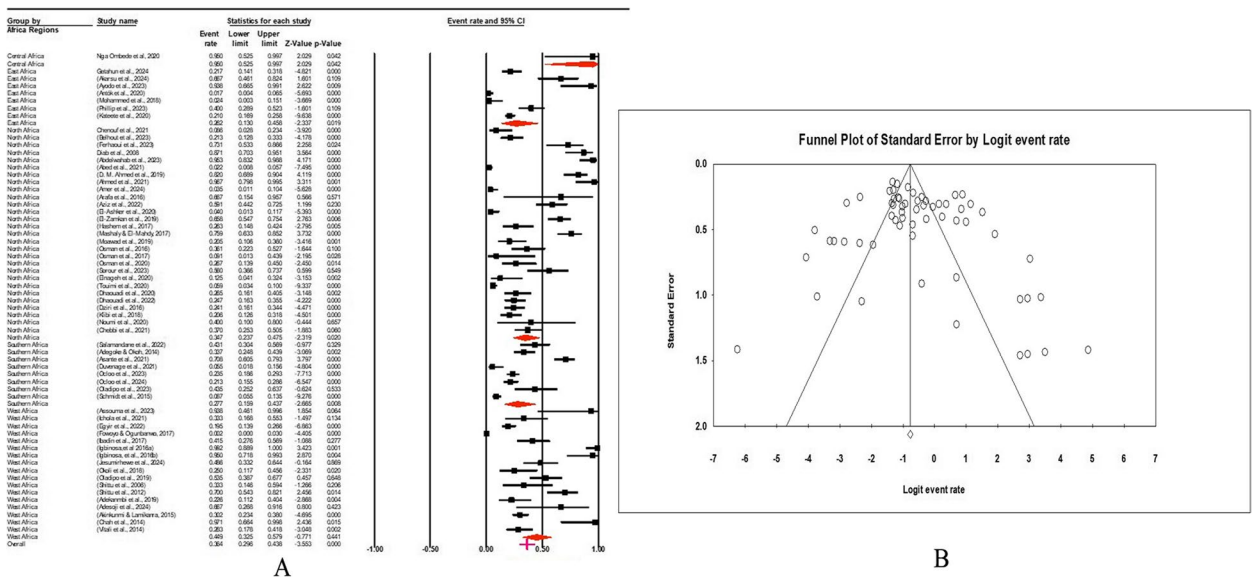

Fig. 7 **A** Forest plot with the adjusted average prevalence of MR-CoNS from various samples in Africa (**B**) Funnel plot of MR-CoNS from various samples in Africa. Legend: Random effects mode (95% CI: -0.51030 – 3.03526; $I^2 = 91.1\%$; $p < 0.0001$). X-axis is the proportion of MR-CoNS reported in individual studies as listed along the Y-axis, with the range of proportion in the 95% confidence interval (CI). I^2 = heterogenicity, $p = p$-value. The estimate of prevalence was calculated by pooling 61 studies

articles were from Egypt ($n = 17$), Nigeria ($n = 15$), South Africa ($n = 7$) Tunisia ($n = 7$) and Algeria ($n = 4$). These countries have reported more studies in previous investigations on *S. aureus* and CoNS [12, 83, 84]. It is important to note that CoNS are considered contaminants in clinical and non-clinical settings, and this perception may be prevalent in many African countries [12]. The diversity of CoNS was notably high, with 36 staphylococcal species reported on the continent. The variety of these species may be attributed to advanced techniques (e.g. mass spectrometry and sequence-based techniques) employed in 34 studies. Different species of CoNS exhibit similar

characteristics [1, 85]. Biochemical tests and semi-automated methods, such as API Staph, VITEK, and BD Phoenix, which assess the reaction of isolates on nutritional, metabolic and enzymatic activities can provide unreliable species identification. For example, one WGS study reported *Staphylococcus borealis* as a colonizer of human faecal samples [46]. *S. borealis* can be misidentified as *S. haemolyticus* by other sequence-based and mass spectrometry methods [86, 87]. Hence, to investigate and understand the diversity of CoNS in Africa, studies utilizing WGS or its combination with mass spectrometry (e.g. MALDI-TOF) techniques are recommended.

The overall prevalence of CoNS in Africa is 27%, with regional prevalences of 39%, 32.0%, 28%, and 15% in East Africa, West Africa, North Africa, and Southern Africa, respectively. This prevalence is similar to other regions of the world, e.g. North and Latin America, with 31% [88] and 36.7% [89], respectively, and 23.2% in Asia [89]. *S. epidermidis* and *S. haemolyticus* were associated with bacteremia [7, 27–30, 37] and skin and soft tissue infections [5, 29, 43] across the African regions. *S. saprophyticus* was mainly linked to urinary tract infections in young adults [1, 10, 29]. These species, including *S. hominis*, have been reported in Europe as the most predominant species associated with infections due to CoNS [11]. *S. xylosus*, *S. chromogenes*, and *M. sciuri* were reported primarily in animals with clinical and subclinical mastitis [13–15, 32, 48, 54]. The widespread occurrence of these CoNS highlights their clinical significance in Africa. CoNS also harbour various antibiotic-resistant genes that can be transferred to other pathogens, including *Staphylococcus aureus* [25]. This situation could potentially increase the incidence of staphylococcal infections in Africa.

The pooled prevalence of MR-CoNS was estimated at 36% in Africa. MR-CoNS was reported in human [5, 7–9, 27, 29, 30, 37, 43] and animal [13, 15, 32, 36, 48, 54, 60] infections in Africa. This observed prevalence aligns with reports from South America (38%), [90], and Europe (37.1%), [91]. The *mecA* was the most commonly detected methicillin resistance gene, while the *mecC* was identified in only four studies. PCR detection of *mecB* was investigated in one study [63], which might be attributed to limited knowledge of the gene. The deployment of WGS to investigate antibiotic resistance gene determinants in clinical and non-clinical settings could enhance the detection of other methicillin resistance gene determinants among staphylococcal isolates. This technique has already facilitated the identification of the *mecA1* gene [35, 53, 74, 76].

The SCC*mec* elements possess the methicillin resistance gene determinants in staphylococci, and *M. sciuri* has been proposed as the ancestral origin of this MGE [1, 11, 92]. Also, cross-species transfer among the staphylococci has been described [93]. Of the 15 SCC*mec* types reported so far, seven types were observed among MR-CoNS in Africa. Specifically, *S. epidermidis* carried SCC*mec* types I, II, III, IV and V, and SCC*mec* type IV was the most common. The widespread prevalence of SCC*mec* type IV among *S. epidermidis* isolates has been documented [23, 94, 95]. This MGE is smaller (21–24 kb) compared to types I–III (34 – 67 kb), with 98–99% homology to the SCC*mec* element reported in *S. aureus* [23, 94]. This observation suggests inter-species transfer of the MGE and could exacerbate the burden of methicillin-resistant *S. epidermidis* and methicillin-resistant *S. aureus* on the continent. The SCC*mec* types II, III, IV and the hybrid SCC*mec-mecC* were identified in some *M. sciuri* isolates. The SCC*mec-mecC* hybrid identified in members of the *M. sciuri* group (*M. sciuri* and *M. lentus*) [20, 70] suggests that the sciuri group may be the ancestral source of *mecA* and *mecC*. This hybrid was 100% homologous within the recombinase region (*ccrB*) in the SCC*mec-mecC* hybrid reported in *S. aureus* in Japan [96]. This observation indicates that this SCC*mec* hybrid has the potential to be transmitted to *S. aureus* isolates of human and animal origins, complicating the treatment of infections caused by the pathogen.

This systematic review has described the epidemiology of MR-CoNS in Africa. We advocate future studies investigating the burden and economic impact of MR-CoNS infections on the continent. Detailed characterization using molecular and proteomic techniques (e.g. WGS, MALDI-TOF) will provide insights into species diversity, SCC*mec* types, and clones across Africa. Such information would be invaluable for infection control experts and policymakers in formulating effective strategies to combat the public health impact of MR-CoNS in the continent. However, these techniques are currently unavailable due to the low resources for research in Africa.

This systematic review had some limitations. First, we did not include publications in other languages (e.g. French and Spanish). Hence, the observations in this systematic review may not be representative of all regions in Africa. Secondly, we did not investigate other antibiotic resistance genes carried on the SCC*mec* elements, the chromosome or plasmids of the MR-CoNS isolates. Thirdly, we did not determine the clonal nature of the MR-CoNS in Africa. Also, this systematic review was not registered on the PROSPERO platform.

Conclusion

This investigation showed that the prevalence of CoNS and MR-CoNS varies across the African regions. However, there are knowledge gaps in many countries. MR-CoNS was primarily associated with *S. epidermidis*, *S.*

haemolyticus and *M. sciuri*, with different SCC*mec* elements. There is a need for the deployment of advanced techniques to assist in gathering comprehensive data on the diversity of CoNS, the genetic determinants involved, SCC*mec* elements, and the potential clones circulating in Africa. This research could enhance preparedness to combat the spread of antibiotic resistance across the continent.

Abbreviations

CoNS	Coagulase-negative staphylococci
MR-CoNS	Methicillin-resistant coagulase-negative staphylococci
SCC*mec*	Staphylococcal cassette chromosome *mec*
WGS	Whole-genome sequencing
MGE	Mobile genetic element
CI	Confidence interval

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-11149-1.

Supplementary Material 1.

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Authors' contributions
Conception, planning and design by TOA, PTQ, AOS and ESD. TOA and NSS worked on the methodology, database search and the screening of articles. TOA, NSS and PTQ collected data, did analysis and interpretation of the data. The initial draft was prepared by TOA and NSS, critical revision of the manuscript by PTQ, AOS and ESD. All the authors provided input, read and agreed to the final draft of the manuscript for publication.

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Data availability
All data generated or analyzed during this study are included in this published article (and its supplementary information files).

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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