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REVIEW

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Clarithromycin-resistant *Helicobacter pylori* in Africa: a systematic review and meta-analysis

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Abstract

Background In 2022, approximately 56.5% of adults and 47.1% of children and adolescents were affected by *Helicobacter pylori* (*H. pylori*) infection in Africa, and clarithromycin-resistant *H. pylori* (CRHp) strains have become global priority pathogens. Therefore, this study aimed to conduct the first comprehensive systematic review and meta-analysis of CRHp in Africa.

Methods This investigation was conducted according to the guidelines of the Preferred Reporting Items for Systematic reviews and Meta-Analyses (The PRISMA 2020). Literature search of electronic databases (Google Scholar, African Journals Online, ResearchGate, PubMed, Embase, and Scopus) was performed using keywords "clarithromycin", "*Helicobacter pylori*", "African country name", "mutation in the 23S rRNA".

Results Sixty-five studies involving 5,313 *H. pylori* strains isolated over 26 years (1997–2022) from 23 African countries were included in this study. The samples from which CRHp was isolated included gastric biopsy (60/63; 95%), and stool (4/63; 6%). The pooled prevalence of CRHp in Africa was 27% (95% CI: 22, 33). There was a steady trend in the prevalence of CRHp isolated in Africa over the 26 years ($R^2 = 0.0001$, $p = 0.92$, slope coefficient of -0.05x). Ten types of 23S rRNA mutations (conferring clarithromycin resistance) were identified, and included mainly A2143G (465 *H. pylori* strains out of 1178 tested) and A2142G (344 *H. pylori* strains out of 1027).

Conclusion To enhance the accuracy and validity of surveillance data for *H. pylori* in Africa, there is an urgent need for implementing standardized microbiological methods for resistance detection. The prevalence of CRHp reported in this study was very similar to the overall global prevalence and there is a need for more representative studies on CRHp in Africa. While waiting for this, the treatment of *H. pylori* infections must be based on the guidelines of the AHMSG first Lagos consensus.

Keywords *Helicobacter pylori*, Clarithromycin resistance, Antimicrobial resistance in Africa, Global priority pathogens, Systematic review, Meta-analysis

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Introduction

Helicobacter pylori, (*H. pylori*) is responsible for one of the most common human bacterial infections worldwide [1, 2]. In 2022, Africa had the highest prevalence of *H. pylori* infection compared to other global regions [2]. The prevalence of *H. pylori* infection in Africa (56.5% for adults and 47.1% for children and adolescents) may be underestimated because of the scarcity of data on asymptomatic *H. pylori* carriage in most African countries [2, 3]. *H. pylori* infections are usually associated with poor sanitation and unclean water supplies [4].

H. pylori is also responsible for approximately 90% of the global burden of non-cardiac gastric cancer [5]. In 2020, the International Agency for Research on Cancer has classified *H. pylori* as a class 1 carcinogen, with a higher incidence of cancer than the human papillomavirus, hepatitis B virus, and hepatitis C virus [6]. To establish and maintain infections, *H. pylori* strains use several virulence factors such as adhesins (*bab*A), urease (*ure* operon), vacuolating cytotoxin (*vac*A), immunodominant antigen (*cag*A), and the induced by contact with epithelium (*ice*A), which are most frequently associated with peptic ulceration and increased production of IL-8 [7, 8].

Advances in medicine have improved the treatment of *H. pylori* infection. In Africa, first-line therapy combines antibiotics (amoxicillin, clarithromycin) with proton pump inhibitors (PPIs), whereas second-line or salvage therapies (levofloxacin-based triple therapy, sequential non-bismuth quadruple therapy, or bismuth-based quadruple therapy) combine antibiotics (amoxicillin, clarithromycin, nitroimidazole, levofloxacin, and tetracycline) with PPIs and bismuth compounds [3].

The antimicrobial resistance has not spared *H. pylori* strains, with global resistance rates of 24% for levofloxacin, 34% for clarithromycin, and 55% for metronidazole [9]. Clarithromycin inhibits *H. pylori* protein synthesis by interacting with the peptidyl transferase ring in the V region of the 23S ribosomal RNA (rRNA) subunit of *H. pylori* strains. Mutations in the 23S rRNA are responsible for clarithromycin resistance [10–12]. The resistance of *H. pylori* to clarithromycin is associated with a sevenfold risk of treatment failure when using a clarithromycin-based regimen [9]. Therefore, in areas with low clarithromycin resistance (< 15%), the treatment algorithm consists of amoxicillin, clarithromycin, and a PPI, whereas second-line therapeutic regimens are used for areas with clarithromycin resistance > 15% [13].

In 2017, the World Health Organization (WHO) released a global priority list of antibiotic-resistant bacteria, and clarithromycin-resistant *H. pylori* (CRHp) strains were ranked as high-priority pathogens for which new antibiotics are urgently needed [14]. Therefore, from an epidemiological standpoint, monitoring the spread of CRHp has become a priority for global public health authorities.

The previous pooled prevalences of CRHp determined in Africa should be taken cautiously since the studies were only limited to a few African countries [9, 15]. To address the lack of quality data on CRHp in Africa, this study aimed to conduct the first comprehensive systematic review and meta-analysis of CRHp in Africa.

Methods

This systematic review and meta-analysis was conducted according to the guidelines of the Preferred Reporting Items for Systematic reviews and Meta-Analyses (The PRISMA 2020) [16].

Literature review

A comprehensive literature search of electronic databases (Google Scholar, African Journals Online, ResearchGate, PubMed, Embase, and Scopus) was performed using keywords "clarithromycin", "*Helicobacter pylori*", "Africa", "African country name", "mutation in the 23S rRNA"). The database search was conducted from March 23, 2024, to April 30, 2024, and the studies written in French and English were included in this systematic review and meta-analysis.

Eligibility criteria

This systematic review and meta-analysis included original peer-reviewed research articles and theses reporting CRHp in African countries. Studies reporting CRHp using both genotypic and phenotypic methods, were included. After identification, duplicate articles were excluded. Reviews, commentaries, perspectives, and non-peer-reviewed articles, reporting CRHp in Africa were also excluded. Furthermore, peer-reviewed research articles and theses on *H. pylori* strains isolated from outside Africa were also excluded.

Quality assessment

Two authors performed the article quality assessment using the Joanna Briggs Institute (JBI) Prevalence Critical Appraisal Tool [17]. The results of the article quality assessment are presented in the Additional file 1. The JBI prevalence appraisal tool includes 10 questions for each article to be answered Yes (Y) or No (N). A positive answer (Y) was worth 10%, and the total number of points that could be obtained for an article was 100%. Studies with a score of ≥ 50% were considered of good quality and were included in the analyses (Additional file 1).

Data extraction

For each study included in this systematic review and meta-analysis, the following data were extracted: country,

authors and references, sample collection period, study design, sample from which the *H. pylori* strains were isolated, methods used to assess clarithromycin resistance, total number of *H. pylori* strains studied, number of CRHp strains, mutations within the 23S rRNA conferring clarithromycin resistance and virulence genes. Two authors conducted the data extraction, and disagreements were resolved by discussion, data cross-checking, and validation.

Data analysis

The pooled prevalences and their *p*-values, forest plots and their *p*-values, funnel plot, and meta-regression were obtained using Stata v17.0 with commands such as '*metaprop*', '*metafunnel*', '*metabias*', and '*meta regress*'. The pooled prevalence were presented with a 95% CI, corresponding *p*-value and forest plot. Funnel plot symmetry and Egger's test statistics were used to evaluate prevalence publication bias [18, 19]. Microsoft Excel 2016 v2.0, was used to perform the remaining statistical analyses, and draw associated graphs. The *p*-values obtained using Microsoft Excel were calculated based on the chi-square proportion comparison test. The level of significance for all statistical tests was set at $p < 0.05$.

Selection of studies

A literature search of public databases (Google Scholar, ResearchGate, African Journals Online, PubMed, Embase, and Scopus), generated 923 studies. Subsequently, 426, 327, 19, 46, and 40 studies were excluded for duplication, data outside Africa, other types of studies (reviews, commentaries, non-peer-reviewed articles and perspective articles), studies reporting bacteria other than *H. pylori*, and studies without any data on clarithromycin resistance, respectively. The remaining 65 studies (64 research articles and one thesis) were included in this systematic review and meta-analysis (Fig. 1). Table 1 shows the data collected from the 65 studies.

Results

Characteristics of included studies

The article quality assessment using the JBI prevalence critical appraisal tool provided an overall risk of bias assessment score of 89.5% (Additional file 1). A total of 5,313 *H. pylori* strains were studied across 65 studies and were isolated over 26 years (1997–2022) from 23 African countries (Fig. 2). Thirty-two studies mentioned the type of study, including 18 (56%) cross-sectional studies, 10 (31%) prospective studies, three (9%) observational studies, and one (3%) case-control study. The number of studies on CRHp per year has increased over the years in Africa (Fig. S1).

Samples carrying CRHp

Sixty-three studies (97%) specified the samples from which CRHp was isolated, including gastric biopsy (60/63; 95%), and stool (4/63; 6%).

Methods used to assess clarithromycin resistance

Sixty-two studies (95%) specified the methods used to assess clarithromycin resistance. The phenotypic methods (48/62; 77%), included the Kirby-Bauer disc diffusion method (22/62; 36%), E-test (20/62; 32%), and agar dilution method (6/62; 10%). Genotypic methods (38/62; 61%), included real-time polymerase chain reaction (RT-PCR) (17/62; 27%), polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) (9/62; 15%), end-point PCR (5/62; 8%), DNA sequencing (5/62; 8%), and the Genotype *Helicobacter* DR Kit (2/62; 3%).

Pooled prevalence of CRHp

A total of 5,313 *H. pylori* strains were studied, of which 1,288 were resistant to clarithromycin. The pooled prevalence of CRHp in Africa was 27% (95% CI: 22, 33). A large discrepancy was reported among the prevalences of CRHp, ranging from 0% (95% CI: 0, 2) to 100% (95% CI: 89, 100), ($I^2 = 95.3\%$, $p < 0.001$) (Fig. S2).

Publication bias

The presence of publication bias on the studies of CRHp in Africa was reported with a bias coefficient of 2.18 (Fig. S3).

Evolution of the prevalence of CRHp over time

Meta-regression of the prevalences of CRHp isolated in Africa over the 26 years did not reveal any significant variation ($R^2 = 0.0001$, $p = 0.92$), with an insignificant downward trend (slope coefficient of -0.05x).

Mutations within the 23S rRNA conferring clarithromycin resistance

Thirty studies (46%) identified ten types of mutations within the 23S rRNA (Table S1). A2143G (carried by 465 *H. pylori* strains out of 1178 tested) and A2142G (344 *H. pylori* strains out of 1027) were by far the most reported 23S rRNA mutations in Africa ($p < 0.0001$) (Table S1).

There was no difference between the prevalence of A2143G and A2142G in Northern Africa ($p = 0.17$) and southern Africa ($p = 0.08$). Nevertheless, the A2143G mutation was significantly more prevalent in Eastern Africa and Central Africa (Table 2). Several studies have reported cases of multiple 23S rRNA mutations in *H. pylori* strains.

Virulence genes

Eleven articles (17%) searched and reported *H. pylori* virulence genes. *cag*A (10/11; 91%) and *vac*A (6/11; 55%)

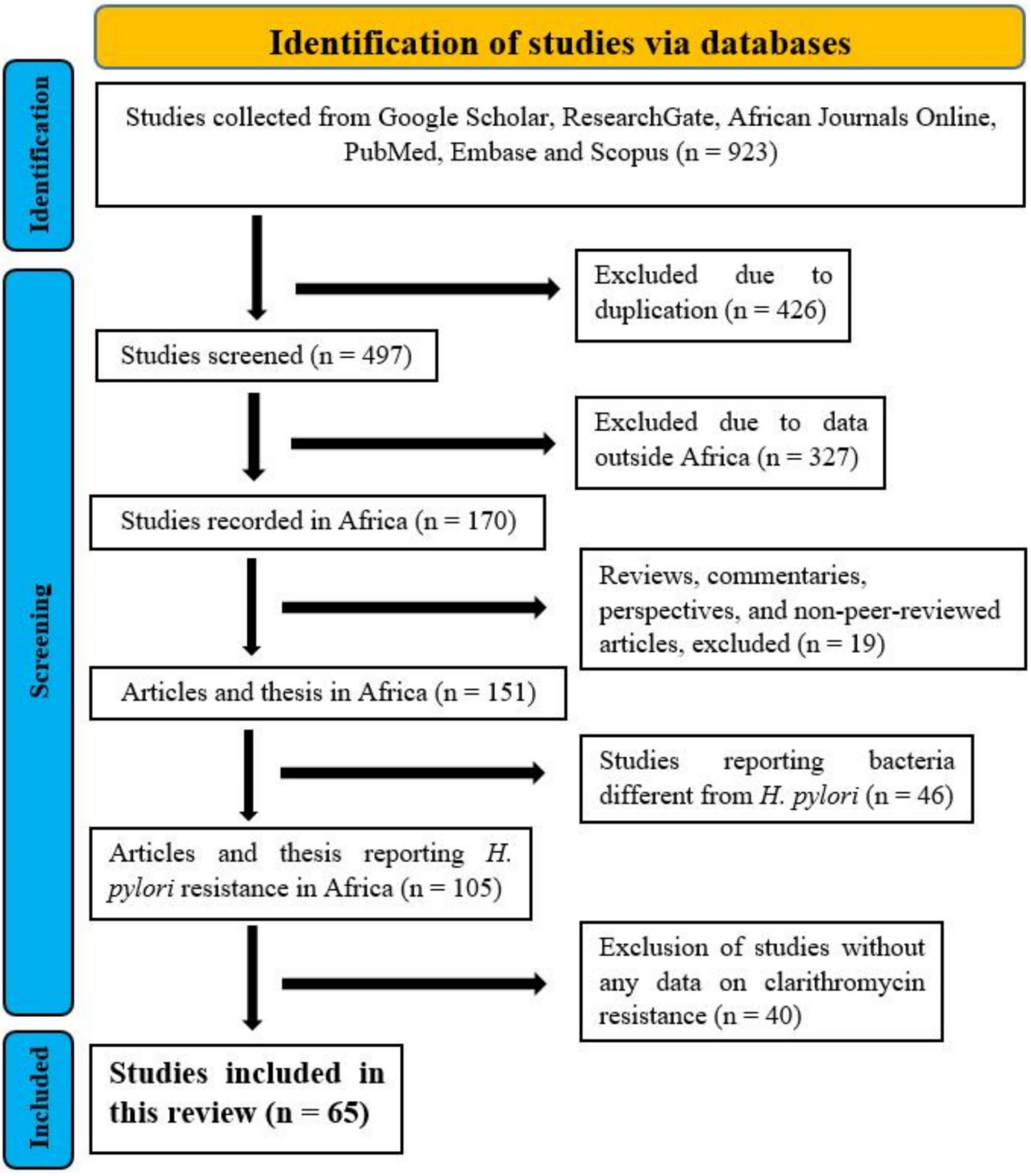

Fig. 1 PRISMA search flow diagram

Table 1 Characteristics of the 65 studies included in this study

Country	Authors and Reference	Strains isolation period	Study design	Sample	Method used to assess clarithromycin resistance	Number of *H. pylori* strains	CRHp	%	mutations in the 23S rRNA	VG
Algeria	Bachir et al. 2018 [35]	2012–2015	NA	gastric biopsies	E-test, agar dilution method	151	38	25.2	NT	*vac*A, *cag*A,
	Djennane-Hadibi et al. 2015 [36]	2008–2014	prospective	gastric biopsies	Scorpion real-time PCR	91	32	35.2	A2143G (26/32; 81%), A2142G (3/32; 9.4%), A2142C (2/32; 6.3%)	NT
	Bachir et al. 2018 [37]	2014–2016	NA	gastric biopsies	E-test, real time PCR	212	53	25	A2143G (69/232), A2142G (69/232)	NT
	Raaf et al. 2017 [38]	2015–2016	prospective study	gastric biopsies	disc diffusion method, E-test, real-time PCR	27	9	33.3	A2143G (14/60), A2142G (14/60)	NT
Burkina Faso	Sia et al. 2018 [39]	2017	prospective	gastric biopsies	Scorpion real time PCR	132	12	9.1	A2143G (12/12)	NT
Cameroon	Kouitche Mabeku et al. 2019 [40]	2013–2015	cross-sectional study	gastric biopsies	Kirby–Bauer disc diffusion method	140	19	13.6	NT	NT
	Ndip et al. 2008 [41]	2006	NA	gastric biopsies	disc diffusion method	132	59	44.7	NT	NT
Chad	Bessimbaye et al. 2021 [42]	2020–2021	observational diagnostic study	gastric biopsie, stool	disc diffusion method	59	10	16.9	NT	NT
Republic of the Congo	Ontsira-Ngoyi et al. 2015 [43]	2013–2014	cross-sectional	gastric biopsies	real-time PCR	56	1	1.8	A2142G (1/1) A2143G (1/1)	NT
Ivory Coast	Diplo et al. 2017 [44]	2015–2016	NA	gastric biopsies	Classic PCR	98	26	26.5	NA	NT
Democratic Republic of Congo	Tshibangu-Kabamba et al. 2020 [45]	2017–2018	NA	gastric biopsies	agar dilution method	102	24	23.5	A2142G (4/24; 16.7%), A2143G (17/24; 70.8%)	NT
Ethiopia	Erkihun et al. 2023 [46]	2019	cross-sectional	gastric biopsies	disc diffusion method	24	16	66.7	NT	NT
	Asrat et al. 2004 [47]	NA	NA	NA	E-test	50	0	0	NT	NT
Egypt	Elrakeeb et al. 2021 [48]	2019–2020	prospective randomized study	gastric biopsies	disc diffusion assay	52	17	32.7	NT	NT

Table 1 (continued)

Country	Authors and Reference	Strains isolation period	Study design	Sample	Method used to assess clarithromycin resistance	Number of *H. pylori* strains	CRHp	%	mutations in the 23S rRNA	VG
Egypt	El Sayed Zaki et al. 2016 [49]	2014–2015	NA	gastric biopsies	disc diffusion assay, PCR-RFLP	72	36	50	A2143G (15/72), A2142G (13.9%; 10/72)	NT
	Ramzy et al. 2016 [50]	2013	NA	gastric biopsies	PCR-RFLP	70	40	57.1	A2142G 39/70), A2143G (1/70)	NT
	Hussien et al. 2022 [34]	2018–2019	NA	gastric biopsies	agar dilution method	19	18	94.7	NT	NT
	Sherif et al. 2004 [51]	2002–2003	NA	gastric biopsies	E-test	48	2	4.2	NT	NT
	Abdallah et al. 2023 [52]	NA	cross-sectional	gastric biopsies	disc diffusion method	30	15	50	NT	NT
	Eshra et al. 2023 [53]	2022	cross-sectional	gastric biopsies	E-test	40	21	52.5	NT	NT
	Hanafy and Seleem, 2019 [54]	2016–2018	observational study	gastric biopsies	E-test, RFLP-PCR	49	12	24.5	A2142G (9/12), A2143G (3/12)	NT
	Abd El Azeem et al. 2017 [55]	NA	NA	stool	disc diffusion method	23	11	47.8	NT	*cag*A, *bab*7 allele of *bab*A2
	Attia et al. 2022 [56]	NA	NA	gastric biopsies	real-time PCR	32	12	37.5	A2142C (4/12), A2143G (12/32)	NT
	Hamza et al. 2018 [57]	NA	NA	stool	PCR-RFLP, disc diffusion method	20	12	60	A2142G (2/12), A2143G (3/12)	*cag*A, *vac*A
	Labeeb and El-khyat, 2019 [58]	NA	cross- sectional	gastric biopsies	agar dilution method	18	9	50	NT	*cag*A
	Abdelsami et al. 2020 [59]	2019–2020	NA	gastric biopsies	E-test, RFLP-PCR	50	27	54	A2142G (5/50), A2143G (21/50)	NT
	Soltan et al. 2018 [60]	2016–2017	cross-sectional	gastric biopsies	RFLP-PCR	71	47	66.2	A2142G (39/71), A2143G (12/71)	NT
	El-Gazzar et al. 2020 [61]	2019–2020	prospective observational study	gastric biopsies	disc diffusion method	28	9	32.1	NT	NT
	El Sayed Zaki et al. 2016 [62]	2015	NA	gastric biopsies	disc diffusion method	69	49	71	NT	NT
	Ghaith et al. 2016 [63]	2013	cross-sectional study	gastric biopsies	RFLP-PCR	70	39	55.7	A2142G (39/70)	NT

Table 1 (continued)

Country	Authors and Reference	Strains isolation period	Study design	Sample	Method used to assess clarithromycin resistance	Number of *H. pylori* strains	CRHp	%	mutations in the 23S rRNA	VG
Egypt	Fathi et al. 2013 [64]	2011–2012	cross-sectional study	gastric biopsies	disc diffusion method, E-test	16	16	100	NT	*ure*C,
	Elzaher et al. 2022 [65]	2018–2021	prospective study	Gastric biopsies	real-time PCR	20	5	25	NA	NA
	Metwally et al. 2022 [66]	2018–2020	cross-sectional study	Gastric biopsies	disc diffusion method	20	8	40	NT	NT
	Diab et al. 2018 [67]	2015–2017	NA	gastric biopsies	RT-PCR	60	4	6.7	A2143G (4/60)	NT
	Mahmoud et al. 2018 [68]	2016–2017	NA	gastric biopsies	disc diffusion method	70	48	68.6	NT	*cag*A, *ice*A1, *vac*A s1, *vac* A s2, *vac*A m
	Awad et al. 2020 [69]	NA	cross-sectional study	gastric biopsies	NA	30	15	50	NT	NT
	Ghazy et al. 2022 [70]	NA	NA	gastric biopsies	RT-PCR	42	27	64.3	23S mutant	*cag*A
Gambia	Secka et al. 2013 [71]	NA	NA	gastric biopsies	agar dilution	64	0	0	NT	NT
Kenya	Kimang'a et al. 2010 [72]	NA	NA	gastric biopsies	E-test	65	0	0	NT	NT
	Lwai-Lume et al. 2005 [73]	2003–2004	cross-sectional descriptive study	gastric biopsies	NA	166	11	6.6	NT	NT
	Kabuthi et al. 2021 [74]	2018–2019	cross-sectional descriptive study	gastric biopsies	E-test	68	9	13.2	NT	NT
Morocco	Bouihat et al. 2016 [75]	2015–2016	prospective	gastric biopsies	E-test, real time scorpion PCR	177	45	25.4	A2142G (29/51; 56.9%); A2143G (20/51; 39.2%) A2142C (4/51; 7.8%)	NT
	Essaidi et al. 2022 [76]	2017–2020	NA	gastric biopsies	PCR - RFLP	96	14	14.6	A2143G	NT
Mozambique	Ismail et al. 2023 [77]	2017–2020	cross-sectional descriptive	gastric biopsies	Standard PCR and sequencing	96	10	10.4	A2142G (2/10), A2143G (8/10)	NT
Mauritania	Khiddi et al. 2020 [78]	2018	NA	gastric biopsies	Real time PCR	76	4	5.3	A2143G (4/4)	*cag*A
Nigeria	Oyedeji et al. 2009 [79]	NA	NA	gastric biopsies	disc diffusion method, E-test, PCR-RFLP, sequencing	186	0	0	NF	NT
Nigeria	Aboderin et al. 2007 [80]	2002–2003 2005–2006	prospective	gastric biopsies	disc diffusion assay	32	32	100	NT	NT
	Bello et al. 2019 [81]	2011–2013	cross-sectional	gastric biopsies	disc diffusion method	109	0	0	NT	NT
	Harrison et al. 2017 [82]	2010–2013	cross-sectional	gastric biopsies	E-test, PCR, sequencing	111	16	14.4	A2143G (1/16), A2144G (2/16), A2143C (2/16), C2196T	*cag*A, *vac*A *s1/m*1
	Ani et al. 1999 [83]	1997–1998	NA	tissue biopsies	E-test	55	7	12.7	NA	NT
	Adeniyi et al. 2012 [84]	NA	NA	gastric biopsies	disc diffusion method	43	3	7	NT	NT
	Palamides et al. 2020* [85]	2015–2018	NA	gastric biopsies	E-test	88	23	26.1	NT	*cag*A, *vac*A

Table 1 (continued)

Country	Authors and Reference	Strains isolation period	Study design	Sample	Method used to assess clarithromycin resistance	Number of *H. pylori* strains	CRHp	%	mutations in the 23S rRNA	VG
Reunion Island	Zemali et al. 2016 [86]	2014	NA	gastric biopsies	real-time PCR	73	9	12.3	A2142C (1/9); A2142G/A2143G (8/9)	NT
Senegal	Seck et al. 2013 [87]	2007–2009	NA	gastric biopsies	E-test, scorpion PCR	108	1	0.9	A2143G (1/1)	NT
South Africa	Palamides et al. 2020* [85]	2015–2018	NA	gastric biopsies	E-test	132	22	16.7	NT	*cag*A, *vac*A
	Tanih et al. 2010 [88]	NA	NA	gastric biopsies	disc diffusion method, agar dilution method	200	40	20	NA	NT
	Tanih and Ndip, 2013 [89]	NA	NA	gastric biopsies	disc diffusion method, GenoType HelicoDR kit	78	12	15.4	A2147G (12/17; 70.6%); A2146C (1/17; 5.9%)	NT
	Tanih et al. 2011 [90]	NA	NA	gastric biopsies	disc diffusion method, end-point PCR, sequencing	200	40	20	A2142G (3/3), A2143G (1/3)	NT
Sudan	Albasha et al. 2021 [91]	2018–2019	NA	gastric biopsies	PCR and DNA sequencing	25	9	36	A2142G (1/9), A2143G (5/9), T2182C (4/9), C2195T (3/9)	NT
Tanzania	Jaka et al. 2019 [92]	2014–2016	cross-sectional study	gastric biopsies	real-time PCR	188	54	28.7	A2143G (32/54), A2142G (22/54), A2142C (1/54), A2143C (1/54)	NT
Tunisia	Ben Mansour et al. 2010 [93]	2005–2007	prospective multicentre study	gastric biopsies	E-test, scorpion real-time PCR	273	42	14.6	A2143G (37/42; 88.1%); A2142G (5/42; 11.9%)	NT
	Ben Mansour et al. 2016 [94]	2009	prospective study	gastric biopsies	E-test	21	3	14.3	NT	NT
	Chtourou et al. 2022 [95]	2017–2020	cross-sectional study	gastric biopsies	Allplex *H. pylori*, ClariR PCR Assay	95	30	31.6	A2143G (90.5% ; 86/95), A2142G (11,6%; 11/95)	NT
Uganda	Angol et al. 2017 [96]	2012–2013	cross-sectional study	stool	GenoType HelicoDR PCR	21	6	28.6	NT	NT
Zambia	Kebotsamang et al. 2024 [97]	NA	case-control study	gastric biopsies	Bosphore *Helicobacter pylori* Genotyping Kit v1 (real-time PCR)	174	48	27.6	A2143G (38/48), A2142G (29/48)	NT

cagA, cytotoxin associated gene A; *vacA*, vacuting cytotoxin A; NA, not available; NT, not tested; *, study including strains from many countries; NF, not found; RFLP, Restriction Fragment Length Polymorphism; CRHp, clarithromycin-resistant *H. pylori;* VG, virulence gene

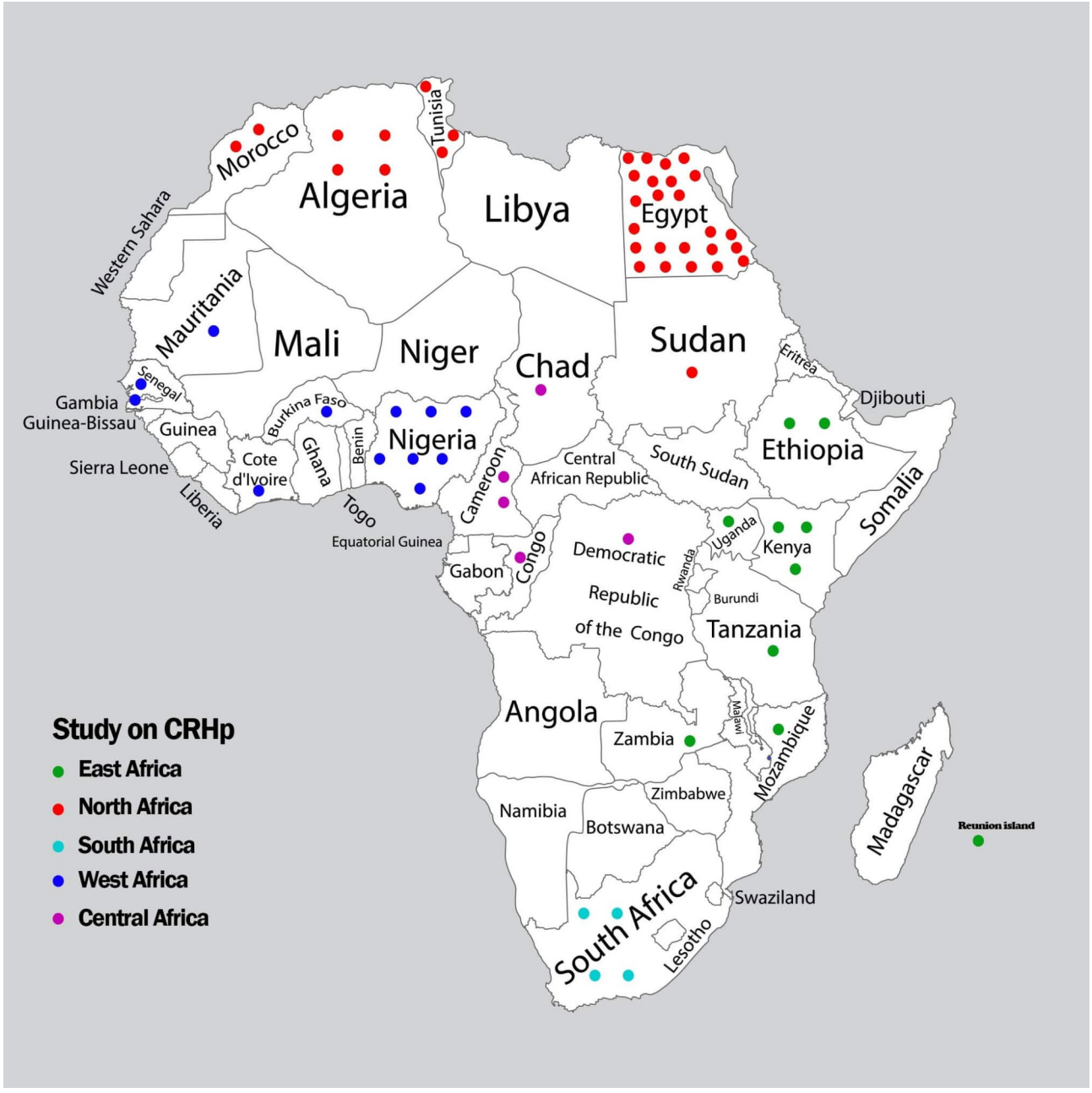

Fig. 2 Map of Africa showing the number of study on CRHp in Africa

Table 2 Distribution of A2143G and A2142G mutations in African regions

Africa and regions	Mutation within the 23S rRNA		*p*-value
	A2143G *n/N* (%)	A2142G *n/N* (%)	
Northern Africa	342/996 (34)	275/878 (31)	0.17
Western Africa	18/33 (55)	0	-
Eastern Africa	86/121 (71)	61/121 (50)	0.001*
Central Africa	18/25 (72)	5/25 (20)	0.0002*
Southern Africa	1/3 (33)	3/3 (100)	0.08
Africa	465/1178 (40)	344/1027 (34)	0.003*

*: significant difference ($p < 0.05$)

were the most reported, followed by *ice*A1 (1/11; 9%), *ure*C (1/11; 9%) and *bab*A2 (1/11; 9%).

Discussion

In the reviewed studies, the agar dilution method, considered the gold standard for antimicrobial susceptibility testing (AST) for *H. pylori*, was used in only 6 of the 65 studies included. In contrast, the Kirby-Bauer disc diffusion method, which is regarded as an unreliable AST method for detecting CRHp, remains the most commonly used method on the African continent (in 22

studies out of 65). This underscores the urgent need for implementing standardized microbiological methods for resistance detection to enhance the accuracy and validity of surveillance data.

The overall pooled prevalence of CRHp reported in this study was 27% (95% CI: 22, 33), and was very similar to the global pooled prevalence of CRHp from 248 articles in 2023 [27.53% (95% CI: 25.41, 29.69)] [20]. The pooled prevalence of CRHp observed in Africa in this systematic review and meta-analysis was slightly lower than that reported for the Asian continent (29.57% and 35.97% in 2023) [85, 86]. However, the CRHp prevalence in Africa was slightly higher than that (22%) reported in the Asia-Pacific region [21], and was the same as that (27%) reported for the Southern Asian region in 2023 [22]. Concerning Europe, the African CRHp pooled prevalence was quite similar to those reported for the European continent, 25% in 2021 [23] and 26.25% in 2023 [20]. The pooled prevalence of CRHp reported in this study was higher than that (23.86%) observed in the American continent in 2023 [20], and was significantly higher than the 10.3% [24] observed for Oceania in 2020 and the 7.02% reported for North America in 2023 [25].

In this study, we reported a steady trend ($R^2 = 0.0001$; $p = 0.92$) for the prevalence of CRHp in Africa for strains isolated from 1997 to 2022, with a slightly negative slope coefficient of -0.05x. This is contrary to most of the trends observed worldwide. An increase from 24.28% in 2010–2017 to 32.14% in 2018–2021 was reported in a global study that included 248 articles in 2023 [20]. In addition, increases in CRHp prevalence were also observed in the South-East Asian Region (13% in 2006–2008 to 21% in 2012–2016) [9], South Asia (21% in 2003–2012 to 30% in 2013–2022) [22], Oceania (6.4% in 1997–2000 to 16.1% in 2000–2013) [24]. Similar to this study, steady trends of CRHp have been reported for Latin America (11% in 1996–2000, 12% in 2001–2005, 14% in 2006–2011, $p = 0.47$) [26]. Furthermore, a decreasing trend in CRHp prevalence was noted for the European continent (25% in 2013–2016 to 20% (2017–2020), $p = 0.002$) [23].

This systematic review and meta-analysis reported ten types of *H. pylori* 23S rRNA mutations conferring clarithromycin resistance in Africa. All the reported 23S rRNA mutations have been already observed worldwide [27–29]. Our results are similar to those reported in Iran: A2143G (46.6%), A2142G (37.2%), and A2142C (5.5%) [30]. However, other 23S rRNA mutations conferring clarithromycin resistance in *H. pylori*, such as A2146G, C2772T, C2759T, G2212A, and A2144G, reported in Brazil [31], Mexico [27], Portugal [32], South Korea [33], and Iraq [34] have not been observed in Africa.

Conclusion

The data reported in this systematic review and meta-analysis showed that the pooled prevalence of CRHp in Africa was very similar to the overall pooled prevalence observed globally. In addition, more representative studies on *H. pylori* are needed in African countries. This can help to appreciate the real extent of antibiotic resistance in *H. pylori* strains. While waiting for further representative studies of the African population to be carried out, the treatment of *H. pylori* infections must be based on the guidelines of the AHMSG first Lagos consensus, for which triple therapy was suggested as this could be tenable.

Supplementary Information

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Supplementary Material 1

Supplementary Material 2

Author contributions

K.M.D. conceptualized and designed the study, helped in data acquisition and analysis, and drafted the manuscript. T.B. helped in data acquisition and analysis. S.S. helped in data analysis. L.L., B.S.B., A.S., and S.D. substantively revised the manuscript. E.E.I., F.P.S. and M.C. provided writing assistance and substantively revised the manuscript. A.E.K. supervised the study and substantively revised the manuscript. S.I.S. supervised the study, and substantively revised the manuscript.

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Data availability

Data is provided within the manuscript or supplementary information files.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

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Competing interests

The authors declare no competing interests.

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