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Prevalence of Colistin Resistance: A Worldwide Meta-Analysis

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ABSTRACT

Background: Colistin is an ancient class of antibiotic which works by rupturing the bacterial cell membrane. Bacteria have developed resistance against colistin antibiotic by various Lipopolysaccharide modification mechanisms. Colistin has long been used as treatment option but its resistance is emerging in developing countries. **Methodology:** A systematic meta-analysis was performed to describe the prevalence of colistin resistance in different regions of the World. Web based search was conducted on platforms like Google scholar, PubMed, Scopus, Web of Science. Data was extracted from 2009-2019. **Results:** A total of 286 articles were identified from different electronic databases from which only 143 articles were selected based on our inclusion criteria. The overall pooled proportion of colistin resistance in different regions of the World was 0.21 (CI 95%: 0.20-0.21). The overall significant heterogeneity was ($I^2=99.54\%$, $p < 0.001$), significant ES=0 ($z=62.53$, $p < 0.001$). Bacterial isolates like *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Escherichia coli* showed highest rates of colistin resistance. **Conclusion:** The performed meta-analysis showed the rates of colistin resistance worldwide. Asia showed high rates of Colsitin resistance. *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa* were the most prevalent isolates. So, an appropriate and regular surveillance program is required and implementations of effective strategies is also needed that address colistin resistance and helps in controlling the spreading of colistin resistance.

Keywords: Colistin, Prevalence, *Metaprop*, Meta-Analysis, Lipopolysaccharide, Heterogeneity, Proportion.

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INTRODUCTION

Antibiotic resistance is the ability of bacteria to protect them from antibiotic attack (1). The last resort of antibiotic to treat infections caused by *Enterobacteriaceae* (MDR) due to resistant caused by carbapenemase is colistin (2). Colistin belongs to polymyxin class of drugs and is a cyclic polycationic heptapeptide (3). It performs its action by attacking on the lipopolysaccharide membrane of gram-negative bacteria. Positively charged residues of colistin are attracted towards lipid portion of lipopolysaccharide due to presence of negatively charged phosphate group (4, 5). Lipid A binds with the calcium and magnesium divalent cations under

normal conditions. This results in the formation and bridging of lipopolysaccharide membrane of gram negative bacteria. Colistin binding affinity with lipid A negative charged group is three times higher than divalent cations of calcium and magnesium therefore colistin compete with these ions and binds to the lipid A. This result in displacement of divalent cations from lipid A. Colistin then reaches in the periplasmic space which termed as self-promoted uptake mechanism (4-6).

Resistance to colistin is rare worldwide. Isolates of colistin resistance are *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii* and *Pseudomonas aeruginosa* (7).

Colistin resistance is caused by several mechanisms. The main cause of colistin resistance is lipopolysaccharides (LPS) modification. There are diverse routes of LPS modification like modification in the outer membrane i.e. porins causes the reduction of LPS negative charge, efflux pump overexpression, capsule polysaccharide overexpression (8), and enzymatic resistance. *Bacillus polymyxa* strains produce colistinase seems to produce resistance to colistin (9). Lipopolysaccharide remodeling in bacterial outer membrane is caused by variations in two regulatory systems, *PhoPQ* and *PmrAB* (10). These genes and operons are responsible for causing mutations in lipopolysaccharides. On the other hand presence of plasmid-mediated genes (*mcr* genes) in different isolates directly produces colistin resistance without any other mechanism of resistance (5). Isolates of Enterobacteriaceae carrying genes of carbapenemase like *NDM* (*NDM1*, *NDM5*, *NDM9*), *VIM1*, *OXA48* and *KPC2* also contains *mcr* gene (11). Sometimes colistin resistance is caused by the overexpression of *MexAB-OprM* and *KpnEF* efflux pump (12). Spread of colistin resistance in different regions of the world is a result of increase usage of this antibiotic to treat infections caused by bacteria like *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Escherichia coli* and *Klebsiella pneumoniae*. Polymyxins has greater rate of resistance in South-East Asia including Korea, Singapore and Mediterranean Sea. In these areas colistin resistance is steadily rising. To stop the growth and spread of colistin resistance, there is an urgent need for efficient infection control methods and prevention. Some nations (such as Japan and South Africa) do not acquire colistin, it is available in its parenteral formulation (as Colistin Methanesulphonate) in few regions of the world like Europe and Australia, while in other regions (such as the Brazil, United States, Singapore, and Malaysia), clinicians may choose between colistin and the parenteral formulation of *Bacillus polymyxin* (13). The purpose of this study is to aware people about distribution and prevalence of colistin resistance worldwide and to check comparative and year wise prevalence in different continents.

METHODOLOGY

Research Design

This meta-analysis research includes different studies reported from different regions of the world. It is a web-based search, which used key words like "colistin resistance worldwide", "colistin resistance genes", "colistin resistance bacterial isolates".

Study Duration

This search was conducted on electronic databases

platforms like Pub-Med, Google scholar, web of science and Scopus and included 143 articles from Jan 2009-Dec 2019. Articles having English language were included in this study. We also screened references cited in 143 articles to check other relevant publications.

Selection Criteria

Three steps were used to select the articles. In first step, abstracts and titles of all the articles were checked excluding the irrelevant articles. In second step, selected articles were again checked with full details. In third step, selected articles were evaluated for meta-analysis by using STATA version 14.1 software.

Inclusion Criteria

Articles were chosen using the following criteria: studies that show prevalence of colistin resistance worldwide, bacterial strains from human samples, relevant national or international articles, and studies showing phenotypic detection methods of colistin resistance and studies that uses molecular detection techniques for colistin resistance genes variants (Figure 1).

Exclusion Criteria

Articles were excluded using following criteria: case reports, review articles, letters, posters, duplicate articles were removed, articles with incomplete information regarding phenotypic detection methods were removed, studies on antibiotics resistance other than colistin were removed, studies on different strains other than humans were removed (Figure 1).

Data Extraction

Data extracted from the selected articles included: country name, publication year, study year, author name, sample size, no. of resistance isolates, phenotypic detection methods including Minimum Inhibitory Concentration (MIC), Disk Diffusion Test, Broth Micro dilution, Epsilometric Test (E-test), Agar Dilution, VITEK and molecular detection techniques for colistin resistance gene variants (Table 1). Extraction and analysis of data were performed twice to remove any conflict (14).

Data Analysis

Metaprop command in STATA version 14.1 was used for statistical analysis to pool the published data for colistin resistance world-wide with computational accurate binomial 95% confidence intervals (CI). I^2 statistics was used to calculate statistical heterogeneity. Using p-values, the results of the meta-analysis were transformed into specified statistical tests. Using a random effects model, the pooled prevalence was estimated. In order to statistically assess publication bias, Begg tests and a funnel plot were used.

Table 1: Distribution of articles regarding Colistin Resistance.

Sr. No	Publication Year	Study Year	Authors	Sample Size	Colistin Resistant Isolates	Phenotypic Detection Test					Molecular Detection Test		
						MIC	Disk Diffusion	Broth Micro dilution	E test	Agar Dilution	VITEK	Genes	Most Prevalent genes
Asia													
1	2009	2006-2007	Suh et al (15)	221	15	Yes	Yes	No	No	No	No	None	None
2	2011	2010	Gill et al (16)	180	69	No	Yes	No	No	No	No	unknown	Unknown
3	2011	2006-2007	Lee et al (17)	215	16	Yes	No	Yes	No	No	Yes	Unknown	Unknown
4	2011	2006-2007	Park et al (7)	33	7	Yes	No	No	No	No	No	pmrA, pmrB, pmrC	pmrB, pmrC
5	2012	2008-2011	Hamzeh et al (18)	260	241	No	Yes	No	No	No	No	unknown	Unknown
6	2013	2012	Bahador et al (19)	94	5	No	Yes	No	No	No	No	blaOXA-51	Unknown
7	2013	unknown	Choi et al (20)	113	51	No	Yes	No	No	No	No	pmrAB, phoPQ, parRS, lpxACD	PmrAB, PhoPQ and ParRS
8	2013	2009	Huangki et al (21)	253	184	No	No	No	No	Yes	No	none	None
9	2013	2008-2011	Lee et al (22)	213	75	No	No	No	Yes	Yes	Yes	Unknown	Unknown
10	2014	unknown	Naparstek et al (23)	46	3	No	Yes	No	No	No	No	aac(3)-II, blaKPC	BlaKPC
11	2014	unknown	Lee et al (24)	4	2	No	Yes	No	No	No	No	pvdQ, pelB, pilY1, cysQ, wbpZ	Unknown
12	2014	Unknown	Kim et al (25)	5	4	No	Yes	Yes	No	No	No	pmrA, pmrB, pmrD, phoP, phoQ	Unknown
13	2014	2008-2011	GÜVEN et al (26)	252	4	No	Yes	No	No	No	No	Unknown	Unknown
14	2015	2013-2015	Mansoor et al (27)	634	231	No	Yes	No	No	No	No	none	None
15	2015	None	Choi et al (28)	6	3	No	No	Yes	No	No	No	pmrB, pbgp,	None
16	2015	2014	Nhung et al (29)	24	14	Yes	No	No	Yes	No	Yes	none	None
17	2015	None	Olaitan et al (30)	5	2	No	Yes	No	No	No	No	NDM-1	None
18	2016	2015-2016	Qadeer et al (31)	568	265	No	Yes	No	No	No	No	Unknown	Unknown
19	2016	2014	Bashir et al (32)	885	3	No	Yes	No	No	No	No	Unknown	Unknown

														<i>pmrB,</i> <i>lpxC,</i> <i>lpxA,</i> <i>lpxD</i>	
20	2016	unknown	Mu et al (33)	4	1	No	Yes	No	No	No	No	No	No	<i>mexB,</i> <i>mexY</i>	Unknown
21	2016	2014	Goli et al (34)	100	68	Yes	Yes	No	No	No	No	No	No	<i>mcr-1</i>	Unknown
22	2016	None	Sonnevend et al (35)	75	8	No	No	Yes	No	No	No	No	No	<i>mcr-1</i>	<i>mcr-1</i>
23	2016	2010-2013	Crawford et al (36)	10	7	No	No	Yes	No	No	No	Yes	NDM-1	None	None
24	2016	None	Yilmaz et al (37)	56	29	No	No	Yes	No	No	No	No	No	none	None
25	2016	2014	Bashie et al (32)	885	3	Yes	Yes	No	No	No	No	No	No	none	None
26	2016	None	Cheng et al (38)	26	17	No	No	No	No	No	Yes	No	No	<i>crrB</i>	<i>PmrC</i>
27	2016	2014-2015	Ni et al (39)	108	31	Yes	No	No	No	No	No	No	No	<i>mcr-1,</i> NDM-1	None
28	2016	2016	Zhaong et al (40)	151	17	No	No	No	No	No	Yes	No	No	<i>blaNDM-</i> 1	<i>mcr-1</i>
29	2016	2008-2009	Sato et al (41)	514	4	No	No	No	No	No	No	No	No	<i>mcr-</i> 1, <i>mcr-2</i>	<i>mcr-1</i>
30	2016	2015	Ye et al (42)	75	3	Yes	No	No	No	No	No	No	No	<i>mcr-1</i>	<i>blaNDM-</i>
31	2016	2010-2013	Crawford et al (43)	10	7	No	No	No	No	No	No	Yes	NDM-1, OXA-48	1, <i>blaOXA-</i> 48	Unknown
32	2016	2012-2013	Kumar et al (44)	1590	122	No	Yes	No	No	No	No	No	No	<i>mrgS</i> <i>e mgrB,</i> <i>phoP/pho</i> Q, <i>pmrA,</i>	Unknown
33	2017	2015-2016	Qamar et al (45)	251	71	No	Yes	No	No	No	No	No	No	<i>pmrB,</i> <i>pmrC, and</i> <i>crrABC,</i> <i>mcr-1</i>	Unknown
34	2017	2014-2015	Aydin et al (46)	1556	109	No	Yes	No	No	No	No	No	No	unknown <i>pmrA,</i> <i>pmrB,</i> <i>pmrC,</i> <i>pmrD,</i>	Unknown
35	2017	2015	Thong et al (47)	31	30	No	Yes	No	No	No	No	No	No	<i>phoP, 83</i> <i>phoQ,</i> <i>mgrB,</i> <i>crrA and</i> <i>crrB</i> <i>blaNDM-</i> 1, <i>blaIMP,</i>	Unknown
36	2017	2014-2016	Cizmeci et al (48)	76	19	No	Yes	No	No	No	No	No	No	<i>blaVIM-</i> like, <i>blaGES-</i> like,	Unknown

37	2017	unknown	Hua et al (49)	2	1	No	No	No	No	No	No	A1S_1983 , hepA, A1S_3026	IpxA, pmrB	
38	2017	2013-2014	Soudeihha et al (50)	100	19	No	Yes	No	Yes	No	No	blaOXA- 23-like, blaOXA- 24-like, blaOXA- 48, blaOXA- 51-like, blaOXA- 58-like, blaGES, blaKPC mcr, mgrB, pmrAB, phoPQ mcr-1, mcr-2, mcr-3, mcr-4,	blaOXA- 23-like, blaOXA- 24-like	
39	2017	2014-2015	Luo et al (51)	1270	40	Yes	No	No	No	No	No	mcr-1		
40	2017	2015-2017	Haeili et al (52)	23	20	No	Yes	No	No	No	No	pmrA, pmrB, phoP, phoQ, mgrB	mgrB	
41	2017	2016	Hu et al (53)	234	5	No	Yes	No	No	No	No	mcr-1,	Unknown	

42	2017	None	Tada et al (54)	18	4	No	No	No	No	No	No	<i>mcr-1</i>	<i>mcr-1</i>	
43	2017	2010-2016	Juhaz et al (55)	504	3	No	No	No	No	No	No	<i>mcr-1</i> , <i>blaSHV-14</i>	None	
44	2017	2017	Tada et al (56)	4	1	No	No	No	No	No	No	<i>blaTEM-1, ampC and aadA1</i>	<i>mcr-1</i>	
45	2017	Unknown	Chew et al (57)	76	48	No	No	Yes	Yes	No	Yes	<i>mcr-1</i> , <i>phoP</i> ,	<i>mcr-1</i>	
46	2017	None	Chung et al (58)	4	2	Yes	No	No	Yes	No	No	<i>pmrA, parR and cprR</i> , <i>mgrB</i> ,	<i>arnB</i>	
47	2017	None	Wang et al (59)	168	33	Yes	No	No	No	No	Yes	<i>pmrB, and phoQ, mcr-1</i>	<i>mcr-1</i>	
48	2017	2012-2013	MiWi et al (60)	77	9	Yes	No	No	No	No	No	<i>blaIMP-6, blaVIM-2</i> , <i>mcr-1</i> ,	<i>blaIMP-6</i>	
49	2018	2016	Singh et al (61)	200	21	No	Yes	No	Yes	No	No	<i>blaNDM-1</i>	<i>mcr-1</i>	
50	2018	2015-2016	Luxmi et al (62)	748	177	No	Yes	No	No	No	No	unknown <i>mcr-1</i> , TEM-1B, CTX-M-1,	Unknown	
51	2018	unknown	Forde et al (63)	267	1	No	Yes	No	No	No	No	<i>aac(3)-Iia, gyrA, drfA</i>	<i>mcr-1</i>	
52	2018	2014-2017	Eiamphungporn et al (64)	317	226	No	Yes	No	No	No	No	<i>mcr-1</i> , <i>pmrB</i> , <i>lpdD</i> ,	Unknown	
53	2018	2013-2016	Farshadzadeh et al (65)	8	4	No	Yes	No	No	No	No	<i>pmrA, pmrC, lpxA, lpxC</i>	<i>pmrB, ipxD</i>	
54	2018	2015-2016	Lu et al (66)	112	5	No	Yes	No	No	No	Yes	<i>mcr-1</i> , <i>pmrB</i>		

														<i>phoQ,</i> <i>pmrB,</i> <i>blaSHV-1,</i> <i>fosA,</i> <i>oqxA,</i> <i>oqxB,</i> <i>blaSHV-3</i> <i>k86,</i> <i>blaSHV-1</i> <i>1, aph(4)-</i> <i>Ia, aac(3)-</i> <i>IVa,</i> <i>aph(3')-Ia,</i> <i>aadA1,</i> <i>aadA2,</i> <i>blaCTX-</i> <i>M-14,</i> <i>cmlA1,</i> <i>dfrA1,</i> <i>dfrA12,,</i> <i>qnrS1,</i> <i>sul1, sul2,</i> <i>sul3,</i> <i>tet(A)</i>
55	2018	2016	Guducuoglu et al (67)	13	9	No	Yes	No	No	No	No	NDM-1, OXA-48	Unknown	
56	2018	2016	Haeili et al (68)	5	3	Yes	Yes	No	No	No	No	<i>pmrA,</i> <i>pmrB,</i> <i>lpxA,</i> <i>lpxC, and</i> <i>lpxD</i>	Unknown	
57	2018	2015-2016	Cao et al (69)	1112	6	No	Yes	No	No	No	No	<i>mcr-1,</i> <i>blaTEM-</i> <i>1B,</i> <i>blaCTX-</i> <i>M14,</i> <i>blaCTX-</i> <i>M132,</i> <i>blaCTX-</i> <i>M55,</i> <i>blaCTX-</i> <i>M123,</i> <i>fosA3,</i> <i>fosA,</i> <i>aph(4)-Ia,</i>	<i>mcr-1</i>	

58	2018	2014-2016	Aghapour et al (70)	900	30	No	Yes	No	No	No	No	<i>sul2,</i> <i>k2oqxA,</i> <i>oqxB,</i> <i>aadA2</i>	None
59	2018	2016-2017	Yonchanghu et al (71)	6497	49	No	No	No	No	No	No	<i>mcr-1,crrB</i>	<i>mcr-3</i>
60	2018	2015-2016	Moubareck et al (72)	13025	89	No	Yes	No	No	No	No	<i>blaOXA-</i> 48-like, <i>blaNDM</i> <i>armaA,</i> <i>rmt, aadA,</i> <i>aac(3)-,</i> <i>aph(3")-</i> <i>Ib, aph(6)-</i> <i>Id,</i> <i>aac(6')-Ib,</i> <i>aac(6')-Ib-</i> <i>cr,</i> <i>blaCTX-</i> M-15, <i>blaSHV-,</i> <i>blaOXA-</i> 1, <i>blaOXA-</i>	<i>blaOXA-48-like</i>
61	2018	2010-2013	Lomonaco et al (73)	10	7	No	Yes	No	No	No	Yes	<i>10,</i> <i>blaOXA-</i> 48, <i>blaNDM-</i> 1, <i>blaTEM-</i> 1, <i>blaCMY-,</i> <i>cmlA5,</i> <i>catA1,</i> <i>qnr, ble,</i> <i>mph, mrx,</i> <i>arr, sul,</i> <i>tet(A),</i> <i>dfrA,</i> <i>mgrB,</i> <i>pmrB</i> <i>mcr-1,</i> <i>blaNDM-</i>	<i>blaCTX-</i> M-15
62	2018	2014-2016	Li et al (74)	7249	7	No	Yes	No	No	No	Yes	<i>5,</i> <i>blaKPC,</i> <i>blaCTX-</i>	<i>blaKPC,</i> <i>blaNDM</i>

													M-65 and <i>blaTEM-</i> 1B, <i>aph</i> (4)-Ia, <i>strA</i> , <i>strB</i> , <i>aadA5</i> , <i>aac</i> (3)-Iid, <i>oqxA</i> , <i>oqxB</i> , <i>fosA</i> , <i>mph</i> (A), <i>sull</i> , <i>sul2</i> , <i>tet</i> (A), <i>dfr</i> A17
63	2018	None	Okdah et al (75)	57	55	Yes	No	No	Yes	No	No	mcr-1	mcr-1
64	2018	2007-2016	Mustapha et al (76)	42	18	No	No	No	No	No	No	pmrA	pmrAB
65	2019	2017-2018	Hameed et al (77)	146	16	No	Yes	No	No	No	No	mcr-1	mcr-1
66	2019	2011-2017	Menekse et al (78)	210	60	Yes	Yes	No	No	No	No	NDM-1	OXA-48
67	2019	2017-2018	Messeron et al (79)	200	38	No	Yes	No	No	No	No	mcr-1	mcr-1
68	2019	2017	Cheong et al (80)	252	13	Yes	Yes	Yes	Yes	No	Yes	pmrA, pmrB, phoP, phoQ	phoQ
Europe													
69	2011	unknown	Wareham et al (81)	6	5	No	No	No	Yes	No	No	Unknown	Unknown
70	2011	unknown	Vila-farres et al (82)	15	13	No	No	Yes	No	No	No	none	None
71	2012	2010-2012	Capone et al (83)	97	89	No	Yes	Yes	No	No	No	blaKPC- 3,VIM-1, CTX-M 1	blaKPC-3
72	2013	2009-2012	Huttner et al (84)	54	24	No	Yes	No	No	No	No	unknown <i>ompK36</i> porin,	Unknown
73	2013	2008-2009	Camacho et al (85)	26	1	No	Yes	No	No	No	No	<i>mgrB</i> , <i>sufB</i> , <islt< i=""> gene, blaDHA-1</islt<>	blaDHA-1
74	2013	None	Cannatelli et al (86)	2	1	Yes	No	No	Yes	No	No	<i>mgrB</i>	None
75	2013	2012	Tamayo et al (87)	66	16	Yes	No	No	No	No	No	<i>ipxA</i> , <i>ipxD</i> blaKPC, blaNDM,	<i>ipxA</i>
76	2014	2013-2014	Monaco et al (88)	197	191	No	Yes	No	No	No	No	blaVIM, and blaOXA-48	blaKPC
77	2014	2011-2012	Gaibani et al (89)	17	8	No	Yes	No	Yes	No	No	KPC3, <i>mgrB</i>	KPC3
78	2014	2008-2011	Agodi et al (90)	26	15	Yes	No	No	No	No	Yes	bla-OXA-	None

79	2014	2011	Cannateli et al (91)	2	1	Yes	No	No	No	No	No	51	<i>pmrA, pmrB, pmrK</i>	None
80	2014	None	Olivgeris et al (92)	254	28	No	Yes	No	Yes	No	Yes		None	None
81	2015	2014-2015	Hasman et al (93)	534	417	No	Yes	No	No	No	No	1B, <i>catA1, dfrA17, floR, fosA, mph(A), rmtB, strA, strB, sul1, sul2, tet(A)</i>	<i>mcr-1 gene</i>	
82	2015	2013	Olaitan et al (30)	267	2	No	No	No	No	No	No	M-2, mutant <i>pmrB gene</i>	<i>pmrB gene</i>	
83	2015	Unknown	Wand et al (94)	12	11	No	Yes	No	No	No	No	<i>lpxA, lpxC, pxD, pmrB, lpxA, lpxC, msbA, pmrA,</i>	<i>pmrB</i>	
84	2015	Unknown	Formosa et al (95)	2	1	No	Yes	No	No	No	No	<i>pmrB, pmrD, phoP, phoQ, arnT, mgrB</i>	<i>mgrB</i>	
85	2015	unknown	Farre's et al (96)	256	128	No	Yes	No	No	No	No	<i>lpxD</i>	<i>lpxD</i>	
86	2015	2009-2013	Dafopoulou et al (97)	61	58	No	No	No	Yes	No	Yes	None	None	
87	2015	2012-2014	Parisi et al (98)	399	97	Yes	No	No	No	No	Yes	NDM, OXA-48, KPC	CPKP	
88	2015	2012-2014	Oikonomou et al (99)	1228	86	Yes	No	No	No	No	Yes	<i>ipxA, ipxC</i>	<i>pmrA and pmrC</i>	
89	2016	2012-2015	Godbole et al (100)	24480	15	No	Yes	No	No	No	No	<i>mcr-1, blaTEM-1,</i>	<i>mcr-1</i>	

90	2016	unknown	Gue'rín et al (101)	124	71	No	Yes	No	No	No	No	<i>blaCTX-M-27,</i> <i>blaCTX-M-14,</i> <i>blaCMY-2, qnrS1</i> <i>phoP, phoQ</i> <i>mcr-1, qnrA, qnrB,</i> <i>qnrS, CTX-M-2a, CTX-M-9a</i> <i>lpxA, lpxC,</i>	Unknown	
91	2016	2010-2012	Wintersdorff et al (102)	122	6	No	No	No	No	No	No	<i>lpxD, ponA, mrcA</i> <i>mgrB, OXA-48, NDM, KPC, CTX-M-15, VIM, IMP</i> <i>pmrA, phoP, phoQ, pmrD, pmrK, pagP, smvR, and smvA</i>	<i>mcr-1</i>	
92	2016	Unknown	Boll et al (103)	15	4	No	No	No	No	No	No	<i>lpxD, ponA, mrcA</i> <i>mgrB, OXA-48, NDM, KPC, CTX-M-15, VIM, IMP</i> <i>pmrA, phoP, phoQ, pmrD, pmrK, pagP, smvR, and smvA</i>	Unknown	
93	2016	2014	Jayol et al (104)	972	42	No	Yes	No	No	No	No	<i>bla OXA-48</i>		
94	2016	None	Lopez-roja et al (105)	11	8	No	No	No	No	No	No	<i>pmrA, phoP, phoQ, pmrD, pmrK, pagP, smvR, and smvA</i>	None	
95	2016	None	Wand et al (106)	6	5	Yes	No	No	No	No	No	<i>pmrK, pmrD</i>		
96	2016	Unknown	Mavroidi et al (107)	135	19	No	Yes	No	No	No	No	<i>mgrB, blaKPC</i>	<i>bla-KPC</i>	
97	2017	2015	Vourli et al (108)	117	108	No	Yes	No	No	No	No	<i>blaOXA-51-like</i>	Unknown	
98	2017	None	Coppi et al (109)	74	61	No	No	Yes	No	No	No	<i>mcr-1, mcr-2</i>	<i>mcr-1</i>	
99	2017	2015	Dona et al (110)	36	3	No	No	No	No	No	No	<i>mcr-1, mcr-2</i>	<i>mcr-1</i>	
100	2017	1996-2016	Jayol et al (111)	25	24	No	Yes	No	Yes	No	No	Unknown	Unknown	
101	2017	2014-2015	Otter et al (112)	40	25	No	No	No	No	Yes	No	<i>mgrB, phoQ, NDM-1</i>	<i>mgrB</i>	

102	2017	2012-2015	Prim et al (113)	13579	91	Yes	Yes	No	No	No	No	<i>mcr-1,</i> <i>mcr-2</i>	<i>mcr-1</i>
103	2017	2014	Cannatelli et al (114)	10	4	Yes	No	No	No	No	No	<i>pmrB,</i> <i>mcr-1</i>	<i>pmrB</i>
104	2018	unknown	Lucas et al (115)	8	7	No	No	No	No	No	No	<i>pmrA,</i> <i>pmrC,</i> <i>eptA</i>	<i>eptA</i>
105	2018	unknown	Servat et al (116)	61	4	No	No	No	Yes	No	No	unknown <i>mcr-1,</i> <i>blaTEM-1b,</i>	Unknown
106	2018	2016	Hannuksela et al (117)	176	93	No	Yes	No	No	No	No	<i>blaCMY-2,</i> <i>qnrB19,</i> <i>dfrA8,</i> <i>strA, strB,</i> <i>sul2, floR</i>	<i>mcr-1</i>
107	2018	2016	Principe et al (118)	3902	35	No	Yes	No	No	No	No	<i>mcr-1, bla</i> TEM	<i>mcr-1</i>
108	2018	2016-2017	Bianco et al (119)	19050	90	No	No	Yes	No	No	No	<i>mcr-1</i>	<i>mcr-1,mcr-2</i>
109	2018	None	Dortek et al (120)	17	9	No	No	No	No	No	No	<i>pmrA,</i> <i>pmrB,</i> <i>pmrC</i>	<i>pmrC</i>
110	2019	unknown	Girlich et al (121)	94	53	No	Yes	No	No	No	No	<i>mcr-2,</i> <i>mcr-5,</i> <i>mcr-1.5,</i> <i>mcr-3.2,</i> Δ <i>mgrB</i>	Unknown
North America													
111	2011	2010	Bogdanovich et al (122)	8	5	No	Yes	No	No	No	No	<i>blaKPC-2</i>	Unknown
112	2012	None	Jernigan et al (123)	12	10	Yes	No	No	No	No	No	None <i>pmrB,</i> <i>adeJ,</i> <i>fusA,</i>	None
113	2013	unknown	Snitkin et al (124)	37	4	No	No	No	No	No	No	<i>csuE,</i> <i>NIA,</i> <i>kdpB, pIF,</i> <i>hutH,</i> <i>feoB,</i> <i>wcaJ, ptk,</i> <i>lysS, rpsB,</i>	<i>pmrB</i>

														<i>relA</i>
114	2013	2010-2011	Hong et al (125)	12	9	Yes	No	No	No	No	No	<i>blaKPC-2,</i> <i>blaSHV-12, and</i> <i>blaTEM-1</i>	None	
115	2013	None	Lee et al (126)	2	1	Yes	No	No	No	No	No	None	None	
116	2013	None	Oleksuik et al (127)	18	6	No	No	Yes	No	No	No	None	None	
117	2013	Unknown	Napier et al (128)	10	6	Yes	Yes	No	No	No	No	<i>pmrB</i>	<i>pmrB</i>	
118	2013	2010-2011	Hindler et al (129)	107	15	No	No	No	Yes	No	No	Unknown	Unknown	
119	2013	Unknown	Lesho et al (130)	28	14	No	Yes	No	No	No	No	<i>pmrA,</i> <i>pmrB,</i> <i>pmrC</i>	<i>pmrB,</i> <i>pmrA1</i>	
120	2015	2007-2014	Qureshi et al (131)	38	20	No	Yes	No	No	No	No	<i>blaOXA-40,</i> <i>blaOXA-58</i>	Unknown	
121	2015	2012-2013	Bradford et al (132)	19719	309	Yes	No	No	No	No	No	CTX-M, SHV, and VEB	KPC	
122	2016	2011-2014	Rojas et al (133)	246	31	No	Yes	No	No	No	No	<i>blaKPC-2,</i> <i>blaKPC-3,</i> <i>blaNDM-1</i>	<i>blaKPC-3</i>	
123	2016	2008-2015	Walkty et al (134)	5571	12	No	Yes	No	No	No	No	<i>mcr-1,</i> <i>mcr-2</i>	<i>mcr-1</i>	
124	2016	2011-2014	Rojas et al (135)	264	41	No	No	Yes	No	No	No	<i>mgrB,</i> <i>mcr-1</i>	<i>mgrB</i>	
125	2017	2012-2014	Gallet et al (136)	32	19	No	No	No	No	No	No	<i>phoPQ,</i> <i>pmrCAB,</i> <i>crab</i>	<i>mgrB</i>	
126	2017	2011-2016	Duin et al (137)	137	12	No	Yes	No	No	No	No	<i>blaVIM,</i> <i>blaIMP,</i> <i>and</i> <i>blaOXA-48</i>	<i>blaKPC-2,</i> <i>blaKPC-3</i>	
127	2017	None	Zhang et al (138)	25	18	Yes	No	No	Yes	No	No	<i>pmrA,</i> <i>pmrB,</i> <i>lpxA, lpxC</i> <i>and lpxD</i>	None	

128	2018	2011-2016	Richter et al (139)	28512	128	Yes	No	No	No	No	No	None	None
129	2018	2016	Zhung et al (140)	134	22	No	No	No	Yes	No	No	<i>mcr-4</i>	<i>mcr genes</i>
130	2011	2005-2008	Maalej et al (141)	150	7	Africa	Yes	Yes	No	Yes	No	Unknown	Unknown
131	2017	Unknown	Sekyere et al (142)	63	44	No	Yes	No	No	No	No	<i>blaNDM-1,</i> <i>blaOXA-232,</i> <i>blaGES-5,</i> <i>CNP-†††,</i> <i>CNP+\$\$\$,</i> <i>blaNDM-5, CNP+ mgrB,</i> <i>blaOXA-48-like,</i> <i>blaOXA-204,</i> <i>blaCMY-4,</i> <i>blaNDM-1,</i> <i>blaCMY-16,</i> <i>blaCTX-M-15</i>	<i>blaNDM-1</i>
132	2017	2015-2016	Mansour et al (143)	940	7	No	Yes	No	No	No	No	<i>bla OXA-48</i>	
133	2014	1996-2013	Rodriguez et al (144)	641	512	South America	No	No	No	Yes	No	None	None
134	2015	unknown	Jayol et al (145)	2	1	No	Yes	No	No	No	No	<i>blaCTX-M-15</i>	Unknown
135	2016	2011-2012	Carrilho et al (146)	127	27	No	Yes	No	No	No	No	<i>pmrB,</i> <i>mgrB,</i> <i>yciM,</i> <i>ipxM,</i> <i>fosA</i>	Unknown
136	2016	2010-2014	Rossi et al (147)	33765	1346	No	No	No	Yes	No	Yes	<i>bla-KPC</i>	<i>bla-KPC</i>
137	2016	Unknown	Leite et al (148)	20	7	No	No	Yes	No	No	No	<i>blaOXA-51-like,</i> <i>blaOXA-23-like,</i> <i>blaOXA-143-like,</i> <i>carO</i>	<i>blaOXA-51-like,</i> <i>carO</i>

138	2017	unknown	Esposito et al (149)	109	86	No	Yes	No	No	No	No	<i>blaIMP</i> , <i>blaVIM</i> , <i>blaNDM</i> , <i>opm33-36</i> , <i>carO</i>	Unknown
139	2017	None	Jayole et al	152	33	No	No	Yes	No	No	No	<i>mcr-1</i> , <i>pmrB</i> , <i>phoQ</i> , <i>mgrB</i> , <i>phoP</i> , <i>crrb</i>	None
140	2014	Unknown	Poirel et al (150)	47	13	No	Yes	No	No	No	No	<i>mgrB</i> , KPC-2, KPC-3, CTX-M-2, CTX-M-15	Unknown
141	2014	2012-2013	Olaitan et al (151)	869	35	No	No	No	No	No	No	<i>phoP</i> , <i>phoQ</i> , <i>pmrB</i>	Unknown
142	2016	Unknown	Nordmann et al (152)	88	52	Yes	No	Yes	No	No	No	<i>mcr-1</i> , <i>mcr-1</i> , <i>mcr-1.2</i> ,	Unknown
143	2018	2014-2016	Wise et al (153)	44407	934	No	Yes	Yes	No	No	No	<i>mcr-1.5</i> , <i>mcr-3.1</i> , <i>mcr-5</i>	<i>mcr-1</i>

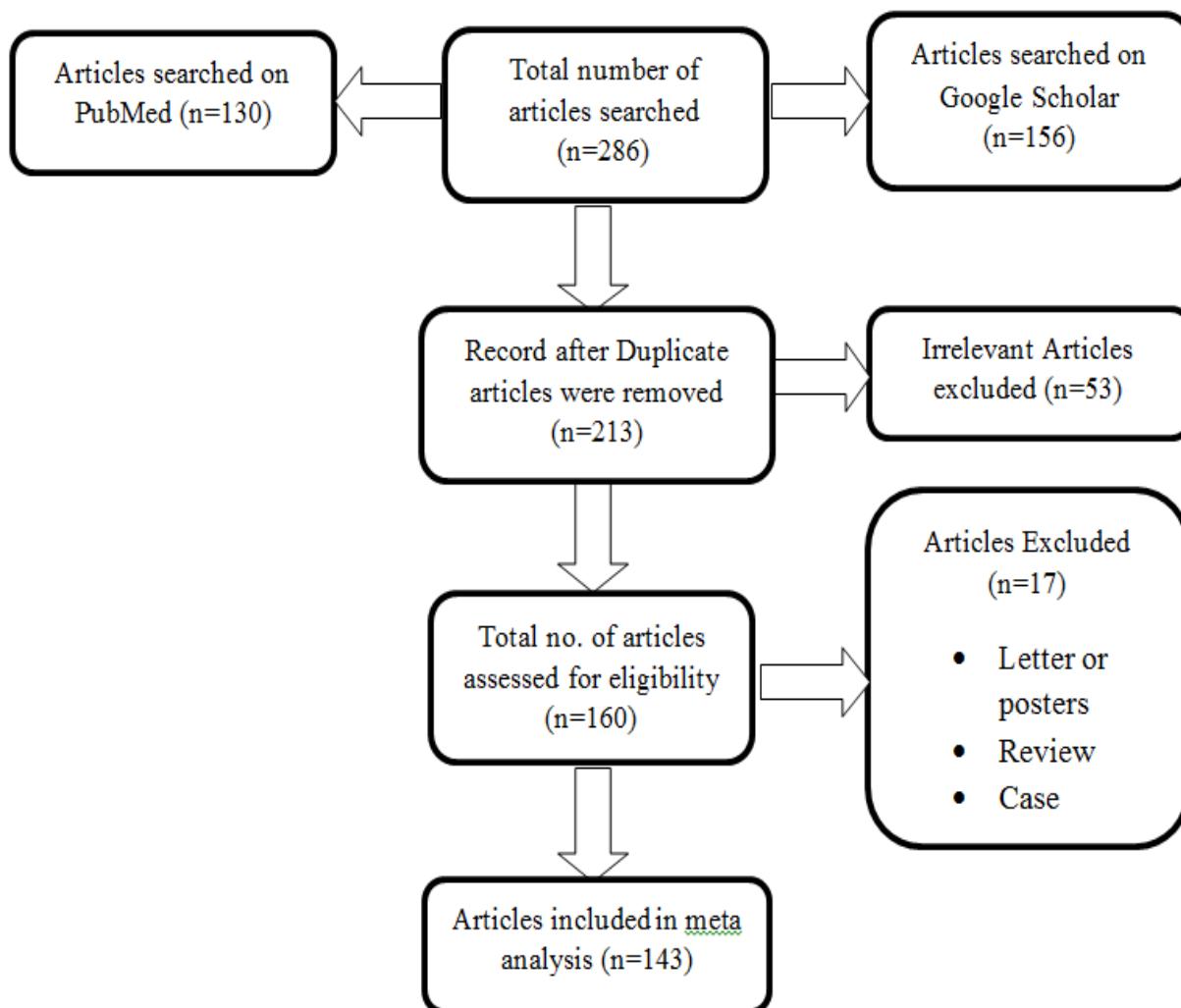


Figure 1: Article selection flowchart by PRISMA guidelines.

RESULTS

Distribution of articles describing Colistin Resistance Worldwide

A total of 286 studies resulted from search on different electronic databases. From which 143 articles were reviewed from five different continents of World i-e 68 (48%) from Asia, 42 (29%) from Europe, 19 (13%) from North America, 3 (2%) from Africa, 7 (5%) from South America, while 4 (3%) all together from different countries of different continents. No studies were found from Australia, Antarctica and Oceania (Table 2 and Figure 2). Maximum number of studies was published from 2015-2017 years (Figure 3).

Prevalence of colistin resistant isolates isolated from human clinical samples in different regions of the World

There were mainly four isolates responsible for Colistin

resistance in clinical samples including *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa*. Among them *Klebsiella pneumoniae* showed highest rate of Colistin resistance about 39% followed by *Acinetobacter baumannii* (26%), *Escherichia coli* (24%) and *Pseudomonas aeruginosa* (11%) (Table 3). Highest rate of colistin resistance was found in Asia by *Klebsiella pneumoniae* (32%), by *Escherichia coli* (25%), by *Acinetobacter baumannii* (25%), *Pseudomonas aeruginosa* (18%). In Europe Colistin resistance by *Klebsiella pneumoniae* was 49%, by *Acinetobacter baumannii* (29%), by *Escherichia coli* (22%), and no resistance was found by *Pseudomonas aeruginosa*. Lowest rate of colistin resistance was found in Africa (Table 3).

Table 2: Distribution of published articles in different regions of the World.

Year	Asia	Europe	North America	Africa	South America	Others	Annual Total Publication
2009-2011	4 (6)	2 (5)	1 (5)	1 (25)	0 (0)	0 (0)	8 (6)
2012-2014	9 (13)	10 (23)	8 (42)	0 (0)	1 (14)	2 (50)	30 (21)
2015-2017	35 (51)	23 (53)	8 (42)	2 (67)	6 (86)	1 (25)	75 (52)
2018-2019	20 (29)	7 (16)	2 (11)	0 (0)	0 (0)	1 (25)	30 (21)
Region Wide	68 (48)	42 (29)	19 (13)	3 (2)	7 (5)	4 (3)	143

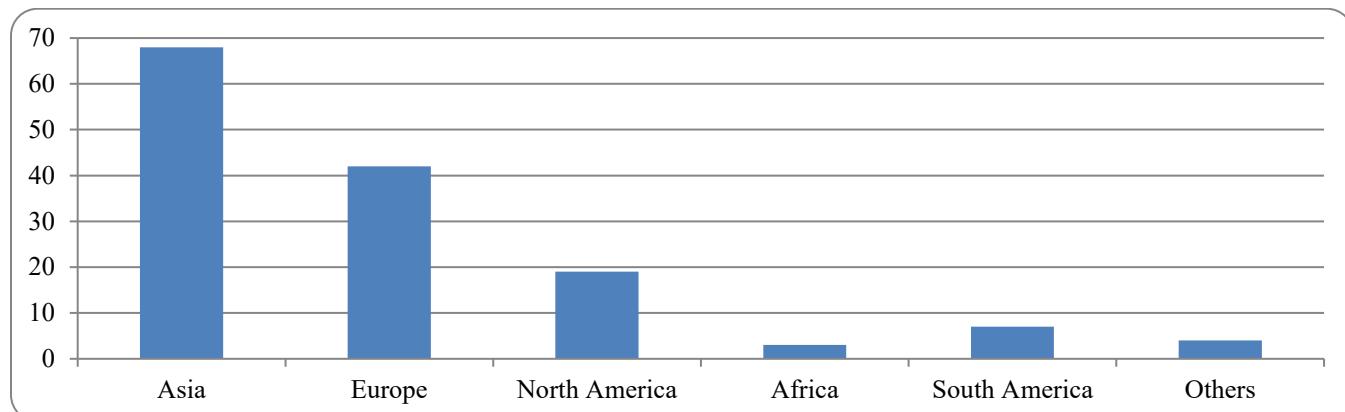


Figure 2: Graphical representation of published articles in different countries.

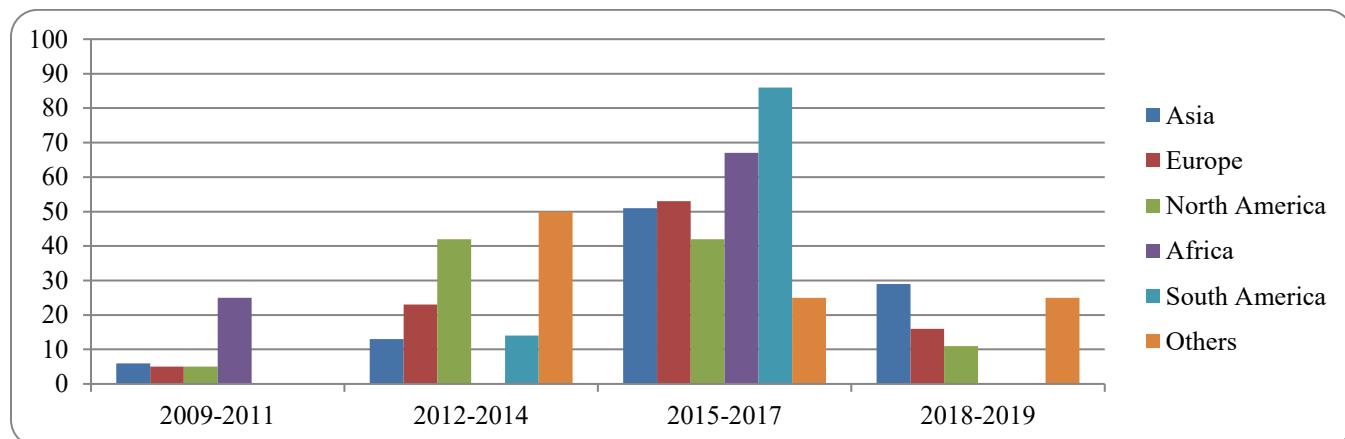


Figure 3: Annual Publication (%) of articles in different regions of the World.

Table 3: Year-wise distribution of bacterial isolates causing Colistin resistance.

Continents	Year	<i>Acinetobacter baumannii</i>	<i>Pseudomonas aeruginosa</i>	<i>Klebsiella pneumonia</i>	<i>Escherichia coli</i>
Asia	2009-2011	1 (2)	2 (9)	1 (1)	0 (0)
	2012-2014	6 (11)	2 (9)	4 (5)	1 (2)
	2015-2017	12 (22)	11 (48)	15 (19)	17 (35)
	2018-2019	7 (13)	4 (17)	14 (18)	8 (16)
Europe	2009-2011	2 (4)	0 (0)	0 (0)	0 (0)
	2012-2014	2 (4)	0 (0)	8 (10)	0 (0)
	2015-2017	8 (15)	0 (0)	12 (15)	9 (18)

	2018-2019	2 (4)	0 (0)	4 (5)	2 (4)
	2009-2011	0 (0)	0 (0)	1 (1)	0 (0)
North America	2012-2014	6 (11)	1 (4)	3 (4)	0 (0)
	2015-2017	2 (4)	0 (0)	5 (6)	3 (6)
	2018-2019	1 (2)	1 (4)	2 (3)	1 (2)
	2009-2011	0 (0)	0 (0)	1 (1)	1 (2)
Africa	2012-2014	0 (0)	0 (0)	0 (0)	0 (0)
	2015-2017	1 (2)	0 (0)	2 (3)	1 (2)
	2018-2019	0 (0)	0 (0)	0 (0)	0 (0)
	2009-2011	0 (0)	0 (0)	0 (0)	0 (0)
South America	2012-2014	0 (0)	0 (0)	0 (0)	0 (0)
	2015-2017	2 (4)	1 (4)	4 (5)	3 (6)
	2018-2019	0 (0)	0 (0)	0 (0)	0 (0)
	2009-2011	0 (0)	0 (0)	0 (0)	1 (2)
Others	2012-2014	0 (0)	0 (0)	2 (3)	0 (0)
	2015-2017	1 (2)	1 (4)	1 (1)	1 (2)
	2018-2019	0 (0)	0 (0)	1 (1)	1 (2)

Prevalence of laboratory detection methods for estimating Colistin Resistance

The most common phenotypic detection methods used to estimate Colistin resistance was MIC, Disc Diffusion, Broth Micro-dilution, E-Test, Agar Dilution and VITEK. Among them Disc Diffusion test was mostly used (42% studies) followed by MIC (24% studies), E test (14% studies), Broth Micro-dilution (13% studies) and VITEK (11% studies). Agar dilution test was used only in 6 (4%) studies (Table 4). Molecular detection tests were also performed which shows genes that are responsible for Colistin resistance. The most prevalent genes were *pmrABC*, *mcr-1*, *phoPQ*, *blaKPC*, *mgrB*, *bla OXA-48* (Table 4).

Prevalence of Colistin resistance and their distribution in different regions of the World

From available data, over-all pooled proportion of

colistin resistance in different regions of the World was 0.21 (CI 95%: 0.20-0.21). Heterogeneity was ($I^2=99.54\%$, $p < 0.001$), ES was 0 ($z=62.53$, $p < 0.001$). The pooled proportion of Colistin resistance in Asia was 0.23 (CI 95%: 0.20-0.21), in Europe was 0.36 (CI 95%: 0.33-0.34), in North America was 0.06 (CI 95%: 0.04-0.05), in Africa was 0.40 (CI 95%: 0.06-0.23), in South America was 0.76 (CI 95%: 0.06-0.41), and in other regions was 0.23 (CI 95%: 0.10-0.17). Heterogeneity for these regions with $p < 0.001$ was 99.35% (Asia), 99.72% (Europe), 97.06% (North America), 98.64% (Africa), 99.78% (South America), and 97.88% (Others). ES was 0 with $p < 0.001$ and $Z=32.41$ (Asia), 42.47 (Europe), 8.56 (North America), 2.72 (Africa), 2.28 (South America) and 5.16 (others) (Figure 4).

Table 4: Proportion estimates of Colistin Resistance.

Study	ES	95% Conf. Interval		% Weight
		Asia		
Suh et al., 2009 (15)	0.07	0.04	0.11	1.13
Gill et al., 2011 (16)	0.38	0.32	0.46	0.52
Lee et al., 2011 (17)	0.07	0.05	0.12	1.09
Park et al., 2011 (7)	0.21	0.11	0.38	0.17
Hamzeh et al., 2012 (18)	0.93	0.89	0.95	1.17
Bahador et al., 2013 (19)	0.05	0.02	0.12	0.88
Choi et al., 2013 (20)	0.45	0.36	0.54	0.36
Huangki et al., 2013 (21)	0.73	0.67	0.78	0.72
Lee et al., 2013 (22)	0.35	0.29	0.42	0.60
Naparstek et al., 2014 (23)	0.07	0.02	0.18	0.52

Lee et al., 2014 (24)	0.50	0.15	0.85	0.02
Kim et al., 2014 (25)	0.80	0.38	0.96	0.03
Guven et al., 2014 (26)	0.02	0.01	0.04	1.52
Mansoor et al., 2015 (27)	0.36	0.33	0.40	1.04
Choi et al., 2015 (28)	0.50	0.19	0.81	0.02
Nhung et al., 2015 (29)	0.58	0.39	0.76	0.09
Olaitan et al., 2015 (30)	0.40	0.12	0.77	0.02
Qadeer et al., 2016 (31)	0.47	0.43	0.51	0.96
Bashir et al., 2016 (32)	0.00	0.00	0.01	1.67
Mu et al., 2016 (33)	0.25	0.05	0.70	0.02
Goli et al., 2016 (34)	0.68	0.58	0.76	0.36
Sonnevend et al., 2016 (35)	0.11	0.06	0.20	0.53
Crawford et al., 2016 (36)	0.70	0.40	0.89	0.05
Yilmaz et al., 2016 (37)	0.52	0.39	0.64	0.20
Bashie et al., 2016 (32)	0.00	0.00	0.01	1.67
Cheng et al., 2016 (38)	0.65	0.46	0.81	0.11
Ni et al., 2016 (39)	0.29	0.21	0.38	0.40
Zhaong et al., 2016 (40)	0.11	0.07	0.17	0.79
Sato et al., 2016 (41)	0.01	0.00	0.02	1.64
Ye et al., 2016 (42)	0.04	0.01	0.11	0.90
Crawford et al., 2016 (43)	0.70	0.40	0.89	0.05
Kumar et al., 2016 (44)	0.08	0.06	0.09	1.57
Qamar et al., 2017 (45)	0.28	0.23	0.34	0.71
Aydin et al., 2017 (46)	0.07	0.06	0.08	1.57
Thong et al., 2017 (47)	0.97	0.84	0.99	0.62
Cizmeci et al., 2017 (48)	0.25	0.17	0.36	0.32
Hua et al., 2017 (49)	0.50	0.09	0.91	0.01
Soudeihia et al., 2017 (50)	0.19	0.13	0.28	0.46
Luo et al., 2017 (51)	0.03	0.02	0.04	1.62
Haeili et al., 2017 (52)	0.87	0.68	0.95	0.18
Hu et al., 2017 (53)	0.02	0.01	0.05	1.46
Tada et al., 2017 (54)	0.22	0.09	0.45	0.10
Juhaz et al., 2017 (55)	0.01	0.00	0.02	1.65
Tada et al., 2017 (56)	0.25	0.05	0.70	0.02
Chew et al., 2017 (57)	0.63	0.52	0.73	0.27
Chung et al., 2017 (58)	0.50	0.15	0.85	0.02
Wang et al., 2017 (59)	0.20	0.14	0.26	0.65
Miwi et al., 2017 (60)	0.12	0.06	0.21	0.51
Singh et al., 2018 (61)	0.10	0.07	0.16	0.93
Luxmi et al., 2018 (62)	0.24	0.21	0.27	1.19
Forde et al., 2018 (63)	0.00	0.00	0.02	1.65
Eiamphungporn et al., 2018 (64)	0.71	0.66	0.76	0.80
Farshadzadeh et al., 2018 (65)	0.50	0.22	0.78	0.03
Lu et al., 2018 (66)	0.04	0.02	0.10	1.02
Guducuoglu et al., 2018 (67)	0.69	0.42	0.87	0.06
Haeili et al., 2018 (68)	0.60	0.23	0.88	0.02
Cao et al., 2018 (69)	0.01	0.00	0.01	1.67
Aghapour et al., 2018 (70)	0.03	0.02	0.05	1.59

Yonchanghu et al., 2018 (71)	0.01	0.01	0.01	1.68
Moubareck et al., 2018 (72)	0.01	0.01	0.01	1.68
Lomonaco et al., 2018 (73)	0.70	0.40	0.89	0.05
Li et al., 2018 (74)	0.00	0.00	0.00	1.68
Okdah et al., 2018 (75)	0.96	0.88	0.99	0.84
Mustapha et al., 2018 (76)	0.43	0.29	0.58	0.15
Hameed et al., 2019 (77)	0.11	0.07	0.17	0.79
Menekse et al., 2019 (78)	0.29	0.23	0.35	0.63
Messeron et al., 2019 (79)	0.19	0.14	0.25	0.73
Cheong et al., 2019 (80)	0.05	0.03	0.09	1.27
Europe				
Wareham et al., 2011 (81)	0.83	0.44	0.97	0.04
Vila-farres et al., 2011 (82)	0.87	0.62	0.96	0.12
Capone et al., 2012 (83)	0.92	0.85	0.96	0.72
Huttner et al., 2013 (84)	0.44	0.32	0.58	0.19
Camacho et al., 2013 (85)	0.04	0.01	0.19	0.49
Cannatelli et al., 2013 (86)	0.50	0.09	0.91	0.01
Tamayo et al., 2013 (87)	0.24	0.16	0.36	0.29
Monaca et al., 2014 (88)	0.97	0.94	0.99	1.34
Gaibani et al., 2014 (89)	0.47	0.26	0.69	0.06
Agodi et al., 2014 (90)	0.58	0.39	0.74	0.10
Cannatelli et al., 2014 (91)	0.50	0.09	0.91	0.01
Olivgeris et al., 2014 (92)	0.11	0.08	0.15	1.02
Hasman et al., 2015 (93)	0.78	0.74	0.81	1.09
Olaitan et al., 2015 (30)	0.01	0.00	0.03	1.61
Wand et al., 2015 (94)	0.92	0.65	0.99	0.14
Formosa et al., 2015 (95)	0.50	0.09	0.91	0.01
Farre's et al., 2015 (96)	0.50	0.44	0.56	0.63
Dafopoulou et al., 2015 (97)	0.95	0.87	0.98	0.73
Parisi et al., 2015 (98)	0.24	0.20	0.29	0.94
Oikonomou et al., 2015 (99)	0.07	0.06	0.09	1.55
Godbole et al., 2016 (100)	0.00	0.00	0.00	1.69
Gue'rin et al., 2016 (101)	0.57	0.48	0.66	0.39
Wintersdorff et al., 2016 (102)	0.05	0.02	0.10	1.02
Boll et al., 2016 (103)	0.27	0.11	0.52	0.07
Jayol et al., 2016 (104)	0.04	0.03	0.06	1.57
Lopez-roja et al., 2016 (105)	0.73	0.43	0.90	0.05
Wand et al., 2016 (106)	0.83	0.44	0.97	0.04
Mavroidi et al., 2016 (107)	0.14	0.09	0.21	0.67
Vourli et al., 2017 (108)	0.92	0.86	0.96	0.83
Coppi et al., 2017 (109)	0.82	0.72	0.89	0.39
Dona et al., 2017 (110)	0.08	0.03	0.22	0.36
Jayol et al., 2017 (111)	0.96	0.80	0.99	0.47
Otter et al., 2017 (112)	0.63	0.47	0.76	0.15
Prim et al., 2017 (113)	0.01	0.01	0.01	1.68
Cannatelli et al., 2017 (114)	0.40	0.17	0.69	0.04
Lucas et al., 2018 (115)	0.88	0.53	0.98	0.07
Servat et al., 2018 (116)	0.07	0.03	0.16	0.62

Hannuksela et al., 2018 (117)	0.53	0.45	0.60	0.49
Principe et al., 2018 (118)	0.01	0.01	0.01	1.68
Bianco et al., 2018 (119)	0.00	0.00	0.01	1.68
Dortek et al., 2018 (120)	0.53	0.31	0.74	0.06
Girlich et al., 2019 (121)	0.56	0.46	0.66	0.31
North America				
Bogdanovich et al 2011 (122)	0.63	0.31	0.86	0.03
Jerigan et al., 2012 (123)	0.83	0.55	0.95	0.08
Snitkin et al., 2013 (124)	0.11	0.04	0.25	0.31
Hong et al., 2013 (125)	0.75	0.47	0.91	0.06
Lee et al., 2013 (126)	0.50	0.09	0.91	0.01
Oleksuik et al., 2013 (127)	0.33	0.16	0.56	0.08
Napier et al., 2013 (128)	0.60	0.31	0.83	0.04
Hindler et al., 2013 (129)	0.14	0.09	0.22	0.58
Lesho et al., 2013 (130)	0.50	0.33	0.67	0.10
Qureshi et al., 2015 (131)	0.53	0.37	0.68	0.14
Bradford et al., 2015 (132)	0.02	0.01	0.02	1.68
Rojas et al., 2016 (133)	0.13	0.09	0.17	0.96
Walkty et al., 2016 (134)	0.00	0.00	0.00	1.68
Rojas et al., 2016 (135)	0.16	0.12	0.20	0.91
Gallet et al., 2017 (136)	0.59	0.42	0.74	0.12
Duin et al., 2017 (137)	0.09	0.05	0.15	0.84
Zhang et al., 2017 (138)	0.72	0.52	0.86	0.11
Richter et al., 2018 (139)	0.00	0.00	0.01	1.68
Zhung et al., 2018 (140)	0.16	0.11	0.24	0.61
Africa				
Maalej et al., 2011 (141)	0.05	0.02	0.09	1.12
Sekyere et al., 2017 (142)	0.70	0.58	0.80	0.25
Mansour et al., 2017 (143)	0.01	0.00	0.02	1.66
South America				
Rodriguez et al., 2014 (144)	0.80	0.77	0.83	1.18
Jayol et al., 2015 (145)	0.50	0.09	0.91	0.01
Carrillho et al., 2016 (146)	0.21	0.15	0.29	0.52
Rossi et al., 2016 (147)	0.04	0.04	0.04	1.68
Leite et al., 2016 (148)	0.35	0.18	0.57	0.08
Esposito et al., 2017 (149)	0.79	0.70	0.86	0.47
Jayole et al., 2017	0.22	0.16	0.29	0.58
Others				
Poirel et al., 2014 (150)	0.28	0.17	0.42	0.20
Olaitan et al., 2014 (151)	0.04	0.03	0.06	1.57
Nordmann et al., 2016 (152)	0.59	0.49	0.69	0.30
Wise et al., 2018 (153)	0.02	0.02	0.02	1.68

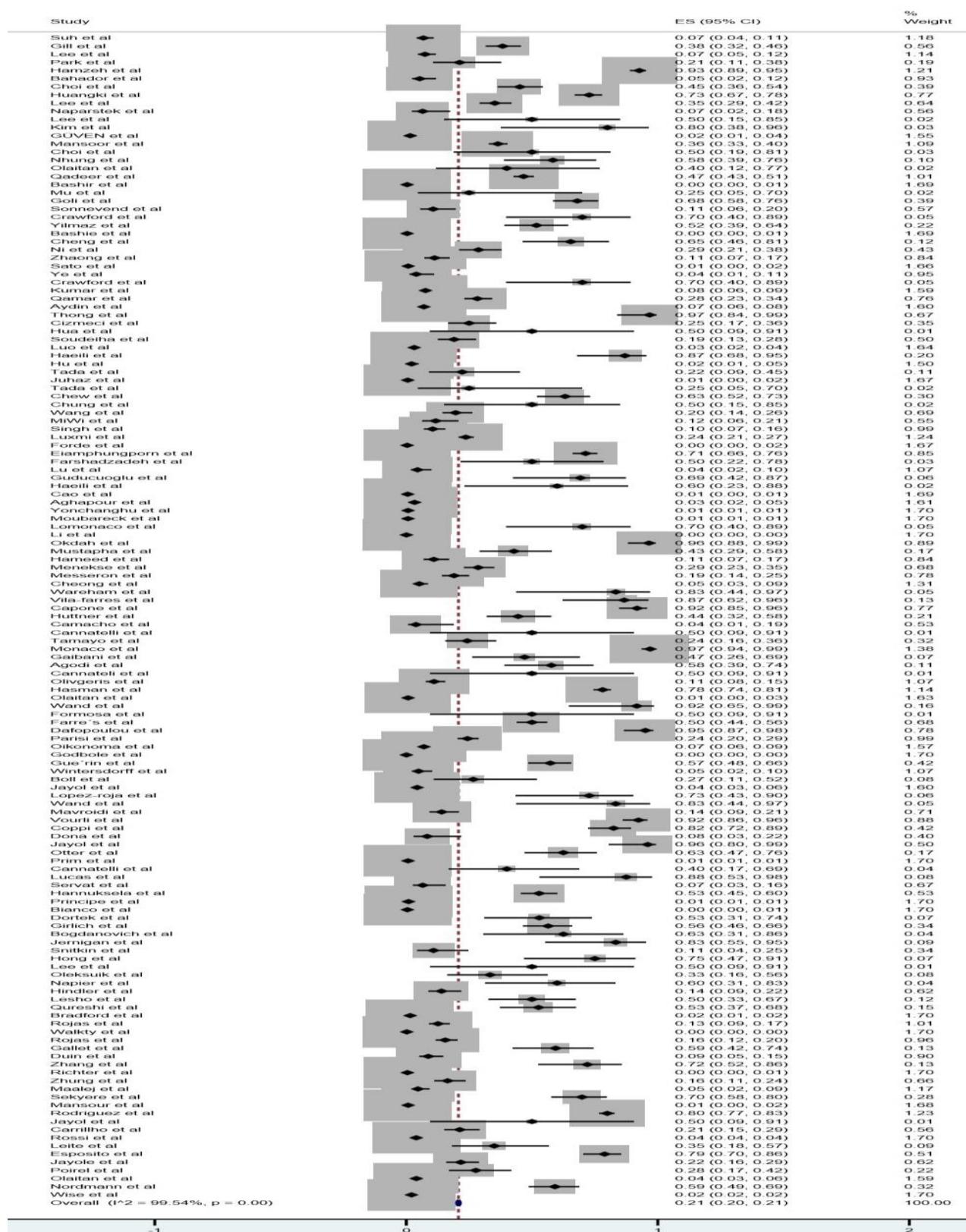


Figure 4: Proportion estimates of Colistin resistance Worldwide. The proportion estimates of colistin resistance have been donated by midpoint of each horizontal line segment. Rhombic mark donates the pooled proportion of all the included studies

DISCUSSION

It is necessary to evaluate the prevalence of colistin resistance in different regions of the world to raise the awareness of multidrug resistant bacteria. Different studies from Asia indicated that there were highest rate of colistin resistance in this region. Colistin resistance had been seen in countries including India (13.8%) (154), Singapore (30%) (155), Philippines (50%) (154), China (92.7%) (156), Iran (11.6%) (157), Korea (27.9%) (158), Turkey (27.5%) (159), Thailand (7.3%) (160) and Pakistan (15%) (161). The bacterial isolate *Klebsiella pneumoniae* was the most prevalent colistin resistance isolate (162). The present study evaluated total 143 studies, according to this study the highest rate of colistin resistance was also found in Asia in *Klebsiella pneumoniae* isolates because large number of studies 48% was conducted in this region. In Asia, *Klebsiella pneumoniae* show highest rate of colistin resistance between years 2015-2017. The rates of *Acinetobacter baumannii*, *Escherichia coli* and *Pseudomonas aeruginosa* colistin resistant isolates are also high in Asia between years 2015-2017.

There were different studies showing rates of colistin resistance in European countries. European countries like United Kingdom reported 3.1% colistin resistance in *Pseudomonas aeruginosa* (163). Spain reported 19.1% strains were resistant to colistin (164). In Romania rates of colistin resistance were 17% in *E.coli* and 11% in *Klebsiella* spp. (165). Rome and Italy reported 36.1% colistin resistance strains of *Klebsiella pneumonia* (83). In this present study about 29% of studies were collected from Europe showing high rates of colistin resistance in *Klebsiella pneumoniae* between years 2015-2017.

A study indicated rates of colistin resistance in isolates of *Acinetobacter baumannii* and *Pseudomonas aeruginosa* was less than 5.5% in North American countries (166). However rates of colistin resistance were high in isolates of *Klebsiella pneumoniae*. In Denmark no resistance to colistin had been observed in *Pseudomonas aeruginosa* isolates (167). Isolates like *Acinetobacter baumannii*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*, *Escherichia coli*, and *Enterobacter* spp showed colistin resistance in Canada (168). And the rate of colistin resistant *Acinetobacter baumannii* were about 4% in Argentina (169). According to the present study, about 13% studies were collected from North America. In North America the most prevalent colistin resistant isolate was *Klebsiella pneumoniae* followed by *Acinetobacter baumannii* and highest rate of resistance was found between years 2012-2017.

Studies from South American countries like Chile and Brazil showed 9% rates of colistin resistance for *Acinetobacter baumannii* and *Pseudomonas aeruginosa* (170). In present study only 5% studies were conducted from South America and most prevalent colistin resistant isolate was *Klebsiella pneumoniae* from years 2015-2017. Studies from African countries like South Africa and Nigeria showed less than 10% colistin resistance (171). A study from Tunisia showed 1.2% colistin resistance for *Klebsiella pneumoniae*, 1.5% for *E. cloacae* and 0.09% for *Escherichia coli* (172). Zimbabwe study reported 53% colistin resistance in isolates of *Pseudomonas aeruginosa* (173). According to this study only 2% studies were conducted in this region and highest rate of colistin resistance was found in *Klebsiella pneumoniae* isolate from years 2015-2017.

Different studies also indicated that the genes that were responsible for causing colistin resistance were *lpxA*, *lpxC*, or *lpxD* in *Acinetobacter baumannii* (174). In *Pseudomonas aeruginosa* *PmrAB*, *PhoPQ* regulatory genes involved in colistin resistance (175) and *mgrB* (86), *blaKPC* (176) were the genes responsible for colistin resistance in *Klebsiella pneumoniae*. According to this present study the most prevalent genes were *pmrABC*, *mcr-1*, *phoPQ*, *blaKPC*, *mgrB*, responsible for causing resistance to colistin. Among them *mcr-1* was the most prevalent one. After that *pmrABC* were most prevalent. The prevalence of *mcr-1* gene was high in Asia followed by Europe. This study contributes to understanding the extent of colistin resistance in isolates of *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa*. Due to various clinical implications the prevalence of colistin resistance should not be minimized. There are many reasons contributing resistance to colistin from 143 studies in different regions of the World. With this limited available information it is difficult to minimize the problem of resistance.

CONCLUSION AND RECOMMENDATIONS

This meta-analysis performed to show rates of colistin resistance in different regions of the World. These studies show frequency of colistin resistance in various continents of the World year wise. No study is present describing colistin resistance in Oceania continent. Bacterial isolates including *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa* showed highest rate of resistance. There is a need for appropriate and regular surveillance program that addresses the issue of resistance to this antibiotic. Implementation of effective

measures including active surveillance activation, highlighting coherent antibiotic strategies in hospitals with hand hygiene to control and stop the spread of colistin resistance in communities and hospitals is required.

DECLARATION

This study is part of BS thesis of Sumaya Mobin.

LIST OF ABBREVIATION

Lipopolysaccharides (LPS), Extended-spectrum β -lactamase (ESBL), multidrug-resistant (MDR), New Delhi metallo- β -lactamase-1 (NDM-1), Epsilometric test (E-Test), Minimum inhibitory concentration (MIC), Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA), Meta-analysis Proportion (*Metaprop*).

AVAILABILITY OF DATA AND MATERIALS

The data sets analyzed during the current study are available from the corresponding author

AUTHORS' CONTRIBUTIONS

SA: designed the study, designed the analysis, SM: Data collection and Manuscript write-up, and IA: manuscript write up, NA: Helped with data collection, AR; data collection.

COMPETING INTERESTS

The authors declare that they have no competing interests.

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