Vancomycin Resistance Enterococcus in Africa in Onehealth approach: A systematic review and meta-analysis

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Abstract

Background Vancomycin resistance enterococci are enterococci that cannot be cured with vancomycin treatment. To combat this resistance, an integrated disciplinary action is mandatory. Therefore, this study aimed to show the prevalence of these agents with the concept of one health approach.

Methods Literature search was conducted on PubMed, Google scholar and Hinari with the term “Vancomycin resistance enterococcus in Africa” in august 1-3, 2019. All available articles exported to “Endnote version 7.1” then to Microsoft word. All the articles checked to meet our criteria for the review. Those articles reported the prevalence of vancomycin resistance Enterococcus and published from 2010 to present in the English language was included for the review. There were 151 articles from the databases; of this, 37 articles included after extensive review with two independent authors.

Result Out of 4112 samples collected, 1527 isolates identified with overall magnitude of VRE as 28.8% (12.9%-44.7%) in Africa with a one-health perspective. The meta-analysis indicates that there was substantial heterogeneity among the articles with consistency index (I^2) =99.9%. A higher rate of Vancomycin resistance enterococci was identified from South Africa 74.8%, followed by Egypt 37.2%. Laboratory method employed for identification showed that a higher rate was from BacTec 98.8%, followed by PCR 59.2%. It is also a non-human sample source was with higher rates of VRE i.e. 32.5%.

Conclusion This meta-analysis indicates there was a high rate of Vancomycin resistance enterococcus in African continent. A lot should be done to prevent and control the transmittion of this resistance gene circulating in the environment.

Introduction

vancomycin-resistant enterococci an enterococci (VRE) that acquired resistance to the antibiotic vancomycin used to treat infection caused by these bacteria [1]. VRE emerged as important nosocomial pathogens since 1987, and there is concern that they may be, or become, endemic in the non-hospital setting, both in human and animal carriers and in the general environment [2]. It advanced to inoffensive colonizer of the gut of humans and animals, ranging from insects to reptiles, birds, and mammals. Whilst they are ubiquitous, they represent a minority population of the healthy human microbiome [3]. Outside the gut, they can disseminate in the environment where they survive in wastewater, slurry and soil contaminated by manure and hence used as indicators of faecal contamination in recreational or drinking water [4].

Members of the genus *Enterococcus* are well-documented pathogens associated with various clinical manifestations, including bacteremia, infective endocarditis, intra-abdominal and pelvic infections, urinary tract infections, and, in rare cases, central nervous system infections [5–7]. Infection with VREs associated with an increased mortality rate, illustrated by a 2.5-fold increase in mortality for patients suffering from VRE bacteremia [8].

The ‘One Health’ concept recognizes that the health of people connected to the health of animals and the environment. Humans, animals, plants, food of animal origin and our environment all potentially constitute overlapping reservoirs of antimicrobial resistance (AMR). Given the serious health threat, a common understanding of AMR, and of the need for a One Health approach to tackle it, are of fundamental importance [9].

VRE is one of this multidrug resistance that needs comprehensive data that indicates the magnitude of VRE in Africa. Therefore, the aim of this study was to compile available data of vancomycin resistance enterococci in Africa in one health perspective.

Methods

Literature Search Strategy

A literature search conducted on PubMed, Google scholar and Hinari with the term “Vancomycin resistance enterococcus in Africa” in august 1–3, 2019. All available articles exported to “Endnote version 7.1” then to Microsoft word. All the articles checked to meet our criteria for the review. Those articles reported the prevalence of vancomycin resistance Enterococcus and published from 2010 to present in the English language was included for the review. There were 151 articles from the databases; of this, 37 articles included after extensive review with two independent authors. Articles failed to fulfill the criteria excluded as presented in *Figure 1* according to the PRISMA protocol 2015.

Data analysis

Excel used for data extraction and then exported to Microsoft word as presented in table 1. Meta-analysis was conducted with OpenMeta analyst software available freely and the result presented as a forest plot in *Figure 2 &3* and in *Table 2*.

Data Quality

The quality of the study included in the review and meta-analysis evaluated with 14 points scoring tool. NIH quality assessment tool for observational and cross-sectional studies in which studies categorized as a good, fair and poor quality based on the internal validity of each article[10].

Heterogeneity and Publication Bias

The heterogeneity of the publication was determined according to the measure of the inconsistency index (I^2). That measures the total variations in the articles was due to heterogeneity rather than by chance with a value of <30%, 30–60%, 61–75% and >75% suggestive of low, moderate, substantial and considerable heterogeneity, respectively [11]. No need for conducting publication bias as the study is considerably heterogeneous as recommended by Hak T. *et al* [12].

Study features

As presented in table 1 studies that conducted in African countries that reported the prevalence of enterococcus and resistance rate for vancomycin, published after 2010. Whatever the sample type and laboratory method employed captured for the review and meta-analysis. The author name, year of publication, country of origin, source of sample (human vs non-human), laboratory method used (culture & polymerase chain reaction (PCR),

PCR only, BacTec, culture only, number of enterococcus isolated and the proportion of vancomycin resistance enterococci isolated was extracted from each articles.

Country of origin for the articles

The country in which the articles originated is indicated as follows, eight (8) articles from each countries, Ethiopia [13–20], and South Africa, [20–28], four (4) articles in each countries Egypt [29–32], and Tunisia [33–36]. Another three articles (3) from each of these countries Morocco [37–39], Tanzania [40–42] and Uganda, [43–45]), two (2) articles from Nigeria, [46, 47] and one (1) article from Algeria [48] were included for the review as presented in *Table 1*.

Results

The magnitude of vancomycin resistance Enterococci

Out of 4112 samples collected, 1527 isolates identified with overall magnitude of VRE 28.8% (12.9%–44.7%) in Africa in a one-health perspective. The meta-analysis indicates that there was substantial heterogeneity among the articles with a consistency index (I^2) = 99.9%.

Subgroup analysis

Country level

The subgroup analysis performed at country level indicates that a high rate of VRE in South Africa 74.8% and the least was from Algeria and Nigeria 2.8% each even if only one article captured from Algeria as presented in *Figure 2*.

Laboratory method

Subgroup analysis of VRE based on the laboratory method in presented in *Table 2* that grouped into culture & polymerase chain reaction (PCR), PCR only, BacTec, culture only. It indicates that the highest rates of VRE even if a single study conducted using BacTec was 98.8 %, followed by using only PCR 59.2%, that conducted using both culture & PCR 38.9% and identified using culture only 7.3 %, chronologically.

Sample Source

As tried to present in *Figure 3* subgroup analysis based on the source of sample conducted by categorizing as non-human and human source. It indicates that a higher rate of VRE was detected from non-human sample sources 32.5% vs 23.3 % human source.

Discussion

Vancomycin is one of the few antibiotics that can be used to treat infections resulting from Gram-positive multidrug-resistant organisms (MDRO) including such as enterococci [49]. In the late 1980s, the emergence of VRE in European hospitals and the isolation of a few years later of VRE from Danish raw minced pork and frozen poultry generated global concern [50]. One Health is the concept that the optimum health for people, animals and the environment can best be ensured through the ongoing cooperative efforts of scientists and practitioners in a variety of disciplines [51].

Our study based on data available in Africa on VRE in a one health perspective in which animal, human, avian and environmental source of samples analyzed to determine the pooled prevalence of VRE. The overall prevalence of VRE was 28.8 % in Africa from different sample sources in a one-health approach. Which is higher than study systematic review and meta-analysis which was conducted in Iran that is 14 % VRE [52]. This difference may be due to the source of the sample we used for the analysis is from different sources. The high rates of this VRE are may be due to the nature of enterococci, which is highly resistant for environmental conditions and different antibiotics [53, 54]. There is no data of systematic review and meta-analysis from other parts of the world including Africa to compare and contrast more with our finding, but the subgroup analysis at country level showed that there is a pronounced difference of VRE in different countries, which ranged from 74.8 % from South Africa to 2.8 % in Algeria.

Our study also performed a subgroup meta-analysis based on the laboratory method used for isolation and identification of Enterococcus & VRE. It showed that the higher the technique used the more sensitive for detection of VRE in which studies conducted with BacTec and PCR leads for isolation of more VRE, whereas those conducted with conventional culture less likely detect VRE. Some studies reported in comparison of PCR and Culture indicates that PCR is more sensitive and specific than later [55, 56].

Sample source in which we categorized in human & non-human source for the sake of subgroup meta-analysis showed that higher rates of VRE were isolated from non-human as compared to a human source. This may be due to most of the articles included based on our inclusion criteria is from non-human sources as different wild & domestic animal wastes or byproducts, poultry, birds, and environmental sample was compiled for analysis. This part of the study strained the one health approach, which is an important way of combating antibiotics resistance which worsens the world know a day's [57].

Conclusion

Our meta-analysis finding from one health perspective showed that there is a high rate of Vancomycin resistance enterococci circulating in Africa based on the available articles. Thus, a means of prevention and control targeting human, animal, avian and environment should be practiced in the continent.

Abbreviations/acronyms

VRE Vancomycin-resistant enterococci

AMR Antimicrobial resistance

PRISMA Preferred Reporting Items for Systematic Reviews and Meta-Analyses

NIH National Heart, Lung, and Blood Institute

PCR Polymerase chain reaction

MDRO multidrug-resistant organisms

Declarations

Ethical Clearance: Not applicable

Consent for publication: Not applicable

Availability of data and material: All the data supporting the findings can be obtained from the corresponding author.

Competing of interest: The authors declare that they have no competing interests

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Authors' contribution: TA: conceived the idea, develop the study plan, extracted data, analyzed the data and prepared the manuscript. MH: Extracted data and revised the manuscript.

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References

- 1.Ramadhan A, Hegedus E: *Survivability of vancomycin resistant enterococci and fitness cost of vancomycin resistance acquisition. Journal of clinical pathology* 2005, *58*(7):744–746.
- 2.Leong KW, Cooley LA, Anderson TL, Gautam SS, McEwan B, Wells A, Wilson F, Hughson L, O'Toole RF: *Emergence of vancomycin-resistant Enterococcus faecium at an Australian hospital: a whole genome sequencing analysis. Scientific reports* 2018, *8*(1):6274.
- 3.Lebreton F, Willems RJ, Gilmore MS: *Enterococcus diversity, origins in nature, and gut colonization.* In: *Enterococci: from commensals to leading causes of drug resistant infection [Internet].* edn.: Massachusetts Eye and Ear Infirmary; 2014.
- 4.Gouliouris T: *The relative importance of human and animal sources of vancomycin-resistant Enterococcus faecium in immunocompromised patients in hospital.* University of Cambridge; 2019.
- 5.Sievert D, Ricks P, Edwards J, Schneider A, Patel J, Srinivasan A, Kallen A, Limbago B, Fridkin S: *National Healthcare Safety Network (NHSN) Team and Participating NHSN Facilities. Antimicrobial-resistant pathogens associated with healthcare-associated infections: summary of data reported to the National Healthcare Safety*

- Network at the Centers for Disease Control and Prevention, 2009–2010. *Infect Control Hosp Epidemiol* 2013, 34(1):1–14.
- 6.Hill EE, Herijgers P, Claus P, Vanderschueren S, Herregods M-C, Peetermans WE: *Infective endocarditis: changing epidemiology and predictors of 6-month mortality: a prospective cohort study. European heart journal* 2006, 28(2):196–203.
- 7.Wang JS, Muzevich K, Edmond MB, Bearman G, Stevens MP: *Central nervous system infections due to vancomycin-resistant enterococci: case series and review of the literature. International Journal of Infectious Diseases* 2014, 25:26–31.
- 8.DiazGranados CA, Zimmer SM, Mitchel K, Jernigan JA: *Comparison of mortality associated with vancomycin-resistant and vancomycin-susceptible enterococcal bloodstream infections: a meta-analysis. Clinical infectious diseases* 2005, 41(3):327–333.
- 9.Ireland's first One Health Report on Antimicrobial Use and Antimicrobial Resistance.
- 10.National habiN: *Quality Assessment Tool for observational cohort and cross-sectional studies. <https://www.nhlbi.nih.gov/health-topics/study-quality-assessment-tools>* 2017.
- 11.Singh S: *How to conduct and interpret systematic reviews and meta-analyses. Clinical and translational gastroenterology* 2017, 8(5):e93.
- 12.Hak T, van Rhee H, Suurmond R: *How to interpret results of meta-analysis. Available at SSRN 3241367* 2016.
- 13.Abamecha A, Wondafrash B, Abdissa A: *Antimicrobial resistance profile of Enterococcus species isolated from intestinal tracts of hospitalized patients in Jimma, Ethiopia. BMC research notes* 2015, 8:213.
- 14.Abebe W, Endris M, Tiruneh M, Moges F: *Prevalence of vancomycin resistant Enterococci and associated risk factors among clients with and without HIV in Northwest Ethiopia: a cross-sectional study. BMC Public Health* 2014, 14(1):185.
- 15.Agegne M, Abera B, Derbie A, Yismaw G, Shiferaw MB: *Magnitude of Vancomycin-Resistant Enterococci (VRE) Colonization among HIV-Infected Patients Attending ART Clinic in West Amhara Government Hospitals. International journal of microbiology* 2018, 2018:7.
- 16.Ali S, Alemayehu M, Dagnew M, Gebrecherkos T: *Vancomycin-Resistant Enterococci and Its Associated Risk Factors among HIV-Positive and -Negative Clients Attending Dessie Referral Hospital, Northeast Ethiopia. International journal of microbiology* 2018, 2018:9.
- 17.Ferede ZT, Tullu KD, Derese SG, Yeshanew AG: *Prevalence and antimicrobial susceptibility pattern of Enterococcus species isolated from different clinical samples at Black Lion Specialized Teaching Hospital, Addis Ababa, Ethiopia. BMC research notes* 2018, 11(1):793.
- 18.Solomon FB, Wadilo FW, Arota AA, Abraham YL: *Antibiotic resistant airborne bacteria and their multidrug resistance pattern at University teaching referral Hospital in South Ethiopia. Annals of clinical microbiology and antimicrobials* 2017, 16(1):29.

- 19.Toru M, Beyene G, Kassa T, Gizachew Z, Howe R, Yeshitela B, Yeshitila B: *Prevalence and phenotypic characterization of Enterococcus species isolated from clinical samples of pediatric patients in Jimma University Specialized Hospital, south west Ethiopia. BMC research notes* 2018, 11(1):281.
- 20.Yilema A, Moges F, Tadele S, Endris M, Kassu A, Abebe W, Ayalew G: *Isolation of enterococci, their antimicrobial susceptibility patterns and associated factors among patients attending at the University of Gondar Teaching Hospital. BMC infectious diseases* 2017, 17(1):276–276.
- 21.Ateba CN, Lekoma KP, Kawadza DT: *Detection of vanA and vanB genes in vancomycin-resistant enterococci (VRE) from groundwater using multiplex PCR analysis. Journal of water and health* 2013, 11(4):684–691.
- 22.Iweriebor BC, Gaqavu S, Obi LC, Nwodo UU, Okoh AI: *Antibiotic susceptibilities of enterococcus species isolated from hospital and domestic wastewater effluents in Alice, eastern cape province of South Africa. Int J Environ Res Public Health* 2015, 12(4):4231–4246.
- 23.Iweriebor BC, Obi LC, Okoh AI: *Virulence and antimicrobial resistance factors of Enterococcus spp. isolated from fecal samples from piggery farms in Eastern Cape, South Africa. BMC microbiology* 2015, 15:136.
- 24.Iweriebor BC, Obi LC, Okoh AI: *Macrolide, glycopeptide resistance and virulence genes in Enterococcus species isolates from dairy cattle. Journal of medical microbiology* 2016, 65(7):641–648.
- 25.Matlou DP, Bissong MEA, Tchatchouang CK, Adem MR, Foka FET, Kumar A, Ateba CN: *Virulence profiles of vancomycin-resistant enterococci isolated from surface and ground water utilized by humans in the North West Province, South Africa: a public health perspective. 2019, 26(15):15105–15114.*
- 26.Molale LG, Bezuidenhout CC: *Antibiotic resistance, efflux pump genes and virulence determinants in Enterococcus spp. from surface water systems. Environmental science and pollution research international* 2016, 23(21):21501–21510.
- 27.Molechan C, Amoako DG, Abia ALK, Somboro AM, Bester LA, Essack SY: *Molecular epidemiology of antibiotic-resistant Enterococcus spp. from the farm-to-fork continuum in intensive poultry production in KwaZulu-Natal, South Africa. Science of The Total Environment* 2019, 692:868–878.
- 28.Tatsing Foka FE, Ateba CN: *Detection of Virulence Genes in Multidrug Resistant Enterococci Isolated from Feedlots Dairy and Beef Cattle: Implications for Human Health and Food Safety. BioMed Research International* 2019, 2019:13.
- 29.Hammad AM, Hassan HA, Shimamoto T: *Prevalence, antibiotic resistance and virulence of Enterococcus spp. in Egyptian fresh raw milk cheese. Food Control* 2015, 50:815–820.
- 30.Hassan RM, Ghaith DM, Ismail DK, Zafer MM: *Reduced susceptibility of Enterococcus spp. isolates from Cairo University Hospital to tigecycline: Highlight on the influence of proton pump inhibitors. Journal of global antimicrobial resistance* 2018, 12:68–72.
- 31.Moemen D, Tawfeek D, Badawy W: *Healthcare-associated vancomycin resistant Enterococcus faecium infections in the Mansoura University Hospitals intensive care units, Egypt. Brazilian journal of microbiology: [publication of the Brazilian Society for Microbiology]* 2015, 46(3):777–783.

- 32.Osman KM, Badr J, Orabi A, Elbehiry A, Saad A, Ibrahim MDS, Hanafy MH: *Poultry as a vector for emerging multidrug resistant Enterococcus spp.: First report of vancomycin (van) and the chloramphenicol-florfenicol (cat-fex-cfr) resistance genes from pigeon and duck faeces. Microbial pathogenesis* 2019, 128:195–205.
- 33.Ben Said L, Klibi N, Dziri R, Borgo F, Boudabous A, Ben Slama K, Torres C: *Prevalence, antimicrobial resistance and genetic lineages of Enterococcus spp. from vegetable food, soil and irrigation water in farm environments in Tunisia. Journal of the science of food and agriculture* 2016, 96(5):1627–1633.
- 34.Ben Yahia H, Chairat S, Hamdi N, Gharsa H, Ben Sallem R, Ceballos S, Torres C, Ben Slama K: *Antimicrobial resistance and genetic lineages of faecal enterococci of wild birds: Emergence of vanA and vanB2 harbouring Enterococcus faecalis. International journal of antimicrobial agents* 2018, 52(6):936–941.
- 35.Dziri R, Lozano C, Ben Said L, Bellaaj R, Boudabous A, Ben Slama K, Torres C, Klibi N: *Multidrug-resistant enterococci in the hospital environment: detection of novel vancomycin-resistant E. faecium clone ST910. Journal of infection in developing countries* 2016, 10(8):799–806.
- 36.Naouel K, Amor I, Rahmouni M, Dziri R, Douja G, Ben Said L, Lozano C, Boudabous A, Karim BS, Mansouri R et al: *Diversity of species and antibiotic resistance among fecal enterococci from wild birds in Tunisia. Detection of vanA-containing Enterococcus faecium isolates. European Journal of Wildlife Research* 2014, 61.
- 37.Bouamama L, Sorlozano A, Laglaoui A, Lebbadi M, Aarab A, Gutierrez J: *Antibiotic resistance patterns of bacterial strains isolated from Periplaneta americana and Musca domestica in Tangier, Morocco. Journal of infection in developing countries* 2010, 4(4):194–201.
- 38.Bouymajane A, Rhazi Filali F, Oulghazi S, Ed-Dra A, Benhallam F, El Allaoui A, Anissi J, Sendide K, Ouhmidou B, Moumni M: *Occurrence, molecular and antimicrobial resistance of Enterococcus spp. isolated from raw cow's milk trade by street trading in Meknes city, Morocco. Germs* 2018, 8(2):77–84.
- 39.Hannaoui I, Barguigua A, Serray B, El Mdaghri N, Timinouni M, Ait Chaoui A, El Azhari M: *Intestinal carriage of vancomycin-resistant enterococci in a community setting in Casablanca, Morocco. Journal of global antimicrobial resistance* 2016, 6:84–87.
- 40.Aamodt H, Mohn SC, Maselle S, Manji KP, Willems R, Jureen R, Langeland N, Blomberg B: *Genetic relatedness and risk factor analysis of ampicillin-resistant and high-level gentamicin-resistant enterococci causing bloodstream infections in Tanzanian children. BMC infectious diseases* 2015, 15:107.
- 41.Katakweba AA, Moller KS, Muumba J, Muhairwa AP, Damborg P, Rosenkrantz JT, Minga UM, Mtambo MM, Olsen JE: *Antimicrobial resistance in faecal samples from buffalo, wildebeest and zebra grazing together with and without cattle in Tanzania. Journal of applied microbiology* 2015, 118(4):966–975.
- 42.Katakweba AAS, Muhairwa AP, Lupindu AM, Damborg P, Rosenkrantz JT, Minga UM, Mtambo MMA, Olsen JE: *First Report on a Randomized Investigation of Antimicrobial Resistance in Fecal Indicator Bacteria from Livestock, Poultry, and Humans in Tanzania. Microbial drug resistance (Larchmont, NY)* 2018, 24(3):260–268.
- 43.Kateete DP, Edolu M, Kigozi E, Kisukye J, Baluku H, Mwiine FN, Najjuka CF: *Species, antibiotic susceptibility profiles and van gene frequencies among enterococci isolated from patients at Mulago National Referral Hospital in Kampala, Uganda. BMC infectious diseases* 2019, 19(1):486.

- 44.Kateete DP, Kabugo U, Baluku H, Nyakarahuka L, Kyobe S, Okee M, Najjuka CF, Joloba ML: *Prevalence and antimicrobial susceptibility patterns of bacteria from milkmen and cows with clinical mastitis in and around Kampala, Uganda. PloS one* 2013, *8*(5):e63413.
- 45.Ngonzi J, Bebell LM, Bazira J: *Risk Factors for Vaginal Colonization and Relationship between Bacterial Vaginal Colonization and In-Hospital Outcomes in Women with Obstructed Labor in a Ugandan Regional Referral Hospital.* 2018, *2018*:6579139.
- 46.Anyanwu M: *Prevalence and Antibigram of Generic Enterococci in Ready-to-Slaughter Beef Cattle. Notulae Scientia Biologicae* 2015, *7*:390–399.
- 47.Ngbede EO, Raji MA, Kwanashie CN, Kwaga JKP: *Antimicrobial resistance and virulence profile of enterococci isolated from poultry and cattle sources in Nigeria. Tropical animal health and production* 2017, *49*(3):451–458.
- 48.Djahmi N, Boutet-Dubois A, Nedjai S, Dekhil M, Sotto A, Lavigne JP: *Molecular epidemiology of Enterococcus sp. isolated in a university hospital in Algeria. Scandinavian journal of infectious diseases* 2012, *44*(9):656–662.
- 49.Faron ML, Ledebouer NA, Buchan BW: *Resistance mechanisms, epidemiology, and approaches to screening for vancomycin-resistant enterococcus in the health care setting. J Clin Microbiol* 2016, *54*(10):2436–2447.
- 50.McEwen SA, Collignon PJ: *Antimicrobial resistance: a One Health perspective. Microbiology spectrum* 2018, *6*(2).
- 51.Kahn LH: *Antimicrobial resistance: a One Health perspective. Transactions of the Royal Society of Tropical Medicine and Hygiene* 2017, *111*(6):255–260.
- 52.Moghimbeigi A, Moghimbeygi M, Dousti M, Kiani F, Sayehmiri F, Sadeghifard N, Nazari A: *Prevalence of vancomycin resistance among isolates of enterococci in Iran: a systematic review and meta-analysis. Adolescent health, medicine and therapeutics* 2018, *9*:177.
- 53.Gold HS: *Vancomycin-Resistant Enterococci: Mechanisms and Clinical Observations. Clinical Infectious Diseases* 2001, *33*:210–219.
- 54.A A Ramadhan EH: *Survivability of vancomycin resistant enterococci and fitness cost of vancomycin resistance acquisition. J Clin Pathol* 2005, *58*:744–746.
- 55.Sloan LM, Uhl JR, Vetter EA, Schleck CD, Harmsen WS, Manahan J, Thompson RL, Rosenblatt JE, Cockerill FR: *Comparison of the Roche LightCycler *vanA*/*vanB* Detection Assay and Culture for Detection of Vancomycin-Resistant Enterococci from Perianal Swabs. Journal of Clinical Microbiology* 2004, *42*(6):2636–2643.
- 56.Deschaght P, De Baere T, Van Simaey L, Van Daele S, De Baets F, De Vos D, Pirnay JP, Vaneechoutte M: *Comparison of the sensitivity of culture, PCR and quantitative real-time PCR for the detection of Pseudomonas aeruginosa in sputum of cystic fibrosis patients. BMC microbiology* 2009, *9*:244.
- 57.Maya Nadimpalli ED-A, 1 David C. Love,2 Lance B. Price,3 Bich-Tram Huynh,1 Jean-Marc Collard,4, Krui Sun Lay LB, 6 Awa Ndir,7 Timothy R. Walsh,8 and Didier Guillemot1; for the Bacterial Infections and antibiotic-Resistant

Diseases, Groupa aYcil-icBS: *Combating Global Antibiotic Resistance: Emerging One Health Concerns in Lower- and Middle-Income Countries. Clinical Infectious Diseases* 2018, 66(6):963–969.

Tables

Table 1 articles that are selected for systematic review and meta- analysis of VRE in Africa

Author	Year	Country	Source of sample	Lab. Method	Enterococcus (N)	VRE (%)
Bouamama <i>et al</i> [13]	2010	Morocco	Flies & cockroaches	Culture	29	0
Djahmi <i>et al</i> [14]	2012	Algeria	Clinical specimen	Culture&PCR	125	4
Ateba <i>et al</i> [15]	2013	South Africa	Ground water	PCR	179	166
Kateete <i>et al</i> [16]	2013	Uganda	Milkmen & Cows mastitis	Culture	24	3
Moemen <i>et al</i> [17]	2014	Egypt	Clinical specimen	Culture	52	12
Abebe <i>et al</i> [18]	2014	Ethiopia	Stool sample	Culture	201	11
Katakweba <i>et al</i> [19]	2014	Tanzania	Buffalo, Zebra, Cattle & wildebeest faecal	Culture&PCR	120	10
Naouel <i>et al</i> [20]	2014	Tunisia	Feces of birds	Culture&PCR	73	6
Anyanwu <i>et al</i> [21]	2015	Nigeria	Cattle rectal swab	Culture	75	5
Iweriebor <i>et al</i> [22]	2015	South Africa	Pig feaces	Culture&PCR	320	320
Aamodt <i>et al</i> [23]	2015	Tanzania	Blood	BacTec	39	39
Hammad <i>et al</i> [24]	2015	Egypt	Milk cheese	Culture&PCR	120	6
Benson <i>et al</i> [25]	2015	South Africa	Hospital waste water	Culture&PCR	62	60
Abamecha <i>et al</i> [26]	2015	Ethiopia	Patients feaces	Culture	142	7
Iweriebor <i>et al</i> [27]	2016	South Africa	Cattles	Culture & PCR	340	340
Dziri <i>et al</i> [28]	2016	Tunisia	Env't sample	Culture	100	6
Ben Said <i>et al</i> [29]	2016	Tunisia	Vegetable,soil&water	Culture	65	4
Nadjette <i>et al</i> [30]	2016	Algeria	Clinical specimen	Culture	85	2
Hannaoui <i>et al</i> [31]	2016	Morocco	Faecal specimen	Culture&PCR	100	21
Molale1&Cornelis [32]	2016	South Africa	Surface water	Culture&PCR	124	86
Emmanuel <i>et al</i> [33]	2016	Nigeria	Rectal swab & manure of poultry& cattle	Culture&PCR	167	0
Yilema <i>et al</i> [34]	2017	Ethiopia	Clinical specimen	Culture	24	10
Solomon <i>et al</i> [35]	2017	Ethiopia	Indoor air sample	Culture	40	3
Katakweba <i>et al</i> [36]	2017	Tanzania	Feces of livestock, poultry & human	Culture&PCR	228	12
Ferede <i>et al</i> [37]	2018	Ethiopia	Clinical specimen	Culture	15	2
Seid <i>et al</i> [38]	2018	Ethiopia	Stool sample	Culture	112	7
Joseph <i>et al</i> [39]	2018	Uganda	Vaginal swab	Culture	49	0
Manamenot <i>et al</i> [40]	2018	Ethiopia	Stool sample	Culture	220	17
Aziz <i>et al</i> [41]	2018	Morocco	Cow milk	Culture&PCR	17	0
Hassan <i>et al</i> [42]	2018	Egypt	Clinical specimen	PCR	67	17
Houssem <i>et al</i> [43]	2018	Tunisia	Wild birds feces	Culture&PCR	79	5
Toru <i>et al</i> [44]	2018	Ethiopia	Clinical specimen	Culture	22	5
Molechan <i>et al</i> [45]	2019	South Africa	Poultry	Culture&PCR	131	0
Daniel <i>et al</i> [46]	2019	South	Water	Culture&PCR	56	44

Africa						
Osman <i>et al</i> [47]	2019	Egypt	Poultry	Culture&PCR	106	101
Kateete <i>et al</i> [48]	2019	Uganda	Clinical specimen	Culture	115	20
Frank <i>et al</i> [49]	2019	South	Feaces, water & soil	Culture&PCR	289	176
Africa						

Table 2-subgroup analysis of VRE based on laboratory methods used employed

Subgroups	Studies	Estimate	Lower -upper bound	Std. error	p- Val	z- Val	Heterogeneity		
							Q(df)	Het. P-val	I ² (%)
Culture & PCR	17	0.389	0.161-0.616	0.116	<0.001	3.35	84591.2(16)	< 0.001	99.98
Culture	17	0.073	0.048- 0.098	0.013	<0.001	5.76	57.5(16)	< 0.001	72.16
PCR	2	0.592	0.068- 1.253	0.337	0.079	1.76	141.7(1)	< 0.001	99.29
BacTec	1	0.988	0.953- 1.022	0.018	NA	NA	NA	NA	NA
Overall	37	0.288	0.129- 0.447	0.081	<0.001		100478.6 (36)	< 0.001	99.96

Figures

Figure 1

the flow daigram for the article selection of vancomycin resistance entrococcus in Africa with a onehealth approach: a systematic review and meta-analysis

Figure 2

shows that the subgroup analysis of VRE at country level

Figure 3

shows the subgroup analysis based on the source of the sample for VRE in Africa

Supplementary Files

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- [PRISMA2009checklist.doc](#)