Environmental Mediation of Colistin Resistance in the African Context. A Systematic Review

Udochukwu Emmanuel Osiogu¹

¹Dr HILLA LIMANN TECHNICAL UNIVERSITY, WA, Ghana

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Although scanty, there are recent reports of colistin resistance especially in infections caused by gram negative organisms such as Escherichia coli, Klebsiella pneumoniae, Salmonella typhi etc. The rising prevalence of AMR in Gram-negative bacteria is a major medical concern with ramifications that will inevitably affect a variety of socioeconomic aspects on a global scale. The fast spread of colistin resistant genes among gram-negative bacteria is particularly alarming since they impart resistance to organisms that have developed resistance to highly conserved and last-resort antibiotics like colistin. The movement of colistin resistance genes into and out of the resistome is a constant that has to be investigated in the context of colistin resistance in Sub-Saharan Africa. This study therefore offers a systematic review of articles delineating how environmental factors contribute to the resistance of gram negative bacteria to colistin and the components involved. In this regard, this study examined the most recent articles (employing PubMed, Science Direct, MEDLINE, EMBASE, Scopus, and Google Scholar) using the following terms and/or text words; “environment”, “Colistin in humans and animals”, “aquatic-based foods”, mobile Colistin resistance gene”, “plasmid-mediated Colistin resistance gene”, “plasmid-borne COL resistance”, “water”, “bacterial isolates”, “mobile COL resistance”, “enterobacteria”, “Gram-negative bacilli”, “wildlife”, and soil sewages” with particular interest in Africa. A total of 847 articles were identified based on search terms. Out of these articles, 26 peer reviewed articles were included, all focusing on Africa. 8 of the articles were from Tunisia with 7 being from Algeria. The remaining span from South Africa, to Egypt, Nigeria and Congo with the least being from Congo. This review confirms the rapid spread of plasmid mediated colistin resistant genes in humans, animals, and the environmental (manure/soil, aquatic, and wildlife) in Africa with mcr-1 as the most common genetic variant and E. coli being the most predominant organism spreading the mcr genes in Africa with Tunisia, Algeria and South Africa reporting the highest occurrence. There is therefore the need for more research into colistin resistance and the launch of an African-wide antibiotic stewardship.