

The Molecular Epidemiology and Genetic Environment of Carbapenemases Detected in Africa

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Abstract

Research articles describing carbapenemases and their genetic environments in Gram-negative bacteria were reviewed to determine the molecular epidemiology of carbapenemases in Africa. The emergence of resistance to the carbapenems, the last resort antibiotic for difficult to treat bacterial infections, affords clinicians few therapeutic options, with a resulting increase in morbidities, mortalities, and healthcare costs. However, the molecular epidemiology of carbapenemases throughout Africa is less described. Research articles and conference proceedings describing the genetic environment and molecular epidemiology of carbapenemases in Africa were retrieved from Google Scholar, Scifinder, Pubmed, Web of Science, and Science Direct databases. Predominant carbapenemase genes so far described in Africa include the blaOXA-48 type, blaIMP, blaVIM, and blaNDM in *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Citrobacter* spp., and *Escherichia coli* carried on various plasmid types and sizes, transposons, and integrons. Class D and class B carbapenemases, mainly prevalent in *A. baumannii*, *K. pneumoniae*, *E. cloacae*, *Citrobacter* spp., and *E. coli* were the commonest carbapenemases. Carbapenemases are mainly reported in North and South Africa as under-resourced laboratories, lack of awareness and funding preclude the detection and reporting of carbapenemase-mediated resistance. Consequently, the true molecular epidemiology of carbapenemases and their genetic environment in Africa is still unknown.