

Title

First author first name followed by surname,¹ * second author first name followed by surname,² third author first name followed by surname,³ etc... according to the number of authors

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A single paragraph of 150-250 words maximum and not broken down into separate headings; objectives, methods, results, and conclusion. The same contents are squeezed into a single paragraph without headings and references.

Example:

First Clinical Case of VIM-1-Producing *Leclercia adecarboxylata*: A case report and literature review

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Leclercia adecarboxylata is a recently recognised emerging pathogen. We describe the first emergence of *L. adecarboxylata* generating VIM-1 in an immunocompetent 63-year-old female patient with an abrupt intracerebral haemorrhage. This case report aimed to narrate the course of infection, management, outcomes and the unique morphological and molecular characteristics of the VIM-1-producing *L. adecarboxylata*. The local laboratory used API E to identify the multi-drug resistant strain in the patient's sample. It was identified using Vitek 2, MALDI-TOF MS and 16S rRNA sequencing after being sent to the central public health laboratory. Vitek 2 was used to conduct antimicrobial susceptibility testing (AST), which employed the AST GN card 215 and the E test. The Clinical and Laboratory Standards Institute served as the foundation for the data interpretation. To validate the isolate's phenotype as a Carbapenem producing Enterobacterials (CPE), the modified Hodge test and the modified Carbapenem inactivation technique were used. Furthermore, multiplex PCR targeting blaOXA-48, blaNDM, blaKPC, blaIMP and blaVIM was used to characterise the CPE genes on a molecular level. Finally, the sanger cycle sequencing technique (BigDye™ Terminator v3.1 - Cycle Sequencing) was used for VIM amplicon to confirm VIM-1. The strain was incorrectly classified as *Citrobacter koseri* by API E (99.9%) and *Pantoea* species by Vitek 2, however *L. adecarboxylata* was verified by MALDI-TOF MS (score 2) and 16S ribosomal RNA analysis. The existence of two populations of resistance genes, VIM-1 and OXA-48, was detected using conventional PCR.