

“High Prevalence of New Delhi Metallo β -Lactamases in Multidrug-Resistant (MDR) *Klebsiella pneumoniae* Sequence Type 101 in Khartoum Hospitals”

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High Prevalence of New Delhi Metallo β -Lactamases in Multidrug-Resistant (MDR) *Klebsiella pneumoniae* Sequence Type 14 in Khartoum Hospitals.

Introduction: The use of carbapenems against extended spectrum beta lactamase (ESBL)-producing Gram-negative microorganisms is increasing in Sudan, which is expected to lead to the emergence of carbapenem-resistant organisms. The current study was carried out to determine the prevalence of carbapenemases-producing *K. pneumoniae* in Khartoum hospitals.

Methods: A total of 120 *k.pneumoniae* isolates were cultured from clinical samples collected from different hospitals in Khartoum, Sudan, from April 2015 to October 2016. Species-confirmation was done using specific PCR primers of *K. pneumoniae*, Pf/Pr1 and Pf/Pr2.

Antibiotic sensitivity was determined by disk diffusion method. Antibiotic resistance sequences were detected using a simple blaNDM PCR and two multiplex PCR to detect the carbapenemase genes, blaIMP, blaKPC, blaVIM, and blaOXA-48, blaGES. Multi Locus Sequence Typing (MLST) was done to identify the sequence typing of MDR *K. pneumoniae*.

Results: 10 isolates were imipenem disk resistant and 28 isolates were meropenem disk resistant. 44 (36.6%) had carbapenemase gene; *K. pneumoniae* ST 14 has three genes Thirty two *K. pneumoniae* isolates were positive for NDM, 10 isolates had OXA48 gene, 3 had VIM and 6 were positive for GES. Six of the 44 with carbapenemases had more than one carbapenemase gene; one isolate was positive for NDM, OXA48 and VIM, two of isolates were positive for NDM and VIM, one had ND and GES and two had both OXA48 and GES.

Conclusion: our results showed an alarmingly high prevalence of cabapenamases and carbapenem resistance among *K. pneumoniae* in Khartoum hospitals. 44 (36.6%) of *K. pneumoniae* isolates studied carried carbapenemases genes, of 10 isolates of which showed resistance to both imipenem and meropenem, eight has carbapenemases (OXA48, NDM, GES) genes. Eighteen were resistant to meropenem, Sixteen of them has carbapenemases (OXA48, NDM, GES, VIM) genes.

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Circulation of influenza A viruses in dromedary camels in Saudi Arabia

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Introduction: Influenza A viruses (IAV) represent a major global challenge to the health of both humans and animals. They can cause severe respiratory diseases and are associated with regular epidemics and occasional pandemics due to their antigenic changes and wide host range. While many aspects of camels had been revealed after the emergence of the Middle East Respiratory Syndrome-Coronavirus (MERS-CoV), it is not really known whether or not these dromedaries could represent unrecognized host of IAV. Given that Saudi Arabia harbors thousands of camels and imports several other thousands from Africa every year, here we set to investigate the presence of IAV in dromedaries in Saudi Arabia.

Materials and Methods: A total of 665 Nasal swabs were collected from domestic and imported dromedary camels between 2017 and 2018. Extracted viral RNA was screened for IAV by RT-PCR and positive samples were sequenced to identify potential IAV in camels in comparison to available sequences in the GenBank database.

Results: Of the 665 samples, 11 samples (1.7%) were positive for IAV, and five samples were used for partial sequencing which confirmed IAV circulation in dromedary camels. Partial sequencing also suggested circulation of H3N8 subtype in which sequences of full gene segments from these viruses were analyzed to further characterize these viruses.

Discussion and Conclusion: While the number of detected IAV in this study is limited (11/665, 1.7%), our data for the first time clearly show that dromedary camels could represent a potential host and zoonotic source of IAV. This work also highlights the importance of enhancing influenza surveillance in camels as well as other animal species to elucidate their possible role in influenza transmission and to better understand the epidemiology of influenza.

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In silico and in vitro Evaluation of new chalcon compounds as anti-leishmania donovani promastigote; molecular modeling approach

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Background: Protozoal infections caused by species which belong to *L. donovani* complex are responsible for the most severe form of leishmaniasis, especially in Sudan and other developing countries. Furthermore, the incidence of leishmaniasis continues to rise due to lack of a vaccine. Drugs commonly used for the treatment of the disease have associated by serious side effects. Thus, there is a need to develop newer drug therapies. Literature revealed that chalcones have potential antiparasitic activity.

