"High Prevalence of New Delhi Metalo β-Lactamases in Multidrug-Resistant (MDR) Klebsiella.pneumoniae Sequence Type 101 in Khartoum Hospitals"

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High Prevalence of New Delhi Metalo 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.pneumoniea.

Results: 10 isolates were imipenem disk resistant and 28 isolates were meropenem disk resistant. 44 (36.6%) had carbapenamase gene; K.pneumoniea 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 carbapenamases had more than one carbapenamase 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 carbapenamases 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 promastigoat; 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 activitiy.

Objective: The aim of this study was to evaluate the antileishmanial activity of new chalcon compounds.

Methods: Biopsies from psitive lymph node aspiration were aseptically inoculated into vacutainers containing Novy-MacNeal-Nicolle (NNN) medium. Cultures were incubated at 25 °C. Promastigotes were transferred into tissue culture flasks containing LIT media supplemented with 10% fetal calf serum (FCS), genatmycin and benzylpenicillin. Promastigote density was adjusted to 2×106 parasites/ml using LIT complete media. A volume of 100 μl from parasite culture was transferred into 96-well microtiter plate. Various concentrations of chalcones solution were added (100 μl) in triplicates. A negative control (DMSO), and positive control (amphotericin B) were treated similarly. The plates were incubated at 25 °C for 72 hours. Parasites were counted by using hemocytometer.

To investigate the molecular mechanism of action of chalcones different leishmania donovani targets were downloaded from protein data bank. The tested compounds were docked into these targets using Sybyl and the corresponding scores were recorded.

Results: Chalcones, at dose range 200–0.05 μg/ml, showed 99.11 ± 1.19– 12.14 ± 2.77% promastigote inhibitory activity, and the positive control showed 94.79 ± 1.96 –18.29 ± 7.61% inhibitory activity at the same dose range. The IC50 values for chalcones rang from0.8 ± 0.09– 0.13 ± 0.05 μg/ml and 0.24 ± 0.02 μg/ml for amphotericin B. In silico study revealed that this activity could be mediated through Adeninephosphoribosyle transferase (Cscore6.21–4.72) inhibition for chalcon.

Conclusion: Chalcone compounds showed promising activity against Leishmania donovani promastigotes when compared to amphotericin B.

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Rapid identification of pathogens from flagged blood cultures by multiplex PCR using the FilmArray system

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Background and purpose: Rapid and accurate identification of pathogens and antibiotic resistance directly from flagged blood cultures could early optimize antibiotic treatment and improve patient outcomes. We compared the results of the FilmArray Blood Culture Identification (BCID) panel with those of conventional methods for organism identification and antibiotic susceptibility.

Methods: A total of 100 randomly selected positive blood cultures (BD BACTEC Plus Aerobic and Anaerobic bottles) were analyzed. The FilmArray BCID panel was used in comparison with the conventional methods with MALDI-TOF MS (Bruker Biotyper) system. This multiplex PCR-based panel can identify 27 targets pathogens, including 19 bacteria and five candida species, and four antibiotic resistance genes (mecA, vanA/vanB, and KPC) from positive blood cultures with one hour. 16S rRNA sequencing analysis for species identification and PCR for detection of resistance gene were conducted for any discrepant results.

Results: Among the 100 flagged blood cultures, 95% of the identification by the multiplex PCR BCID panel were consistent with the identification with standard-of-care methods with MALDI-TOF MS results. One isolate of K. pneumonae identified 16S rRNA sequencing analysis was identified as K. oxytoca by multiplex PCR BCID panel and K. pneumonae by MALDI-TOF MS. One isolate of Klebsiella spp. identified 16S r-RNA sequencing analysis was identified as K. pneumoniae by multiplex PCR BCID panel and K. variicola by MALDI-TOF MS. Five vancomycin-resistant enterococci that were with positive for vanA/vanB genes and one Klebsila pneumoniae isolates positive for KPC gene were correctly identified by the FilmArray BCID panel. Among the 12 Staphylococcus species with positive mecA gene identified by the FilmArray BCID panel, three (one methicillin-susceptible S. aureus and two methicillin-susceptible coagulase-negative staphylococci) were mecA negative by other PCR method (75% accuracy).

Conclusion: The FilmArray BCID panel shows good correlation with blood culture identification and antibiotic resistance detection performed by conventional methods.

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Circulation of Non-MERS Coronaviruses in Imported Camels In Saudi Arabia

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Background and purpose: Coronaviruses (CoVs) are important human and animal pathogens causing around one-third of the community-acquired upper respiratory tract infections in humans and huge economic loss in animals. While the discovery of SARS-CoV triggered the search for new CoVs in animals, the recent emergence of MERS-CoV in humans and dromedary camels increased the interest in the discovery of novel CoVs as well as other viruses in dromedaries. So far, at least two additional new CoVs have been discovered in dromedaries including DcCoV UAE-HKU23 and human CoV-229E-related camel alpha-CoV. In this study, we investigated the possible carriage of other non-MERS CoVs in imported camels into Saudi Arabia which is a major importer of dromedary camels from Africa.

Methods: Approximately 337 nasal swabs were collected from dromedary camels at the port of entry in the western region of Saudi Arabia. Viral RNA was extracted from samples and screened for coronaviruses using RT-PCR. Positive samples were sequenced to identify circulating coronaviruses.

Results: Out of 337 tested samples, 28 samples were positive for coronaviruses by RT-PCR. Partial sequencing of these viral genome showed that at least 2 camels were infected with human CoV-229E-related camel alpha-CoV. Partical sequencing of remaining samples did not reveal any known coronaviruses. Full genome of these viruses was sequenced and analyzed to further characterize these viruses.

Conclusion: Our data show that that co-infection or concurrent infection with MERS-CoV as well as other CoVs is not uncommon in imported African camels in Saudi Arabia and might result in recombination and/or possible emergence of novel CoVs. Therefore, it is highly recommended to establish enhanced surveillance for CoVs in imported camels to better understand their role in CoVs epidemiology in Saudi Arabia.

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