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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