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

Methods: Biopsies from positive lymph node aspiration were aseptically inoculated into vacuutainers 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), gentamycin 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 ranged from 0.8 ± 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 Adeninereceptorsinfluence phosphorylase 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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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 DcoV 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. Partial 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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