

Veille scientifique Maladies tropicales négligées

Semaine 0316 au 22 janvier 2023

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Dengue, chikungunya et maladie à virus Zika

Differential proteomics of Zika virus (ZIKV) infection reveals molecular changes potentially involved in immune system evasion by a Brazilian strain of ZIKV.

Tatara JM, Rosa RL, Varela APM, Teixeira TF, Sesterheim P, Gris A, Driemeier D, Moraes ANS, Berger M, Peña RD, Roehe PM, Souza DOG, Guimarães JA, Campos AR, Santi L, Beys-da-Silva WO.

20-01-2023

Arch Virol.

https://pubmed.ncbi.nlm.nih.gov/36658439/

Zika virus (ZIKV) is an arbovirus that was responsible for multiple outbreaks from 2007 to 2015. It has been linked to cases of microcephaly in Brazil in 2015, among other neurological disorders. Differences among strains might be the reason for different clinical outcomes of infection. To evaluate this hypothesis, we performed a comparative proteomic analysis of Vero cells infected with the African strain MR766 (ZIKVAFR) and the Brazilian strain 17 SM (ZIKVBR). A total of 550 proteins were identified as differentially expressed in ZIKVAFR- or ZIKVBR-infected cells compared to the control. The main findings included upregulation of immune system pathways (neutrophil degranulation and adaptive/innate immune system) and potential activation of immune-system-related pathways by ZIKVAFR (mTOR, JAK-STAT, NF-κB, and others) compared with the ZIKVBR/control. In addition, phagocytosis by macrophages and engulfment of leukocytes were activated in ZIKVAFR infection. An in vivo analysis using an immunocompetent C57BL/6N mouse model identified interstitial pneumonia with neutrophil infiltration in the lungs only in mice infected with ZIKVBR at 48 hours postinfection, with a significant amount of virus detected. Likewise, only animals infected with ZIKVBR had viral material in the cytoplasm of lung macrophages. These results suggest that activation of the immune system by ZIKVAFR infection may lead to faster viral clearance by immune cells.

Sinococuline, a bioactive compound of Cocculus hirsutus has potent antidengue activity.

Shukla R, Ahuja R, Beesetti H, Garg A, Aggarwal C, Chaturvedi S, Nayyar K, Arora U, Lal AA, Khanna N. 19-01-2023

Sci Rep.

https://pubmed.ncbi.nlm.nih.gov/36658277/

Dengue virus (DENV) infection has increased worldwide, with over 400 million infections annually, and has become a serious public health concern. Several drug candidates, new and repurposed, have failed to meet the primary efficacy endpoints. We have recently shown that Aqueous Extract of the stem of Cocculus hirsutus (AQCH) was effective in vitro and in vivo against DENV and was safe in humans. We now report that an active ingredient of AQCH, Sinococuline, protects against the antibody-

mediated secondary-DENV infection in the AG129 mouse model. DENV infection markers were assessed, viz. serum viremia and vital organs pathologies-viral load, proinflammatory cytokines and intestinal vascular leakage. The treatment with Sinococuline at 2.0 mg/kg/day; BID (twice a day), was the most effective in protecting the severely DENV-infected AG129 mice. Also, this dose effectively reduced serum viremia and tissue-viral load and inhibited the elevated expression levels of proinflammatory cytokines (TNF- α and IL-6) in several vital organs. Based on these findings, it could be explored further for pre-clinical and clinical developments for the treatment of dengue.

Interferon-induced restriction of Chikungunya virus infection.

Suzuki Y.

Feb-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36657882/

CRISPR mediated transactivation in the human disease vector Aedes aegypti.

Bui M, Dalla Benetta E, Dong Y, Zhao Y, Yang T, Li M, Antoshechkin IA, Buchman A, Bottino-Rojas V, James AA, Perry MW, Dimopoulos G, Akbari OS.

19-01-2023

PLoS Pathog.

https://pubmed.ncbi.nlm.nih.gov/36656895/

As a major insect vector of multiple arboviruses, Aedes aegypti poses a significant global health and economic burden. A number of genetic engineering tools have been exploited to understand its biology with the goal of reducing its impact. For example, current tools have focused on knocking-down RNA transcripts, inducing lossof-function mutations, or expressing exogenous DNA. However, methods for transactivating endogenous genes have not been developed. To fill this void, here we developed a CRISPR activation (CRISPRa) system in Ae. aegypti to transactivate target gene expression. Gene expression is activated through pairing a catalyticallyinactive ('dead') Cas9 (dCas9) with a highly-active tripartite activator, VP64-p65-Rta (VPR) and synthetic guide RNA (sgRNA) complementary to a user defined target-gene promoter region. As a proof of concept, we demonstrate that engineered Ae. aegypti mosquitoes harboring a binary CRISPRa system can be used to effectively overexpress two developmental genes, even-skipped (eve) and hedgehog (hh), resulting in observable morphological phenotypes. We also used this system to overexpress the positive transcriptional regulator of the Toll immune pathway known as AaRel1, which resulted in a significant suppression of dengue virus serotype 2 (DENV2) titers in the mosquito. This system provides a versatile tool for research pathways not previously possible in Ae. aegypti, such as programmed overexpression of endogenous genes, and may aid in gene characterization studies and the development of innovative vector control tools.

Field Evaluation of In2Care Mosquito Traps to Control Aedes aegypti and Aedes albopictus (Diptera: Culicidae) in Hawai'i Island.

Brisco KK, Jacobsen CM, Seok S, Wang X, Lee Y, Akbari OS, Cornel AJ.

19-01-2023

J Med Entomol.

https://pubmed.ncbi.nlm.nih.gov/36656078/

Aedes aegypti Linnaeus and Aedes albopictus Skuse are vectors of dengue virus and responsible for multiple autochthonous dengue outbreaks in Big Island, Hawai'i. Control of Ae. aegypti and Ae. albopictus has been achieved in In2Care trap trials, which motivated us to investigate this potential control approach in the Big Island. Our In2Care trial was performed in the coastal settlement of Miloli'i in the southwest of Big Island where both Ae. aegypti and Ae. albopictus are found. This trial starting in the second week of July and ending in the last week of October 2019 fell within the traditional wet season in Miloli'i. No significant reduction in egg or adult counts in our treatment areas following 12 wk of two In2Care trap placements per participating household were observed. In fact, an increase in numbers of adults during the trial reached levels that required the local mosquito abatement program to stop the In2Care trap trial and institute a thorough source reduction and treatment campaign. The source reduction campaign revealed a large variety and quantity of water sources competed with the oviposition cups we had placed, which likely lowered the chances of our oviposition cups being visited by pyriproxyfen-contaminated Aedes adults exiting the In2Care traps.

Chaperonin TRiC/CCT Participates in Mammarenavirus Multiplication in Human Cells via Interaction with the Viral Nucleoprotein.

Sakabe S, Witwit H, Khafaji R, Cubitt B, de la Torre JC. 19-01-2023

J Virol.

https://pubmed.ncbi.nlm.nih.gov/36656012/

The eukaryotic chaperonin containing tailless complex polypeptide 1 ring complex (CCT, also known as TCP-1 Ring Complex, TRiC/CCT) participates in the folding of 5% to 10% of the cellular proteome and has been involved in the life cycle of several viruses, including dengue, Zika, and influenza viruses, but the mechanisms by which the TRiC/CCT complex contributes to virus multiplication remain poorly understood. Here, we document that the nucleoprotein (NP) of the mammarenavirus lymphocytic choriomeningitis virus (LCMV) is a substrate of the human TRiC/CCT complex, and that pharmacological inhibition of TRIC/CCT complex function, or RNAi-mediated knockdown TRIC/CCT complex subunits, inhibited LCMV multiplication in human cells. We obtained evidence that the TRiC/CCT complex is required for the production of NPcontaining virus-like particles (VLPs), and the activity of the virus ribonucleoprotein (vRNP) responsible for directing replication and transcription of the viral genome. Pharmacological inhibition of the TRIC/CCT complex also

restricted multiplication of the live-attenuated vaccine candidates Candid#1 and ML29 of the hemorrhagic fever causing Junin (JUNV) and Lassa (LASV) mammarenaviruses, respectively. Our findings indicate TRIC/CCT complex is required mammarenavirus multiplication and is an attractive candidate for the development of host directed antivirals human-pathogenic mammarenaviruses. IMPORTANCE Host-directed antivirals have gained great interest as an antiviral strategy to counteract the rapid emergence of drug-resistant viruses. The chaperonin TRIC/CCT complex has been involved in the life cycle of several viruses, including dengue, Zika, and influenza viruses. Here, we have provided evidence that the TRIC/CCT chaperonin complex participates mammarenavirus infection via its interaction with the viral NP. Importantly, pharmacological inhibition of TRiC/CCT function significantly inhibited multiplication of LCMV and the distantly related mammarenavirus JUNV in human cells. Our findings support that the TRiC/CCT complex is required for multiplication of mammarenaviruses and that the TRiC/CCT complex is an attractive host target for the development of antivirals against human-pathogenic mammarenaviruses.

ASVAC2022 : 8th Asian Vaccine Conference.

Galagoda GCS, Perera J, de Silva R, Wickramasinghe HT, Dasanayake D, Bravo L, Ismail Z, Goh DYT, Nelson EAS. 19-01-2023

Hum Vaccin Immunother.

https://pubmed.ncbi.nlm.nih.gov/36655357/

Aiming to further the Immunization Partners in Asia Pacific (IPAP)'s vision of a world where no one suffers from a vaccine preventable disease, the 8th Asian Vaccine Conference (ASVAC 2022) was held in Colombo, Sri Lanka and virtually from 15 to 18, September 2022 (www.asianvaccine.com). This conference followed those held in Siem Reap, Cambodia (2009), Manila, Philippines (2010), Jakarta, Indonesia (2011), Cebu, Philippines (2013), Hanoi, Vietnam (2015), Singapore (2017) and Naypyidaw and Yangon, Myanmar (2019). The ASVAC2022 themed "Immunization: in Era of Pandemics," commenced with the EPI Managers' Workshop, followed by preconference workshops and Vaccinology Masterclass, followed by the main conference featuring 5 plenary lectures, 6 partner-led symposia, free paper and poster presentations, and industry-supported lunch and evening sessions. There were over 1830 registered participants, with 112 attending in person and 998 virtually from 63 countries. The conference was organized by IPAP and hosted by the Vaccine and Infectious Disease Forum of Sri Lanka, Sri Lanka College of Pediatricians, Sri Lanka College of Microbiologists and College of General Practitioners of Sri Lanka, with the support of the Ministry of Health, Sri Lanka. The 9th ASVAC is scheduled to be held in Davao City, Philippines in late 2023.

Application of reaction-diffusion equations for modeling human and breeding site attraction movement behavior of Aedes aegypti mosquito.

Richter O, Nguyen A, Nguyen T.

05-09-2022

Math Biosci Eng.

https://pubmed.ncbi.nlm.nih.gov/36654028/

This paper shows how biological population dynamic models in the form of coupled reaction-diffusion equations with nonlinear reaction terms can be applied to heterogeneous landscapes. The presented systems of coupled partial differential equations (PDEs) combine the dispersal of disease-vector mosquitoes and the spread of the disease in a human population. Realistic biological dispersal behavior is taken into account by applying chemotaxis terms for the attraction to the human host and the attraction of suitable breeding sites. These terms are capable of generating the complex active movement patterns of mosquitoes along the gradients of the attractants. The nonlinear initial boundary value problems are solved numerically for geometries of heterogeneous landscapes, which have been imported from geographic information system data to construct a general-purpose finite-element solver for systems of coupled PDEs. The method is applied to the dispersal of the dengue disease vector for Aedes aegypti in a small-scale rural setting consisting of small houses and different breeding sites, and to a large-scale section of the suburban zone of a metropolitan area in Vietnam. Numerical simulations illustrate how the setup of model equations and geographic information can be used for the assessment of control measures, including the spraying patterns of pesticides and biological control by inducing male sterility.

Chikungunya and Lyme vaccines make headway.

[No authors listed]

Jan-2023

Nat Biotechnol.

https://pubmed.ncbi.nlm.nih.gov/36653502/

Synergistic antibacterial and mosquitocidal effect of Passiflora foetida synthesized silver nanoparticles.

Palanisamy DS, Gounder BS, Selvaraj K, Kandhasamy S, Alqahtani T, Alqahtani A, Chidambaram K, Arunachalam K, Alkahtani AM, Chandramoorthy HC, Sharma N, Rajeshkumar S, Marwaha L.

09-01-203

Braz J Biol.

https://pubmed.ncbi.nlm.nih.gov/36651434/

Dynamics of a dengue disease transmission model with two-stage structure in the human population.

Li-Martín A, Reyes-Carreto R, Vargas-De-León C. lan-2023

Math Biosci Eng.

https://pubmed.ncbi.nlm.nih.gov/36650797/

Age as a risk factor is common in vector-borne infectious diseases. This is partly because children depend on adults to take preventative measures, and adults are less susceptible to mosquito bites because they generally

spend less time outdoors than children. We propose a dengue disease model that considers the human population as divided into two subpopulations: children and adults. This is in order to take into consideration that children are more likely than adults to be bitten by mosquitoes. We calculated the basic reproductive number of dengue, using the next-generation operator method. We determined the local and global stability of the disease-free equilibrium. We obtained sufficient conditions for the global asymptotic stability of the endemic equilibrium using the Lyapunov functional method. When the infected periods in children and adults are the same, we that the endemic equilibrium is globally asymptotically stable in the interior of the feasible region when the threshold quantity $\$ R $0 > 1\$. Additionally, we performed a numerical simulation using parameter values obtained from the literature. Finally, a local sensitivity analysis was performed to identify the parameters that have the greatest influence on changes in \$ (R 0) \$, and thereby obtain a better biological interpretation of the results.

Blood transfusion in severe dengue infection: a case series.

Kularatne SAM, Dalugama C, Rajapakse M, Warnasooriya S, Pathirage M, Ralapanawa U, Jayalath T. 18-01-2023

J Med Case Rep.

https://pubmed.ncbi.nlm.nih.gov/36650590/

Determinants of exposure to Aedes mosquitoes: a comprehensive geospatial analysis in peri-urban Cambodia.

Parker DM, Medina C, Bohl J, Lon C, Chea S, Lay S, Kong D, Nhek S, Man S, Doehl JSP, Leang R, Kry H, Rekol H, Oliveira F, Minin VM, Manning JE.

14-01-2023

Acta Trop.

https://pubmed.ncbi.nlm.nih.gov/36649803/

Aedes mosquitoes are some of the most important and globally expansive vectors of disease. Public health efforts are largely focused on prevention of human-vector contact. A range of entomological indices are used to measure risk of disease, though with conflicting results (i.e. larval or adult abundance does not always predict risk of disease). There is a growing interest in the development and use of biomarkers for exposure to mosquito saliva, including for Aedes spp, as a proxy for disease risk. In this study, we conduct a comprehensive geostatistical analysis of exposure to Aedes mosquito bites among a pediatric cohort in a peri-urban setting endemic to dengue, Zika, and chikungunya viruses. We use demographic, household, and environmental variables (the flooding index (NFI), land type, and proximity to a river) in a Bayesian geostatistical model to predict areas of exposure to Aedes aegypti bites. We found that hotspots of exposure to Ae. aegypti salivary gland extract (SGE) were relatively small (< 500 m and sometimes < 250 m) and stable across the two-year study period. Age was negatively associated with antibody responses to Ae. aegypti SGE. Those living in agricultural settings had lower

antibody responses than those living in urban settings, whereas those living near recent surface water accumulation were more likely to have higher antibody responses. Finally, we incorporated measures of larval and adult density in our geostatistical models and found that they did not show associations with antibody responses to Ae. aegypti SGE after controlling for other covariates in the model. Our results indicate that targeted house- or neighborhood-focused interventions may be appropriate for vector control in this setting. Further, demographic and environmental factors more capably predicted exposure to Ae. aegypti mosquitoes than commonly used entomological indices.

Quassinoids from Eurycoma longifolia with antiviral activities by inhibiting dengue virus replication.

He X, Zheng Y, Tian C, Wen T, Yang T, Yu J, Fang X, Fan C, Liu J, Yu L.

05-01-2023

Phytomedicine.

https://pubmed.ncbi.nlm.nih.gov/36649670/

Background: Dengue caused by dengue virus (DENV) spreads rapidly around the world. However, there are no worldwide licensed vaccines or specific antivirals to combat DENV infection. Quassinoids are the most characteristic components of Eurycoma longifolia, which have been reported to display a variety of biological activities. However, whether guassinoids exert anti-DENV activities remains unknown. Purpose: To test the quassinoids of E. longifolia for their activity against DENV and to clarify the potential mechanisms. Methods: The quassinoids from E. longifolia were isolated by chromatography techniques, and their chemical structures were elucidated by spectroscopic analysis. The anti-DENV activities of quassinoids on baby hamster kidney cells BHK-21 were determined by lactate dehydrogenase (LDH) assay. The synthesis of progeny virus was measured by plaque assay. The expression levels of envelope protein (E) and non-structural protein 1 (NS1) were evaluated by qRT-PCR, Western blot and immunofluorescence assays. Molecular docking was used to screen the potential targets of the most active quassinoid against DENV-2, and surface plasmon resonance analysis was employed to confirm the direct binding between the most active quassinoid and potential target. Results: Twenty-four quassinoids, including three new quassinoids (1 - 3), were isolated from the ethanol extract of E. longifolia. Quassinoids 4, 5, 9, 11, 12, 15, 16, 17, 19 and 20 significantly reduced the LDH release at the stages of viral binding and entry or intracellular replication. Among them, 19 (6α -hydroxyeurycomalactone, 6α -HEL) exhibited the best anti-DENV-2 activities with an EC_{50} value of 0.39 \pm 0.02 μ M. Further experiments suggested that 6α-HEL remarkably inhibited progeny virus synthesis and mRNA and protein expression levels of E and NS1 of DENV-2. Time-of-drug-addition assay suggested that 6α -HEL inhibited intracellular replication of DENV-2 at an early stage. Moreover, 6α -HEL was shown to interact with NS5-RdRp domain at a binding affinity of -8.15 kcal/mol. SPR assay further verified $6\alpha\text{-HEL}$ bound to RdRp protein with an equilibrium dissociation constant of 1.49 \times 10-7 M.

Conclusion: Ten quassinoids from E. longifolia showed anti-DENV activities at processes of virus binding and entry or intracellular replication. The most active quassinoid 6α -HEL exerts the anti-DENV-2 activities at intracellular replication stage by directly targeting the NS5-RdRp protein. These results suggest that 6α -HEL could be a promising candidate for the treatment of DENV-2 infection.

Chikungunya: risks for travellers.

Simon F, Caumes E, Jelinek T, Lopez-Velez R, Steffen R, Chen LH.

16-01-2023

J Travel Med.

https://pubmed.ncbi.nlm.nih.gov/36648431/

Rhizophora mucronata Lam., a halophyte from Mauritius Island, inhibits the entry of Zika virus in human cells (A549)- an in vitro and in silico analysis.

Sadeer NB, Haddad JG, Ezzat MO, Desprès P, Abdallah HH, Zengin G, Alshamrani IM, Barnawi J, Khalid A, Abdalla AN, Le Van B, El Kalamouni C, Mahomoodally MF.

17-01-2023

J Biomol Struct Dyn.

https://pubmed.ncbi.nlm.nih.gov/36648248/

The recent appearance of Zika virus (ZIKV) in Brazil should serve as a wake-up call to international authorities, as it poses a threat to global public health. In the present study, we investigated whether a mangrove plant, Rhizophora mucronata Lam. (R. mucronata) collected in Mauritius, possesses anti-ZIKV activity at the non-cytotoxic doses. ZIKVMC-MR766NIID (ZIKVGFP) was used for assessing anti ZIKV activity. In silico docking (Autodock 4) and molecular simulation were performed on collected data. Using a recombinant ZIKV expressing reporter green fluorescent protein(GFP) protein, we discovered that fruit and root methanolic, decocted fruit and root extracts were effective inhibitors of ZIKV infection in human epithelial A549 cells at negligible cytotoxicity. The mechanisms by which such extracts prevented ZIKV infection are linked to the inability of the virus to attach to the host cell surface. The outcomes of this study were supported by the docking calculations in which some of the dominant compounds have shown high binding affinity against ZIKV. The scientific data gathered in this study might pave the way for the future development of possible R. mucronata inhibitors to combat ZIKV.f Communicated by Ramaswamy H. Sarma.

Severe Rhabdomyolysis Leading to Acute Kidney Injury in a Case of Dengue Fever.

Thacker JP, Nimbalkar S, Chaudhari AJ.

Jan-Feb 2022

Saudi J Kidney Dis Transpl.

https://pubmed.ncbi.nlm.nih.gov/36647994/

Rhabdomyolysis is not a well-known complication in dengue fever and only a few cases are reported. We report

a patient of dengue, with severe body ache and myalgia, passed reddish-brown urine with a very high creatine-phosphokinase level. He also developed oliguria, hypertension, and raised creatinine. This suggests rhabdomyolysis occurred which led to acute kidney injury. This can complicate otherwise stable patients with dengue and affect the outcome. This complication needs to be explored when a similar clinical picture is encountered.

Identification of desoxyrhapontigenin as a novel antiviral agent against congenital Zika virus infection.

Yu W, Zhang B, Hong X, Cai H, Wang Y, Lu J, Hu X, Cao B. 13-01-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36646387/

Zika virus (ZIKV) infection arises as a global health threat owing to its association with Guillain-Barre syndrome and microcephaly in adults and fetuses since the most recent epidemics. Although extraordinary efforts have been underway globally to identify safe and effective treatments for ZIKV, therapeutic progressions seem to remain stagnant, especially for treating congenital ZIKV infection. Bio-compounds from medicinal plants evolutionarily optimized as drug-like molecules offer eligible sources of pharmaceuticals and lead drugs to fight against viral infections. Here, we identified desoxyrhapontigenin (DES), a naturally occurring bioactive product, as the strongest inhibitory compound against ZIKV infection among six conventional polyphenols in vitro. We also leveraged the trophoblast cell line, human trophoblast stem cells, and complex placental organoid models to provide solid evidence to support the anti-ZIKV bioactivity of DES. Notably, DES treatment effectively reduced the ZIKV burden in serum and target tissues, and correspondingly improved ZIKV-induced pathologic changes including weight loss, tissue inflammation, cell apoptosis, and adverse pregnancy outcomes, while it did not lead to obvious toxicity in both adult and pregnant mice. Furthermore, mechanistic studies revealed that DES could suppress ZIKV entry via dual mechanisms of direct targeting ZIKV E proteins and downregulating putative ZIKV receptors. These findings elucidate a previously unappreciated protective role of desoxyrhapontigenin against ZIKV infection both in vitro and in vivo, which shed light on the development of a novel and potent treatment for congenital ZIKV infection.

An alternating transmission model between mice and mosquitoes for genetic study of Dengue virus.

Zhu X, Jiang Y, Zhang H, Li C, Xing D, Guo X, Zhao T. 13-01-2023

Acta Trop.

https://pubmed.ncbi.nlm.nih.gov/36646237/

Rapidly increased incidence and prevalence of dengue virus serotype 2 (DENV-2) in recent decades highlight the need for better understanding of the selective pressures that drive genetic and phenotypic changes in this virus. We simulated the transfer of DENV-2 between human hosts and mosquito vectors by horizontally transmitting the

virus between suckling mice and Aedes aegypti (Linnaeus, Diptera: Culicidae). A total of 3 cycles of alternating transmission were performed and 3 passages of virus population were harvested from the infected sucking mice. The viral titer in mice brain and infectivity to mosquitoes of theses viral populations were tested. The genome of the viruses was also sequenced. Results showed that viral titer were similar and infection rate in the mosquitoes were not significantly different among those 3 passages. This in vivo model could be utilized to explore virus evolution and genetic variance in alternating transmission.

Paediatric dengue shock syndrome and acute respiratory failure: a single-centre retrospective study.

Preeprem N, Phumeetham S.

Nov-2022

BMJ Paediatr Open.

https://pubmed.ncbi.nlm.nih.gov/36645744/

Pharmacophore-based virtual screening and in-silico study of natural products as potential DENV-2 RdRp inhibitors.

Roney M, Huq AKMM, Issahaku AR, Soliman MES, Hossain MS, Mustafa AH, Islam MA, Dubey A, Tufail A, Mohd Aluwi MFF, Tajuddin SN.

16-01-2023

J Biomol Struct Dyn.

https://pubmed.ncbi.nlm.nih.gov/36645141/

Dengue fever is a significant public health concern throughout the world, causing an estimated 500,000 hospitalizations and 20,000 deaths each year, despite the lack of effective therapies. The DENV-2 RdRp has been identified as a potential target for the development of new and effective dengue therapies. This research's primary objective was to discover an anti-DENV inhibitor using in silico ligand- and structure-based approaches. To begin, a ligand-based pharmacophore model was developed, and 130 distinct natural products (NPs) were screened. Docking of the pharmacophore-matched compounds were performed to the active site of DENV-2 RdRp protease. Eleven compounds were identified as potential DENV-2 RdRp inhibitors based on docking energy and binding interactions. ADMET and drug-likeness were done to predict their pharmacologic, pharmacokinetic, and drug-likeproperties . Compounds ranked highest in terms of pharmacokinetics and drug-like appearances were then subjected to additional toxicity testing to determine the leading compound. Additionally, MD simulation of the lead compound was performed to confirm the docked complex's stability and the binding site determined by docking. As a result, the lead compound (compound-108) demonstrated an excellent match to the pharmacophore, a strong binding contact and affinity for the RdRp enzyme, favourable pharmacokinetics, and drug-like characteristics. In summary, the lead compound identified in this study could be a possible DENV-2 RdRp inhibitor that may be further studied on in vitro and in vivo models to develop as a drug candidate.Communicated by Ramaswamy H. Sarma.

Triple Infection with Dengue, Chikungunya and Malaria.

Goel A, Bansal R, Bansal P.

Jul-Dec 2022 Trop Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36643985/

Co-circulation of all the four Dengue virus serotypes during 2018-2019: first report from Eastern Uttar Pradesh, India.

Behera SP, Bhardwaj P, Deval H, Srivastava N, Singh R, Misra BR, Agrawal A, Kavathekar A, Kant R. 09-01-2023

PeerJ.

https://pubmed.ncbi.nlm.nih.gov/36643644/

Dengue fever is an endemic disease in India, transmitted by an infected mosquito bite. In India, the number of concurrent infections and the circulation of multiple dengue virus (DENV) serotypes has increased in recent decades. Molecular surveillance among the DENV serotype is important to keep track of the circulating serotypes, evolutionary changes, and key mutations that can alter the diagnostics. The current study included patients admitted for dengue in the Eastern Uttar Pradesh (E-UP) region during 2018-2019. The genetic characterization of the circulating DENV was accomplished through partial CprM (511 bp) gene amplification via reverse transcriptase polymerase chain reaction and sequencing. Phylogenetic analysis revealed the circulation of all four DENV1-4 serotypes. DENV-2 was the most abundant serotype (44%, 27/61), followed by DENV-3 (32%, 20/61). DENV-1 had a 16% (10/61) predominance, while DENV-4 (6%, 4/61) was found to be the least abundant serotype. DENV-2 genotypes were distributed among lineages I (7.4%), II (85%) and III (7.4%) of genotype IV, DENV-3 to lineage III of genotype III, DENV-1 to genotype III; DENV-2 to lineage B (75%) and C (25%) of genotype I. This primary report on the co-circulation of DENV1-4 serotypes from the E-UP region highlights the requirement of continuous molecular surveillance for monitoring circulating DENV serotypes.

A Critical Analysis of Intracranial Hemorrhage (ICH) as a Fatal Complication of Dengue Fever.

Siahaan AMP, Tandean S, Nainggolan BWM, Tarigan J, Sitanggang JS.

16-01-2023

J Korean Neurosurg Soc.

https://pubmed.ncbi.nlm.nih.gov/36642946/

Effects of gamma radiation on the vector competence of Aedes aegypti (diptera: Culicidae) to transmit Zika virus.

da Silva EB, de Mendonça CM, Guedes DRD, Paiva MHS, Mendonça JA, Dias ESF, Florêncio SGL, Amaral A, Netto AM, Lopes CFJA, de Melo-Santos MAV.

11-01-2023

Acta Trop.

https://pubmed.ncbi.nlm.nih.gov/36640923/

One of the limitations of the Sterile Insect Technique (SIT), conventionally performed by ionizing radiation, regards separating males from females, which is not 100% effective. Some irradiated females may be released together with males in the field at SIT. The present study aimed to evaluate the influence of ionizing radiation on the ability of Aedes aegypti mosquitoes to transmit the Zika virus after exposing female pupae to a 40 Gy of gamma radiation. The results suggest that the genetic damage induced by exposure of females to this dose level promotes their total sterility, but it does not influence their vector competence. However, our data point out that ionizing radiation may decrease the proportion of infective mosquitoes.

Flavivirus prM interacts with MDA5 and MAVS to inhibit RLR antiviral signaling.

Sui L, Zhao Y, Wang W, Chi H, Tian T, Wu P, Zhang J, Zhao Y, Wei ZK, Hou Z, Zhou G, Wang G, Wang Z, Liu Q.

13-01-2023 Cell Biosci.

https://pubmed.ncbi.nlm.nih.gov/36639652/

prM-reactive antibodies reveal a role for partially mature virions in dengue virus pathogenesis.

A Dowd K, Sirohi D, D Speer S, VanBlargan LA, Chen RE, Mukherjee S, Whitener BM, Govero J, Aleshnick M, Larman B, Sukupolvi-Petty S, Sevvana M, Miller AS, Klose T, Zheng A, Koenig S, Kielian M, Kuhn RJ, Diamond MS, Pierson TC.

17-07-2023

Proc Natl Acad Sci U S A.

https://pubmed.ncbi.nlm.nih.gov/36638211/

Cleavage of the flavivirus premembrane (prM) structural protein during maturation can be inefficient. The contribution of partially mature flavivirus virions that retain uncleaved prM to pathogenesis during primary infection is unknown. To investigate this question, we characterized the functional properties of newlygenerated dengue virus (DENV) prM-reactive monoclonal antibodies (mAbs) in vitro and using a mouse model of DENV disease. Anti-prM mAbs neutralized DENV infection in a virion maturation state-dependent manner. Alanine scanning mutagenesis and cryoelectron microscopy of anti-prM mAbs in complex with immature DENV defined two modes of attachment to a single antigenic site. In vivo, passive transfer of intact anti-prM mAbs resulted in an antibody-dependent enhancement of disease. However, protection against DENV-induced lethality was observed when the transferred mAbs were genetically modified to inhibit their ability to interact with Fcy receptors. These data establish that in addition to mature forms of the virus, partially mature infectious prM+ virions can also contribute to pathogenesis during primary DENV infections.

Assessing dengue fever risk in Costa Rica by using climate variables and machine learning techniques. Barboza LA, Chou-Chen SW, Vásquez P, García YE, Calvo JG, Hidalgo HG, Sanchez F.

13-01-2023

PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/36638136/

Health care seeking during travel: an analysis by the GeoSentinel surveillance network of travel medicine providers.

Piyaphane W, Stoney RJ, Asgeirsson H, Appiah GD, Díaz-Menéndez M, Barnett ED, Gautret P, Libman M, Schlagenhauf P, Leder K, Plewes K, Grobusch MP, Huits R, Mavunda K, Hamer DH, Chen LH.

13-01-2023

J Travel Med.

https://pubmed.ncbi.nlm.nih.gov/36637429/

Rapid molecular assays for the detection of the four dengue viruses in infected mosquitoes.

Ahmed M, Pollak NM, Hugo LE, van den Hurk AF, Hobson-Peters J, Macdonald J.

19-07-2022

Gates Open Res.

https://pubmed.ncbi.nlm.nih.gov/36636741/

The pantropic emergence of severe dengue disease can partly be attributed to the co-circulation of different dengue viruses (DENVs) in the same geographical location. Effective monitoring for circulation of each of the four DENVs is critical to inform disease mitigation strategies. In low resource settings, this can be effectively achieved by utilizing inexpensive, rapid, sensitive and specific assays to detect viruses in mosquito populations. In this study, we developed four rapid DENV tests with direct applicability for low-resource virus surveillance in mosquitoes. The test protocols utilize a novel sample preparation step, a singletemperature isothermal amplification, and a simple lateral flow detection. Analytical sensitivity testing demonstrated tests could detect down to 1,000 copies/µL of virusspecific DENV RNA, and analytical specificity testing indicated tests were highly specific for their respective virus, and did not detect closely related flaviviruses. All four DENV tests showed excellent diagnostic specificity and sensitivity when used for detection of both individually infected mosquitoes and infected mosquitoes in pools of uninfected mosquitoes. With individually infected mosquitoes, the rapid DENV-1, -2 and -3 tests showed 100% diagnostic sensitivity (95% CI = 69% to 100%, n=8 for DENV-1; n=10 for DENV 2,3) and the DENV-4 test showed 92% diagnostic sensitivity (CI: 62% to 100%, n=12) along with 100% diagnostic specificity (CI: 48-100%) for all four tests. Testing infected mosquito pools, the rapid DENV-2, -3 and -4 tests showed 100% diagnostic sensitivity (95% CI = 69% to 100%, n=10) and the DENV-1 test showed 90% diagnostic sensitivity (55.50% to 99.75%, n=10) together with 100% diagnostic specificity (CI: 48-100%). Our tests reduce the operational time required to perform mosquito infection status surveillance testing from > two hours to only 35 minutes, and have potential to improve accessibility of mosquito screening, improving monitoring and control strategies in low-income countries most affected by dengue outbreaks.

Wolbachia RNase HI contributes to virus blocking in the mosquito Aedes aegypti.

Hussain M, Zhang G, Leitner M, Hedges LM, Asgari S. 19-12-2022

iScience.

https://pubmed.ncbi.nlm.nih.gov/36636344/

The endosymbiotic bacterium Wolbachia pipientis blocks replication of several arboviruses in transinfected Aedes aegypti mosquitoes. However, the mechanism of virus blocking remains poorly understood. Here, we characterized an RNase HI gene from Wolbachia, which is rapidly induced in response to dengue virus (DENV) infection. Knocking down w RNase HI using antisense RNA in Wolbachia-transinfected mosquito cell lines and A. aegypti mosquitoes led to increased DENV replication. Furthermore, overexpression of wRNase HI, in the absence of Wolbachia, led to reduced replication of a positive sense RNA virus, but had no effect on a negative sense RNA virus, a familiar scenario in Wolbachia-infected cells. Altogether, our results provide compelling evidence for the missing link between early Wolbachia-mediated virus blocking and degradation of viral RNA. These findings and the successful pioneered knockdown of Wolbachia genes using antisense RNA in cell line and mosquitoes enable new ways to manipulate and study the complex endosymbiont-host interactions.

Cost-analysis of real time RT-PCR test performed for COVID-19 diagnosis at India's national reference laboratory during the early stages of pandemic mitigation.

Minhas N, Gurav YK, Sambhare S, Potdar V, Choudhary ML, Bhardwaj SD, Abraham P.

11-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36630456/

Real-time reverse transcription polymerase chain reaction (rRT-PCR) is one of the most accurate and extensively used laboratory procedures for diagnosing COVID-19. This molecular test has high diagnostic accuracy (sensitivity and specificity) and is considered as the gold standard for COVID-19 diagnosis. During COVID-19 surge in India, rRT-PCR service was encouraged and supported by the government of India through existing healthcare setup at various levels of healthcare facilities. The primary purpose of this research was to determine the per-unit cost of providing COVID-19 rRT-PCR services at the national reference laboratory at ICMR-National Institute of Virology in Pune during the early phase of COVID-19 pandemic mitigation, from the provider's perspective. The monthly cost for rRT-PCR testing as well as an estimated annual average unit cost for testing that takes account of peaks and troughs in pandemic were investigated. The time frame used to estimate unit cost was one year (July 2020-June 2021). For data collection on all resources spent during the early phase of pandemic, a conventional activity-based bottom-up costing technique was used.

Capital costs were discounted and annualized over the estimated life of the item. Apportioning statistics were selected for cost heads like human resources, capital, and equipment based on time allocation, sharing of services, and utilization data. The data was also used to understand the breakdown of costs across inputs and over time and different levels of testing activity. During the initial phase of pandemic mitigation, the per unit cost of providing the COVID-19 rRT-PCR test was estimated to be ₹566 (\$7.5) in the month of July 2020, where the total 56318 COVID-19 rRT-PCR tests was performed. The major proportion (87%) of funds was utilized for procuring laboratory consumables, followed by HR (10%), and it was least for stationary & allied items (0.02%). Unit cost was found to be the most sensitive to price variations in lab consumables (21.7%), followed by the number of samples tested (3.9%), salaries paid to HR (2.6%), price of equipment (0.23%), and building rental price (0.14%) in a univariate sensitivity analysis. The unit cost varies over the period of the pandemic in proportion with the prices of consumables and inversely proportional with number of tests performed. Our study would help the Government to understand the value for money they invested for laboratory diagnosis of COVID-19, budget allocation, integration and decentralization of laboratory services so as to help for achieving universal health coverage.

Alterations in deglutition in children with congenital Zika virus syndrome.

Rios D, Rios M, Nóbrega AC, Oliveira LB, Vaz D, Sales H, Almeida BL, Lopes LS, Siqueira IC, Lucena R. 06-01-2023

Codas.

https://pubmed.ncbi.nlm.nih.gov/36629551/

Longitudinal proteomic profiling of the inflammatory response in dengue patients.

Garishah FM, Boahen CK, Vadaq N, Pramudo SG, Tunjungputri RN, Riswari SF, van Rij RP, Alisjahbana B, Gasem MH, van der Ven AJAM, de Mast Q. 03-01-2023

PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/36595532/

Background: The immunopathogenesis of dengue virus (DENV) infection remains incompletely understood. To increase our understanding of inflammatory response in non-severe dengue, we assessed longitudinal changes in the inflammatory proteome in patients with an acute DENV infection. Methods: Using a multiplex proximity extension assay (PEA), we measured relative levels of 368 inflammatory markers in plasma samples from hospitalized patients with non-severe DENV infection in the acute (n = 43) and convalescence (n = 35) phase of the infection and samples of healthy controls (n = 10). **Results:** We identified 203 upregulated and 39 downregulated proteins in acute versus convalescent plasma samples. The upregulated proteins had a strong representation of interferon (IFN) and IFN-inducible effector proteins, cytokines (e.g. IL-10, IL-33) and cytokine receptors, chemokines, pro-apoptotic proteins (e.g. granzymes) and

endothelial markers. A number of differentially expressed proteins (DEPs) have not been reported in previous studies. Functional network analysis highlighted a central role for IFNy, IL-10, IL-33 and chemokines. We identified different novel associations between inflammatory proteins and circulating concentrations of the endothelial glycocalyx disruption surrogate marker syndecan-1. Conclusion: This unbiased proteome analysis provides a comprehensive insight in the inflammatory response in DENV infection and its association with glycocalyx disruption.

5-(Perylen-3-ylethynyl)uracil as an antiviral scaffold: Potent suppression of enveloped virus reproduction by 3-methyl derivatives in vitro.

Chistov AA, Chumakov SP, Mikhnovets IE, Nikitin TD, Slesarchuk NA, Uvarova VI, Rubekina AA, Nikolaeva YV, Radchenko EV, Khvatov EV, Orlov AA, Frolenko VS, Sukhorukov MV, Kolpakova ES, Shustova EY, Galochkina AV, Streshnev PP, Osipov EM, Sapozhnikova KA, Moiseenko AV, Brylev VA, Proskurin GV, Dokukin YS, Kutyakov SV, Aralov AV, Korshun VA, Strelkov SV, Palyulin VA, Ishmukhametov AA, Shirshin EA, Osolodkin DI, Shtro AA, Kozlovskaya LI, Alferova VA, Ustinov AV.

Jan-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36581049/

Management of Dengue: An Updated Review.

Tayal A, Kabra SK, Lodha R.

Feb-2023

Indian J Pediatr.

https://pubmed.ncbi.nlm.nih.gov/36574088/

Dengue is an important public health problem with a wide clinical spectrum. The World Health Organization classifies dengue into probable dengue, dengue with warning signs, and severe dengue. Severe dengue, characterized by plasma leakage, severe bleeding, or organ impairment, entails significant morbidity and mortality if not treated timely. There are no definitive curative medications for dengue; management is supportive. Judicious fluid resuscitation during the critical phase of dengue is the cornerstone of management. Crystalloids are the initial fluid of choice. Prophylactic platelet transfusion is not recommended. Organ involvement in severe dengue should be carefully looked for and managed. Secondary hemophagocytic lymphohistiocytosis is a potentially fatal complication of dengue that needs to be recognized, as specific management with steroids or intravenous immunoglobulin may improve outcomes. Several compounds with anti-dengue potential are being studied; no anti-dengue drug is available so far.

Infection and disruption of placental multidrug resistance (MDR) transporters: Implications for fetal drug exposure.

Andrade CBV, Lopes LVA, Ortiga-Carvalho TM, Matthews SG, Bloise E.

15-01-2023

Toxicol Appl Pharmacol.

https://pubmed.ncbi.nlm.nih.gov/36526072/

P-glycoprotein (P-gp, encoded by the ABCB1 gene) and breast cancer resistance protein (BCRP/ABCG2) are efflux multidrug resistance (MDR) transporters localized at the syncytiotrophoblast barrier of the placenta and protect the conceptus from drug and toxin exposure throughout pregnancy. Infection is an important modulator of MDR expression and function. This review comprehensively examines the effect of infection on the MDR transporters, P-gp and BCRP in the placenta. Infection PAMPs such as bacterial lipopolysaccharide (LPS) and viral polyinosinicpolycytidylic acid (poly I:C) and single-stranded (ss)RNA, as well as infection with Zika virus (ZIKV), Plasmodium berghei ANKA (modeling malaria in pregnancy - MiP) and polymicrobial infection of intrauterine tissues (chorioamnionitis) all modulate placental P-gp and BCRP at the levels of mRNA, protein and or function; with specific responses varying according to gestational age, trophoblast type and species (human vs. mice). Furthermore, we describe the expression and localization profile of Toll-like receptor (TLR) proteins of the innate immune system at the maternal-fetal interface, aiming to better understand how infective agents modulate placental MDR. We also highlight important gaps in the field and propose future research directions. We conclude that alterations in placental MDR expression and function induced by infective agents may not only alter the intrauterine biodistribution of important MDR substrates such as drugs, toxins, hormones, cytokines, chemokines and waste metabolites, but also impact normal placentation and adversely affect pregnancy outcome and maternal/neonatal health.

External Validation and Comparison of Two Dengue Severity Scores in Pediatric Patients.

Chandra S, Budiputri CL, Meliani F, Muljono MP, Heriyanto RS, Juliansen A, Octavius GS.

Feb-2023

Indian J Pediatr.

https://pubmed.ncbi.nlm.nih.gov/36515807/

RBM24 inhibits the translation of SARS-CoV-2 polyproteins by targeting the 5'-untranslated region.

Yao Y, Sun H, Chen Y, Tian L, Huang D, Liu C, Zhou Y, Wang Y, Wen Z, Yang B, Chen X, Pei R.

Jan-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36464077/

SARS-CoV-2 is a betacoronavirus with single-stranded positive-sense RNA, which is a serious global threat to human health. Understanding the molecular mechanism of viral replication is crucial for the development of antiviral drugs. The synthesis of viral polyproteins is a crucial step in viral progression. The synthesis of viral polyproteins in coronaviruses is regulated by the 5'-untranslated region (UTR); however, the detailed regulatory mechanism needs further investigation. The

present study demonstrated that the RNA binding protein. RBM24, interacts with the RNA genome of SARS-CoV-2 via its RNA recognition submotifs (RNPs). The findings revealed that RBM24 recognizes and binds to the GUGUG element at stem-loop 4 (SL4) in the 5'-UTR of SARS-CoV-2. The interaction between RBM24 and 5'-UTR prevents 80S ribosome assembly, which in turn inhibits polyproteins translation and the replication of SARS-CoV-2. Notably, other RNA viruses, including SARS-CoV, MERS-CoV, Ebolavirus, rhinovirus, West Nile virus, Zika virus, Japanese encephalitis virus, yellow fever virus, hepatitis C virus, and human immunodeficiency virus-1 also contain one or several G(U/C/A)GUG sequences in the 5'-UTR, which is also targeted by RBM24. In conclusion, the present study demonstrated that RBM24 functions by interacting with the 5'-UTR of SARS-CoV-2 RNA, and elucidated that RBM24 could be a host restriction factor for SARS-CoV-2 and other RNA viruses.

Paradox between adequate sanitation and rainfall in dengue fever cases.

Oliveira JB, Murari TB, Nascimento Filho AS, Saba H, Moret MA, Cardoso CAL.

20-02-2023

Sci Total Environ.

https://pubmed.ncbi.nlm.nih.gov/36455745/

Background: Dengue fever is a tropical disease and a major public health concern, and almost half of the world's population lives in areas at risk of contracting this disease. Climate change is identified by WHO and other international health authorities as one of the primary factors that contribute to the rapid spread of dengue fever. Methods: We evaluated the effect of sanitation on the cross-correlation between rainfall and the first symptoms of dengue in the city of Mato Grosso do Sul, which is in a state in the Midwest region of Brazil, and employed the time-lagged detrended cross-correlation analysis (DCCAC) method. Results: Co-movements were obtained through the time-phased DCCAC to analyze the effects of climatic variables on arboviruses. The use of a time-lag analysis was more robust than DCCAC without lag to present the behavior of dengue cases in relation to accumulated precipitation. Our results show that the cross-correlation between rain and dengue increased as the city implemented actions to improve basic sanitation in the city. Conclusion: With climate change and the increase in the global average temperature, mosquitoes are advancing beyond the tropics, and our results show that cities with improved sanitation have a high correlation between dengue and annual precipitation. Public prevention and control policies can be targeted according to the period of time and the degree of correlation calculated to structure vector control and prevention work in places where sanitation conditions are adequate.

The life cycle of the alphaviruses: From an antiviral perspective.

Skidmore AM, Bradfute SB.

Jan-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36436722/

Advances in Computational Methods to Discover New NS2B-NS3 Inhibitors Useful Against Dengue and Zika Viruses.

Dos Santos Nascimento IJ, da Silva Rodrigues ÉE, da Silva MF, de Araújo-Júnior JX, de Moura RO. 2022

Curr Top Med Chem.

https://pubmed.ncbi.nlm.nih.gov/36415099/

The Flaviviridae virus family consists of the genera Hepacivirus, Pestivirus, and Flavivirus, with approximately 70 viral types that use arthropods as vectors. Among these diseases, dengue (DENV) and zika virus (ZIKV) serotypes stand out, responsible for thousands of deaths worldwide. Due to the significant increase in cases, the World Health Organization (WHO) declared DENV a potential threat for 2019 due to being transmitted by infected travelers. Furthermore, ZIKV also has a high rate of transmissibility, highlighted in the outbreak in 2015, generating consequences such as Guillain-Barré syndrome and microcephaly. According to clinical outcomes, those infected with DENV can be asymptomatic, and in other cases, it can be lethal. On the other hand, ZIKV has severe neurological symptoms in newborn babies and adults. More serious symptoms include microcephaly, brain calcifications, intrauterine growth restriction, and fetal death. Despite these worrying data, no drug or vaccine is approved to treat these diseases. In the drug discovery process, one of the targets explored against these diseases is the NS2B-NS3 complex, which presents the catalytic triad His51, Asp75, and Ser135, with the function of cleaving polyproteins, with specificity for basic amino acid residues, Lys- Arg, Arg-Arg, Arg-Lys or Gln-Arg. Since NS3 is highly conserved in all DENV serotypes and plays a vital role in viral replication, this complex is an excellent drug target. In recent years, computer-aided drug discovery (CADD) is increasingly essential in drug discovery campaigns, making the process faster and more costeffective, mainly explained by discovering new drugs against DENV and ZIKV. Finally, the main advances in computational methods applied to discover new compounds against these diseases will be presented here. In fact, molecular dynamics simulations and virtual screening is the most explored approach, providing several hit and lead compounds that can be used in further optimizations. In addition, fragment-based drug design and quantum chemistry/molecular mechanics (QM/MM) provides new insights for developing anti-DENV/ZIKV drugs. We hope that this review offers further helpful information for researchers worldwide and stimulates the use of computational methods to find a promising drug for treating DENV and ZIKV.

Clinical Features of COVID-19, Dengue, and Influenza among Adults Presenting to Emergency Departments and Urgent Care Clinics-Puerto Rico, 2012-2021.

Wong JM, Volkman HR, Adams LE, Oliveras García C, Martinez-Quiñones A, Perez-Padilla J, Bertrán-Pasarell J, Sainz de la Peña D, Tosado-Acevedo R, Santiago GA, Muñoz-Jordán JL, Torres-Velásquez BC, Lorenzi O, Sánchez-González L, Rivera-Amill V, Paz-Bailey G.

21-12-2022

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36410319/

Therapeutic targeting of organelles for inhibition of Zika virus replication in neurons.

Ojha D, Basu R, Peterson KE.

Jan-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36396026/

Perinatal Transmission of Dengue Infection among Dengue Hemorrhagic Fever Outbreaks in Southern Vietnam: The First Case Managed at Tu Du Hospital and Review of Literature.

Pham TH, Nguyen PN, Ho QN.

14-11-2023

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36375466/

Dengue hemorrhagic fever is a high-risk pathology in pregnancy, leading to an increased mortality rate for both the mother and baby. Perinatal transmission of dengue infection may occur during the labor stage of the febrile phase, despite its extreme rarity. In the present case, a young female patient with pregnancy at 39 weeks 3 days of gestational age was hospitalized because of dengue hemorrhagic fever. Upon monitoring, her platelet count gradually decreased to a very low of 13,000 mm3 on the third day of fever. However, her platelet count increased soon afterwards. On the eighth day of admission, she was delivered by emergency cesarean section due to acute fetal distress. The female neonate was promptly assessed by the pediatric team upon cesarean surgery. The neonate was diagnosed with vertical transmission of dengue infection based on positive dengue virus nonstructural protein 1 antigen, and low platelet count was found on the first day postpartum. When there is a high suspicion of perinatal transmission, closely monitoring the newborn helps to avoid the adverse outcomes and mortality for the infant. Herein, we thoroughly report an unusual case of maternal-fetal transmission of dengue during pregnancy at our maternity hospital.

Surveillance of Aedes aegypti and Aedes albopictus (Diptera: Culicidae) as a Method for Prevention of Arbovirus Transmission in Urban and Seaport Areas of the Southern Coast of Brazil.

Acero-Sandoval MA, Palacio-Cortés AM, Navarro-Silva MA.

12-01-2023

J Med Entomol.

https://pubmed.ncbi.nlm.nih.gov/36305159/

Entomological surveillance is a traditional method to measure presence, distribution, and seasonal variation of vectors in urban areas, and is essential to targeted control activities to prevent arbovirus transmission. Ovitraps as one of the main components of surveillance programs, enable determination of female oviposition behavior, as well as identification of seasonal variations of the vector. The goals of this study were 1) to detect the mosquitos (Aedes aegypti Linnaeus) and (Aedes albopictus Skuse) (Diptera:Culicidae), in Paranaguá city, 2) to assess ovitrap positive index (OPI), egg density index (EDI), and their relationship with meteorological variables, and 3) to evaluate the vertical transmission of dengue, Zika, and chikungunya in Ae. aegypti and Ae. albopictus. The study was carried out in urban areas of Paranaguá city, an important port region of Brazil, from June 2017 to November 2018. The city was divided into 16 areaclusters. Three-hundred and thirty-one ovitraps were installed monthly, remaining for four days in selected places. Kernel density maps were done to compare the spatiotemporal distribution of collected eggs. Areas which maintained constant oviposition associated with vector activity were identified and were found to overlap the area-clusters with the highest EDI. As viral RNA was not detected, vertical transmission was likely not a maintenance mechanism of arbovirus circulation in Ae. aegypti and Ae. albopictus vectors. This study reiterates the importance, efficiency, and feasibility of ovitraps to monitor the presence and dynamics of Aedes spp. populations.

Reactivity of DENV-positive sera against recombinant envelope proteins produced in bacteria and eukaryotic cells.

Santos Souza HF, Zaneti AB, da Silva Almeida B, Martinho JA, Yamamoto MM, Rosa DS, Slhessarenko RD, Boscardin SB.

Feb-2023

Immunol Res.

https://pubmed.ncbi.nlm.nih.gov/36192522/

Dengue is a mosquito-borne disease endemic in many tropical and subtropical countries. It is caused by the dengue virus (DENV) that can be classified into 4 different serotypes (DENV-1-4). Early diagnosis and management can reduce morbidity and mortality rates of severe forms of the disease, as well as decrease the risk of larger outbreaks. Hiperendemicity in some regions of the world and the possibility that some people develop a more severe form of disease after a secondary infection caused by antibody-dependent enhancement justify the need to understand more thoroughly the antibody response induced against the virus. Here, we successfully produced a recombinant DENV-2 envelope (E) protein and its domains (EDI/II and EDIII) in two distinct expression systems: the Drosophila S2 insect cell system and the BL21 (DE3) pLySs bacterial system. We then evaluated the reactivity of sera from patients previously infected with DENV to each recombinant protein and to each domain separately. Our results show that the E protein produced in Drosophila S2 cells is recognized more frequently than the protein produced in bacteria. However, the recognition of E protein produced in bacteria correlates better with the DENV-2 sera neutralization capacity. The results described here emphasize the differences observed when antigens produced in bacteria or eukaryotic cells are used and may be useful to gain more

insight into the humoral immune responses induced by dengue infection.

Dengue fever on the rise in Southeast Asia.

Alied M, Nguyen D, Abdul Aziz JM, Vinh DP, Huy NT.

Feb-2023

Pathog Glob Health.

https://pubmed.ncbi.nlm.nih.gov/36036222/

Safety of Dengue Vaccine?

de Silva A.

13-01-2032

Clin Infect Dis.

https://pubmed.ncbi.nlm.nih.gov/36048521/

Safety and immunogenicity of Zika virus vaccine: A systematic review of clinical trials.

Yeasmin M, Molla MMA, Masud HMAA, Saif-Ur-Rahman KM.

Jan-2023

Rev Med Virol.

https://pubmed.ncbi.nlm.nih.gov/35986594/

Several phase-1 clinical trials have been performed to evaluate the safety and efficacy of candidate anti-Zika vaccines. In this systematic review, we systematically evaluated the safety and immunogenicity of candidate vaccines, which would aid researchers in formulating an effective vaccination strategy for phase-2 trials based on current evidence. A literature search was conducted using the electronic databases MEDLINE through Pubmed. Web of Science, and Cochrane Database for relevant studies on candidate anti-zika vaccines. Studies on animal models were excluded from our study. Healthy individuals who were administered candidate Zika vaccines to evaluate the immune response and adverse events (AEs) compared to placebo were considered. Data were extracted, tabulated, and analysed using Microsoft Excel, while the risk of bias plots were generated using tidyverse and Robvis packages in R-studio. A total of five phase-1 clinical trials were included in our analysis comprising of studies on inactivated. viral vector, and DNA vaccines. Immunogenicity ranged from 10% to 100% after vaccination with the lowest seroconversion rate (10%) and geometric mean titre (GMT) (6.3: 95% confidence interval (CI):3.7-10.8) observed among recipients of single-dose inactivated anti-zika vaccine (ZPIV). For DNA vaccines, the seroconversion rate ranged from 60% to 100% with the highest seroconversion rate (100%) and GMT (2871; 95% CI:705.3-11688) observed among recipients of three shots of high dose GLS-5700 vaccine. For viral vector vaccine (Ad26.ZIKV.001) seroconversion rate (100%) and GMT peaked after two shots with both low and high-dose vaccines. In all those studies AEs were mostly local including injection site pain, erythema, and itching. The most common systemic AEs included fever, myalgia, nausea, and fatigue. In phase-1 clinical trials, all candidate vaccines were found to be highly immunogenic and relatively safe, especially when administered in higher doses and with the help of needle-free devices.

Seroepidemiological Reconstruction of Long-term Chikungunya Virus Circulation in Burkina Faso and Gabon.

Lim JK, Ridde V, Agnandji ST, Lell B, Yaro S, Yang JS, Hoinard D, Weaver SC, Vanhomwegen J, Salje H, Yoon IK. 11-01-2023

J Infect Dis.

https://pubmed.ncbi.nlm.nih.gov/35710849/

Chikungunya virus (CHIKV) is a major public health concern worldwide. However, infection levels are rarely known, especially in Africa. We recruited individuals from Ouagadougou, Burkina Faso and Lambaréné, Gabon (age range, 1-55 years), tested their blood for CHIKV antibodies, and used serocatalytic models to reconstruct epidemiological histories. In Ouagadougou, 291 of 999 (29.1%) individuals were seropositive, ranging from 2% among those aged <10 years to 66% in those aged 40-55 years. We estimated there were 7 outbreaks since the 1970s but none since 2001, resulting in 600 000 infections in the city, none of which were reported. However, we could not definitively conclude whether infections were due to CHIKV or o'nyong-nyong, another alphavirus. In Lambaréné, 117 of 427 (27%) participants were seropositive. Our model identified a single outbreak sometime since 2007, consistent with the only reported CHIKV outbreak in the country. These findings suggest sporadic outbreaks in these settings and that the burden remains undetected or incorrectly attributed.

The expression of circulating hsa-miR-126-3p in dengue-infected Thai pediatric patients.

Sriprapun M, Rattanamahaphoom J, Sriburin P, Chatchen S, Limkittikul K, Sirivichayakul C.

Feb-2023

Pathog Glob Health.

https://pubmed.ncbi.nlm.nih.gov/35708203/

Circulating hsa-miRNA-126 (CmiR-126) has been reported to involve in the pathogenesis of many infectious diseases including dengue virus infection. However, no prior study has been conducted to describe more details in dengueinfected pediatric patients. This study aimed to describe CmiR-126-3p in dengue-infected pediatric patients during the febrile and convalescent phases. Additionally, the correlations between CmiR-126-3p and other relevant clinical laboratory factors were investigated. Sixty pairedserum specimens collected during febrile and convalescent phases were retrieved from patients with dengue fever (DF) (n = 30) and dengue hemorrhagic fever (DHF) (n = 30). Thirty paired-serum specimens collected from non-dengue acute febrile illness patients (AFI) were included as the control group. CmiR-126-3p was determined using reverse transcription quantitative realtime polymerase-chain reaction (RT-qPCR). Relative miRNA expression was calculated as 2-ACt using CmiR-16-5p for data normalization. CmiR-126-3p expression during febrile and convalescent phases in dengue-infected patients was significantly lower than AFI (p < 0.05). However, miRNA levels were not different (p > 0.05)compared between DF and DHF and between primary and secondary infection. CmiR-126-3p levels in DF in the

convalescent were significantly higher than in the febrile phase (p=0.025). No association between CmiR-126-3p and hematocrit, WBC level, platelet count, WBC differential count or dengue viral load was observed (p>0.05). The data suggest that hsa-miR-126-3p involved in pathogenesis of dengue infection and may be a promising early and late biomarker for DENV infection. However, hsa-miR-126-3p alone cannot be used as a predictor for dengue severity.

The relationship between chikungunya virus and the kidneys: A scoping review.

Costa DMDN, Gouveia PADC, Silva GEB, Neves PDMM, Vajgel G, Cavalcante MAGM, Oliveira CBL, Valente LM, Silveira VMD.

Jan-2023

Rev Med Virol.

https://pubmed.ncbi.nlm.nih.gov/35521644/

Several atypical forms of chikungunya fever (CHIK) have been described, including neurological, cardiac and renal involvement. These forms may be related to high morbidity and mortality rates. This scoping review based on the PubMed, Scopus, and WOS databases aims to identify and summarise all the available evidence regarding the clinical and histopathological presentations and risk factors associated with kidney injury related to CHIK, as well as the clinical impact. Thus, a total of 54 papers were selected from 1606 initial references after applying the defined inclusion criteria. Data on the association between kidney injury and CHIK are scarce, with studies only conducted in the acute phase of the disease, lacking further characterisation. Kidney injury incidence in hospitalised patients using the Kidney Disease Improving Global Outcomes criteria varies from 21% to 45%, being higher among patients with atypical and severe manifestations. Although acute kidney injury does not seem to be related to viraemia, it may be related to higher mortality. Few studies have described the renal histopathological changes in the acute phase of CHIK, with prevalent findings of acute interstitial nephritis with mononuclear infiltrate, glomerular congestion and nephrosclerosis. Only one study assessed the kidney function of patients in the subacute and chronic phases of CHIK. Additionally, individuals with comorbidities, including chronic kidney disease, may be among those with a greater risk of presenting worse outcomes when affected by CHIK. The results described herein may contribute to better understand the relationship between the kidneys and chikungunya virus.

SARS-CoV-2 and dengue virus coinfection: Epidemiology, pathogenesis, diagnosis, treatment, and management.

Prapty CNBS, Rahmat R, Araf Y, Shounak SK, Noor-A-Afrin, Rahaman TI, Hosen MJ, Zheng C, Hossain MG. Jan-2023

Rev Med Virol.

https://pubmed.ncbi.nlm.nih.gov/35238422/

SARS-CoV-2 and dengue virus co-infection cases have been on the rise in dengue-endemic regions as coronavirus disease 2019 (COVID-19) spreads over the

world, posing a threat of a co-epidemic. The risk of comorbidity in co-infection cases is greater than that of a single viral infection, which is a cause of concern. Although the pathophysiologies of the two infections are different, the viruses have comparable effects within the body, resulting in identical clinical symptoms in the case of coinfection, which adds to the complexity. Overlapping symptoms and laboratory features make proper differentiation of the infections important. However, specific biomarkers provide precise results that can be utilised to diagnose and treat a co-infection, whether it is simply COVID-19, dengue, or a co-infection. Though their treatment is distinguished, it becomes more complicated in circumstances of co-infection. As a result, regardless of whatever infection the first symptom points to, confirmation diagnosis of both COVID-19 and dengue should be mandatory, particularly in dengue-endemic regions, to prevent health deterioration in individuals treated for a single infection. There is still a scarcity of concise literature on the epidemiology, pathophysiology, diagnosis, therapy, and management of SARS-CoV-2 and dengue virus co-infection. The epidemiology of SARS-CoV-2 and dengue virus co-infection, the mechanism of pathogenesis, and the potential impact on patients are summarised in this review. The possible diagnosis with biomarkers, treatment, and management of the SARS-CoV-2 and dengue viruses are also discussed. This review will shed light on the appropriate diagnosis, treatment, and management of the patients suffering from SARS-CoV-2 and dengue virus co-infection.

Chemical composition, antioxidant, antimicrobial and antiviral activities of the leaf extracts of Syzygium myrtifolium.

Ahmad MA, Lim YH, Chan YS, Hsu CY, Wu TY, Sit NW. 30-12-2021

Acta Pharm.

https://pubmed.ncbi.nlm.nih.gov/36651512/

Rage

Sheep scrapie and deer rabies in England prior to 1800.

Ness A, Aiken J, McKenzie D.

Dec-2023

Prion.

https://pubmed.ncbi.nlm.nih.gov/36654484/

Eighteenth-century England witnessed the emergence of two neurological diseases in animals. Scrapie, a transmissible spongiform encephalopathy, is a fatal neurodegenerative disease of sheep and goats that appears in classical and atypical forms. Reports of classical scrapie in continental Europe with described symptoms date back to 1750 in what is now western Poland. However, two major outbreaks of scrapie appeared in England prior to the 1800s. References to a sheep disease with a resemblance to scrapie first appear in Southwestern England between 1693 and 1722 and in the East Midlands between 1693 and 1706. Concurrent with the descriptions of scrapie in sheep was a neurological disease of deer first

appearing in the East of England. Two 18th-century writers remarked on the symptomatic similarities between the sheep and deer neurological diseases. Multiple outbreaks of the unknown deer disease existing as early as 1772 are examined and are identified as rabies.

Multisectoral prioritization of zoonotic diseases in Haryana (India) using one health approach.

Thukral H, Shanmugasundaram K, Riyesh T, Kumar N, Singha H, Gambhir D, Laura A, Tiwari S, Gulati BR. 03-01-2023

Prev Vet Med.

https://pubmed.ncbi.nlm.nih.gov/36642015/

Zoonotic diseases have huge livestock and public health burden worldwide, including India. Prioritizing zoonotic diseases is one of the important tasks under 'One Health' as it facilitates effective policy making, proper allocation of resources and promotion of multisectoral collaboration. Although some efforts have been made to prioritizing zoonotic diseases at national level in India, it is important to identify priority diseases in regional settings due to wide variation in climate and demography of different states. Therefore, the present study aims to prioritize zoonotic diseases for the state of Haryana (India). One Health Zoonotic Disease Prioritization (OHZDP) tool was used in this study to prioritize zoonotic diseases. Based on literature review of the past 23 years (2000-2022) on prevalence, morbidity, and mortality of zoonotic diseases, twenty-three high-scoring zoonotic diseases in Haryana and neighboring states of India were initially shortlisted for prioritization. A three-day participatory workshop was conducted involving 17 experts representing the Health, Animal Husbandry and Wildlife departments of Haryana. The Analytical Hierarchy Process (AHP) was used to rank the criteria, which were used to score the selected diseases using the decision tree analysis. The participants selected the following 7 criteria along with their relative weights to score the diseases: (1) Severity of disease in humans, (2) Severity of disease in animals, (3) Presence of disease in the region, (4) Transmission and outbreak potential, (5) Socio-economic impact, (6) Availability of interventions, and (7) Existing inter-sectoral collaboration for surveillance and reporting. The top scoring eight diseases selected as priority zoonotic diseases for Haryana were rabies, Japanese encephalitis, bovine tuberculosis, leptospirosis, avian influenza (H5N1), brucellosis, glanders and Influenza A (H1N1). Sensitivity analysis did not reveal any significant variation in prioritization results by varying criteria weights. This is the first systemic attempt to prioritize zoonotic diseases in the state and this will help in formulating effective monitoring, prevention, and control strategies for zoonotic diseases in the regional settings.

Rabies virus P protein binds to TBK1 and interferes with the formation of innate immunity-related liquid condensates.

Scrima N, Le Bars R, Nevers Q, Glon D, Chevreux G, Civas A, Blondel D, Lagaudrière-Gesbert C, Gaudin Y. 04-01-2023

Cell Rep.

https://pubmed.ncbi.nlm.nih.gov/36640307/

Viruses must overcome the interferon-mediated antiviral response to replicate and propagate into their host. Rabies virus (RABV) phosphoprotein P is known to inhibit interferon induction. Here, using a global mass spectrometry approach, we show that RABV P binds to TBK1, a kinase located at the crossroads of many interferon induction pathways, resulting in innate immunity inhibition. Mutations of TBK1 phosphorylation sites abolish P binding. Importantly, we demonstrate that upon RABV infection or detection of dsRNA by innate immunity sensors, TBK1 and its adaptor proteins NAP1 and SINTBAD form dynamic cytoplasmic condensates that have liquid properties. These condensates can form larger aggregates having ring-like structures in which NAP1 and TBK1 exhibit locally restricted movement. P binding to TBK1 interferes with the formation of these structures. This work demonstrates that proteins of the signaling pathway leading to interferon induction transiently form liquid organelles that can be targeted by viruses.

RABIES DIAGNOSIS AND RESPONSE TO VACCINATION IN SOUTHERN TAMANDUA (TAMANDUA TETRADACTYLA).

Cushing AC, Sheldon J, Martinelli L, Grome H, Souza M, Dunn J, Craig LE, Carlson A, Niezgoda M, Satheshkumar PS, Wallace R.

Jan-2023

J Zoo Wildl Med.

https://pubmed.ncbi.nlm.nih.gov/36640082/

Health care seeking during travel: an analysis by the GeoSentinel surveillance network of travel medicine providers.

Piyaphane W, Stoney RJ, Asgeirsson H, Appiah GD, Díaz-Menéndez M, Barnett ED, Gautret P, Libman M, Schlagenhauf P, Leder K, Plewes K, Grobusch MP, Huits R, Mavunda K, Hamer DH, Chen LH.

13-01-2023

J Travel Med.

https://pubmed.ncbi.nlm.nih.gov/36637429/

Background: International travellers may seek care abroad to address health problems that arise during their trip or plan healthcare outside their country of residence as medical tourists. Methods: Data were collected on travellers evaluated at GeoSentinel Network sites who reported healthcare during travel. Both unplanned and planned healthcare were analysed, including the reason and nature of healthcare sought, characteristics of the treatment provided, and outcomes. Travellers that presented for rabies post-exposure prophylaxis were described elsewhere and were excluded from detailed analysis. Results: From May 2017 through June 2020, after excluding travellers obtaining rabies post-exposure prophylaxis (n = 415), 1093 travellers reported care for a medical or dental issue that was an unanticipated part of the travellers' planned itinerary (unplanned healthcare). Travellers who sought unplanned healthcare abroad had frequent diagnoses of acute diarrhoea, dengue,

falciparum malaria, and unspecified viral syndrome, and obtained care in 131 countries. Thirty-four (3%) reported subsequent deterioration and 230 (21%) reported no change in condition; a third (n = 405; 37%) had a pre-travel health encounter. Forty-one travellers had sufficient data on planned healthcare abroad for analysis. The most common destinations were the US, France, Dominican Republic, Belgium, and Mexico. The top reasons for their planned healthcare abroad were unavailability of procedure at home (n = 9; 19%), expertise abroad (n = 9; 19%), lower cost (n = 8; 17%), and convenience (n = 7; 15%); a third (n = 13; 32%) reported cosmetic or surgical procedures. Early and late complications occurred in 14 (33%) and 4 (10%) travellers, respectively. Four travellers (10%) had a pre-travel health encounter. Conclusions: International travellers encounter health problems during travel that often could be prevented by pre-travel consultation. Travellers obtaining planned healthcare abroad can experience negative health consequences associated with treatments abroad, for which pre-travel consultations could provide advice and potentially help to prevent complications.

"BACACIX", a spatial index combining proxies of bovine and badger space use associated with extended Mycobacterium bovis circulation in France.

Marsot M, Bernard C, Payne A, Rossi S, Ruette S, Desvaux S, Richomme C, Bouchez-Zacria M, Durand B. 14-12-2022

Prev Vet Med.

https://pubmed.ncbi.nlm.nih.gov/36543069/

To better prevent and control multi-host pathogen circulation over large areas, it is essential to identify patterns of disease persistence within host communities involved in pathogen circulation at a macroscale. The aim of this study was to design and calculate "BACACIX", a spatial index of indirect contacts between cattle and badgers, two species involved in the circulation of Mycobacterium bovis, one of the main causative agents of bovine tuberculosis (bTB), in some areas of France. The index combined spatial models of land use distribution (the probable distribution defining animal use of space) based on pasture location for cattle, and based on land cover for badgers, with proxies for animal density for both species. For badgers, we used two series of census data of badger setts in two regions of France to evaluate our model of badger space use distribution (also known as utilization distribution), and analyzed the relationship between BACACIX and the upsurge of bovine tuberculosis observed in several regions of France during the decade after the country obtained the officially bTB-free status in 2001. We observed high values of BACACIX from the southwest to the northeast of France and from Brittany to the Channel coast. Conversely, in two areas (north-central area and Mediterranean coast), index values were low, suggesting that indirect cattle-badger contacts were unlikely. In the two series of census data of badger setts that we analyzed, 96.5% and 87% of the global positioning system (GPS) locations of badger setts, respectively were located in the calculated badger space use distribution. A logistic regression model showed that after controlling bTB over the previous decade, the value of the index was positively associated with the risk of cattle outbreaks between 2001 and 2010 (OR = 1.57). In addition, the risk of bTB occurrence in cattle decreased when the pasture area outside the badger space use distribution increased. In the future, the spatial index of indirect cattle-badger contacts we propose could help to better target bTB surveillance and control in France.

Trachome

Association of trachoma with vision-related quality of life in children.

Eleiwa TK, Elsaadani IA, Elhusseiny AM. Jan-2023 *Ocul Surf*.

https://pubmed.ncbi.nlm.nih.gov/36379422/

Combined Surgical Strategies Adjusted to Clinical Evaluations for Severe Upper Eyelid Cicatricial Entropion and Trichiasis.

Zhang L, Hou Z, Li Y, Li D. 13-01-2023 J Craniofac Surg.

https://pubmed.ncbi.nlm.nih.gov/36635852/

Background: The management of cicatricial entropion and trichiasis represents a therapeutic challenge. The authors determined the long-term stability of combined surgical procedures in severe cases. Methods: The authors retrospectively studied consecutive patients with severe upper eyelid cicatricial entropion and trichiasis treated between 2019 and 2021 at Beijing Tongren Eye Center. Combined surgical procedures adjusted to clinical evaluations were performed. Clinical characteristics, procedures, and surgical outcomes were retrieved. Results: The authors included data on 58 eyelids (25 left and 33 right) from 39 patients (19 males and 20 females). The mean age was 54.81 years. Follow-up averaged 20.67 months. Common diagnoses were chemical injury, trachoma, and chronic conjunctivitis. Seven eyelids with eyelid margin entropion were successfully treated using anterior lamellar recession and gray line split. Seven eyelids with eyelid margin entropion and posterior lamellar deficits were effectively treated using anterior lamellar recession, gray line split, and posterior lamellar lengthening. Thirty-eight eyelids with recalcitrant eyelid margin entropion were treated using anterior lamellar recession and gray line split with graft, with a success rate of 94.74% and 89.47%, 3 and 6 months after the operation, respectively. Six eyelids with recalcitrant eyelid margin entropion and posterior lamellar deficits were effectively treated using anterior lamellar recession, gray line split with graft, and posterior lamellar lengthening. Among various grafts, pediculated orbicularis muscle was significantly different from banked sclera or resected tarsus (P = 0.011, P < 0.001).

Perceptions of ophthalmologists on the impact of trachoma in Egypt: a mixed-methods, nationwide survey.

Nayel Y, Taylor M, Montasser AS, Elsherif M, Diab MM. 17-01-2023

BMC Infect Dis.

https://pubmed.ncbi.nlm.nih.gov/36650425/

Ulcère de Buruli

Gold Panning-Related Chronic Cutaneous Ulcers in Guinea, West Africa.

Keita ML, Kaba A, Telly Diallo I, Kesso Bah M, Sagno M, Goumane A, Bouam A, Drancourt M.

12-12-2023

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36509061/

Lèpre

Wheat ergot fungus-derived and modified drug for inhibition of intracranial aneurysm rupture due to dysfunction of TLR-4 receptor in Alzheimer's disease.

Debnath S, Sharma D, Chaudhari SY, Sharma R, Shaikh AA, Buchade RS, Kesari KK, Abdel-Fattah AM, Algahtani M, Mheidat M, Alsaidalani R, Paul T, Sayed AA, Abdel-Daim MM.

19-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36656815/

Background: Alzheimer's disease (AD) is a form of dementia that strikes elderly people more frequently than it does younger people. The cognitive skills and memory of Alzheimer's sufferers continue to deteriorate over time. Recent studies have shown that patients with AD have greater amounts of inflammatory markers in their bodies, which suggests that inflammation occurs early on in the progression of the disease. There is a possibility that Aß oligomers and fibrils can be recognised by TLRs, in addition to the microglial receptors CD14, CD36, and CD47. When Aß binds to either CD36 or TLR4, it sets off a chain reaction of inflammatory chemokines and cytokines that ultimately results in neurodegeneration. Diabetes and Alzheimer's disease have both been recently related to TLR4. The activation of TLR4 has been connected to a variety of clinical difficulties that are associated with diabetes, in addition to the internal environment of the body and the microenvironment of the brain. TLR4 inhibitors have been shown in clinical investigations to not only lessen the likelihood of getting sick but also to increase the average longevity. Result: In this work we used molecular docking and molecular dynamics modelling to investigate the effectiveness of FDA-approved antidiabetic plant derived drugs in combating the TLR4 receptor. Molecular docking experiments were used to make a prediction regarding the interactions involving most important Bromoergocryptine Mesylate. With a binding affinity of - 8.26 kcal/mol, it stood out from the other candidates as the one with the greatest potential. To verify the interaction pattern that takes place between 2-Bromoergocryptine Mesylate and the TLR4 receptor, a molecular dynamic simulation was run at a time scale of 150 nanoseconds. Because of this, 2-Bromoergocryptine Mesylate was able to make substantial contact with the active site, which led to increased structural stability during the process of the complex's dynamic development. **Conclusion:** As a result of this, the results of our research may be relevant for future research into the efficacy of 2-bromoergocryptine mesylate as a potential lead treatment for TLR4 receptors in intracranial aneurysm rupture in AD.

Analysis of molecular resistance to azole and echinocandin in Candida species in patients with vulvovaginal candidiasis.

Lotfali E, Erami M, Fattahi M, Nemati H, Ghasemi Z, Mahdavi E.

Jun-2022

Curr Med Mycol.

https://pubmed.ncbi.nlm.nih.gov/36654793/

Progressive neuropathy in patients with lepromatous leprosy after multidrug therapy.

Penna PS, Pitta IJR, Vital RT, Hacker MAVB, Salles AM, Pinheiro RO, Antunes SLG, Sarno EN, Jardim MR.

16-01-2023

Mem Inst Oswaldo Cruz.

https://pubmed.ncbi.nlm.nih.gov/36651454/

Background: The lepromatous pole is a stigmatising prototype for patients with leprosy. Generally, these patients have little or no symptoms of peripheral nerve involvement at the time of their diagnosis. However, signs of advanced peripheral neuropathy would be visible during the initial neurological evaluation and could worsen during and after multidrug therapy (MDT). Disabilities caused by peripheral nerve injuries greatly affect these patients' lives, and the pathophysiological mechanisms underlying nerve damage remain unclear. Objectives: To evaluate the outcome of peripheral neuropathy in patients with lepromatous leprosy (LL) and persistent neuropathic symptoms years after completing MDT. Methods: We evaluated the medical records of 14 patients with LL who underwent nerve biopsies due to worsening neuropathy at least four years after MDT. Findings: Neuropathic pain developed in 64.3% of the patients, and a neurological examination showed that most patients had alterations in the medium- and large-caliber fibers at the beginning of treatment. Neurological symptoms and signs deteriorated despite complete MDT and prednisone or thalidomide use for years. Nerve conduction studies showed that sensory nerves were the most affected. Main conclusions: Patients with LL can develop progressive peripheral neuropathy, which continues to develop even when they are on longterm anti-inflammatory and immunosuppressive therapy.

Successful treatment of cutaneous Mycobacterium chelonae infection by

switching from levofloxacin to sitafloxacin.

Murakami T, Aozasa N, Fukano H, Miyamoto Y, Ishii N, Tsunemi Y, Nakamura K.

18-01-2023

J Dermatol.

https://pubmed.ncbi.nlm.nih.gov/36651085/

Integration of COVID-19 and TB screening in Kampala, Uganda: healthcare provider perspectives.

Semitala FC, Katwesigye R, Kalibbala D, Mbuliro M, Lalitha R, Owachi D, Atine E, Nassazi J, Turyahabwe S, Sekadde M.

17-01-2023

Implement Sci Commun.

https://pubmed.ncbi.nlm.nih.gov/36650596/

Not all Black Fungus is Mucormycosis: A challenging case of Medicopsis Romeroi.

Bhardwaj N, Parvathy N, Kaur H, Handa S, Srinivasan R. 17-01-2023

Cytopathology.

https://pubmed.ncbi.nlm.nih.gov/36648323/

The prevalence of invasive fungal infections is increasing especially in immunocompromised individuals. These are associated with high morbidity even with adequate antifungal therapy. We report an unusual case of Medicopsis romeroi species of phaeohyphomycosis wherein fine needle aspiration cytology enabled a rapid diagnosis and emergent treatment.

Impacts of language barriers on healthcare access and quality among Afaan Oromoo-speaking patients in Addis Ababa, Ethiopia.

Olani AB, Olani AB, Muleta TB, Rikitu DH, Disassa KG. 16-01-2023

BMC Health Serv Res.

Background: Ethiopia is a multilingual and multinational federation with Addis Ababa serving as both the capital city of Oromia regional state and the seat of the Ethiopian federal government. Nevertheless, only Amharic is considered as the working language of the city and federal offices, including hospitals. As a result, Afaan Oromoospeaking patients may be facing language barriers in the healthcare settings in Addis Ababa. Language barriers have the capacity to affect patients' experience of care and treatment outcomes. This study, hence, examined the impacts of language barriers on the healthcare access and quality for the Afaan Oromoo-speaking patients in public hospitals in Addis Ababa. Methods: In-depth interviews with patients (N = 27) and key informant interviews with healthcare providers (N = 9) were conducted in six public hospitals found in Addis Ababa. All the interviews were audio-taped and transcribed verbatim. A thematic analysis technique was employed to address the study objectives. Results: The study participants indicated the widely existing problem of language discordance between patients and healthcare providers. The impacts of

language barriers on the patients include preventable medical errors, low treatment adherence, low healthseeking behavior, additional treatment cost, increased length of hospital stays, weak therapeutic relation, social desirability bias, less confidence, and dissatisfaction with the healthcare. For the healthcare providers, language barriers are affecting their ability to take patient history, perform diagnoses and provide treatment, and have also increased their work burden. The use of ad hoc interpreters sourced from bilingual/multilingual patients, patient attendants, volunteer healthcare providers, and other casual people has been reported to deal with the problem of language barriers. Conclusion: A significant number of Afaan Oromoo-speaking patients are facing language barriers in accessing quality healthcare in public hospitals in Addis Ababa, and this constitutes structural violence. As a way out, making Afaan Oromoo an additional working language of the public hospitals in Addis Ababa, the assignment of professional interpreters, and a hiring system that promotes the recruitment of qualified multi-lingual healthcare providers are suggested.

Dermoscopy of Darier's disease in dark phototypes: an observational study by the International Dermoscopy Society Task Force on "Imaging in Skin of Color".

Errichetti E, Ankad BS, Lallas A, Chauhan P, Nayak M, Usatine RP, Bhat Y, Vinay K, Akay BN, Kelati A, Enechukwu NA, Ogunbiyi A, Behera B.

16-01-2023

J Eur Acad Dermatol Venereol.

https://pubmed.ncbi.nlm.nih.gov/36645849/

Lucio phenomenon in an adolescent female.

da Silva Martins P, Paixão AG, Mesquita MB, de Souza E Silva NS, Quintella LP, Carvalho Gonçalves ML, D'ávila Freitas A, Ferreira CP.

Dec-2022

Wounds.

https://pubmed.ncbi.nlm.nih.gov/36645661/

Clusters of risk for the occurrence of leprosy and disabilities in children under 15 years of age in Cuiabá: a geospatial study.

Martoreli Júnior JF, Ramos ACV, Berra TZ, Nascimento MCD, Tavares RBV, Moura HSD, Mello DF, Alves JD, Arcêncio RA.

09-01-2023

Rev Bras Epidemiol.

https://pubmed.ncbi.nlm.nih.gov/36629618/

Judicialization of the right to health with a focus on neglected tropical diseases: dimensions and challenges in Piauí State, Northeastern Brazil, 2000-2020.

Andrade NRN, Nunes CFO, Ferreira AF, Araújo CEL, Albuquerque FB, Silva JAMD, Araújo Filho FJ, Freire PS, Ramos AN Jr.

Jan-2023

Cien Saude Colet.

https://pubmed.ncbi.nlm.nih.gov/36629581/

This article aims to analyse the magnitude and profile of legal demands for public health goods and services, also verifying the presence of legal demands for neglected tropical diseases (NTDs) in the State of Piauí between 2000-2020. Cross-sectional descriptive study based on the databases of the Court of Justice of Piauí on lawsuits demanding from the Direct Public Administration, goods and health services. A total of 6,658 lawsuits were initially identified. After eligibility analysis, 1,384 cases (20.8%) were analysed, with an increase in demand from 2017. We highlight the characteristics: origin in the capital Teresina (614; 44.4%), 40 to 59 years of age (372; 26.9%), female (761; 55.0%), farmers (123; 8.9%), public legal assistance (1,063; 76.8%), upheld (594; 42.9%). Five (5; 0.4%) lawsuits for NTDs, one visceral leishmaniasis requesting transportation, with granting, four for leprosy (two medicines, one granted, other extinguished without resolution of the merit, one consultation and one exam granted). The judicialization of the right to health is expressive and growing in the State of Piauí. The low demand related to NTDs may translate into limited access not only to health care, but also to the judiciary.

[Leprosy and vulnerability: a scoping review].

Jesus ILR, Montagner MI, Montagner MÂ, Alves SMC, Delduque MC.

Jan-2023

Cien Saude Colet.

https://pubmed.ncbi.nlm.nih.gov/36629560/

The objective of this work was to review published scientific works on leprosy as a public health problem in Brazil, and the marker of vulnerability for people with the disease. A scoping review was carried out with the descriptor 'leprosy AND vulnerability', on the Virtual Health Library (BVS) database. A total of 29 articles published between January 2016 and December 2020 that met the inclusion criteria were selected. The results pointed to scientific papers published in indexed journals and with different impact factors, with emphasis on the fact that most of the selected publications appear in iournals with impact metrics that are not very significant in the eyes of the international community, even though they have national impact. The majority of the studies had municipal coverage, with emphasis on cities in the North and Northeast of Brazil. The works addressed vulnerability in leprosy using different typologies.

Effect of adipose derived stromal vascular fraction on leprosy neuropathy: A Preliminary report.

Sirait SP, Bramono K, Menaldi SL, Pawitan JA, Indriatmi W, Aninditha T.

03-01-2023

PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/36595533/

Epidemiological Characteristics and Factors Associated with Cure of Leprosy in Chongqing, China, from 1949 to 2019.

Wang Y, Xiao D, Wu M, Qing L, Yang T, Xiao P, Deng D. 21-12-2022

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36410327/

A prospective case control study of resistance to rifampicin, dapsone and ofloxacin in Type 1 and Type 2 leprosy reactions and the therapeutic impact of modified treatment regimen on reactions.

Muddebihal A, Sardana K, Khurana A, Sachdeva S, Singh I, Ahuja M, Sharma R.

Feb-2023

J Eur Acad Dermatol Venereol.

https://pubmed.ncbi.nlm.nih.gov/36308057/

Successful management of a toddler with toxic epidermal necrolysis in a dermatology intensive care unit.

Mitra D, Singh GK, Bhatnagar A, Mitra B, Talukdar K, Patil C.

Feb-2023

Int J Dermatol.

https://pubmed.ncbi.nlm.nih.gov/35638318/

Dietary strategies for chronic spontaneous urticaria: an evidence-based review.

Podder I, Jaiswal S, Das A.

Feb-2023

Int J Dermatol.

https://pubmed.ncbi.nlm.nih.gov/34826140/

Although the relationship between diet and chronic spontaneous urticaria (CSU) remains elusive, several patients seek dietary modifications as they are easy and cost-effective. Adequate patient education and counseling are crucial as modified diets may be beneficial for a subset of antihistamine refractory CSU patients, and no modality currently exists to identify these patients. Elimination of food items based exclusively on patient history may lead to unnecessary restrictions in most cases resulting in nutritional deficiencies and impaired quality of life. Several dietary strategies have been tried till date with varying rates of success and evidence. This review highlights the various dietary strategies along with their levels of evidence, which may help the treating dermatologists and physicians to counsel CSU patients and make evidencebased treatment decisions. There is grade A recommendation for the elimination of food additives (artificial pseudoallergens), personalized diets, vitamin D supplementation. Diamine oxidase supplementation and probiotics (in children), grade B recommendation for dietary elimination of red meat, fish and their products, natural pseudoallergens (fruits, vegetables, and spices), and low-histamine diet, while dietary elimination of gluten (with concomitant celiac disease) has grade C recommendation. Notably, elimination diets should be continued for at least 3 consecutive weeks to assess their effectiveness.

Trypanosomes (trypanosomiase et maladie de Chagas)

Enzymatic production of a suite of human milk oligosaccharides directly in milk.

Perna VN, Meier S, Meyer AS.

13-01-2023

Enzyme Microb Technol.

https://pubmed.ncbi.nlm.nih.gov/36657310/

Human milk oligosaccharides (HMOs) denote specific glycans in human breast milk. They function as prebiotics, immune modulating, and antimicrobial agents in the gut of breastfed infants, and certain HMOs even promote the cognitive development of the baby. HMOs are virtually absent in cow's milk and hence in infant formula, which provides a huge incentive for identifying ways in which HMOs can be produced to improve infant formulas. Here, we show that different sialylated and fucosylated HMOs can be generated in cow's milk via different simultaneous enzymatic transglycosylation reactions catalyzed by an engineered sialidase (EC 3.2.1.18, from Trypanosoma rangeli) and an 1,2- α -L-fucosidase (EC 3.2.1.63, from Tannerella forsinthia) acting on the lactose in the milk and on casein glycomacropeptide, two types of commercially available HMOs, i.e. 2'-fucosyllactose and lacto-Nneotetraose, added to the milk. We also outline the details of the individual reactions in aqueous systems, demonstrate that the enzymatic reactions can be accomplished at 5 °C, and validate the products formed by LC-MS and NMR analysis. Enzymatic production of HMOs directly in milk provides opportunities for enriching milk and infant formulas and extends the use of enzymatic transglycosylation reactions to synthesis of HMOs in milk and eventually in other beverages.

TriTrypDB: An integrated functional genomics resource for kinetoplastida.

Shanmugasundram A, Starns D, Böhme U, Amos B, Wilkinson PA, Harb OS, Warrenfeltz S, Kissinger JC, McDowell MA, Roos DS, Crouch K, Jones AR.

19-01-2023

PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/36656904/

An atypical Trypanosoma lewisi infection in a 22-day-old neonate from India: An emergent zoonosis.

Jain P, Goyal V, Agrawal R.

Jan-Mar 2023

Indian J Pathol Microbiol.

https://pubmed.ncbi.nlm.nih.gov/36656242/

Lipase-Catalyzed Synthesis and Biological Evaluation of N-Picolineamides as Trypanosoma cruzi Antiproliferative Agents.

García FF, Musikant D, Escalona JL, Edreira MM, Liñares GG.

03-01-2023

ACS Med Chem Lett.

https://pubmed.ncbi.nlm.nih.gov/36655123/

In our search for new safe antiparasitic agents, an enzymatic pathway was applied to synthesize a series of N-pyridinylmethyl amides derived from structurally different carboxylic acids. Thirty derivatives, including 11 new compounds, were prepared through lipase-catalyzed acylation in excellent yields. In order to optimize the synthetic methodology, the impact of different reaction parameters was analyzed. Some compounds were evaluated as antiproliferative agents against Trypanosoma cruzi, the parasite responsible for American trypanosomiasis (Chagas' disease). Some of them showed significant activity as parasite proliferation inhibitors. Amides derived from 2-aminopicoline and stearic and elaidic acids were as potent as nifurtimox against the amastigote form of *T. cruzi*, the clinically relevant form of the parasite. Even more, a powerful synergism between nifurtimox and N-(pyridin-2-ylmethyl)stereamide was observed, almost completely inhibiting the proliferation of the parasite. Besides, the obtained compounds showed no toxicity in Vero cells, making them excellent potential candidates as lead drugs.

Detection of Trypanosoma cruzi DTUs TcI and TcIV in two outbreaks of orally-transmitted Chagas disease in the Northern region of Brazil.

Freitas VLT, Piotto MR, Esper HR, Nakanishi EYS, Fonseca CA, Assy JGPL, Berreta OCP, França FOS, Lopes MH. 16-01-2023

Rev Inst Med Trop Sao Paulo.

https://pubmed.ncbi.nlm.nih.gov/36651468/

This study describes the laboratory investigation of two acute Chagas disease outbreaks that occurred in the riverside communities of Marimarituba and Cachoeira do Arua, in the Santarem municipality, Para State, located in the Northern region of Brazil, and occurred in March 2016 and August 2017, respectively. The generation of data regarding the diversity of Trypanosoma cruzi parasites circulating in the Amazon region is key for understanding the emergence and expansion of Chagas disease. This study aimed to identify T. cruzi Discrete Typing Units (DTUs) involved in two outbreaks of acute Chagas disease (ACD) directly from the patient's biological sample. Nested and multiplex PCR targeting the $24S\alpha$ (rRNA) and miniexon genes, respectively, were used to identify T. cruzi DTU in blood samples from patients diagnosed with ACD. The samples with positive cPCR were submitted for analysis for T. cruzi DTUs, which included 13 samples from the patients with ACD by oral transmission and two samples collected from two newborns of two women with ACD, from Marimarituba and Cachoeira do Arua. The samples were classified as T. cruzi TcIV, from

Marimarituba's outbreak, and T. cruzi Tcl, from Cachoeira do Arua's outbreak. The molecular identification of T. cruzi may increase understanding of the role of this parasite in Chagas disease's emergence within the Amazon region, contributing to the improvement of the management of this important, but also neglected, disease.

pH-responsive phthalate cashew gum nanoparticles for improving drugs delivery and anti-Trypanosoma cruzi efficacy.

de Jesus Oliveira AC, Silva EB, de Oliveira TC, de Oliveira Silva Ribeiro F, Nadvorny D, de Freitas Oliveira JW, Borrego-Sánchez A, da Franca Rodrigues KA, Silva MS, Rolim-Neto PJ, Viseras C, Silva-Filho EC, da Silva DA, Chaves LL, de La Roca Soares MF, Soares-Sobrinho JL. 14-01-2023

Int J Biol Macromol.

https://pubmed.ncbi.nlm.nih.gov/36649864/

Nanotechnology is a crucial technology in recent years has resulted in new and creative applications of nanomedicine. Polymeric nanoparticles have increasing demands in pharmaceutical applications and require high reproducibility, homogeneity, and control over their properties. Work explores the use of cashew phthalate gum (PCG) as a particle-forming polymer. PCG exhibited a pH-sensitive behavior due to the of acid groups on its chains, and control drug release. We report the development of nanoparticles carrying benznidazole. Formulations were characterized by DLS, encapsulation efficiency, drug loading, FTIR, pH-responsive behavior, release, and in vitro kinetics. Interaction between polymer and drug was an evaluated by molecular dynamics. Morphology was observed by SEM, and in vitro cytotoxicity by MTT assay. Trypanocidal effect for epimastigote and trypomastigote forms was also evaluated. NPs responded to the slightly basic pH, triggering the release of BNZ. In acidic medium, they presented small size, spherical shape, and good stability. It was indicated NP with enhanced biological activity, reduced cytotoxicity, high anti T. cruzi performance, and pH-sensitive release. This work investigated properties related to the development and enhancement of nanoparticles. PCG has specific physicochemical properties that make it a promising alternative to drug delivery, however, there are still challenges to be overcome.

Trypanosoma cruzi Survey in Poached Pichis (Zaedyus pichiy; Mammalia, Cingulata) from Mendoza, Argentina.

Morales ME, Martín CM, Cattan PE, Superina M. 17-01-2023

J Wildl Dis.

https://pubmed.ncbi.nlm.nih.gov/36648759/

The transmission cycles of Trypanosoma cruzi, the causative agent of Chagas disease, include a wide variety of mammals and hematophagous triatomine insects. Infection with this blood parasite has been confirmed in many armadillo species; however, information on infection in Zaedyus pichiy, a small armadillo that inhabits

areas endemic to Chagas disease, is scarce. Our objective was to determine the infection frequency and parasite load of T. cruzi in 49 wild Z. pichiy confiscated dead from poachers in Mendoza, Argentina, 2010-2017. We detected T. cruzi DNA in 32 of 49 armadillos (65%) using real-time PCR, confirming infection with T. cruzi in a high proportion of confiscated pichis. No differences were found related to sex, age, or ecoregion origin of the assessed pichis. Parasite loads ranged between <0.1 and 8.88 parasite equivalents/microgram cardiac tissue. Additional studies on the infection status of Z. pichiy are needed to determine their role in the maintenance of the sylvatic transmission cycle and the potential zoonotic risk from hunted pichis.

Multifunctional organometallic compounds for the treatment of Chagas disease: Re(I) tricarbonyl compounds with two different bioactive ligands.

Soba M, Scalese G, Casuriaga F, Pérez N, Veiga N, Echeverría GA, Piro OE, Faccio R, Pérez-Díaz L, Gasser G, Machado I, Gambino D.

17-01-2023
Dalton Trans.

https://pubmed.ncbi.nlm.nih.gov/36648116/

Chagas' disease (American Trypanosomiasis) is an ancient and endemic illness in Latin America caused by the protozoan parasite Trypanosoma cruzi. Although there is an urgent need for more efficient and less toxic chemotherapeutics, no new drugs to treat this disease have entered the clinic in the last decades. Searching for metal-based prospective antichagasic drugs, in this work, multifunctional Re(I) tricarbonyl compounds bearing two different bioactive ligands were designed: a polypyridyl NN derivative of 1,10-phenanthroline and a monodentate azole (Clotrimazole CTZ or Ketoconazol KTZ). Five fac-[Re(CO)3(NN)(CTZ)](PF6) compounds and a fac-[Re(CO)3(NN)(KTZ)](PF6) were synthesized and fully characterized. They showed activity against epimastigotes (IC50 3.48-9.42 μ M) and trypomastigotes of T. cruzi (IC50 0.61-2.79 µM) and moderate to good selectivity towards the parasite compared to the VERO mammalian cell model. In order to unravel the mechanism of action of our compounds, two potential targets were experimentally and theoretically studied, namely DNA and one of the enzymes involved in the parasite ergosterol biosynthetic pathway, CYP51 (lanosterol 14-α-demethylase). As hypothesized, the multifunctional compounds shared in vitro a similar mode of action as that disclosed for the single bioactive moieties included in the new chemical entities. Additionally, two relevant physicochemical properties of biological interest in prospective drug development, namely lipophilicity and stability in solution in different media, were determined. The whole set of results demonstrates the potentiality of these Re(I) tricarbonyls as promising candidates for further antitrypanosomal drug development.

Case report: diagnosis of chronic Chagas cardiomyopathy using a multimodality imaging approach.

Li SX, Soles EO, Sharma PS, Rao AK.

06-01-2023

Eur Heart J Case Rep.

https://pubmed.ncbi.nlm.nih.gov/36644453/

Case Report: Chagas Disease in a Traveler Who Developed Esophageal Involvement Decades after Acute Infection.

Beatty NL, Alcala RF, Luque NA, Radetic M, Joshi-Guske P, Alakrad E, Forsyth CJ, Hamer DH.

16-01-2023

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36646072/

Travelers to Chagas disease endemic regions of Latin America may be at risk for Trypanosoma cruzi infection. We report a 67-year-old woman who screened positive for T. cruzi infection while donating blood. The patient had a history of an unusual febrile illness and marked swelling of the face sustained at age 10 after camping in northern Mexico that led to a 3-week hospitalization without a diagnosis. More than 4 decades later, rapid diagnostic tests and commercial and confirmatory serology for Chagas disease were all positive for T. cruzi infection. On evaluation, the patient described a progressive chronic cough, gastroesophageal reflux, and dysphagia for > 10 years. There was no evidence of any cardiac complications. However, esophageal manometry demonstrated significant dysmotility, with 90% of swallows being ineffective with evidence of esophageal pressurization and retrograde peristalsis in several swallows, suggesting early autonomic disruption due to Chagas disease esophagopathy. In this report, we highlight the importance of travel-related Chagas disease among travelers to endemic regions and the need to further identify potential risks of transmission among this at-risk population.

Epididymitis in mice experimentally infected with Trypanosoma equiperdum: a histopathological and immunohistochemical study.

Tanaka Y, Suganuma K, Watanabe K, Kobayashi Y. 13-01-2023

J Comp Pathol.

https://pubmed.ncbi.nlm.nih.gov/36642054/

Blood parasites (Trypanosoma, Leucocytozoon, Haemoproteus) in the Eurasian sparrowhawk (Accipiter nisus): diversity, incidence and persistence of infection at the individual level.

Svobodová M, Čepička I, Zídková L, Kassahun A, Votýpka J, Peške L, Hrazdilová K, Brzoňová J, Voříšek P, Weidinger K.

14-01-2023

Parasit Vectors.

https://pubmed.ncbi.nlm.nih.gov/36641440/

DOCUMENTATION OF TRYPANOSOMA EVANSI IN CAPTIVE TIGERS AND LIONS IN PUNJAB (2016-2018), PAKISTAN.

Khan MA, Shabir S, Azeem S, Gill W, Ashraf K, Azhar M, Rashid I, Ashraf M, Avais M, Ahmad AS, Younas M, Badshah A, Ahmad S, Akbar H.

Jan-2023

J Zoo Wildl Med.

https://pubmed.ncbi.nlm.nih.gov/36640086/

Trypanosoma evansi is an important hemoparasite of a variety of animal species worldwide. This parasite is a threat to the health of domestic animals as well as wild animals, particularly those managed in captivity. The current study investigated the presence of T. evansi in captive tigers (Panthera tigris tigris) and lions (Panthera leo) in Pakistan. In total, 24 blood samples from 11 tigers and 3 lions (n = 14) were collected during the course of roughly 3 yr (2016-2018). Eighteen samples were subjected to both microscopic and molecular evaluation for the presence of *T. evansi*; the remaining 6 samples were processed for PCR only. Of the 18 samples tested by both methods, 3 (16%) and 8 (44%) were positive by microscopy and PCR, respectively. This highlights the higher sensitivity of PCR over microscopy for detection of trypanosomes. Of the 24 total samples evaluated by PCR, 12 (50%) were positive. The three sequences obtained showed 99% identity with variant surface glycoprotein genes of the different isolates of T. evansi. The sensitivity, specificity, positive predictive value, and negative predictive value of microscopy in identifying T. evansi was 37.5, 100, 100, and 66.7%, respectively, considering PCR as the gold standard. We recommend rigorous monitoring of captive tigers and lions for hemoparasites, particularly in winter and early spring in areas with high infection rate of this parasite, preferably via PCR.

Effect of statins on inflammation and cardiac function in patients with chronic Chagas disease: A protocol for pathophysiological studies in a multicenter, placebo-controlled, proof-of-concept phase II trial.

Campos-Estrada C, Urarte E, Denegri M, Villalón L, González-Herrera F, Kemmerling U, Maya JD.

13-01-2023 *PLoS One*.

https://pubmed.ncbi.nlm.nih.gov/36638112/

Protozoal meningoencephalitis and myelitis in 4 dogs associated with Trypanosoma cruzi infection.

Landsgaard KA, Milliron SM, Faccin M, Broughton CA, Auckland LD, Edwards JF, Hamer SA, Hensel ME.

13-01-2023

Vet Pathol.

https://pubmed.ncbi.nlm.nih.gov/36636956/

American trypanosomiasis is caused by the zoonotic protozoa *Trypanosoma cruzi* and primarily results in heart disease. Organisms also infect the central nervous system

(CNS). The Texas A&M University veterinary teaching hospital archive was searched for dogs with CNS disease with intralesional protozoal amastigotes. This study summarizes 4 cases of dogs with disseminated trypanosomiasis and CNS involvement confirmed by quantitative polymerase chain reaction (qPCR) with T. cruzi primers. Clinical signs included lethargy, respiratory distress, tetraparesis, and seizures. Central nervous system lesions included meningeal congestion (1/4), necrosis with hemorrhage in the spinal cord gray and white matter (2/4), and histiocytic meningoencephalitis (4/4), and meningomyelitis (2/4) with intralesional and intracellular protozoal. Genotyping identified 1 case of T. cruzi discrete typing unit (DTU) Tcl and 2 cases as TclV, both are common variants in the United States. Trypanosomiasis should be considered a differential diagnosis for dogs with CNS signs in T. cruzi-endemic areas.

[Evaluation of Ex Vivo Cultivation Potentials of Trypanosoma cruzi, Leishmania tropica ve Toxoplasma gondii Parasites in J774, Vero and HeLa Cell Lines].

Yıldırım A, Özbilgin A, Yereli K.

Jan-2023

Mikrobiyol Bul.

https://pubmed.ncbi.nlm.nih.gov/36636847/

Three obligate intracellular protozoan parasite species, namely Trypanosoma cruzi, Leishmania tropica and Toxoplasma gondii, causative agents of Chagas disease, Leishmaniasis and toxoplasmosis, respectively, which are responsible for significant morbidity and mortality and reside in macrophage cells, affect more than half of the world's population in connection with socio-economic and geographical factors and also causes neglected parasitic diseases of increasing importance. This study aimed to evaluate the ex vivo cultivation potential of T.cruzi, L.tropica and T.gondii parasites in J774, Vero and HeLa cells and to reproduce in a short time and in large amounts without losing their virulence properties. Ex vivo experimental models were created by infecting J774, Vero and HeLa cell lines confluently produced in cell culture flasks with T.cruzi, L.tropica and T.gondii parasites. In ex vivo cultivation, one passage was applied for seven days and three times in a row. Cells removed from the surface after each passage were plated on eight-well chamber slides. Giemsa stained slides were prepared and infection rates were evaluated by light microscopic examination. At the end of the study, it was observed that all three cell lines could be infected with T.cruzi, L.tropica and T.gondii parasites, and infection rates increased in all cell lines after consecutive passages. As a result of ex vivo cultivation, the best cell lines from which T.cruzi and L.tropica strains grew, were J774, Vero and HeLa, and HeLa, J774 and Vero cell lines for T.gondii strain, respectively (p<0.05). Trypanosoma cruzi, L.tropica and T.gondii parasites were successfully grown in J774, Vero and HeLa cell lines by ex vivo culture method in a short time and in large amounts without losing their virulence properties. Cell lines with the best ex vivo cultivation potential for T.cruzi and L.tropica parasites were J774, Vero and HeLa, respectively, while HeLa, J774 and Vero for T.gondii. It is thought that the data obtained in this regard will contribute to many studies on the development of vaccines, drugs and new diagnostic kits.

Hammerhead ribozyme-based Uinsertion and deletion RNA editing assays for multiplexing in HTS applications.

Rostamighadi M, Mehta V, Hassan Khan R, Moses D, Salavati R.

Feb-202

RNA.

https://pubmed.ncbi.nlm.nih.gov/36456183/

Leishmaniose

TriTrypDB: An integrated functional genomics resource for kinetoplastida.

Shanmugasundram A, Starns D, Böhme U, Amos B, Wilkinson PA, Harb OS, Warrenfeltz S, Kissinger JC, McDowell MA, Roos DS, Crouch K, Jones AR.

19-01-2023

PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/36656904/

Leishmania: an urgent need for new treatments.

eBioMedicine.

Jan-2023

EBioMedicine

https://pubmed.ncbi.nlm.nih.gov/36653110/

Raising the suspicion of a nonautochthonous infection: identification of Leishmania guyanensis from Costa Rica exhibits a Leishmaniavirus related to Brazilian north-east and French Guiana viral genotypes.

Mata-Somarribas C, Quesada-López J, Matamoros MF, Cervantes-Gómez C, Mejía A, Chacón K, Bendig I, Campos R, Quesada-Morera R, Cantanhêde LM, Pereira LOR, Cupolillo E.

16-01-2023

Mem Inst Oswaldo Cruz.

https://pubmed.ncbi.nlm.nih.gov/36651455/

Everything old is new again: a case series of pediatric cutaneous leishmaniasis in Portland, Maine.

Jubulis J, Goddard A, Seiverling E, Kimball M, McCarthy C.

05-12-2022

J Trop Pediatr.

https://pubmed.ncbi.nlm.nih.gov/36647897/

Leishmaniasis has varying clinical manifestations and treatment regimens, dependent on species and host. Old world leishmaniasis, found primarily in Africa and Asia, may be associated with visceral disease, while new world

disease, primarily in Latin America, may be associated with mucocutaneous disease. We present a case series of pediatric African patients with New World cutaneous leishmaniasis. Data extraction was performed via chart review, of children with cutaneous leishmaniasis presenting to the pediatric infectious diseases clinic in Portland, ME. Biopsy specimens were sent to the federal center for disease control (CDC) for identification via polymerase chain reaction (PCR) and culture. Five cases of cutaneous leishmaniasis were diagnosed in pediatric patients (ages 1-17 years) in Maine during the study period. Leishmaniasis was not initially suspected; thus, time to diagnosis was 1-4 months, Two patients were diagnosed with Leishmania panamensis, one with Leishmania brasiliensis, one with Leishmania sp. and one with mixed infection (L. panamensis and Leishmania mexicana). One patient was managed with surgical excision only, one was observed off therapy, and three were treated with ketoconazole. This case series highlights the importance of a high index of suspicion in migrant patients. Detailed travel history and epidemiologic knowledge is essential to diagnosis, as patients may present with forms of illness not congruent with their country of origin.

Superparamagnetic Iron Oxide-Labeled Leishmania major Can Be Traced in Fibroblasts.

Yektaeian N, Zare S, Radfar AH, Hatam G.

04-01-2023

J Parasitol Res.

https://pubmed.ncbi.nlm.nih.gov/36643716/

[Epidemiological investigation on a visceral leishmaniasis case in Zhengzhou City of Henan Province].

Yang CY, Zhao XM, Lu DL, Zhang YQ, Qian JH, Wang X, Li SH, He ZQ, Qian D, Liu Y, Ji PH, Zhou RM, Zhang HW.

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642906/

In vitro miltefosine and amphotericin B susceptibility of strains and clinical isolates of Leishmania species endemic in Brazil that cause tegumentary leishmaniasis.

Ferreira BA, Coser EM, Saborito C, Yamashiro-Kanashiro EH, Lindoso JAL, Coelho AC.

13-01-2023

Exp Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36642298/

Tegumentary leishmaniasis encompasses a spectrum of clinical manifestations caused by the parasitic protozoa of the genus Leishmania. In Brazil, there are at least seven Leishmania species that are endemic and responsible for this set of clinical manifestations of the disease. Current treatment is limited to a restricted number of drugs that in general have several drawbacks including parenteral use, toxicity, and severe side effects. Amphotericin B is considered a second-line drug for tegumentary

leishmaniasis in Brazil, while miltefosine was recently approved for clinical use in the treatment of this disease. In this study, we investigated the in vitro susceptibility of Leishmania strains representative of the species endemic to Brazil, as well as a panel of thirteen clinical isolates of tegumentary leishmaniasis, to both amphotericin B and miltefosine. A moderate variation in the susceptibility to both drugs was found, where the EC_{50} values varied from 11.43 to 52.67 μM for miltefosine and from 12.89 to 62.36nM for amphotericin B in promastigotes, while for the intracellular amastigotes, values ranged from 1.08 to 9.60 μM and from 1.69 to 22.71 nM for miltefosine and amphotericin B respectively. Furthermore, the clinical isolates and strains of the subgenus Viannia were evaluated for the presence of Leishmania RNA virus 1 (LRV1), as this is an important factor associated with disease severity and treatment outcome. These findings provide a preclinical dataset of the activity of these drugs against the causative species of tegumentary leishmaniasis in Brazil.

In Vitro and In Silico Studies of Kinase Inhibitor of MAPK3 Protein to Determine Leishmania martiniquensis Treatment.

Aiebchun T, Rasri N, Kiriwan D, Siripattanapipong S, Choowongkomon K.

13-01-2023

Acta Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36637694/

[Evaluation of Ex Vivo Cultivation Potentials of Trypanosoma cruzi, Leishmania tropica ve Toxoplasma gondii Parasites in J774, Vero and HeLa Cell Lines].

Yıldırım A, Özbilgin A, Yereli K.

Jan-2023

Mikrobivol Bul.

https://pubmed.ncbi.nlm.nih.gov/36636847/

Three obligate intracellular protozoan parasite species, namely Trypanosoma cruzi, Leishmania tropica and Toxoplasma gondii, causative agents of Chagas disease, Leishmaniasis and toxoplasmosis, respectively, which are responsible for significant morbidity and mortality and reside in macrophage cells, affect more than half of the world's population in connection with socio-economic and geographical factors and also causes neglected parasitic diseases of increasing importance. This study aimed to evaluate the ex vivo cultivation potential of T.cruzi, L.tropica and T.gondii parasites in J774, Vero and HeLa cells and to reproduce in a short time and in large amounts without losing their virulence properties. Ex vivo experimental models were created by infecting J774, Vero and HeLa cell lines confluently produced in cell culture flasks with T.cruzi, L.tropica and T.gondii parasites. In ex vivo cultivation, one passage was applied for seven days and three times in a row. Cells removed from the surface after each passage were plated on eight-well chamber slides. Giemsa stained slides were prepared and infection rates were evaluated by light microscopic examination. At

the end of the study, it was observed that all three cell lines could be infected with T.cruzi, L.tropica and T.gondii parasites, and infection rates increased in all cell lines after consecutive passages. As a result of ex vivo cultivation, the best cell lines from which T.cruzi and L.tropica strains grew, were J774, Vero and HeLa, and HeLa, J774 and Vero cell lines for T.gondii strain, respectively (p<0.05). Trypanosoma cruzi, L.tropica and T.gondii parasites were successfully grown in J774, Vero and HeLa cell lines by ex vivo culture method in a short time and in large amounts without losing their virulence properties. Cell lines with the best ex vivo cultivation potential for T.cruzi and L.tropica parasites were J774, Vero and HeLa, respectively, while HeLa, J774 and Vero for T.gondii. It is thought that the data obtained in this regard will contribute to many studies on the development of vaccines, drugs and new diagnostic kits.2

Anti Leishmanial Effect of Plantago psyllium (Ovate) and White Vinegar on Leishmania major Lesion in BALB/c Mice.

Moshfe A, Karami K, Bahmani M, Naghmachi M, Askarian S, Rezaei A, Zare R, Jamshidi A.

31-03-2022

J Arthropod Borne Dis.

https://pubmed.ncbi.nlm.nih.gov/36633698/

Identification of cuticle and midgut fungal microflora of phlebotomine sandflies collected in Tunisia.

Layouni S, Remadi L, Chaâbane-Banaoues R, Haouas N, Babba H.

12-01-2023

Arch Microbiol.

https://pubmed.ncbi.nlm.nih.gov/36633698/

Asymptomatic Leishmania infection in humans: A systematic review.

Pederiva MMC, Santos SMD, Rivarola LGS, Guerreiro VJ, Lopes KS, Lima Junior MSDC, Neitzke-Abreu HC.

331-12-2023

J Infect Public Health.

https://pubmed.ncbi.nlm.nih.gov/36630836/

Tephrosia toxicaria (Sw.) Pers. extracts: Screening by examining aedicidal action under laboratory and field conditions along with its antioxidant, antileishmanial, and antimicrobial activities.

Sá GCDS, da Silva LB, Bezerra PVV, da Silva MAF, Inacio CLS, Paiva WS, E Silva VPM, Cordeiro LV, Oliveira JWF, Silva MS, Lima EO, Moreira FJC, Rocha HAO, Barra PB, Ximenes MFFM, Uchôa AF.

11-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36630475/

An increase in the incidence of arboviral, microbial and parasitic infections, and to disorders related to oxidative

stress has encouraged the development of adjuvant therapies based on natural formulations, such as those involving plant extracts. Thus, to expand the repertoire of the available therapeutic options, this study aimed to describe the versatility of Tephrosia toxicaria (Sw.) (Pers., 1807) extracts for the control of arbovirus vectors, as well as their antioxidant, antileishmanial, and antimicrobial potential. Among the aqueous and hydroethanolic extracts obtained, the hydroethanolic extract from roots (RHA) was identified as the most active larvicide extract demonstrating, respectively, the lowest concentration (mg/mL) for 50%, 90% and 99% of Aedes aegypti (L., 1762) and Aedes albopictus (S., 1894) larvae, observed at 24 h (0.33, 0.84 and 1.80; 0.32, 0.70 and 1.32) and 48 h (0.17, 0.51 and 1.22; 0.26, 0.47 and 0.78) postexposure. Field assays revealed that RHA (0.84 mg/mL) is a potential oviposition deterrent, reducing egg-laying by approximately 90%. RHA (0.1 mg/mL) also exhibited antioxidant activity for the following tests: total antioxidant capacity (286.86 mg AAE/g), iron (87.16%) and copper (25.64%) chelation, and superoxide scavenging (10%). In the cell culture assays, RHA (0.1 mg/mL) promoted regeneration of metabolic activity (92% cell viability) in cells exposed to oxidative stress. Furthermore, RHA displayed weak antileishmanial activity (IC50 = 3.53 mg/mL) against Leishmania amazonensis and not exhibit antimicrobial activity. The extraction favored the concentration of carbohydrates in RHA, in addition to lectins and protease inhibitors, with molecular masses estimated between 10 and 24 kDa. Cytotoxicity and phytotoxicity analyses of RHA suggested its biosecurity. Thus, RHA is a multivalent extract with insecticide and antioxidant properties at low and safe concentrations. However, others studies on its indirect toxic effects are ongoing to ensure the complete safety of RHA.

Revisiting the Burden Borne by Fumarase: Enzymatic Hydration of an Olefin.

Bellur A, Das S, Jayaraman V, Behera S, Suryavanshi A, Balasubramanian S, Balaram P, Jindal G, Balaram H.

17-01-2023

Biochemistry.

https://pubmed.ncbi.nlm.nih.gov/36595439/

Fumarate hydratase (FH) is a remarkable catalyst that decreases the free energy of the catalyzed reaction by 30 kcal mol⁻¹, much larger than most exceptional enzymes with extraordinary catalytic rates. Two classes of FH are observed in nature: class-I and class-II, which have different folds, yet catalyze the same reversible hydration/dehydration reaction of the dicarboxylic acids fumarate/malate, with equal efficiencies. Using class-I FH from the hyperthermophilic archaeon Methanocaldococcus jannaschii (Mj) as a model along with comparative analysis with the only other available class-I FH structure from Leishmania major (Lm), we provide insights into the molecular mechanism of catalysis in this class of enzymes. The structure of MjFH apo-protein has been determined, revealing that large intersubunit rearrangements occur across apo- and holo-protein forms, with a largely preorganized active site for substrate binding. Site-directed mutagenesis of active site residues,

kinetic analysis, and computational studies, including density functional theory (DFT) and natural population analysis, together show that residues interacting with the carboxylate group of the substrate play a pivotal role in catalysis. Our study establishes that an electrostatic network at the active site of class-I FH polarizes the substrate fumarate through interactions with its carboxylate groups, thereby permitting an easier addition of a water molecule across the olefinic bond. We propose a mechanism of catalysis in FH that occurs through transition-state stabilization involving the distortion of the electronic structure of the substrate olefinic bond mediated by the charge polarization of the bound substrate at the enzyme active site.

Functional characterization and immunogenicity of a novel vaccine candidate against tick-borne encephalitis virus based on Leishmania-derived virus-like particles.

Zimna M, Brzuska G, Salát J, Svoboda P, Baranska K, Szewczyk B, Růžek D, Krol E.

Jan-2023

Antiviral Res.

https://pubmed.ncbi.nlm.nih.gov/36581050/

Design, synthesis, in vitro - In vivo biological evaluation of novel thiazolopyrimidine compounds as antileishmanial agent with PTR1 inhibition.

Istanbullu H, Bayraktar G, Karakaya G, Akbaba H, Perk NE, Cavus I, Podlipnik C, Yereli K, Ozbilgin A, Debelec Butuner B, Alptuzun V.

05-02-2023

Eur J Med Chem.

https://pubmed.ncbi.nlm.nih.gov/36577215/

Improved synthesis of deoxyalpinoid B and quantification of antileishmanial activity of deoxyalpinoid B and sulforaphane.

Leary E, Anderson ET, Keyes JK, Huskie TR, Blake DJ, Miller KA.

18-01-2023

Bioorg Med Chem.

https://pubmed.ncbi.nlm.nih.gov/36565668/

A new oral self-emulsifying drug delivery system improves the antileishmania efficacy of fexinidazole in vivo.

Damasio DSDN, Antunes PA, Lages EB, Morais-Teixeira E, Vital KD, Cardoso VN, Fernandes SOA, Aguiar MG, Ferreira LAM.

25-01-2023

Int J Pharm.

https://pubmed.ncbi.nlm.nih.gov/36549405/

The aim of this study was to develop, characterize and evaluate the in vivo oral efficacy of self-emulsifying drug delivery systems (SEDDS) containing fexinidazole (FEX) in

the experimental treatment of visceral leishmaniasis (VL). The developed FEX-SEDDS formulation presented as a clear, yellowish liquid, with absence of precipitate. The droplet size, polydispersion index and zeta potential after dilution in water (1:200) was of 91 \pm 3 nm, 0.242 \pm 0.005 and -16.7 \pm 0.2, respectively. In the simulated gastric and intestinal media, the FEX-SEDDS had a size of 97 \pm 1 and 106 ± 9 nm, respectively. The FEX retention in droplet after SEDDS dilution in simulated gastrointestinal media was almost 100 %. Antileishmanial efficacy studies showed that FEX-SEDDS was the only treatment able to significantly (p < 0.05) reduce the parasite burden in the liver and spleen of animals experimentally infected with Leishmania infantum. Our intestinal permeability data suggest that FEX-SEDDS showed no evidence of injury to the intestinal mucosa. These findings suggest that FEX-SEDDS can be a promising oral alternative for the treatment of VL caused by L. infantum.

Inspection of in-house designed novel thiochromone amino-acid conjugate derivatives as Lm-NMT inhibitor - An insilico analysis.

Johri S, Kumar BK, Dey S, Faheem, Balana-Fouce R, Gowri Chandra Sekhar KV, Kunjiappan S, Murugesan S.

Mar-2023

J Mol Graph Model.

https://pubmed.ncbi.nlm.nih.gov/36542915/

Leishmaniasis is a complex neglected tropical disease caused by various leishmanial parasites that primarily affect the world's poorest people. A limited number of standard medications are available for this disease that has been used for several decades, which have drawbacks such as resistance, higher cost, and patient compliance, making it difficult to reach the poor. The search for novel chemical entities to treat leishmaniasis has led to targetbased scaffold research. Thiochromone moieties in conjugation with aromatic amino acids have been considered for the study, along with possible substitutions of the electron-withdrawing and electron-donating groups. N-myristoyl transferase (NMT) has been selected as the molecular target for the study responsible for protein-protein interaction and ribosylation of proteins necessary for the growth inside the human body of the parasite. The designed novel thiochromone analogs were docked against the selected leishmanial NMT using theinsilico methods, physicochemical and toxicity properties were predicted, and Structure-Activity Relationship was also established in-silico. Finally, a molecular dynamics simulation study for 100 ns gave an idea about the stability $\,$ of the protein-ligand complex. A time frame analysis of each 10 ns confirmation was also studied to understand better the putative binding pattern designed analogs.

Holanamine, a Steroidal Alkaloid from the Bark of Holarrhena pubescens Wall. ex G. Don Inhibits the Growth of Leishmania donovani by Targeting DNA Topoisomerase 1B.

Goel N, Gupta VK, Garg A, Bhoumik A, Biswas R, Natarajan R, Majumder HK, Jaisankar P.

13-01-2023 ACS Infect Dis.

https://pubmed.ncbi.nlm.nih.gov/36417798/

Case Report: Simple Nodular Cutaneous Leishmaniasis Caused by Autochthonous Leishmania (Mundinia) orientalis in an 18-Month-Old Girl: The First Pediatric Case in Thailand and Literature Review.

Anugulruengkitt S, Songtaweesin WN, Thepnarong N, Tangthanapalakul A, Sitthisan M, Chatproedprai S, Wititsuwannakul J, Likitnukul S, Jariyapan N, Weedall GD, Siriyasatien P, Preativatanyou K.

21-12-2022

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36410322/

We report an autochthonous case of simple, localized cutaneous leishmaniasis in a healthy 18-month-old girl from southern Thailand. The patient presented with a solitary chronic cutaneous nodular lesion on her left cheek for approximately 1 year. Histopathological dissection of the cheek skin biopsy demonstrated remarkably nodular and interstitial infiltrates of lymphocytes and histiocytes full of intracellular oval-shaped amastigotes, consistent with cutaneous leishmaniasis. The Leishmania promastigotes were also cultured successfully from the lesion biopsy and were designated with the WHO code MHOM/TH/2021/CULE5. Using internal transcribed spacer 1-specific polymerase chain reaction, the parasite DNA was demonstrated in both saliva and lesion biopsy. Based on the BLASTn and phylogenetic analysis, the parasite was identified as Leishmania orientalis, clustered in the Mundinia subgenus. The patient responded well to a 6-week course of oral itraconazole, without recurrence. To our knowledge, this is the fourth case of autochthonous leishmaniasis resulting from L. orientalis and the youngest patient of leishmaniasis ever reported in Thailand. More importantly, we also demonstrate the clinical course of the lesion according to the timeline before and after treatment, which can help physicians better understand and provide an accurate diagnosis with appropriate treatment of this emerging parasitic disease.

The discovery and characterization of two novel structural motifs on the carboxy-terminal domain of kinetoplastid RNA editing ligases.

Moses D, Mehta V, Salavati R.

Feb-2023

RNA.

https://pubmed.ncbi.nlm.nih.gov/36400447/

Nyssomyia whitmani (Diptera: Psychodidae) Activity From Sunset to Sunrise: A Two-Year Study in a Rural Area in Northeast Argentina.

Fernández MS, Cueto GR, Manteca-Acosta M, Salomón OD.

12-01-2023

 ${\it J~Med~Entomol}.$

https://pubmed.ncbi.nlm.nih.gov/36308521/

We model the nocturnal patterns of the main vector of Leishmania braziliensis (Vianna) in the Paranaense region of South America, Nyssomyia whitmani (Antunes & Coutinho). Occurrence and abundance variation were analyzed by hourly periods, and in relation to sunrise and sunset to avoid differences in luminosity at fixed times throughout the year. The possible role of climatic and environmental variables on nocturnal activity curves was explored. A rotating light trap was operated biweekly in the peridomestic henhouse of a farm in Puerto Iguazú, from May 2016 to May 2018. Ny. whitmani, is the predominant Phlebotominae species (6,720 specimens captured), and is present throughout the night and seasons. Generalized additive models of nocturnal abundance of Ny. whitmani show a bell shape with an acrophase in the early evening. Models of abundance distribution as a function of total abundance showed significant nonlinear variations, only for the tertile of highest vector abundance, in the curves by hourly periods, and related to dawn, while female abundance relative to total abundance showed an asymptotic increasing curve, suggesting density-dependent events with abundance thresholds. Finally, temperature was the variable that best explained the pattern of abundance distribution of Ny. whitmani during the night, although triggers for scotophase activity due to internal clocks or luminosity could not be ruled out. The relationship of activity and abundance with climatic variables would also explain the nights of extraordinary abundance, and therefore of greater probability of vector-human and vector-reservoir contacts.

Phlebotomine Fauna (Diptera: Psychodidae) and Infection by Leishmania spp. in Forest Fragments of a University Campus, Western Amazon.

Carneiro ACG, de Souza EA, Barroso EP, de Ávila MM, Melchior LAK, Rocha RDC, Shimabukuro PHF, Galati EAB, Brilhante AF.

12-01-2023

J Med Entomol.

https://pubmed.ncbi.nlm.nih.gov/36305744/

Cysticercose

Intraocular and neuro-cysticercosis with diffuse stromal choroiditis.

Das D, Bhattacharjee H, Bhattacharjee K, Barman MJ, Islam S, Das BC, Deshmukh S, Deka A, Chirania P, Kumari N.

Jan-Mar 2023

Indian J Pathol Microbiol.

https://pubmed.ncbi.nlm.nih.gov/36656228/

Updated spatial analysis of areas of occurrence of bovine cysticercosis in the state of Espírito Santo, Brazil.

Gomes JB, de Avelar BR, Martins IVF. 12-12-2022 Braz J Vet Med.

https://pubmed.ncbi.nlm.nih.gov/36654814/

The risk of bovine cysticercosis is mutable over time, since population habits, local infrastructure, and bovine herd size change through the years. Hence, the aim of this study was to update the risk map of bovine cysticercosis occurrence in Espírito Santo State, Brazil, by choosing the following risk factors: inadequate sewer service; bovine population per municipality; risk of flooding; and land use and occupation, examined with a mathematical model using the GIS program ArcGis 10.5. The risk map of occurrence demonstrated that the state is composed of 12.8, 24.5, 36.2 and 26.5% of areas of very high, high, medium, and low risk, respectively. The northern area stood out for areas of very high risk, with the cities of Linhares and São Mateus accounting for 99% of the area with this classification. Of the state's 78 municipalities, 15 had a portion of their territory with very high risk, 11 had over 50% of the territory with high risk and all except Irupi (100% of low risk) had some percentage of medium risk. These findings demonstrate the areas where actions to prevent bovine cysticercosis should be preferentially conducted.

Anterior segment optical coherence tomography and ultrasound biomicroscopy in the diagnosis of subconjunctival mycosis mimicking nodular scleritis.

Vishwakarma P, Murthy SI, Joshi V, Mishra DK. 17-01-2023

BMJ Case Rep.

https://pubmed.ncbi.nlm.nih.gov/36653048/

A female patient in her 20s presented with a bulbar conjunctival mass lesion that was diagnosed as nodular scleritis. It was treated with topical and oral steroids in another hospital. Imaging was done using anterior segment optical coherence tomography and ultrasound biomicroscopy, which helped to rule out scleritis and subconjunctival cysticercosis. Histopathology of the excision biopsy specimen revealed fungal filaments. Topical antifungals were started, and the condition resolved without recurrence after therapy. Although rare, infections should be considered in the differential diagnosis of conjunctival mass lesions. Imaging can help to rule out other entities and guide towards appropriate management.

Cysticercosis and co-incidence with COVID-19.

Mungmunpuntipantip R, Wiwanitkit V.

Jul-Dec 2022

Trop Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36643991/

Taenia solium taeniasis/cysticercosis in Guatemala: a prevalent public health problem?

Hernández-Chea RD, Morales-Ramírez P, Hernández M, Toledo A, Hun A, Sciutto E, Fleury A.

Feb-2023

Pathog Glob Health.

https://pubmed.ncbi.nlm.nih.gov/35657099/

Dracunculose

Structures of the xyloglucans in the monocotyledon family Araceae (aroids).

Hsiung SY, Li J, Imre B, Kao MR, Liao HC, Wang D, Chen CH, Liang PH, Harris PJ, Hsieh YSY.

17-01-2023

Planta.

https://pubmed.ncbi.nlm.nih.gov/36650257/

The xyloglucans of all aquatic Araceae species examined had unusual structures compared with those of other noncommelinid monocotyledon families previously examined. The aquatic Araceae species Lemna minor was earlier shown to have xyloglucans with a different structure from the fucogalactoxyloglucans of other non-commelinid monocotyledons. We investigated 26 Araceae species (including L. minor), from five of the seven subfamilies. All seven aquatic species examined had xyloglucans that were unusual in having one or two of three features: < 77% XXXG core motif [L. minor (Lemnoideae) and Orontium aquaticum (Orontioideae)]; no fucosylation [L. minor (Lemnoideae), Cryptocoryne aponogetonifolia, and Lagenandra ovata (Aroideae, Rheophytes clade)]; and > 14% oligosaccharide units with S or D side chains [Spirodela polyrhiza and Landoltia punctata (Lemnoideae) and Pistia stratiotes (Aroideae, Dracunculus clade)]. Orontioideae and Lemnoideae are the two most basal subfamilies, with all species being aquatic, and Aroideae is the most derived. Two terrestrial species [Dieffenbachia seguine and Spathicarpa hastifolia (Aroideae, Zantedeschia clade)] also had xyloglucans without fucose indicating this feature was not unique to aquatic species.

Melatonin Treatment Enhances the Growth and Productivity of Useful Metabolites in the In Vitro Culture of Spirodela polyrhiza.

Ko J, Ryu JE, Noh SW, Choi HK. 16-01-2023

J Agric Food Chem.

https://pubmed.ncbi.nlm.nih.gov/36647270/

MXene $(Ti_3C_2T_x)$ /cellulose nanofiber/polyaniline film as a highly conductive and flexible electrode material for supercapacitors.

Yuan T, Zhang Z, Liu Q, Liu XT, Miao YN, Yao CL. 15-03-2023

Carbohvdr Polvm.

https://pubmed.ncbi.nlm.nih.gov/36641165/

In recent years, supercapacitors based on cellulose nanofiber (CNF) films have received considerable attention for their excellent flexibility, lightweight, and unique structure. In this study, MXene $(Ti_3C_2T_x)$ /CNF/polyaniline (PANI) hybrid films with good

conductivity and flexibility were prepared by a convenient vacuum filtration method. Combined with PANI, MXene creates an open structure with high conductivity, which facilitates ion and electron transport among the materials and provides the composite with high electrochemical activity. The MXene/CNF/PANI electrode presents a high areal specific capacitance of 2935 mF cm⁻² at the current density of 1 mA cm⁻², excellent cycling stability with high capacitance retention of 94 % after 2000 cycles at 10 mA cm⁻² and high electrical conductivity (634.4 S·cm⁻¹). As a further application of this film, it is used as a free-standing electrode to fabricate a quasi-solid-state supercapacitor with high performance, which has an ultra-thin thickness of 0.344 mm, a significantly high areal specific capacitance (522 mF cm⁻²) at 5 mA cm⁻², a high areal energy density of 94.7 μWh·cm⁻² and a high areal power density of 573 μW·cm⁻². This work shows the great potential of the developed high-performance and flexible cellulose-based composites for fabricating electrodes as well as supercapacitors.

Evidence for the role of sound on the growth and signal response in duckweed.

Ye Z, Yang R, Xue Y, Xu Z, He Y, Chen X, Ren Q, Sun J, Ma X, Hu J, Yang L.

31-12-2022

Plant Signal Behav.

https://pubmed.ncbi.nlm.nih.gov/36634685/

Intercropping of Pinellia ternata (herbal plant) with Sedum alfredii (Cd-hyperaccumulator) to reduce soil cadmium (Cd) absorption and improve yield.

Ng CWW, So PS, Wong JTF, Lau SY.

21-12-2022

Environ Pollut.

https://pubmed.ncbi.nlm.nih.gov/36565916/

Echinococcose

Pulmonary Hydatid Cyst in Children and Adults: Diagnosis and Management.

Aydin Y, Ulas AB, Ahmed AG, Eroglu A.

Dec-2022

Eurasian J Med.

https://pubmed.ncbi.nlm.nih.gov/36655457/

Hydatid cyst disease induced by Echinococcus granulosus is a parasitic disease known since ancient times. Today, it continues to be seen in many countries and creates serious problems. The lung is the second most frequently affected organ by hydatid cysts after the liver. Lung involvement is more prevalent in children than adults, and the growth of the cyst is faster in children. Hydatid cysts are mostly seen in the right lower lobe of the lung. Common symptoms are chest pain, cough, and shortness of breath, with the most diagnostic symptom being the expectoration of cyst fluid or membranes. In endemic areas, the diagnosis of hydatid cysts can usually be made easily by clinical findings, serology tests, and radiological

findings. When the hydatid cyst ruptures and becomes complicated, it is clinically and radiologically confused with many diseases, especially lung cancer. Surgery is accepted as primary treatment of lung hydatid cysts all over the world. The surgical approach is related to several factors such as the size of the cyst, whether it is intact or complicated, unilateral or bilateral, solitary or multiple, and the presence of destruction of the lung parenchyma. Although it is stated by some surgeons that capitonnage is not required, the most frequently applied surgical technique is cystotomy and capitonnage. Pulmonary resection should be avoided as much as possible, particularly in children. Albendazole or mebendazole treatment in pulmonary hydatid cyst is generally used after surgery and to prevent recurrences.

Diagnostic and Management Perspectives in Alveolar Echinococcosis: Review of Literature.

Aydin F, Yalcin A, Karaman A, Sade R, Ozturk G, Alper F. Dec-2022

Eurasian J Med.

https://pubmed.ncbi.nlm.nih.gov/36655439/

Alveolar echinococcosis is a life-threatening zoonotic disease caused by Echinococcus multilocularis. The disease usually primarily involves the liver and shows tumor-like growth. Early diagnosis of alveolar echinococcosis is difficult because the disease is usually asymptomatic in the early stages. Untreated cases are fatal and result in death within 10 years of liver involvement. In the diagnosis of alveolar echinococcosis, the patient's medical history, radiological imaging findings, and serological and histopathological tests are used together. Radiological imaging methods are very important for early diagnosis and differential diagnosis of the disease. In this article, we wanted to review the diagnosis and treatment of alveolar echinococcosis and emphasize the importance of keeping it in mind, especially in cystic lesions of the liver, and the importance of early diagnosis of the disease.

Anatomical-Based Imaging of Cystic Echinococcosis and Review of the Current Literature.

Yesilyurt M, Esdur V.

Dec-2022

Eurasian J Med.

https://pubmed.ncbi.nlm.nih.gov/36655438/

Echinococcosis is a zoonosis caused by cestodes of the genus Echinococcus. This serious disease continues to be an important public health problem as it is endemic in many parts of the world. Cystic disease affects many organs in the body, most commonly the liver. Hydatid disease can cause a diverse spectrum of symptoms, from asymptomatic infection to potential death. In the presence of clinical suspicion, the diagnosis is made by serology and imaging methods. Imaging findings can range from completely cystic lesions to completely solid appearance and calcification. The imaging method to be used depends on the involved organ and the stage of the

cyst. The updated recommendations of the World Health Organization-Echinococcosis Informal Working Group for the stage and treatment of human echinococcosis have had important implications. Accordingly, there are 4 approaches to the clinical management of hydatid disease: surgery, percutaneous techniques and drug therapy for active cysts, and a "watch and wait" approach for inactive cysts. Since it directly affects the treatment, it is necessary to be familiar with the imaging findings of the cyst, especially in endemic areas.

The anti-echinococcal activity of crocin in mice experimentally infected with Echinococcus granulosus.

Aghighi K, Heidarpour M, Borji H.

14-01-2023

Exp Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36649915/

Herbal preparations have good medicinal value for potential use as therapeutic agents in cystic echinococcosis. The efficiency of crocin in the case of cystic echinococcosis was investigated, and compared with that of albendazole, one of the few licensed antiechinococcosis drugs that served as a positive control. Five months after infecting BALB/C mice with E. granulosus sensu lato the experimental group was divided into 7 subgroups containing 10 animals each: 1- Crocin 80 (80 mg/kg), 2- Crocin 40 (40 mg/kg), 3- Crocin 10 (10 mg/kg), 4- Albendazole (200 mg/kg), 5- Crocin 10 (10 mg/kg) +Albendazole (100 mg/kg), 6- Crocin 20 (20 mg/kg) +Albendazole (50 mg/kg), 7- the control (infected and untreated). After two weeks of daily treatment, significant reductions of cysts' weights, sizes, and total numbers concerning the control group were achieved by treatment with crocin 80, crocin 40, crocin 10, crocin 10 + ABZ100, crocin 20+ ABZ50 and ABZ200 (p < 0.05). Moreover, there was no difference concentrations of crocin and those treated with albendazole,. The concentration of bilirubin was higher in the control group than all treated groups with crocin, significantly. However, the ALT activity showeda significant decrease in the crocin 10 group, compared to the crocin 80, crocin 40, crocin 10 + ABZ100, crocin 20 + ABZ50, control groups (p < 0.05). Based on our results, the administration of crocin used at 10 mg/kg concentrations seems a hopeful applicant for the treatment of cystic echinococcosis.

A survey of gastrointestinal parasites in dogs illegally entering the UK (2015-2017).

Fisher MA, Rees B, Capner C, Pritchard S, Holdsworth PA, Fitzgerald RA.

11-01-2023

Vet Rec Open.

https://pubmed.ncbi.nlm.nih.gov/36643053/

[Hepatic cystic echinococcosis complicated with tuberculous empyema misdiagnosed as hepatic and pulmonary cystic echinococcosis: one case report].

Li WD, Pang MQ, Li CQ, Xu K, Dong Y, Zhao WQ, Wang Y, Fan HN.

09-11-2022

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642912/

Hepatic cystic echinococcosis is a chronic parasitic disease caused by the infection with the larvae of *Echinococcus granulosus* in human or animal liver tissues. As a chronic active infectious disease, tuberculous empyema mainly invades the pleural space and then causes visceral and parietal pleura thickening. It is rare to present comorbidity for hepatic cystic echinococcosis and tuberculous empyema. This case report presents a case of hepatic cystic echinococcosis complicated with tuberculous empyema misdiagnosed as hepatic and pulmonary cystic echinococcosis, aiming to improve clinicians' ability to distinguish this disorder.

[Mechanism of hepatic fibrosis associated with Echinococcus: a review].

Zhang RJ, Pang HS, Li JZ, Luo ZH, Ai L, Song P, Cai YC, Lu Y, Mo XJ, Chen MX, Chen JX.

09-11-2022

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642908/

Echinococcosis is a zoonotic parasitic disease caused by Echinococcus infections, and this disorder may cause fibrosis of multiple vital organs, which may further progress into cirrhosis. Early-stage hepatic fibrosis is reversible, and unraveling the mechanisms underlying hepatic fibrosis induced by Echinococcus infections is of great significance for the prevention and treatment of early-stage hepatic fibrosis. Recently, the studies pertaining to hepatic fibrosis associated with Echinococcus infections focus on cytokines and immune cells. This review summarizes the advances in the mechanisms underlying host immune cells- and cytokinesmediated hepatic fibrosis in humans or mice following Echinococcus infections.

[Prevalence of Echinococcus infection in small mammals captured from Shiqu County, Sichuan Province from 2015 to 2020].

He W, Yang L, Wang Q, Yu WJ, Liao S, Liu Y, Zhong B, Luo ZH, Wang Q.

06-01-2023

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642901/

Primary costal hydatid cyst resembling urolithiasis: A case report.

Reza E, Hesam A, Sara S, Mahbod I, Shahab R. 12-01-2023

Int J Surg Case Rep.

https://pubmed.ncbi.nlm.nih.gov/36640468/

Introduction: Hydatid disease (HD) is a zoonotic infection caused by echinococcus granulosus tapeworms. HD accounts for approximately one million cases worldwide. HD is more prevalent in endemic areas, such as the

Mediterranean region. Presentation of case: A middleaged male patient presented with right flank pain for years. His vital signs and physical examination were unremarkable. The whole-body bone scan revealed an area along the sixth rib's posterior arch with increased metabolic activity and CT and MRI were compatible with a hydatid cyst. The cyst was surgically resected and irrigation of the area with hypertonic saline was done. Medical treatment with albendazole was initiated and the patient had no complications. Discussion: Bone involvement is an uncommon finding in HD and involvement of the ribs is even more scarce. Surgical resection complemented with medical treatment is the preferred approach. **Conclusion:** In the Mediterranean and middle eastern regions, high infection rates with E. granulosis are evident hence, uncommon manifestations of the disease should be regarded. Although renal stones are far more prevalent when in endemic areas of HD, the physician should also consider skeletal HD as a differential diagnosis.

Can Echinococcus granulosus-Derived MicroRNAs be Biomarkers for Diagnosis and Follow-up of Cystic Echinococcosis Patients?

Fasihi Karami M, Beiromvand M, Rafiei A, Dayer D, Rahdar M, Bahreini A, Dastyar AA.

13-01-2023

Acta Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36637695/

Proteomics investigation of human sera for determination of postoperative indicators of pulmonary cystic echinococcosis.

Sadjjadi FS, Hajjaran H, Sedaghat B, Mardani P, Sadjjadi SM.

11-01-2023

J Cardiothorac Surg.

https://pubmed.ncbi.nlm.nih.gov/36631795/

THERAPEUTIC APPROACH OF COMPLICATED HYDATID DISEASE: ROLE OF ENDOSCOPIC RETROGRADE CHOLANGIOPANCREATOGRAPHY IN CHOLANGIOHYDATIDOSIS.

González-Arboleda F, Pizarro F, Lindner C, Caqueo F.

09-01-2023

Arg Bras Cir Dig.

https://pubmed.ncbi.nlm.nih.gov/36629682/

Modeling, molecular dynamics and docking studies of a full-length Echinococcus granulosus 2DBD nuclear receptor.

Cancela S, Esteves A, Alvite G, Paulino M.

07-01-2022

J Biomol Struct Dyn.

https://pubmed.ncbi.nlm.nih.gov/34994278/

Nuclear receptors are ligand-activated transcription factors capable of regulating the expression of complex gene networks. The family includes seven subfamilies of protein with a wide phylogenetic distribution. A novel subfamily with two DNA-binding domains (2DBDs) has first reported in Schistosoma mansoni (Platyhelminth, Trematoda). Employing an ab initio protocol and homology modeling methods, the full-length 3D structure of the Eg2DBD α .1 nuclear receptor from Echinococcus granulosus (Platyhelminth, Cestoda) was generated. The model analysis reveals the presence of the conserved three-layered alpha-helical sandwich structure in the ligand binding domain, and a particularly long and flexible hinge region. Molecular dynamics simulations were performed previous to dock a conformational library of fatty acids and retinoic acids. Our results indicate that oleic and linoleic acids are suitable ligands to this receptor. The ligand-protein complex is stabilized mainly by hydrogen bonds and hydrophobic interactions. The fact that 2DBD nuclear receptors have not been identified in vertebrates confers particular interest to these nuclear receptors, not only concerning their structure and function but as targets of new anthelmintic drugs.Communicated by Ramaswamy H. Sarma.

Trématodoses d'origine alimentaire (clonorchiase, opisthorchiase, fasciolase et paragonimose

Copper chloride and copper sulphate in combination with nitroxynil against gastrointestinal nematodes of ruminants: a possible hitchhiking synergic effect at low concentrations.

Juliana Ribeiro Dolenga C, Dos Anjos A, José Arruda E, Beltrão Molento M.

16-01-2023

Int J Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36657612/

caused by Haemonchus spp. Trichostrongylus spp. are major health problems for sheep and cattle. The objective of this study was to determine the efficacy of copper chloride (CuCl₂), and copper sulphate (CuSO₄) at 2.0, 7.0, 30.0, 125.0, 500.0, and 2000.0 μM formulations, and nitroxynil 34% (NTX) at 0.235 mM against gastrointestinal nematodes (GINs) of ruminants. Hence, the in vitro egg hatch test (EHT), the larval development test (LDT), and the larval migration inhibition test (LMIT) were used. Haemonchus spp. (52%) and Trichostrongylus spp. (38%) were the most frequently found parasites. The data fitted a concentrationdependent shape with the highest efficacies of CuCl₂ and CuSO₄ at 95.2 and 97.3% for parasites collected from sheep, and 95.8 and 93.4% from cattle, respectively. The combination of the 50% inhibitory concentration (IC₅₀) of

CuCl $_2$ and CuSO $_4$ and the IC $_{10}$ of NTX showed up to a 52% increase in efficacy above the expected additive results, demonstrating a synergic/drug enhancer interaction. NTX may retain Cu-II ions by complexation, in a hitchhiking mechanism carrying the salts across the parasite cell wall, causing oxidative stress as a consequence of free radical production and cell damage. Synergy data between NTX and CuCl $_2$, and CuSO $_4$ represent a viable opportunity to develop new formulations for combating parasites of ruminants (i.e., Fasciola hepatica, Haemonchus spp., and Oesophagostomum spp.).

Diagnosis of helminths depends on worm fecundity and the distribution of parasites within hosts.

Crellen T, Haswell M, Sithithaworn P, Sayasone S, Odermatt P, Lamberton PHL, Spencer SEF, Déirdre Hollingsworth T.

25-01-2023

Proc Biol Sci.

https://pubmed.ncbi.nlm.nih.gov/36651047/

[Global distribution and transmission of Fasciola].

Yao JW, Jia TW.

05-01-2023

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642909/

As a global zoonotic disease, fascioliasis is a serious threat to human and animal health and animal husbandry development. The complexity of the classification and identification of Lymnaeidae, the intermediate host of *Fasciola*, notably the emergence of its sibling species, leads to misunderstanding of geographical distribution and transmission potential of *Fasciola*. This review introduces the classification of flukes of the family Fasciolidae, describes the geographical distribution of *F. hepatica* and *F. gigantic*, and discusses the co-evolution of *Fasciola* and Lymnaeidae host snails, and the effects of human activities and ruminant migration on global spread and transmission of *Fasciola*. In addition, we revisit the intermediate host snails of *Fasciola* in Africa based on the latest molecular biological evidence.

Effects of Clonorchis sinensis combined with Hepatitis B virus infection on the prognosis of patients with Hepatocellular Carcinoma following Hepatectomy.

Li YK, Zhao JF, Yang CL, Zhan GH, Zhang J, Qin SD, Zhou M, Li MJ, Huang JT, Kong FY, Huang H, Chen JH, Xiang BD. 13-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36638133/

Effects of Health Literacy Promotion Programs for Preventing Opisthorchiasis and Cholangiocarcinoma: a Systematic Review and Meta-analysis.

Moonsan S, Songserm N, Woradet S, Suksatan W. 13-01-2023

J Cancer Educ.

https://pubmed.ncbi.nlm.nih.gov/36637714/

Cholangiocarcinoma (CCA), caused mainly by Opisthorchis viverrini (OV) infection, is a public health issue. Health literacy can play a significant role in preventing OV and CCA and adopting preventive behaviors. Therefore, this study aimed to evaluate, summarize, and synthesize the current evidence on health literacy programs for preventing OV and CCA.A systematic literature search, with Thai and English languages, was performed using electronic databases through PubMed, Google Scholar, ThaiJo, ThaiLis, and Embase to identify studies examining health literacy programs to prevent OV and CCA. We followed PRISMA 2020 guidelines. In addition, we used the RevMan software to perform a meta-analysis to analyze effect sizes using a fixed-effects model and measures of heterogeneity using Cochran's Q and I². This meta-analysis included seven studies that met the criteria. The results showed that the people who received a program had an increased health literacy overall and in each aspect with a statistically significant (p < 0.001). So, health literacy programs can assist people in understanding their health and gaining access to health information and services. Additionally, the effect of programs (communication abilities, self-management, media and information literacy, and decision-making in practice) can help prevent OV and CCA. As a result, multi-disciplinary healthcare teams are crucial to developing preventive programs to prevent OV and CCA. Further studies need to be done and applied to these programs to modify behavior to avoid other diseases.

Microscopic alterations in Fasciola hepatica treated with the essential oils of Pelargonium graveolens and Citrus aurantium.

de Mello AB, Baccega BF, Martins FO, da Rosa Farias NA, de Giacometi M, da Fonseca RN, de Oliveira Hübner S, Soares MP, Oliveira CB.

Feb-2023

Vet Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36565643/

Fasciolosis is one of the most important parasitic diseases in animal health, affecting mainly ruminants, causing economic and productivity losses. This study aimed to evaluate the in vitro ovicidal and adulticidal activity of essential oils (EOs) from Pelargonium graveolens (geranium) and Citrus aurantium (sour orange) on Fasciola hepatica. Performed Gas Chromatography of EOs P. graveolens and C. aurantium, with major compound, citronellol (31.37 %) and limonene (93.89 %), respectively. For the cytotoxicity assay, the sour orange EO showed to be promising when used in lower concentrations. For the ovicidal tests, the eggs were incubated with geranium EOs at concentrations from 4.5 to 0.03375 mg/mL and sour orange at concentrations from 4.25 to 0.031875 mg/mL, along with controls. The viable eggs were counted on the 14th day post-incubation. Adult forms of F. hepatica were incubated containing the EOs and observed for 24 h after treatment, as well as the control groups. Later the

specimens were fixed for histological analysis. Geranium and sour orange EOs in trematode eggs at the concentrations tested were 100 % effective in inactivating hatching (p < 0.05) when compared to the untreated control. In the adulticidal test, the essential oil of P. graveolens at both concentrations tested (0.0675 and 0.03375) within 15 h, promoted the death of flukes. For C. aurantium, 18 h was enough to inactivate all specimens, up to a concentration of 0.06375. The histological analysis, observed the accumulation of liquid in the tegument in the specimens incubated in C. aurantium and P. graveolens, with vacuolization in the tegument and spines, preventing externalization. The results of the study present OEs with efficient ovicidal and adulticidal activity.

Filariose lymphatique

Coverage and compliance of mass drug administration in lymphatic filariasis amidst the COVID-19 pandemic: A community based epidemiological study.

Chakraborty S, Bhattacharya T.

Jul-Dec 2022

Trop Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36643986/

Novel genome sequences and evolutionary dynamics of the North American anopheline species Anopheles freeborni, Anopheles crucians, Anopheles quadrimaculatus, and Anopheles albimanus.

Henderson C, Kemirembe K, McKeand S, Bergey C, Rasgon JL.

12-12-2023

G3 (Bethesda).

https://pubmed.ncbi.nlm.nih.gov/36377778/

Anopheles mosquitoes are the principal vectors for malaria and lymphatic filariasis, and evidence for arboviral transmission under laboratory and natural contexts has been demonstrated. Vector management approaches an understanding of the ecological, epidemiological, and biological contexts of the species in question, and increased interest in gene drive systems for vector control applications has resulted in an increased need for genome assemblies from understudied mosquito vector species. In this study, we present novel genome assemblies for Anopheles crucians, Anopheles freeborni, Anopheles albimanus, and Anopheles quadrimaculatus and examine the evolutionary relationship between these species. We identified 790 shared single-copy orthologs between the newly sequenced genomes and created a phylogeny using 673 of the orthologs, identifying 289 orthologs with evidence for positive selection on at least 1 branch of the phylogeny. Gene ontology terms such as calcium ion signaling, histone binding, and protein acetylation identified as being biased in the set of selected genes. These novel genome sequences will be useful in developing our understanding of the diverse biological traits that drive vectorial capacity in anophelines.

Onchocercose

Sores of boreal moose reveal a previously unknown genetic lineage of parasitic nematode within the genus Onchocerca.

Benedict BM, Barboza PS, Crouse JA, Groch KR, Kulpa MR, Thompson DP, Verocai GG, Wiener DJ.

11-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36630399/

Long-standing reports of open sores on the hind legs of moose (Alces alces) have been recorded in Alaska (as well as Canada, Europe, and Michigan), eliciting concerns about causes and infection. We used histological and genomic methods to investigate the sores from 20 adult moose on the Kenai Peninsula, Alaska. We paired this with thermal imagery and molt scoring of adult moose to further describe sore formation and understand its timing. Severe, ulcerative and eosinophilic dermatitis was found in all moose with sores present, and microfilariae within intraepidermal pustules were additionally found in four samples. Genetic analysis of sores from moose revealed a previously unknown genetic lineage of Onchocerca. Adult moose molt and lose their barrier of protection against flies in June and July during peak fly activity, leaving them vulnerable and allowing the development of sores. In summary, our results indicate that the cause for the sores on the hindleg of moose is a previously unknown genetic lineage of Onchocerca, probably transmitted by black flies, in timing with the molt cycle of adult moose. These sores leave moose exposed to pathogens, making them vulnerable, and challenging their health and fitness.

Two Nigerian States (Plateau and Nasarawa) Have Eliminated Transmission of Human Onchocerciasis-A Report of Post-Ivermectin Mass Drug Administration Surveillance.

Miri ES, Eigege A, Kahansim B, Nwodu K, Sambo Y, Mancha B, Adelamo S, Umaru J, Kadimbo J, Danboyi J, Mafuyai H, Makata E, Akpan N, Akilah J, Igbe M, Coalson J, Rakers L, Griswold E, Unnasch TR, Nwoke BEB, Noland GS. Richards FO.

30-11-2022

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36450227/

Schistosomiase

Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for differential identification of adult Schistosoma worms.

Ebersbach JC, Sato MO, de Araújo MP, Sato M, Becker SL, Sy I.

19-01-2023

Parasit Vectors.

https://pubmed.ncbi.nlm.nih.gov/36658630/

Background: Schistosomiasis is a major neglected tropical disease that affects up to 250 million individuals worldwide. The diagnosis of human schistosomiasis is mainly based on the microscopic detection of the parasite's eggs in the feces (i.e., for Schistosoma mansoni or Schistosoma japonicum) or urine (i.e., for Schistosoma haematobium) samples. However, these techniques have limited sensitivity, and microscopic expertise is waning outside endemic areas. Matrix-assisted desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry (MS) has become the gold standard diagnostic method for the identification of bacteria and fungi in many microbiological laboratories. Preliminary studies have recently shown promising results for parasite identification using this method. The aims of this study were to develop and validate a species-specific database for adult Schistosoma identification, and to evaluate the effects of different storage solutions (ethanol and RNAlater) on spectra profiles. Methods: Adult worms (males and females) of S. mansoni and S. japonicum were obtained from experimentally infected mice. Species identification was carried out morphologically and by cytochrome oxidase 1 gene sequencing. Reference protein spectra for the creation of an in-house MALDI-TOF MS database were generated, and the database evaluated using new samples. We employed unsupervised (principal component analysis) and supervised (support vector machine, k-nearest neighbor, Random Forest, and partial least squares discriminant analysis) machine learning algorithms for the identification and differentiation of the Schistosoma species. Results: All the spectra were correctly identified by internal validation. For external validation, 58 new Schistosoma samples were analyzed, of which 100% (58/58) were correctly identified to genus level (log score values ≥ 1.7) and 81% (47/58) were reliably identified to species level (log score values \geq 2). The spectra profiles showed some differences depending on the storage solution used. All the machine learning algorithms classified the samples correctly. Conclusions: MALDI-TOF MS can reliably distinguish adult S. mansoni from S. japonicum.

Understanding perceptions of schistosomiasis and its control among highly endemic lakeshore communities in Mayuge, Uganda.

Mujumbusi L, Nalwadda E, Ssali A, Pickering L, Seeley J, Meginnis K, Lamberton PHL.

19-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36656869/

The role of the host gut microbiome in the pathophysiology of schistosomiasis.

Stark KA, Rinaldi G, Cortés A, Costain A, MacDonald AS, Cantacessi C.

19-01-2023

Parasite Immunol.

https://pubmed.ncbi.nlm.nih.gov/36655799/

Schistosomiasis model with treatment, habitat modification and biological control.

Nur W, Trisilowati T, Suryanto A, Kusumawinahyu WM. 19-09-2022

Math Biosci Eng.

https://pubmed.ncbi.nlm.nih.gov/36654068/

Schistosomiasis is a parasitic disease caused by Schistosoma worm infection. Some species of snails can serve as the intermediate hosts for the parasite. Numerous interventions have been performed to repress the snail population. One of them is the use of molluscicide. Nevertheless, it is debated that molluscicide intervention has negative impacts on the ecosystem. To investigate the impact of more environmentally friendly interventions, we develop a schistosomiasis model with treatment, habitat modification and biological control. The biological control agent examined in our model is a snail predator. Moreover, to investigate the impact of snail habitat modification, we assume that the snail population grows logistically. We show that all solutions of our model are non-negative and bounded. We also study the existence and stability conditions of equilibrium points. The basic reproduction numbers are determined using the next-generation operator. Linearization combined with the Routh-Hurwitz criterion is used to prove the local stability condition of disease-free equilibrium points. Bifurcation theory is applied to investigate the local stability condition of the endemic equilibrium points. To examine the global behavior of our model, we use asymptotically autonomous system theory and construct a Lyapunov function. We perform several numerical simulations to validate and support our deductive results. Our results show that early treatment can reduce the basic reproduction number and schistosomiasis cases. In addition, modifying snail habitat and releasing the snail predator at the snail habitat can reduce schistosomiasis prevalence. We suggest using snail predators which can hunt and kill snails effectively as a biological control agent.

Schistosomiasis of liver graft as a differential diagnosis of abnormal liver tests after transplantation: report of two cases.

Falcão LTM, Batista AD, Maranhão EC, Santos SSFD, Madeiro VRV, Moura FM, Lyra CHA.

16-01-2023

Rev Inst Med Trop Sao Paulo.

https://pubmed.ncbi.nlm.nih.gov/36651463/

Schistosomiasis is a major health problem that affects over 200 million people worldwide. There are few reports of Schistosoma mansoni found in liver transplants as well as scarce information about the course of the disease and the long-term effects on the graft. Herein, we report two cases of schistosomiasis in liver transplant recipients who presented abnormal serum liver enzymes, with evidence of gradual improvement after antiparasitic treatment. Furthermore, we discuss the possible role of screening the parasite infection in potential liver transplant recipients from endemic areas.

Planarians to schistosomes: an overview of flatworm cell-types and regulators.

Lee J

16-01-2023

J Helminthol.

https://pubmed.ncbi.nlm.nih.gov/36644809/

Schistosomiasis remains a major neglected tropical disease that afflicts over 200 million people globally. Schistosomes, the aetiological agent of schistosomiasis, are parasitic flatworms that propagate between molluscan and mammalian hosts. Inside the mammalian host. schistosomes rapidly grow over 100-fold in size and develop into a sexually mature male or female that thrives in the bloodstream for several decades. Recent work has identified schistosome stem cells as the source that drives parasite transmission, reproduction and longevity. Moreover, studies have begun to uncover molecular programmes deployed by stem cells that are essential for tissue development and maintenance, parasite survival and immune evasion. Such programmes are reminiscent of neoblast-driven development and regeneration of planarians, the free-living flatworm relative of schistosomes. Over the last few decades, research in planarians has employed modern functional genomic tools that significantly enhanced our understanding of stem cell-driven animal development and regeneration. In this review, we take a broad stroke overview of major flatworm organ systems at the cellular and molecular levels. We summarize recent advances on genetic regulators that play critical roles in differentiation and maintenance of flatworm cell types. Finally, we provide perspectives on how investigation of basic parasite biology is critical to discovering new approaches to battle schistosomiasis.

[Investigation on prevalence of Schistosoma japonicum infections in wild mice in Shitai County, Anhui Province, 2018].

He JC, Chen XF, Wang TP, Gao FH, Tao W, Dai B, Ding SJ, Liu T, Li Y, Wang H, Mao WF, Zhang LS, Xu XJ, Zhang SQ. 30-08-2022

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642903/

[Comparison of pathogenicity and gene expression profiles between adult Schistosoma japonicum isolated from hilly and marshland and lake regions of Anhui Province].

Wu JL, Hu MC, Wang Q, Liu DH, Zhang LS, Zhu L, Sun CS, Cao ZG, Wang TP.

09-12-2022

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642897/

Objective: To compare the differences in pathogenicity and gene expression profiles between adult *Schistosoma japonicum* isolated from hilly and marshland and lake regions of Anhui Province, so as to provide the scientific evidence for formulating the precise schistosomiasis

control strategy in different endemic foci. Methods: C57BL/6 mice were infected with cercariae of *S. japonicum* isolates from Shitai County (hilly regions) and Susong County (marshland and lake regions) of Anhui Province in 2021, and all mice were sacrificed 44 days post-infection and dissected. The worm burdens, number of S. japonicum eggs deposited in the liver, and the area of egg granulomas in the liver were measured to compare the difference in the pathogenicity between the two isolates. In addition, female and male adult S. japonicum worms were collected and subjected to transcriptome sequencing, and the gene expression profiles were compared between Shitai and Susong isolates of S. japonicum. The differentially expressed genes (DEGs) were subjected to Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses. Results: The total worm burdens [(14.50 \pm 3.96) worms/mouse vs. (16.10 \pm 3.78) worms/mouse; t = 0.877, P = 0.392], number of female and male paired worms [(4.50 \pm 0.67) worms/mouse vs. (5.10 \pm 1.45) worms/mouse; t = 1.129, P = 0.280], number of unpaired male worms [(5.50 ± 4.01) worms/mouse vs. (5.60 ± 1.69) worms/mouse; t = 0.069, P = 0.946], number of eggs deposited in per gram liver [(12 116.70 \pm 6 508.83) eggs vs. (16 696.70 \pm 4 571.56) eggs; t = 1.821, P = 0.085], and area of a single egg granuloma in the liver [(74 359.40 \pm 11 766.34) μ m² vs. (74 836.90 \pm 13 086.12) μ m²; t =0.081, P = 0.936] were comparable between Shitai and Susong isolates of S. japonicum. Transcriptome sequencing identified 584 DEGs between adult female worms and 1 598 DEGs between adult male worms of Shitai and Susong isolates of *S. japonicum*. GO enrichment analysis showed that the DEGs between female adults were predominantly enriched in biological processes of stimulus response, cytotoxicity, multiple cell biological processes, metabolic processes, cellular processes and signaling pathways, cellular components of cell, organelles and cell membranes and molecular functions of binding and catalytic ability, and KEGG enrichment analysis showed that these DEGs were significantly enriched in pathways of vascular endothelial growth factor signaling, glutathione metabolism, arginine and proline metabolism. In addition, the DEGs between male adults were predominantly enriched in biological processes of signaling transduction, multiple cell biological processes, regulation of biological processes, metabolic processes, development processes and stimulus responses, cellular components of extracellular matrix and cell junction and molecular functions of binding and catalytic ability, and these DEGs were significantly enriched in pathways of Wnt signaling, Ras signaling, natural killer cells-mediated cytotoxicity, extracellular matrix-receptor interactions and arginine biosynthesis.

Conclusions: There is no significant difference in the pathogenicity between *S. japonicum* isolates from hilly and marshland and lake regions of Anhui Province; however, the gene expression profiles vary significantly between *S. japonicum* isolates.

[Recombinant Schistosoma japonicum egg ribonuclease SjCP1412 inhibits the activation of LX-2 hepatic stellate cells in vitro].

Li QF, Song LJ, Yang YY, Dong PP, Mei CJ, Li YX, Zhang JF, Xiong C, Yu CX, Yang K.

05-01-2023

Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. https://pubmed.ncbi.nlm.nih.gov/36642896/

Burden and risk factors for Schistosoma mansoni infection among primary school children: A quantitative schoolbased cross-sectional survey in Busega district, Northern Tanzania.

Ogweno G, Mushi V, Silvestri V, Bonaventura W, Justine NC, Noah M, Yoram F, Mohamed H, Tarimo D.

12-01-2023

PLoS One.

https://pubmed.ncbi.nlm.nih.gov/36634114/

High Sensitivity of Mobile Phone Microscopy Screening for Schistosoma haematobium in Azaguié, Côte d'Ivoire.

Coulibaly JT, Silue KD, Armstrong M, Díaz de León Derby M, D'Ambrosio MV, Fletcher DA, Keiser J, Fisher K, Andrews JR, Bogoch II.

12-12-2022

Am J Trop Med Hyg.

https://pubmed.ncbi.nlm.nih.gov/36509050/

Schistosomiasis infections continue to impact African settings disproportionately, and there is an urgent need for novel tools to evaluate infection control and elimination strategies at the community level. Mobile phone microscopes are portable and semiautomated devices with multiple applications for screening neglected tropical diseases. In a community-based schistosomiasis screening program in Azaguié, Côte d'Ivoire, mobile phone microscopy demonstrated a sensitivity of 85.7% (95% CI: 69.7-95.2%) and specificity of 93.3% (95% CI: 87.7-96.9%) for Schistosoma haematobium identification compared with conventional light microscopy, and 95% sensitivity (95% CI: 74.1-99.8%) with egg concentrations of five or more per 10 mL of urine. Mobile phone microscopy is a promising tool for schistosomiasis control and elimination efforts.

Modeling, molecular dynamics and docking studies of a full-length Echinococcus granulosus 2DBD nuclear receptor.

Cancela S, Esteves A, Alvite G, Paulino M. 07-01-2022 J Biomol Struct Dyn.

https://pubmed.ncbi.nlm.nih.gov/34994278/

Helminthiases transmises par le sol (ascaridiose, trichuriase, ankylostomiase)

An Overview of Ascariasis Involvement in Gallbladder Disease: A Systematic Review of Case Reports.

Inyang B, Koshy FS, George K, Poudel P, Chalasani R, Goonathilake MR, Waqar S, George S, Jean-Baptiste W, Yusuf Ali A, Mohammed L.

15-12-2022

Cureus.

https://pubmed.ncbi.nlm.nih.gov/36654632/

Ascaris lumbricoides is the most common type of helminth infection in humans. It affects more than one billion of the world's population. Children living in developing nations are prone to ascariasis, presenting with obstructive biliary illnesses. Migration of Ascaris worms through the major duodenal papilla to the hepatobiliary system leads to symptoms of biliary colic and complications along the biliary tree. In April 2022, we performed a systematic review of case reports to identify and examine cases of gallbladder ascariasis worldwide. A methodical search using PubMed, Semantic Scholar, ScienceDirect, and Directory of Open Access Journals yielded 2773 studies. After duplicate removal, title, abstract, and content screening, retrieval, and quality assessment, 13 studies met the criteria for this systematic review of case reports. The cases and results from these 13 studies revealed gallbladder ascariasis in different age groups worldwide. This systematic review discusses ascariasis, explicitly highlighting its presence in the gallbladder, symptomatic presentation, laboratory/imaging findings, complications, and approach to management.

Occurrence of gastrointestinal parasites in dogs from Cuiabá, Mato Grosso.

Souza CTV, Dorr AP, Silva VLB, Silva FL, Silva EBD, Ramos DGS, Pacheco RC, Sousa VRF.

13-01-2023

Rev Bras Parasitol Vet.

https://pubmed.ncbi.nlm.nih.gov/36651423/

Gastrointestinal parasitism by helminths and protozoa poses risks to animal and human health owing to clinical changes and transmission of potentially zoonotic agents. Thus, the present study aimed to verify the occurrence of gastrointestinal parasites in dogs from the municipality of Cuiabá, Mato Grosso, Brazil, using coproparasitological tests. From June 2021 to April 2022, faecal samples were collected from domestic dogs at the Veterinary Hospital and Animal Protection Shelters in the Cuiabá municipality. A semi-structured questionnaire was applied to the owners and those responsible for the shelters to analyse the factors associated with gastrointestinal parasitism. A total of 353 faecal samples were collected and subjected to parasitological flotation and sedimentation techniques. Data were analysed using the chi-squared test and

exploratory factorial analysis. The occurrence of gastrointestinal parasitism was 22.66% and the parasites found alone or in mixed infections were Ancylostoma spp., Trichuris vulpis, Toxocara spp., Dipylidium caninum, Cystoisospora spp., Giardia duodenalis, and coccidia. It was concluded that the occurrence of gastrointestinal parasites in dogs is frequent, and the variables associated with these infections were source origin, breed, age, coexistence with other animals, and dull fur.

High Prevalence of Hookworm Species and Associated Factors among Soil-Transmitted Helminth-Infected Household Contacts in Burie Zuria District, Northwest Ethiopia: A Community-Based Cross-Sectional Study.

Assefa G, Alemu M, Ayehu A.

07-01-2023

Biomed Res Int.

https://pubmed.ncbi.nlm.nih.gov/36647545/

Gut Parasites of medical importance harboured by Musca domestica in Calabar, Nigeria.

Otu-Bassey IB, Efretuei GK, Mbah M.

Jul-Dec 2022

Trop Parasitol.

https://pubmed.ncbi.nlm.nih.gov/36643981/

Assessment of cetyl-trimethylammonium bromide (CTAB) based method for the extraction of soiltransmitted helminth DNAs from stools for molecular dagnostic of soiltransmitted helminthiasis.

Kamdem CN, Fogue PS, Tiofack AAZ, Mewamba EM, Womeni HM, Koffi M, Simo G.

Jan-2023

J Microbiol Methods.

https://pubmed.ncbi.nlm.nih.gov/36565938/

Although several protocols were developed to extract DNA for soil-transmitted helminthiasis diagnostic, amplifying these extracts remains challenging due to DNA polymerase inhibitors. This study aimed to assess a DNA extraction method for efficient detection of soiltransmitted helminth species by determining stool mass and the type of DNA polymerase that can be used for this extraction method. For this study, 141 stool samples harbouring soil-transmitted eggs and 50 samples without egg were obtained from school-aged children of Makenene in the Centre region of Cameroon. DNA was extracted from 10, 20, 40 and 80 mg of stool using commercial kit and/or cetyltrimethylammonium bromide (CTAB)-based method. The amount of stool for molecular diagnostic of soil-transmitted helminthiasis was determined by amplifying Ascaris lumbricoides DNA. The performances of three DNA polymerases and CTAB-based method were assessed by amplifying DNA of different soiltransmitted helminth species. For this study, 94 stools with A. lumbricoides eggs. 39 with Trichuris trichuria and 15 with hookworm were analyzed. DNA of A. lumbricoides, T. trichuria, Necator americanus and Ancylostoma duodenale were detected in 97.9% of extracts from stools harbouring soil-transmitted helminth eggs. transmitted helminth DNAs were significantly ($X^2 = 17.66$; df = 3; p (00001) more amplified in extracts from 10 and 20 mg than those from 40 and 80 mg. The amplification rate with "Q5 high fidelity DNA polymerase" was significantly ($X^2 = 30.54$; df = 2; p < 0.00001) higher than that of other DNA polymerases. Multiplex-PCR confirmed co-infections of A. lumbricoides with either T. trichuria or N. americanus. The extraction cost for the CTAB-based method was \$1.45. This method appeared is reliable and 3 times cost effective than commercial kit. Its combination with the "Q5 high fidelity DNA polymerase" may improve soil-transmitted helminthiasis diagnostic.

Gale

Case of concurrence of bullous pemphigoid and Norwegian scabies.

Wang X, Liu Y, Li J, Bao F, Chen M. 16-12-2023

Parasite Immunol.

https://pubmed.ncbi.nlm.nih.gov/36645298/

Bullous pemphigoid (BP) with scabies is a condition rarely encountered in clinical practice, and when it is encountered, it is often due to the use of immunosuppressants. This paper is a report on a patient with bullous pemphigoid (BP) and scabies, who developed scabs after taking dexamethasone. It should be noted that bullous pemphigoid antibody is necessary, which can distinguish bullous pemphigoid with scabies and bullous scabies, and the treatment options for the two diseases are different.

Morsures de serpent

Evaluation of the properties of Bungarus caeruleus venom and checking the efficacy of antivenom used in Bangladesh for its bite treatment.

Alam MJ, Maruf MMH, Iqbal MA, Hasan M, Sohan MSR, Shariar MR, Haidar IKA, Chowdhury MAW, Ghose A, Hoque KMF, Reza MA.

03-01-2023

Toxicon X.

https://pubmed.ncbi.nlm.nih.gov/36654657/

As a disaster-prone country with unique geographical features, snake biting is a major public health concern in Bangladesh. The primary reasons of mortality from snakebite include late presentation to the hospital, low efficacy of antivenom, and a lack of adequate management facilities. Because snake venom characteristics vary depending on geographical location, antivenom should be manufactured from snakes native to the region in which it would be administered. *Bungarus caeruleus* is a highly venomous snake contributing to the

major snakebite issue in Bangladesh. Therefore, the neutralization efficacy of the antivenom against B. caeruleus venom was evaluated in the current study along with the characterization of venom. For biological characterization of venom, RP-HPLC and SDS-PAGE profiling, hemolytic activity, hemorrhagic activity, phospholipases A₂ (PLA₂) activity, edema inducing activity and histopathological observations were carried out following standard protocol. LD₅₀ of the venom was calculated along with neutralization potency of Incepta antivenom through probit analysis. Results showed that venom possesses phospholipase A2 activity, hemolytic activity and edema inducing activity while hemorrhagic activity was absent in the skin of envenomed mice. alterations including Histopathological congestion and infiltrations were observed in envenomed mice organs after hematoxylin and eosin staining. Neutralization study showed that Incepta polyvalent antivenom could neutralize (potency 0.53 mg/ml) the lethal effect in *in vitro* study on mice. Further investigation on snakebite epidemiology and clinical observations of the envenomed patients will help in combating the snakebite problem more efficiently.

Using a gradient boosted model for case ascertainment from free-text veterinary records.

Kennedy U, Paterson M, Clark N.

10-01-2023

Prev Vet Med.

https://pubmed.ncbi.nlm.nih.gov/36638610/

Case ascertainment for prevalence and incidence studies from veterinary clinical data poses a major challenge because medical notes are not consistently structured or complete. Using natural language processing (NLP) and machine learning, this study aimed to obtain accurate case recognition for feline upper respiratory tract infections (primarily caused by viruses such as feline herpes virus (FHV-1) and feline calici virus (FCV), and bacteria such as Chlamydophila felis, Mycoplasma felis and Bordetella bronchiseptica using retrospective electronic veterinary records from the Royal Society for Prevention of Cruelty to Animals, Queensland (RSPCA Qld). Data cleaning and NLP on eight years of free-text veterinary records from RSPCA Queensland was carried out to derive text-based predictors. The NLP steps included sorting records by length of stay, vectorising, tokenising and spell checking against a bespoke veterinary database. A gradient boosted model (GBM) was trained to predict the probability of each animal having a diagnosis of upper respiratory infection. A manually annotated dataset was used for training the algorithm to learn dominant patterns between predictors (frequencies of n-grams) and responses (manual binary case classification). The GBM's performance was tested against an out of sample validation dataset, and model agnostics were used to interrogate the model's learning process. The GBM used patient-level frequencies of 1250 unique n-grams as predictor variables and was able to predict the probability of cases in the validation dataset with an accuracy of 0.95 (95% CI 0.92, 0.97) and F1 score of 0.96. Predictors that exerted the highest influence on the model included frequencies of "doxycycline", "flu", "sneezing", "doxybrom" and "ocular". The trained GBM was deployed on the full dataset spanning eight years, comprising 60,258 clinical entries. The prevalence in the full dataset was predicted to be 23.59%, which is in line with domain expertise from practicing veterinarians at the shelter. Case ascertainment is a crucial step for further epidemiological study of cat flu. Ultimately, this tool can be extended to other clinical procedures, conditions, and diseases such as intensive care treatment due to snake bites and tick paralysis, physical injuries such as orthopaedic fractures or chest injuries and labour-intensive infectious diseases like parvovirus, canine cough, and ringworm, all of which require prolonged quarantine and care.

Venom-induced consumptive coagulopathy leading to thrombotic microangiopathy following Echis carinatus sochureki bite: is snake antivenom effective?

Parihar V, Mittal A, Vikarn V, Didel S, Singh K. 05-12-2022

J Trop Pediatr.

https://pubmed.ncbi.nlm.nih.gov/36629498/

The incidence of thrombotic microangiopathy (TMA) following snake bite is reported to be ranging from 3.6 to 15%. We report a 10-year-old boy who developed TMA and due to venom-induced consumptive coagulopathy (VICC) despite receiving adequate and timely doses of snake antivenom following a bite of saw-scaled viper (Echis carinatus sochureki). VICC was managed by plasmapheresis. Though snake bite envenomationassociated renal complications are not uncommon, possibility of TMA should be considered early during management. Our patient developed TMA with subsequent acute cortical necrosis after saw-scaled viper bite despite an adequate and timely dose of snake antivenom which emphasizes the ineffectiveness of antivenom against the venom of given snake species leading to long-term complications.