



Veille scientifique

Maladies tropicales négligées

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14 au 20 août 2023

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Cysticercose

Metagenomic next-generation sequencing in the diagnosis of neurocysticercosis: A case report.

Xu WB, Fu JJ, Yuan XJ, Xian QJ, Zhang LJ, Song PP, You ZQ, Wang CT, Zhao QG, Pang F.

16-07-2023

World J Clin Cases.

<https://pubmed.ncbi.nlm.nih.gov/37584000/>

Seropositivity to Cysticercosis in School-Age Children Living in a Low-Income Municipality in the Midwest Region of Brazil.

Moraes D, Santos ÉAD, Mendes JAA, Barcelos ISDC, De Souza JBA, De Fátima Gonçalves-Pires MDR, Costa-Cruz JM, Rodrigues RM.

Avr-Juin 2023

Iran J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37583630/>

Background: Human cysticercosis (CC) is a global public health problem, especially in Latin America, including Brazil. We aimed to analyze the seroprevalence of CC among school-age children and adolescents. **Methods:** We analyzed the presence of specific IgG antibodies against *Taenia solium* metacestodes in 500 serum samples from elementary school children and adolescents in Jataí City, state of Goiás, Brazil. IgG antibodies against the antigenic extract of the parasite were detected and analyzed by ELISA, and specific peptides were identified by confirmatory Western Blotting test. **Results:** Of the 500 study participants, 205 (41%) were male, and 295 (59%) were female. Participants aged between 4 and 18 years (mean age 8.4 years). The percentage of serum samples reactive by ELISA was 37.2%. These samples were analyzed by Western Blotting, which confirmed that the seropositivity rate was 6.2% (95% CI 2.4-14.7) in 31 samples reactive for CC-specific bands, determined in serum samples from 18 male (5-11 years old) and 13 female (4-12 years old) students. **Conclusion:** The CC seroprevalence demonstrated in schoolchildren suggests that this parasitosis is endemic in the study area. Further investigations are necessary to clarify the local epidemiology of this parasitosis.

Quantitative risk assessment for human *Taenia solium* taeniasis/cysticercosis exposure through consumption of pork in Mpwapwa District of Dodoma Region, Tanzania.

Mulilo MA, Mwape KE, M'kandawire E, Mkupasi EM.

Mai-2023

Vet World.

<https://pubmed.ncbi.nlm.nih.gov/37576769/>

Colloidal/Calcified Neurocysticercosis at University Hospital of KSA: A Case Series.

Nazish S, Almuhanha M.

May-2023

Ethiop J Health Sci.

<https://pubmed.ncbi.nlm.nih.gov/37576167/>

Background: Neurocysticercosis (NCC) is considered the most common central nervous system (CNS) helminthic infection. The prevalence of NCC cases in the Middle East has increased in recent years. Thirty-nine cases of NCC were reported between 2003-2011 in the Arabian Peninsula, among, five cases being from the kingdom Saudi Arabia (KSA). Most of the cases reported from the KSA were presented with seizures, and they belonged to expatriate workers or their related contacts. In this case series, we presented three cases of colloidal/calcified NCC.

Cases: Our patients were diagnosed with NCC based on epidemiologic exposure, clinical features, and typical radiological findings. Stool samples for ova and parasites were negative in all three cases. Among these cases, two patients were immigrants and belonged to endemic areas, and third case who is the youngest in this series was a Saudi, without any history of exposure to any source.

Results: The first and the third cases were treated with Albendazole and Dexamethasone. We did not offer any medication regarding NCC in the second case as he had asymptomatic NCC and the disease was inactive so did not mandate anti-helminth medication. **Conclusion:** NCC in KSA, like in non-endemic countries, is not a rare or unusual infection anymore, presenting with seizures or incidental findings in an asymptomatic state. Vigilant diagnostic protocols with efficient diagnostic tools are required for detecting carriers of the adult form of the parasite. Timely detection of these carriers can avoid further spread and its related complications in the Saudi population.

Sexual dimorphism in the murine model of extraparenchymal neurocysticercosis.

Moreira CAA, Murayama LHV, Martins TC, Oliveira VT, Generoso D, Machado VMV, Batah SS, Fabro AT, Bazan R, Zanini MA, Sciutto E, Fleury A, Hamamoto Filho PT.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37428312/>

Neurocysticercosis is a heterogeneous disease, and the patient's sex seems to play a role in this heterogeneity. Hosts' sexual dimorphism in cysticercosis has been largely explored in the murine model of intraperitoneal *Taenia crassiceps* cysticercosis. In this study, we investigated the sexual dimorphism of inflammatory responses in a rat model of extraparenchymal neurocysticercosis caused by *T. crassiceps*. *T. crassiceps* cysticerci were inoculated in the subarachnoid space of Wistar rats (25 females, 22 males). Ninety days later, the rats were euthanized for histologic, immunohistochemistry, and cytokines studies. Ten animals also underwent a 7-T magnetic resonance imaging (MRI). Female rats presented a higher concentration of immune cells in the arachnoid-brain interface, reactive astroglia in the periventricular region, in situ pro-inflammatory cytokine (interleukin [IL]-6) and anti-inflammatory cytokine (IL-10), and more intense hydrocephalus on MRI than males. Intracranial hypertension signals were not observed during the observational period. Overall, these results suggest sexual

dimorphism in the intracranial inflammatory response that accompanied T. crassiceps extraparenchymal neurocysticercosis.

Neurocysticercosis: A rare cause of a single brain granuloma.

Vargas-Urbina J, Martinez-Silva R, Anicama-Lima W.

25-08-2023

Med Clin (Barc).

<https://pubmed.ncbi.nlm.nih.gov/37296044/>

Dengue, chikungunya et maladie à virus Zika

Structural and functional characterization of Aedes aegypti pupal cuticle protein that controls dengue virus infection.

Huang Q, Gavor E, Tulsian NK, Fan J, Lin Q, Mok YK, Kini RM, J S.

18-08-2023

Protein Sci.

<https://pubmed.ncbi.nlm.nih.gov/37593853/>

The pupal cuticle protein from *Aedes aegypti* (AaPC) inhibits dengue virus (DENV) infection; however, the underlying mechanism of this inhibition remains unknown. Here, we report that AaPC is an intrinsically disordered protein and interacts with domain I/II of the DENV envelope protein via residues Asp59, Asp61, Glu71, Asp73, Ser75 and Asp80. AaPC can directly bind to and cause the aggregation of DENV, which in turn blocks virus infection during the virus-cell fusion stage. AaPC may also influence viral recognition and attachment by interacting with human immune receptors DC-SIGN and CD4. These findings enhance our understanding of the role of AaPC in mitigating viral infection and suggest that AaPC is a potential target for developing inhibitors or antibodies to control dengue virus infection. This article is protected by copyright. All rights reserved.

Molecular detection of dengue and chikungunya viruses in surveillance of wild-caught Aedes mosquitoes in Punjab, North India.

Kaura T, Sarkar S, Sharma V, Mewara A, Devi S, Singh N, Kaur K, Sehgal R, Ratho RK, Grover GS.

18-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37593844/>

Scrub Typhus in Children: A Prospective Observational Study in a Tertiary Care Hospital in Eastern India.

Kumar Jana J, Krishna Mandal A, Gayen S, Mahata D, Alam Mallick MS.

16-07-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37593313/>

Retracted: Recurrent Neural Networks for Feature Extraction from Dengue Fever.

And Alternative Medicine EC.

09-08-2023

Evid Based Complement Alternat Med.

<https://pubmed.ncbi.nlm.nih.gov/37593039/>

Chikungunya virus cell-to-cell transmission is mediated by intercellular extensions in vitro and in vivo.

Yin P, Davenport BJ, Wan JJ, Kim AS, Diamond MS, Ware BC, Tong K, Couderc T, Lecuit M, Lai JR, Morrison TE, Kielian M.

17-08-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37591996/>

Chikungunya virus (CHIKV) has recently emerged to cause millions of human infections worldwide. Infection can induce the formation of long intercellular extensions that project from infected cells and form stable non-continuous membrane bridges with neighbouring cells. The mechanistic role of these intercellular extensions in CHIKV infection was unclear. Here we developed a co-culture system and flow cytometry methods to quantitatively evaluate transmission of CHIKV from infected to uninfected cells in the presence of neutralizing antibody. Endocytosis and endosomal acidification were critical for virus cell-to-cell transmission, while the CHIKV receptor MXRA8 was not. By using distinct antibodies to block formation of extensions and by evaluation of transmission in HeLa cells that did not form extensions, we showed that intercellular extensions mediate CHIKV cell-to-cell transmission. In vivo, pre-treatment of mice with a neutralizing antibody blocked infection by direct virus inoculation, while adoptive transfer of infected cells produced antibody-resistant host infection. Together our data suggest a model in which the contact sites of intercellular extensions on target cells shield CHIKV from neutralizing antibodies and promote efficient intercellular virus transmission both in vitro and in vivo.

How habitat factors affect an Aedes mosquitoes driven outbreak at temperate latitudes: The case of the Chikungunya virus in Italy.

Solimini A, Virgillito C, Manica M, Poletti P, Guzzetta G, Marini G, Rosà R, Filipponi F, Scognamiglio P, Vairo F, Caputo B.

17-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37590255/>

ARCA: the interactive database for arbovirus reported cases in the Americas.

Meneses MV, Riva A, Salemi M, Mavian C.

16-08-2023

BMC Bioinformatics.

<https://pubmed.ncbi.nlm.nih.gov/37587443/>

Background: Accurate case report data are essential to understand arbovirus dynamics, including spread and evolution of arboviruses such as Zika, dengue and chikungunya viruses. Given the multi-country nature of arbovirus epidemics in the Americas, these data are not often accessible or are reported at different time scales (weekly, monthly) from different sources. **Results:** We developed a publicly available and user-friendly database for arboviral case data in the Americas: ARCA. ARCA is a relational database that is hosted on the ARCA website. Users can interact with the database through the website by submitting queries through the website, which generates displays results and allows users to download these results in different, convenient file formats. Users can choose to view arboviral case data through a table which contains the number of cases for a particular week, a plot, or through a map. **Conclusion:** Our ARCA database is a useful tool for arboviral epidemiology research allowing for complex queries, data visualization, integration, and formatting.

Erratum for the Review "Insights into dengue immunity from vaccine trials".

Ooi EE, Kalimuddin S.

16-08-2023

Sci Transl Med.

<https://pubmed.ncbi.nlm.nih.gov/37585506/>

Towards the invasion of wild and rural forested areas in Gabon (Central Africa) by the Asian tiger mosquito *Aedes albopictus*: Potential risks from the one health perspective.

Obame-Nkoghe J, Roiz D, Ngangue MF, Costantini C, Rahola N, Jiolle D, Lehmann D, Makaga L, Ayala D, Kengne P, Paupy C.

16-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37585443/>

Background: Since its first record in urban areas of Central-Africa in the 2000s, the invasive mosquito, *Aedes albopictus*, has spread throughout the region, including in remote villages in forested areas, causing outbreaks of *Aedes*-borne diseases, such as dengue and chikungunya. Such invasion might enhance *Ae. albopictus* interactions with wild animals in forest ecosystems and favor the spillover of zoonotic arboviruses to humans. The aim of this study was to monitor *Ae. albopictus* spread in the wildlife reserve of La Lopé National Park (Gabon), and evaluate the magnitude of the rainforest ecosystem colonization. **Methodology:** From 2014 to 2018, we used ovitraps, larval surveys, BG-Sentinel traps, and human landing catches along an anthropization gradient from La Lopé village to the natural forest in the Park. **Conclusions:** We detected *Ae. albopictus* in gallery forest up to 15 km away from La Lopé village. However, *Ae. albopictus* was significantly more abundant at anthropogenic sites than in less anthropized areas. The number of eggs laid by *Ae. albopictus* decreased progressively with the distance from the forest fringe up to 200m inside the forest. Our results

suggested that in forest ecosystems, high *Ae. albopictus* density is mainly observed at interfaces between anthropized and natural forested environments. Additionally, our data suggested that *Ae. albopictus* may act as a bridge vector of zoonotic pathogens between wild and anthropogenic compartments.

Hypoxia dampens innate immune signalling at early time points and increases Zika virus RNA levels in iPSC-derived macrophages.

Schilling M, Vaughan-Jackson A, James W, McKeating JA.

16-08-2023

J Gen Virol.

<https://pubmed.ncbi.nlm.nih.gov/37584553/>

Nepal's worst dengue outbreak is a wake-up call for action.

Bijukchhe SM, Hill M, Bch BM, Adhikari B, Shrestha A, Shrestha S.

16-08-2023

J Travel Med.

<https://pubmed.ncbi.nlm.nih.gov/37584474/>

Evaluating the strategies to control SARS-CoV-2 Delta variant spread in New Caledonia, a zero-COVID country until September 2021.

Ochida N, Dupont-Rouzeyrol M, Moury PH, Demaneuf T, Gourinat AC, Mabon S, Jouan M, Cauchemez S, Mangeas M.

30-06-2023

IJID Reg.

<https://pubmed.ncbi.nlm.nih.gov/37583482/>

Objectives: New Caledonia, a former zero-COVID country, was confronted with a SARS-CoV-2 Delta variant outbreak in September 2021. We evaluate the relative contribution of vaccination, lockdown, and timing of interventions on healthcare burden. **Methods:** We developed an age-stratified mathematical model of SARS-CoV-2 transmission and vaccination calibrated for New Caledonia and evaluated three alternative scenarios. **Results:** High virus transmission early on was estimated, with R_0 equal to 6.6 (95% confidence interval [6.4-6.7]). Lockdown reduced R_0 by 73% (95% confidence interval [70-76%]). Easing the lockdown increased transmission (39% reduction of the initial R_0); but we did not observe an epidemic rebound. This contrasts with the rebound in hospital admissions (+116% total hospital admissions) that would have been expected in the absence of an intensified vaccination campaign (76,220 people or 34% of the eligible population were first-dose vaccinated during 1 month of lockdown). A 15-day earlier lockdown would have led to a significant reduction in the magnitude of the epidemic (-53% total hospital admissions). **Conclusion:** The success of the response against the Delta variant epidemic in New Caledonia was due to an effective lockdown that provided additional time for people to vaccinate. Earlier lockdown would have greatly mitigated the magnitude of the epidemic.

Repurposing of investigational cancer drugs: Early phase discovery of dengue virus NS2B/NS3 protease inhibitors.

Saleem HN, Kousar S, Jiskani AH, Sohail I, Faisal A, Saeed M.

15-08-2023

Arch Pharm (Weinheim).

<https://pubmed.ncbi.nlm.nih.gov/37582646/>

Identification of 3, 4-dihydroxy complexes as potential antiviral via DFT, molecular docking, molecular dynamics and MM/PBSA against rabies and dengue receptors.

Sinha P, Yadav AK.

14-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37580968/>

The quest to identify antiviral drug candidates for dengue and rabies viral diseases is a great challenge for the researchers. While different research is being conducted on the repurposed drugs against these two viruses, no drug compound has gained success in treating them. Therefore, in this study, 3, 4-dihydroxy complexes have been virtually designed to investigate their antiviral properties and analyze their efficiency in interaction with the concerned viral diseases. DFT calculations are carried out to study the electronic and thermodynamic properties to understand the stability and reactivity of the reported compounds. These compounds were subjected to molecular docking studies to understand the binding interactions with NS5 Dengue virus mRNA 2'-O-methyltransferase and phosphoprotein C-terminal domain of Rabies virus. MD simulation, hydrogen bond analysis, and MM/PBSA were performed at 100 ns to support the obtained docking results. Communicated by Ramaswamy H. Sarma.

Co-Infection between Dengue Virus and SARS-CoV-2 in Cali, Colombia.

Agudelo-Rojas OL, Rebellón-Sánchez DE, Llanos Torres J, Zapata-Vásquez IL, Rodríguez S, Robles-Castillo S, Tejada Vega A, Parra-Lara LG, Rosso F.

14-08-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37580025/>

The co-occurrence of COVID-19 with endemic diseases is a public health concern that may affect patient prognosis and outcomes. The objective of this study was to describe the clinical characteristics of patients with dengue virus (DENV) and SARS-CoV-2 co-infections and compare their outcomes against those of COVID-19 patients without dengue. A cross-sectional study was conducted in patients with SARS-CoV-2 infection who attended a single center in Cali, Colombia, from March 2020 to March 2021. All patients who were tested by both real-time polymerase chain reaction for SARS-CoV-2 and IgM/NS1 for DENV were included. Dengue was diagnosed as having either an IgM- or an NS1- positive test. A total of 90 patients were included (72 with COVID-19 only and 18 with co-infection).

Patients with co-infection had more dyspnea (61.1% versus 22.2%; $P = 0.003$) as well as higher oxygen desaturation (53.3% versus 13.4%; $P = 0.002$) and neutrophil-to-lymphocyte ratio (5.59 versus 3.84; $P = 0.038$) than patients with COVID-19 alone. The proportion of patients classified with moderate to severe COVID-19 was higher in the co-infection group (88.3% versus 47.8%; $P = 0.002$). Also, co-infection was associated with an increased need for mechanical ventilation ($P = 0.06$), intensive care unit (ICU) initial management ($P = 0.02$), and ICU admission during hospitalization ($P = 0.04$) compared with COVID-19 only. The ICU mortality rate was 66.6% in patients with co-infection versus 29.4% in patients infected with only SARS-CoV-2 ($P < 0.05$). The possibility of DENV and SARS-CoV2 co-infection occurred in the convergence of both epidemic waves. Co-infection was associated with worse clinical outcomes and higher mortality in ICU-admitted patients than in patients with the COVID-19 only.

Tropism and immune response of chikungunya and zika viruses: An overview.

Ravindran S, Lahon A.

12-08-2023

Cytokine.

<https://pubmed.ncbi.nlm.nih.gov/37579710/>

Zika virus (ZIKV) and chikungunya virus (CHIKV) are two medically important vector-borne viruses responsible for causing significant disease burden in humans, including neurological sequelae/complications. Besides sharing some common clinical features, ZIKV has major shares in causing microcephaly and brain malformations in developing foetus, whereas CHIKV causes chronic joint pain/swelling in infected individuals. Both viruses have a common route of entry to the host body, i.e., dermal site of inoculation through the bite of an infected mosquito and later taken up by different immune cells for further dissemination to other areas of the host body that lead to a range of immune responses via different pathways. The immune responses generated by both viruses have similar characteristics with varying degrees of inflammation and activation of immune cells. However, the overall response of immune cells is not fully explored in the context of ZIKV and CHIKV infection. The knowledge of cellular tropism and the immune response is the key to understanding the mechanisms of viral immunity and pathogenesis, which may allow to develop novel therapeutic strategies for these viral infections. This review aims to discuss recent advancements and identify the knowledge gaps in understanding the mechanism of cellular tropism and immune response of CHIKV and ZIKV.

Correction: Clinical Characteristics and Outcomes Among Travelers With Severe Dengue.

[No authors listed]

15-08-2023

Ann Intern Med.

<https://pubmed.ncbi.nlm.nih.gov/37579313/>

Network Analysis of Hosts and Vectors in the Multiple Transmissions of Flavivirus.

Nieto-Rabiela F, Esponda F, Roche B, Suzán G.

09-08-2023

Vector Borne Zoonotic Dis.

<https://pubmed.ncbi.nlm.nih.gov/37579044/>

Background: It is well established that infection patterns in nature can be driven by host, vector, and symbiont communities. One of the first stages in understanding how these complex systems have influenced the incidence of vector-borne diseases is to recognize what are the major vertebrate (*i.e.*, hosts) and invertebrate (*i.e.*, vectors) host species that propagate those microbes. Such identification opens the possibility to identify such essential species to develop targeted preventive efforts. **Methods:** The goal of this study, which relies on a compilation of a global database based on published literature, is to identify relevant host species in the global transmission of mosquito-borne flaviviruses, such as West Nile virus, St. Louis virus, Dengue virus, and Zika virus, which pose a concern to animal and public health. **Results:** The analysis of the resulting database involving 1174 vertebrate host species and 46 reported vector species allowed us to establish association networks between these species. Three host species (*Mus musculus*, *Sapajus flavius*, *Sapajus libidinosus*, etc.) have a much larger centrality values, suggesting that they play a key role in flavivirus community interactions. **Conclusion:** The methods used and the species detected as relevant in the network provide new knowledge and consistency that could aid health officials in rethinking prevention and control strategies with a focus on viral communities and their interactions. Other infectious diseases that harm animal and human health could benefit from such network techniques.

Craniofacial and dental features in children aged 3-5 years with congenital Zika syndrome.

Díaz C, Aragón N, Lopez-Medina E, Arango MC, Dávalos D, Contreras-Rengifo A.

14-08-2023

Clin Oral Investig.

<https://pubmed.ncbi.nlm.nih.gov/37578656/>

Coding Therapeutic Nucleic Acids from Recombinant Proteins to Next-Generation Vaccines: Current Uses, Limitations, and Future Horizons.

Harisa GI, Faris TM, Sherif AY, Alzhrani RF, Alanazi SA, Kohaf NA, Alanazi FK.

14-08-2023

Mol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37578574/>

Assessment of antibacterial drug utilization patterns and antibiogram in infectious diseases: a prospective cross-sectional study.

Nilay S, Shreya P, Vivek S.

14-08-2023

Naunyn Schmiedebergs Arch Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37578516/>

Background: Antibacterial drugs are successful in combating most types of infections. Irrational use and higher consumption of these drugs can give rise to the antibiotic resistance globally. **Objective:** To evaluate antibacterial drug prescribing patterns and antibiogram in infectious disease cases admitted to the hospital. **Methods:** A cross-sectional, observational study was conducted from September 2019 to February 2020 among inpatients ward at the hospital after ethical approval. All the data was analysed by the mean and percentage values using Microsoft excel.

Results: Out of 250 admitted patients, males and females were 156 (62%) and 94 (38%) respectively. The majority of patients 79 (32%) belonged to the age group of 20-40 years. The majority of prescriptions reported were for viral fever 48 (19%), lower respiratory tract infections 40 (16%) and dengue 33 (13%). Antibacterial drugs administered through the intravenous route and the oral route were 301 (83%) and 63 (17%) respectively. The most frequently utilized antibacterial drugs were beta-lactam class ceftriaxone 149 (60%) and the fixed-dose combination, amoxicillin plus clavulanic acid 65 (26%). Further highly prescribed antibacterial drugs were metronidazole 52 (21%), azithromycin 36 (15%), and levofloxacin 24 (10%). In Gram-negative bacteria, *Escherichia coli* 6 (30%) contributed majorly, while in Gram-positive coagulase-negative, *Staphylococci* 6 (30%) contributed the highest growth of bacteria for the specific infections in the admitted cases. **Conclusion:** Ceftriaxone and the amoxicillin-clavulanic acid combination were highly prescribed among all antibacterial drugs, followed by metronidazole and azithromycin. The current study showed that in the antibiogram pattern, *Escherichia coli* and coagulase-negative *Staphylococci* contributed significantly as causative organisms for infectious disease cases. The present study highlighted demographic distribution, infectious diseases with their antibacterial drug utilization patterns and antibiogram assessment in the admitted patients.

The La Crosse virus class II fusion glycoprotein ij loop contributes to infectivity and replication in vitro and in vivo.

Thannickal SA, Spector SN, Stapleford KA.

14-08-2023

J Virol.

<https://pubmed.ncbi.nlm.nih.gov/37578236/>

A low-background, fluorescent assay to evaluate inhibitors of diverse viral proteases.

Leonard RA, Rao VN, Bartlett A, Froggatt HM, Luftig MA, Heaton BE, Heaton NS.

14-08-2023

J Virol.

<https://pubmed.ncbi.nlm.nih.gov/37578235/>

Antigenic diversity and dengue disease risk.

Wang L, Huang A, Katzelnick L, Lefrancq N, Escoto AC, Duret L, Chowdhury N, Jarman R, Conte M, Berry I, Fernandez S, Klungthong C, Thaisomboonsuk B, Santarattiwong P, Vandepitte W, Whitehead S, Cauchemez S, Cummings D, Salje H.

02-08-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37577717/>

Many pathogens continuously change their protein structure in response to immune-driven selection, resulting in weakened protection. In addition, for some pathogens such as dengue virus, poorly targeted immunity is associated with increased risk of severe disease, through a mechanism known as antibody-dependent enhancement. However, it remains a mystery whether the antigenic distance between an individual's first infection and subsequent exposures dictate disease risk, explaining the observed large-scale differences in dengue hospitalisations across years. Here we develop an inferential framework that combines detailed antigenic and genetic characterisation of viruses, and hospitalised cases from 21 years of surveillance in Bangkok, Thailand to identify the role of the antigenic profile of circulating viruses in determining disease risk. We find that the risk of hospitalisation depends on both the specific order of infecting serotypes and the antigenic distance between an individual's primary and secondary infections, with risk maximised at intermediate antigenic distances. These findings suggest immune imprinting helps determine dengue disease risk, and provides a pathway to monitor the changing risk profile of populations and to quantifying risk profiles of candidate vaccines.

The interplay between vector microbial community and pathogen transmission on the invasive Asian tiger mosquito, *Aedes albopictus*: current knowledge and future directions.

Garrido M, Veiga J, Garrigós M, Martínez-de la Puente J.

27-07-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37577425/>

The invasive Asian tiger mosquito *Aedes albopictus* is nowadays broadly distributed with established populations in all continents except Antarctica. In the invaded areas, this species represents an important nuisance for humans and, more relevant, it is involved in the local transmission of pathogens relevant under a public health perspective. *Aedes albopictus* is a competent vector of parasites such as *Dirofilaria* and viruses including dengue virus, Zika virus, and chikungunya virus, among others. The mosquito microbiota has been identified as one of the major drivers of vector competence, acting upon relevant vector functions as development or immunity. Here, we review the available literature on the interaction between *Ae. albopictus* microbiota and pathogen transmission and identify the knowledge gaps on the topic. Most studies are strictly focused on the interplay between pathogens and *Wolbachia*

endosymbiont while studies screening whole microbiota are still scarce but increasing in recent years, supported on Next-generation sequencing tools. Most experimental trials use lab-reared mosquitoes or cell lines, exploring the molecular mechanisms of the microbiota-pathogen interaction. Yet, correlational studies on wild populations are underrepresented. Consequently, we still lack sufficient evidence to reveal whether the microbiota of introduced populations of *Ae. albopictus* differ from those of native populations, or how microbiota is shaped by different environmental and anthropic factors, but especially, how these changes affect the ability of *Ae. albopictus* to transmit pathogens and favor the occurrence of outbreaks in the colonized areas. Finally, we propose future research directions on this research topic.

Dengue, Chikungunya, and Zika: The Causes and Threats of Emerging and Re-emerging Arboviral Diseases.

Soni S, Gill VJS, Anusheel, Singh J, Chhabra J, Gill GJS, Bakshi R.

11-07-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37575782/>

The recent emergence and re-emergence of viral infections transmitted by vectors, Zika, chikungunya, dengue, and others, is a cause for international concern. Here, we provide a summary of the current understanding of the transmission, clinical features, diagnosis, global burden, and the likelihood of future epidemics by these viruses. Arboviruses transmitted by mosquitoes are challenging to diagnose and can have surprising clinical complications. Dengue, chikungunya, and Zika are the most important diseases caused by arboviruses worldwide, especially in tropical and subtropical regions. These are transmitted to humans by day-biting *Aedes aegypti* and *Aedes albopictus* mosquitoes. In India, the increase in the incidence of dengue and chikungunya cases is primarily linked to the dissemination of *Aedes aegypti*. A rapid and accurate diagnosis is paramount for effectively controlling dengue outbreaks. As there is no vaccination or specific treatment available for these viruses, vector control is the only comprehensive solution available.

Continued dominance of dengue virus serotype 2 during the recent Central India outbreaks (2019-2021) with evidence of genetic divergence.

Agarwal A, Ganvir R, Kale D, Chaurasia D, Kapoor G.

13-08-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37574815/>

Multifaceted contributions of Dicer2 to arbovirus transmission by *Aedes aegypti*.

Merkling SH, Crist AB, Henrion-Lacritick A, Frangeul L, Couderc E, Gausson V, Blanc H, Bergman A, Baidaliuk A, Romoli O, Saleh MC, Lambrechts L.

11-08-2023

Cell Rep.

<https://pubmed.ncbi.nlm.nih.gov/37573505/>

Arthropod-borne viruses (arboviruses) transmitted by *Aedes aegypti* mosquitoes are an increasing threat to global health. The small interfering RNA (siRNA) pathway is considered the main antiviral immune pathway of insects, but its effective impact on arbovirus transmission is surprisingly poorly understood. Here, we use CRISPR-Cas9-mediated gene editing in vivo to mutate Dicer2, a gene encoding the RNA sensor and key component of the siRNA pathway. The loss of Dicer2 enhances early viral replication and systemic viral dissemination of four medically significant arboviruses (chikungunya, Mayaro, dengue, and Zika viruses) representing two viral families. However, Dicer2 mutants and wild-type mosquitoes display overall similar levels of vector competence. In addition, Dicer2 mutants undergo significant virus-induced mortality during infection with chikungunya virus. Together, our results define a multifaceted role for Dicer2 in the transmission of arboviruses by *Ae. aegypti* mosquitoes and pave the way for further mechanistic investigations.

Prospective study to compare results of FIA (fluorescent immunoassay) test with gold standard ELISA test in Dengue NS1 patients admitted in a tertiary care hospital.

Kulkarni P, Taklikar S, Turbadkar D.

Sept-Oct 2023

Indian J Med Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37573050/>

Outbreak investigation of Dengue like fever in rural area of Rajasthan.

Sharma P, Sharma M, Bhomia N, Sharma H, Deeba F, Sharma RK, Singh R, Sharma RP, Malhotra B.

Sept-Oct 2023

Indian J Med Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37573049/>

During October 2020, suddenly many cases were reported with Dengue like illness in Sahawa village, Rajasthan. Blood samples collected from 68 patients were tested for Dengue NS1 antigen and IgM antibodies for Dengue, Chikungunya, Scrub typhus, Leptospira and Brucella by ELISA, Dengue, Chikungunya and Zika viral RNA by multiplex Polymerase Chain Reaction (PCR), 41.17% samples were positive for Dengue; 25% were positive by Dengue PCR, 17.64% for NS1 Ag, 14.70% for IgM ELISA, 20.58% were positive for antibodies either for Scrub typhus (4.41%), Leptospira (7.35%) or Brucella (10.29%). Dengue was seen in 41.17% cases and other etiological agents in 20.58% cases.

Associating biological context with protein-protein interactions through text mining at PubMed scale.

Sosa DN, Hintzen R, Xiong B, de Giorgio A, Fauqueur J, Davies M, Lever J, Altman RB.

10-08-2023

J Biomed Inform.

<https://pubmed.ncbi.nlm.nih.gov/37572825/>

In Silico Characterisation of the Aedes aegypti Gustatory Receptors.

Bibi M, Hussain A, Ali F, Ali A, Said F, Tariq K, Yun BW.

31-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37569638/>

Aedes aegypti, also known as the dengue mosquito or the yellow fever mosquito, is the vector of dengue, chikungunya, Zika, Mayaro and yellow fever viruses. The *A. aegypti* genome contains an array of gustatory receptor (GR) proteins that are related to the recognition of taste. In this study, we performed in silico molecular characterization of all 72 *A. aegypti* GRs reported in the latest version of *A. aegypti* genome AaegL5. Phylogenetic analysis classified the receptors into three major clads. Multiple GRs were found to encode multiple transcripts. Physicochemical attributes such as the aliphatic index, hydropathicity index and isoelectric point indicated that *A. aegypti* gustatory receptors are highly stable and are tailored to perform under a variety of cellular environments. Analysis for subcellular localization indicated that all the GRs are located either in the extracellular matrix or the plasma membrane. Results also indicated that the GRs are distributed mainly on chromosomes 2 and 3, which house 22 and 49 GRs, respectively, whereas chromosome 1 houses only one GR. NCBI-CDD analysis showed the presence of a highly conserved 7tm_7 chemosensory receptor protein superfamily that includes gustatory and odorant receptors from insect species *Anopheles gambiae* and *Drosophila melanogaster*. Further, three significantly enriched ungapped motifs in the protein sequence of all 72 *A. aegypti* gustatory receptors were found. High-quality 3D models for the tertiary structures were predicted with significantly higher confidence, along with ligand-binding residues. Prediction of S-nitrosylation sites indicated the presence of target cysteines in all the GRs with close proximity to the ligand-binding sites within the 3D structure of the receptors. In addition, two highly conserved motifs inside the GR proteins were discovered that house a tyrosine (Y) and a cysteine (C) residue which may serve as targets for NO-mediated tyrosine nitration and S-nitrosylation, respectively. This study will help devise strategies for functional genomic studies of these important receptor molecules in *A. aegypti* and other mosquito species through in vitro and in vivo studies.

Levels and Predictors of Proactive Practical Experience to Solve COVID-19 among Public Health Officers in Primary Care Units in the Upper Southern Region, Thailand: An Explanatory Mixed Methods Approach.

Sangpoom S, Adesina F, Kaewchandee C, Sikanna K, Noppapak N, Maneerattanasak S, Shohaimi S, Suwanbamrung C.

31-07-2023

Int J Environ Res Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37569027/>

estimateR: an R package to estimate and monitor the effective reproductive number.

Scire J, Huisman JS, Grosu A, Angst DC, Lison A, Li J, Maathuis MH, Bonhoeffer S, Stadler T.

11-08-2023

BMC Bioinformatics.

<https://pubmed.ncbi.nlm.nih.gov/37568078/>

Genotyped functional screening of soluble Fab clones enables in-depth analysis of mutation effects.

Oksanen S, Saarinen R, Korkiakoski A, Lamminmäki U, Huovinen T.

11-08-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37567990/>

Monoclonal antibodies (mAbs) and their fragments are widely used in therapeutics, diagnostics and basic research. Although display methods such as phage display offer high-throughput, affinities of individual antibodies need to be accurately measured in soluble format. We have developed a screening platform capable of providing genotyped functional data from a total of 9216 soluble, individual antigen binding fragment (Fab) clones by employing next-generation sequencing (NGS) with hierarchical indexing. Full-length, paired variable domain sequences (VL-VH) are linked to functional screening data, enabling in-depth analysis of mutation effects. The platform was applied to four phage display-selected scFv/Fab screening projects and one site-saturation VH affinity maturation project. Genotyped functional screening simultaneously enabled the identification of affinity improving mutations in the VH domain of Fab 49A3 recognizing Dengue virus non-structural protein 1 (NS1) serotype 2 and informed on VH residue positions which cannot be changed from wild-type without decreasing the affinity. Genotype-based identification revealed to us the extent of intraclonal signal variance inherent to single point screening data, a phenomenon often overlooked in the field. Moreover, genotyped screening eliminated the redundant selection of identical genotypes for further study and provided a new analysis tool to evaluate the success of phage display selections and remaining clonal diversity in the screened repertoires.

Prevalence and outcomes of Myocarditis in dengue viral fever: A systematic review and Meta-analysis.

Farrukh AM, Ganipineni VDP, Jindal U, Chaudhary A, Puar RK, Ghazarian K, Corrales VV, Alarcón SE, Remala K, Thota N, Vijayan S, Rathore SS.

09-08-2023

Curr Probl Cardiol.

<https://pubmed.ncbi.nlm.nih.gov/37567490/>

Application of medical information system to identify dengue outbreak factors: Insights from a hyperendemic city in Malaysia.

Keat-Chuan Ng C, Linus-Lojikip S, Mohamed K, Hss AS.

Sept-2023

Int J Med Inform.

<https://pubmed.ncbi.nlm.nih.gov/37549500/>

Background: Dengue is widespread globally, but it is more severe in hyperendemic regions where the virus, its vectors, and its human hosts naturally occur. The problem is particularly acute in cities, where outbreaks affect a large human population living in a wide array of socio-environmental conditions. Controlling outbreaks will rely largely on systematic data collection and analysis approaches to uncover nuances on a city-by-city basis due to the diversity of factors. **Objective:** The main objective of this study is to consolidate and analyse the dengue case dataset amassed by the e-Dengue web-based information system, developed by the Ministry of Health Malaysia, to improve our epidemiological understanding. **Methods:** We retrieved data from the e-Dengue system and integrated a total of 18,812 cases from 2012 to 2019 (8 years) with meteorological data, geoinformatics techniques, and socio-environmental observations to identify plausible factors that could have caused dengue outbreaks in Ipoh, a hyperendemic city in Malaysia. **Results:** The rainfall trend characterised by a linearity of $R^2 > 0.99$, termed the "wet-dry steps", may be the unifying factor for triggering dengue outbreaks, though it is still a hypothesis that needs further validation. Successful mapping of the dengue "reservoir" contact zones and spill-over diffusion revealed socio-environmental factors that may be controlled through preventive measures. Age is another factor to consider, as the platelet and white blood cell counts in the "below 5" age group are much greater than in other age groups. **Conclusions:** Our work demonstrates the novelty of the e-Dengue system, which can identify outbreak factors at high resolution when integrated with non-medical fields. Besides dengue, the techniques and insights laid out in this paper are valuable, at large, for advancing control strategies for other mosquito-borne diseases such as malaria, chikungunya, and Zika in other hyperendemic cities elsewhere globally.

Peptidomimetic Oligomers Targeting Membrane Phosphatidylserine Exhibit Broad Antiviral Activity.

Tate PM, Mastrodomenico V, Cunha C, McClure J, Barron AE, Diamond G, Mounce BC, Kirshenbaum K.

11-08-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37530426/>

The development of durable new antiviral therapies is challenging, as viruses can evolve rapidly to establish resistance and attenuate therapeutic efficacy. New compounds that selectively target conserved viral features are attractive therapeutic candidates, particularly for combating newly emergent viral threats. The innate immune system features a sustained capability to combat pathogens through production of antimicrobial peptides (AMPs); however, these AMPs have shortcomings that can preclude clinical use. The essential functional features of AMPs have been recapitulated by peptidomimetic oligomers, yielding effective antibacterial and antifungal agents. Here, we show that a family of AMP mimetics,

called peptoids, exhibit direct antiviral activity against an array of enveloped viruses, including the key human pathogens Zika, Rift Valley fever, and chikungunya viruses. These data suggest that the activities of peptoids include engagement and disruption of viral membrane constituents. To investigate how these peptoids target lipid membranes, we used liposome leakage assays to measure membrane disruption. We found that liposomes containing phosphatidylserine (PS) were markedly sensitive to peptoid treatment; in contrast, liposomes formed exclusively with phosphatidylcholine (PC) showed no sensitivity. In addition, chikungunya virus containing elevated envelope PS was more susceptible to peptoid-mediated inactivation. These results indicate that peptoids mimicking the physicochemical characteristics of AMPs act through a membrane-specific mechanism, most likely through preferential interactions with PS. We provide the first evidence for the engagement of distinct viral envelope lipid constituents, establishing an avenue for specificity that may enable the development of a new family of therapeutics capable of averting the rapid development of resistance.

Synthesis of Isolated DNA Aptamer and Its Application of AC-Electrothermal Flow-Based Rapid Biosensor for the Detection of Dengue Virus in a Spiked Sample.

Park H, Lee H, Lee M, Baek C, Park JA, Jang M, Kwon Y, Min J, Lee T.

16-08-2023

Bioconjug Chem.

<https://pubmed.ncbi.nlm.nih.gov/37527337/>

Role of endoplasmic reticulum stress-related unfolded protein response and its implications in dengue virus infection for biomarker development.

Das B, Samal S, Hamdi H, Pal A, Biswas A, Behera J, Singh G, Behera CK, Sahoo DP, Pati S.

15-09-2023

Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/37517582/>

Assessing the role of Ndel1 oligopeptidase activity in congenital Zika syndrome: Potential predictor of congenital syndrome endophenotype and treatment response.

Christoff RR, Nani JV, Lessa G, Rabello T, Rossi AD, Krenn V, Higa LM, Tanuri A, Garcez PP, Hayashi MAF.

August-2023

J Neurochem.

<https://pubmed.ncbi.nlm.nih.gov/37497817/>

Maternal infections are among the main risk factors for cognitive impairments in the offspring. Zika virus (ZIKV) can be transmitted vertically, causing a set of heterogeneous birth defects, such as microcephaly, ventriculomegaly and corpus callosum dysgenesis. Nuclear distribution element like-1 (Ndel1) oligopeptidase controls

crucial aspects of cerebral cortex development underlying cortical malformations. Here, we examine Ndel1 activity in an animal model for ZIKV infection, which was associated with deregulated corticogenesis. We observed here a reduction in Ndel1 activity in the forebrain associated with the congenital syndrome induced by ZIKV isolates, in an in utero and postnatal injections of different inoculum doses in mice models. In addition, we observed a strong correlation between Ndel1 activity and brain size of animals infected by ZIKV, suggesting the potential of this measure as a biomarker for microcephaly. More importantly, the increase of interferon (IFN)-beta signaling, which was used to rescue the ZIKV infection outcomes, also recovered Ndel1 activity to levels similar to those of uninfected healthy control mice, but with no influence on Ndel1 activity in uninfected healthy control animals. Taken together, we demonstrate for the first time here an association of corticogenesis impairments determined by ZIKV infection and the modulation of Ndel1 activity. Although further studies are still necessary to clarify the possible role(s) of Ndel1 activity in the molecular mechanism(s) underlying the congenital syndrome induced by ZIKV, we suggest here the potential of monitoring the Ndel1 activity to predict this pathological condition at early stages of embryos or offspring development, during while the currently employed methods are unable to detect impaired corticogenesis leading to microcephaly. Ndel1 activity may also be possibly used to follow up the positive response to the treatment, such as that employing the IFN-beta that is able to rescue the ZIKV-induced brain injury.

Galidesivir Triphosphate Promotes Stalling of Dengue-2 Virus Polymerase Immediately Prior to Incorporation.

Deshpande S, Huo W, Shrestha R, Sparrow K, Wood JM, Evans GB, Harris LD, Kingston RL, Bulloch EMM.

11-08-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37488090/>

Mechanical transmission of dengue virus by Aedes aegypti may influence disease transmission dynamics during outbreaks.

Li HH, Su MP, Wu SC, Tsou HH, Chang MC, Cheng YC, Tsai KN, Wang HW, Chen GH, Tang CK, Chung PJ, Tsai WT, Huang LR, Yueh YA, Chen HW, Pan CY, Akbari OS, Chang HH, Yu GY, Marshall JM, Chen CH.

August-2023

EBioMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37487418/>

Background: Dengue virus outbreaks are increasing in number and severity worldwide. Viral transmission is assumed to require a minimum time period of viral replication within the mosquito midgut. It is unknown if alternative transmission periods not requiring replication are possible. **Methods:** We used a mouse model of dengue virus transmission to investigate the potential of mechanical transmission of dengue virus. We investigated minimal viral titres necessary for development of

symptoms in bitten mice and used resulting parameters to inform a new model of dengue virus transmission within a susceptible population. **Findings:** Naïve mice bitten by mosquitoes immediately after they took partial blood meals from dengue infected mice showed symptoms of dengue virus, followed by mortality. Incorporation of mechanical transmission into mathematical models of dengue virus transmission suggest that this supplemental transmission route could result in larger outbreaks which peak sooner. **Interpretation:** The potential of dengue transmission routes independent of midgut viral replication has implications for vector control strategies that target mosquito lifespan and suggest the possibility of similar mechanical transmission routes in other disease-carrying mosquitoes. **Funding:** This study was funded by grants from the National Health Research Institutes, Taiwan (04D2-MMMOST02), the Human Frontier Science Program (RGP0033/2021), the National Institutes of Health (1R01AI143698-01A1, R01AI151004 and DP2AI152071) and the Ministry of Science and Technology, Taiwan (MOST104-2321-B-400-016).

Acetylation of the NS3 helicase by KAT5y is essential for flavivirus replication.

Serman T, Chiang C, Liu G, Sayyad Z, Pandey S, Volcic M, Lee H, Muppala S, Acharya D, Goins C, Stauffer SR, Sparrer KMJ, Gack MU.

09-08-2023

Cell Host Microbe.

<https://pubmed.ncbi.nlm.nih.gov/37478852/>

Insights into the structure, functional perspective, and pathogenesis of ZIKV: an updated review.

Bhat EA, Ali T, Sajjad N, Kumar R, Bron P.

Sept-2023

Biomed Pharmacother.

<https://pubmed.ncbi.nlm.nih.gov/37473686/>

Unique Immune Blood Markers Between Severe Dengue and Sepsis in Children.

Salgado DM, Rivera GM, Pinto WA, Rodríguez J, Acosta G, Castañeda DM, Vega R, Perdomo-Celis F, Bosch I, Narváez CF.

01-09-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/37463399/>

Treatment with sofosbuvir attenuates the adverse neurodevelopmental consequences of Zika virus infection in infant rhesus macaques.

Medina A, Rusnak R, Richardson R, Zimmerman MG, Suthar M, Schoof N, Kovacs-Balint Z, Mavigner M, Sanchez M, Chahroudi A, Raper J.

15-08-2023

J Neuroimmunol.

<https://pubmed.ncbi.nlm.nih.gov/37451078/>

Phospholipid binding of the dengue virus envelope E protein segment containing the conserved His residue.

Villalaín J.

Oct-2023

Biochim Biophys Acta Biomembr.

<https://pubmed.ncbi.nlm.nih.gov/37437754/>

Flaviviruses encompass many important human pathogens, including Dengue, Zika, West Nile, Yellow fever, Japanese encephalitis, and Tick-borne encephalitis viruses as well as several emerging viruses that affect millions of people worldwide. They enter cells by endocytosis, fusing their membrane with the late endosomal one in a pH-dependent manner, so membrane fusion is one of the main targets for obtaining new antiviral inhibitors. The envelope E protein, a class II membrane fusion protein, is responsible for fusion and contains different domains involved in the fusion mechanism, including the fusion peptide. However, other segments, apart from the fusion peptide, have been implicated in the mechanism of membrane fusion, in particular a segment containing a His residue supposed to act as a specific pH sensor. We have used atomistic molecular dynamics to study the binding of the envelope E protein segment containing the conserved His residue in its three different tautomer forms with a complex membrane mimicking the late-endosomal one. We show that this His-containing segment is capable of spontaneous membrane binding, preferentially binds electronegatively charged phospholipids and does not bind cholesterol. Since Flaviviruses have caused epidemics in the past, continue to do so and will undoubtedly continue to do so, this specific segment could characterise a new target that would allow finding effective antiviral molecules against DENV virus in particular and Flaviviruses in general.

FEN1-aided recombinase polymerase amplification (FARPA) for one-pot and multiplex detection of nucleic acids with an ultra-high specificity and sensitivity.

Ma Y, Wu H, Chen S, Xie C, Hu J, Qi X, Ma X, Chu Y, Shan J, Lu Y, Cui L, Zou B, Zhou G.

01-10-2023

Biosens Bioelectron.

<https://pubmed.ncbi.nlm.nih.gov/37354713/>

SARS-CoV-2 and Dengue Coinfection in Filipino Children: Epidemiology Profile, Clinical Presentation and Outcomes.

Pantig FMT, Clemens SAC, Clemens R, Maramba-Lazarte CC, Madrid MAC.

01-09-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/37314214/>

Background: The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in dengue-endemic regions has raised concern on the possibility of coinfection, especially in children who bear the highest burden of illness. This study determined the incidence and described the profile of Filipino children with SARS-CoV-2

and dengue coinfection, and compared disease severity and outcome in children with coinfection to a matched group of children with SARS-CoV-2 mono-infection. **Methods:** This was a retrospective matched cohort study of pediatric patients 0-18 years old diagnosed with SARS-CoV-2 and dengue coinfection or SARS-CoV-2 mono-infection in the Philippines and reported to the Surveillance and Analysis of Coronavirus disease 2019 (COVID-19) in Children Nationwide registry from March 01, 2020 to June 30, 2022. **Results:** A total of 3,341 SARS-CoV-2 infections in children were reported. The SARS-CoV-2 and dengue coinfection incidence is 4.34% (n = 145). We matched 120 coinfections to mono-infections according to age, gender and timing of infection. More coinfection cases were classified as mild or moderate COVID-19, whereas more asymptomatic cases were seen in those with mono-infection. Rates were similar for severe and critical COVID-19 in both groups. Coinfections predominantly presented with typical dengue symptoms rather than COVID-19 symptoms and laboratory parameters. No differences in outcomes were observed between coinfection and mono-infection. The case fatality rates are 6.7% for coinfection and 5.0% for mono-infection. **Conclusions:** One in every 25 SARS-CoV-2 infections had a dengue coinfection. Continued surveillance is needed to establish the interaction of SARS-CoV-2 and dengue virus, evaluate the impact of COVID-19 and/or dengue vaccination on coinfection and monitor complications of coinfection.

In Vitro and In Vivo Models for Drug Transport Across the Blood-Testis Barrier.

Hau RK, Wright SH, Cherrington NJ.

Sept-2023

Drug Metab Dispos.

<https://pubmed.ncbi.nlm.nih.gov/37258305/>

The blood-testis barrier (BTB) is a selectively permeable membrane barrier formed by adjacent Sertoli cells (SCs) in the seminiferous tubules of the testes that develops intercellular junctional complexes to protect developing germ cells from external pressures. However, due to this inherent defense mechanism, the seminiferous tubule lumen can act as a pharmacological sanctuary site for latent viruses (e.g., Ebola, Zika) and cancers (e.g., leukemia). Therefore, it is critical to identify and evaluate BTB carrier-mediated drug delivery pathways to successfully treat these viruses and cancers. Many drugs are unable to effectively cross cell membranes without assistance from carrier proteins like transporters because they are large, polar, and often carry a charge at physiologic pH. SCs express transporters that selectively permit endogenous compounds, such as carnitine or nucleosides, across the BTB to support normal physiologic activity, although reproductive toxicants can also use these pathways, thereby circumventing the BTB. Certain xenobiotics, including select cancer therapeutics, antivirals, contraceptives, and environmental toxicants, are known to accumulate within the male genital tract and cause testicular toxicity; however, the transport pathways by which these compounds circumvent the BTB are largely unknown. Consequently, there is a need to identify the

clinically relevant BTB transport pathways in in vitro and in vivo BTB models that recapitulate human pharmacokinetics and pharmacodynamics for these xenobiotics. This review summarizes the various in vitro and in vivo models of the BTB reported in the literature and highlights the strengths and weaknesses of certain models for drug disposition studies. **SIGNIFICANCE STATEMENT:** Drug disposition to the testes is influenced by the physical, physiological, and immunological components of the blood-testis barrier (BTB). But many compounds are known to cross the BTB by transporters, resulting in pharmacological and/or toxicological effects in the testes. Therefore, models that assess drug transport across the human BTB must adequately account for these confounding factors. This review identifies and discusses the benefits and limitations of various in vitro and in vivo BTB models for preclinical drug disposition studies.

Dengue Shock Syndrome with Acute Liver Failure- A Stormy Presentation of Congenital Dengue.

Subashri P, G B, Rao PVR.

Sept-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37256450/>

Neonatal Chikungunya - An Emerging Tale of Neonatal Encephalopathy.

Kr A, Bandiya P, Hs N.

Sept-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37248382/>

Elucidating cellular interactome of chikungunya virus identifies host dependency factors.

Yin P, Jian X, Liu Y, Liu Y, Lv L, Cui H, Zhang L.

Aug-2023

Virol Sin.

<https://pubmed.ncbi.nlm.nih.gov/37182691/>

Development of disposable electrode for the detection of mosquito-borne viruses.

Nasrin F, Khoris IM, Chowdhury AD, Muttaqin SE, Park EY.

Aug-2023

Biotechnol J.

<https://pubmed.ncbi.nlm.nih.gov/37127933/>

Mimotope discovery as a tool to design a vaccine against Zika and dengue viruses.

Cuevas-Juárez E, Liñan-Torres A, Hernández C, Kopylov M, Potter CS, Carragher B, Ramírez OT, Palomares LA.

Sept-2023

Biotechnol Bioeng.

<https://pubmed.ncbi.nlm.nih.gov/37058415/>

Vaccine development against dengue virus is challenging because of the antibody-dependent enhancement of infection (ADE), which causes severe disease. Consecutive

infections by Zika (ZIKV) and/or dengue viruses (DENV), or vaccination can predispose to ADE. Current vaccines and vaccine candidates contain the complete envelope viral protein, with epitopes that can raise antibodies causing ADE. We used the envelope dimer epitope (EDE), which induces neutralizing antibodies that do not elicit ADE, to design a vaccine against both flaviviruses. However, EDE is a discontinuous quaternary epitope that cannot be isolated from the E protein without other epitopes. Utilizing phage display, we selected three peptides that mimic the EDE. Free mimotopes were disordered and did not elicit an immune response. After their display on adeno-associated virus (AAV) capsids (VLP), they recovered their structure and were recognized by an EDE-specific antibody. Characterization by cryo-EM and enzyme-linked immunosorbent assay confirmed the correct display of a mimotope on the surface of the AAV VLP and its recognition by the specific antibody. Immunization with the AAV VLP displaying one of the mimotopes induced antibodies that recognized ZIKV and DENV. This work provides the basis for developing a Zika and dengue virus vaccine candidate that will not induce ADE.

Membraneless Organelles and Condensates Orchestrate Innate Immunity Against Viruses.

Boccaccio GL, Thomas MG, García CC.

15-08-2023

J Mol Biol.

<https://pubmed.ncbi.nlm.nih.gov/36702393/>

The cellular defense against viruses involves the assembly of oligomers, granules and membraneless organelles (MLOs) that govern the activation of several arms of the innate immune response. Upon interaction with specific pathogen-derived ligands, a number of pattern recognition receptors (PRRs) undergo phase-separation thus triggering downstream signaling pathways. Among other relevant condensates, inflammasomes, apoptosis-associated speck-like protein containing a caspase-recruitment domain (ASC) specks, cyclic GMP-AMP synthase (cGAS) foci, protein kinase R (PKR) clusters, ribonuclease L-induced bodies (RLBs), stress granules (SGs), processing bodies (PBs) and promyelocytic leukemia protein nuclear bodies (PML NBs) play different roles in the immune response. In turn, viruses have evolved diverse strategies to evade the host defense. Viral DNA or RNA, as well as viral proteases or proteins carrying intrinsically disordered regions may interfere with condensate formation and function in multiple ways. In this review we discuss current and hypothetical mechanisms of viral escape that involve the disassembly, repurposing, or inactivation of membraneless condensates that govern innate immunity. We summarize emerging interconnections between these diverse condensates that ultimately determine the cellular outcome.

Effect of carpaine, a major alkaloid from *Carica papaya* leaves, on dengue virus-2 infection and replication-an in-vitro and in-silico study.

Alagarasu K, Puneekar M, Patil P, Kasabe B, Kakade M, Davuluri KS, Cherian S, Parashar D.

Août-2023

Phytother Res.

<https://pubmed.ncbi.nlm.nih.gov/36587936/>

Identification of potential inhibitors of Zika virus targeting NS3 helicase using molecular dynamics simulations and DFT studies.

Mishra SS, Kumar N, Karkara BB, Sharma CS, Kalra S.

Août-2023

Mol Divers.

<https://pubmed.ncbi.nlm.nih.gov/36063275/>

Despite the various research efforts towards the drug discovery program for Zika virus treatment, no antiviral drugs or vaccines have yet been discovered. The spread of the mosquito vector and ZIKV infection exposure is expected to accelerate globally due to continuing global travel. The NS3-Hel is a non-structural protein part and involved in different functions such as polyprotein processing, genome replication, etc. It makes an NS3-Hel protein an attractive target for designing novel drugs for ZIKV treatment. This investigation identifies the novel, potent ZIKV inhibitors by virtual screening and elucidates the binding pattern using molecular docking and molecular dynamics simulation studies. The molecular dynamics simulation results indicate dynamic stability between protein and ligand complexes, and the structures keep significantly unchanged at the binding site during the simulation period. All inhibitors found within the acceptable range having drug-likeness properties. The synthetic feasibility score suggests that all screened inhibitors can be easily synthesizable. Therefore, possible inhibitors obtained from this study can be considered a potential inhibitor for NS3 Hel, and further, it could be provided as a lead for drug development.

Emerging and Re-emerging Infectious Diseases in the WHO Eastern Mediterranean Region, 2001-2018.

Mostafavi E, Ghasemian A, Abdinasir A, Nematollahi Mahani SA, Rawaf S, Salehi Vaziri M, Gouya MM, Minh Nhu Nguyen T, Al Awaidey S, Al Ariqi L, Islam MM, Abu Baker Abd Farag E, Obtel M, Omondi Mala P, Matar GM, Asghar RJ, Barakat A, Sahak MN, Abdulmonem Mansouri M, Swaka A.

01-08-2023

Int J Health Policy Manag.

<https://pubmed.ncbi.nlm.nih.gov/33904695/>

Dracunculose

Extraction of Functional Compounds from Tarragon (*Artemisia dracunculus* L.) by Deep Eutectic Solvents at Different Properties.

Gerçek YC, Kutlu N, Çelik S, Gıdık B, Bayram S, Ecem Bayram N.

13-08-2023

Chem Biodivers.

<https://pubmed.ncbi.nlm.nih.gov/37574459/>

Taro Roots: An Underexploited Root Crop.

Ferdaus MJ, Chukwu-Munsen E, Foguel A, da Silva RC.

27-07-2023

Nutrients.

<https://pubmed.ncbi.nlm.nih.gov/37571276/>

Taro (*Colocasia esculenta*) is a root crop that remains largely underutilized and undervalued despite its abundance and affordability. In comparison to other root vegetables, such as potatoes, yams, carrots, and cassava, taro stands out as a plentiful and low-cost option. As global hunger increases, particularly in Africa, it becomes essential to address food insecurity by maximizing the potential of existing food resources, including taro, and developing improved food products derived from it. Taro possesses a wealth of carbohydrates, dietary fiber, vitamins, and minerals, thereby making it a valuable nutritional source. Additionally, while not a significant protein source, taro exhibits higher protein content than many other root crops. Consequently, utilizing taro to create food products, such as plant-based milk alternatives, frozen desserts, and yogurt substitutes, could play a crucial role in raising awareness and increasing taro production. Unfortunately, taro has been stigmatized in various cultures, which has led to its neglect as a food crop. Therefore, this review aims to highlight the substantial potential of taro as an economical source of dietary energy by exploring the rich fiber, potassium, vitamin C, protein, and other micronutrient content of taro, and providing a foundation for the formulation of novel food products. Furthermore, this paper assesses the nutritional benefits of taro, its current utilization, and its antinutritional properties. It emphasizes the need for further research to explore the various applications of taro and improve on-farm processing conditions for industrial purposes.

Transcriptomic and Functional Analyses of Two Cadmium Hyper-Enriched Duckweed Strains Reveal Putative Cadmium Tolerance Mechanisms.

Yang GL, Huang L, Yang X, Li Z, Liao HM, Mao K, Liu ZJ, Geng HY, Cao Q, Tan AJ.

29-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37569533/>

Cadmium (Cd) is one of the most toxic metals in the environment and exerts deleterious effects on plant growth and production. Duckweed has been reported as a promising candidate for Cd phytoremediation. In this study, the growth, Cd enrichment, and antioxidant enzyme activity of duckweed were investigated. We found that both high-Cd-tolerance duckweed (HCD) and low-Cd-tolerance duckweed (LCD) strains exposed to Cd were hyper-enriched with Cd. To further explore the underlying molecular mechanisms, a genome-wide transcriptome analysis was performed. The results showed that the growth rate, chlorophyll content, and antioxidant enzyme activities of duckweed were significantly affected by Cd

stress and differed between the two strains. In the genome-wide transcriptome analysis, the RNA-seq library generated 544,347,670 clean reads, and 1608 and 2045 differentially expressed genes were identified between HCD and LCD, respectively. The antioxidant system was significantly expressed during ribosomal biosynthesis in HCD but not in LCD. Fatty acid metabolism and ethanol production were significantly increased in LCD. Alpha-linolenic acid metabolism likely plays an important role in Cd detoxification in duckweed. These findings contribute to the understanding of Cd tolerance mechanisms in hyperaccumulator plants and lay the foundation for future phytoremediation studies.

Effect of pressure treatment duration on the rheological characteristics of dry-heated alocasia starch in the presence of monosaccharide and disaccharide.

Roy D, Kumar KJ.

15-08-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37414314/>

The current work investigated the impact of different pressure processing times (5, 10, and 15 min) at 120 psi on the rheological behavior of a mixture of dry-heated *Alocasia macrorrhizos* starch with monosaccharide and disaccharide. Shear-thinning behavior was exhibited by the samples in steady shear evaluation and the highest viscosity was observed in the 15 min pressure treated samples. In the initial phase of amplitude sweep measurement, samples exhibited strain dependency but later they remain unaffected with applied deformation. The greater value of Storage modulus (G') than loss modulus (G'') ($G' > G''$) indicating the weak gel-like behavior. Increasing in pressure treatment duration enhanced the value of G' and G'' with applied frequency and found maximum at 15 min. In temperature sweep measurement the G' , G'' as well as complex viscosity curves increased initially and then decreased after achieving peak temperature. However, the rheological parameters of the samples treated under long pressure processing time were found to be improved during temperature sweep measurements. The resulting extremely viscous, pressure-treated dry-heated *Alocasia macrorrhizos* starch-saccharides combination has a variety of uses in different pharmaceuticals as well as in food industries.

Protective effects of Typhonii Rhizoma in rheumatoid arthritis rats revealed by integrated metabolomics and network pharmacology.

Zhang X, Wang B, Chen S, Fu Y.

Sept-2023

Biomed Chromatogr.

<https://pubmed.ncbi.nlm.nih.gov/37161606/>

Echinococcosis

Cladistics of *Echinococcus granulosus* Sensu Stricto Genotypes Infecting the Slaughtered Pigs.

Moudgil AD, Nehra AK, Vohra S, Kumari A, Moudgil P.
17-08-2023

Acta Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37592063/>

Purpose: *Echinococcus granulosus* sensu stricto (s. s.) consists of the most widespread genotypes (G1, G3) implicated in human cystic echinococcosis worldwide. The present study aimed to evaluate the role of pigs in the transmission dynamics of *E. granulosus* s. s. genotypes, including the phylogenetics, evolutionary divergence and haplotype network analyses of north Indian pig isolates along with GenBank™ archived sequences. **Methods:** In total, 223 slaughtered pigs were thoroughly screened for the presence of hydatid cysts. The amplification of the partial mitochondrial cytochrome C oxidase subunit 1 gene was performed for the molecular confirmation and phylogenetics of the retrieved metacestodes. **Results:** The molecularly confirmed and sequenced present study isolates (n = 2) clustered with the *E. granulosus* genotype G3. The very low evolutionary divergence values (< 0.0027) of the present study isolates with *E. granulosus* genotype G3 indicated the absence of diverged lineages. The significantly negative values of Tajima's D (-2.598) and Fu and Li's D (-4.054) of the overall dataset and for the Asian sequences signified an expansion of population size. The overall dataset exhibited low nucleotide (0.067 ± 0.055) and high haplotype (0.574 ± 0.015) diversities, also alluding to demographic expansion. The haplotype network showed that the pig isolates from South America and Europe constituted the predominant haplotype, Hap_2 along with Hap_3 and Hap_6, primarily associated to *E. granulosus* genotype G1; whereas, the Indian isolates formed different haplotypes (Hap_1 and Hap_5) belonging to genotype G3. **Conclusions:** The present study highlighted the important role of pigs in the transmission of *E. granulosus* s. s., which is of paramount significance given the public health and economic impact of cystic echinococcosis.

A Disseminated Echinococcosis Patient with Five Years Survival from Turkey: A Case Report.

Karakök T, Ata N, Kiliç EK, Kinikli S.

Avr-Juin 2023

Iran J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37583632/>

Echinococcosis is a parasitic disease characterized by cysts in especially liver and lung. We report a long-term survival of a 44-year-old female patient with disseminated echinococcal disease involving the brain, lung, liver, spleen, kidney, mediastinum, thyroid gland, parotid gland, pancreas, peritoneum, rectus muscle, pararenal area, left thigh, skin and breast tissue from Turkey in 2016.

Zoonotic Transmission of Hepatic Hydatid Cyst from Domestic Dogs: A Case Report from an Urban-Marginal Area in Ecuador.

Coello Peralta RD, Coello Cuntó RA, Yancha Moreta C, Guerrero Lapo GE, Vinuesa Sierra RL, León Villalba LR, Pazmiño Gómez BJ, Gómez Landires EA, Ramallo G.

14-08-2023

Am J Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37574793/>

Diaphragmatic perforation as a result of cystic echinococcosis in an HIV positive migrant.

Schwarz C, Schmidbauer V, Lagler H, Stremitzer S, Kaczirek K, Langenberger H, Chromy D, Auer H, Gschwantler M.

11-08-2023

J Travel Med.

<https://pubmed.ncbi.nlm.nih.gov/37565821/>

Establishment and application of unbiased in vitro drug screening assays for the identification of compounds against *Echinococcus granulosus* sensu stricto.

Kaethner M, Preza M, Kaempfer T, Zumstein P, Tamponi C, Varcasia A, Hemphill A, Brehm K, Lundström-Stadelmann B.

04-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37540716/>

Application and evaluation of native antigen B from *Echinococcus granulosus* sensu stricto and *E. canadensis* alone or mixture for serodiagnosis of human G1-G3 and G6/G7 genotypes cystic echinococcosis sera, using ELISA and Western blotting.

Sharifi Y, Sadjjadi SM, Jafari SH, Nikoupour Deilami H, Mardani P, Solgi R.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37438467/>

Cystic echinococcosis (CE) is one of the most important helminthic diseases in the world with different genotypes distribution. The application of specific genotype antigens together with sera from patients with specific cyst genotypes have not been reported, so far. The present study aimed to apply and evaluate native AgB from *Echinococcus granulosus* sensu stricto (Eg) and *Echinococcus canadensis* (Ec) alone or mixture for serodiagnosis of human G1-G3 and G6/G7 genotypes cystic echinococcosis sera, using ELISA and Western blotting. A total of 47 human sera along with 47 human CE cysts were collected. CE genotypes were determined. Native AgB were prepared from *E. granulosus* s.s and *E. canadensis* genotypes. ELISA and Western blot were performed on human specific G1-G3 and G6/G7

genotypes sera. Species specific native AgB were used alone or mixed. The sensitivity of ELISA using alone and mixed 1Eg-1Ec, 1Eg-2Ec, and 2Eg-1Ec of native AgB from *E. granulosus* s.s and *E. canadensis* genotypes for human G1-G3 sera were 92.10, 89.47, 97.37, 100, and 100%, respectively; while using AgBs, alone and mixed for human G6/G7 sera were 100%. The sensitivity of Western blotting using native AgB of *E. granulosus* s.s and *E. canadensis* genotypes alone and mixed 2Eg-1Ec were 78.95% and 100% for human G1-G3 and G6/G7 genotypes sera, respectively. The mixture of AgB from *Echinococcus granulosus sensu stricto* and *Echinococcus canadensis* genotypes increased ELISA sensitivity for the diagnosis of human CE. Preparation and application of native AgB from specific and prevalent genotypes of CE in endemic regions is recommended.

Dimerization, host-parasite communication and expression studies of an *Echinococcus granulosus* 2DBD nuclear receptor.

Blanco V, Mozzo B, Alvite G.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37395819/>

Nuclear receptors (NRs) are ligand-modulated transcription factors that regulate various biological processes, such as metabolism, development and reproduction. Although NRs with two DNA-binding domains (2DBD) were identified in *Schistosoma mansoni* (Platyhelminth, Trematoda) more than fifteen years ago, these proteins have been poorly studied. 2DBD-NRs could become attractive therapeutic targets to combat parasitic diseases such as cystic echinococcosis since this type of protein is absent in vertebrate hosts. Cystic echinococcosis is a worldwide zoonosis caused by the larval stage of the parasitic platyhelminth *Echinococcus granulosus* (Cestoda) that generates an important public health problem and a significant economic loss. Recently, our research group identified four 2DBD-NRs in *E. granulosus*, named Eg2DBD α , Eg2DBD α .1 (an isoform of Eg2DBD α), Eg2DBD β , and Eg2DBD γ . This work demonstrated that Eg2DBD α .1 forms homodimers through the E and F regions, whereas its interaction with EgRXR β could not be detected. In addition, the stimulation of Eg2DBD α .1 homodimerization by intermediate host serum was shown, suggesting that at least one lipophilic molecule from bovine serum could bind to Eg2DBD α .1. Finally, Eg2DBDs expression studies in the protoscolex larval stage were performed, indicating that Eg2dbd γ is not expressed, whereas Eg2dbd α has the highest expression level followed by Eg2dbd β and Eg2dbd α .1 in decreased order. Overall, these findings provide new insights into the mechanism of action of Eg2DBD α .1 and its potential role in host-parasite communication.

An unexpected guest: Pulmonary echinococcosis diagnosed by intraoperative frozen section examination. A case report and literature review.

Maggioni G, Bonis A, Schiavon M, Giraudo C, Lunardi F, Pezzuto F, Calabrese F.

Aug-2023

Pathol Res Pract.

<https://pubmed.ncbi.nlm.nih.gov/37343377/>

Echinococcosis is caused by tapeworms belonging to the *Echinococcus* genus. The most common site of infection is the liver although it may involve almost any organ. Symptoms of pulmonary echinococcosis vary depending on the location and structure of the cyst. While uncomplicated cysts usually appear at imaging as well-defined homogeneous lesions with fluid content and smooth walls of variable thickness, complicated lesions may have a more heterogeneous content with higher density making more difficult the distinction from malignancies or other infections. Hereby we describe the case of a 61-year-old Northern African male admitted to our tertiary center for left upper chest pain who then underwent a chest computed tomography (CT) scan which demonstrated a large hypodense lesion, with smooth and thick walls, in the upper left lobe. The following magnetic resonance confirmed the homogeneous fluid content, and the 18 F- fluorodeoxyglucose-positron emission tomography/CT demonstrated a mild uptake of the walls. According to these findings, the main differential diagnoses at imaging included bronchogenic cyst, synovial sarcoma, and pulmonary hematoma although the patient denied any recent trauma. Given the large size and clinical symptoms he underwent surgery. Intra-operative frozen section, supported by imprint cytology, excluded the presence of malignancy while suggested an echinococcal laminar exocyst. The final pathological examination confirmed the diagnosis of echinococcosis (i.e., *Echinococcus granulosus* protoscolex). After surgery he was treated with albendazole and at the six-month follow-up he was in good clinical conditions. Our case highlights the importance of considering rare infections, particularly in individuals from endemic areas. Frozen tissue analyses can be a diagnostic challenge and often require ancillary tools such as imprint cytology and serial sections for more sensitive and accurate diagnosis.

Pulmonary Cystic Echinococcosis in a Child Presenting in the United Kingdom with Fever and Chest Pain: A Brief Report and Discussion on Management.

Lees EA, Ives A, Fowler D, Lakhoo K, Grant D, Kelly D, Paulus S, Segal S, Gilchrist JJ, Kew A, Chiodini P, Kadambari S.

01-09-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/37200507/>

Filariose lymphatique

Soil-transmitted helminths: A critical review of the impact of co-infections and implications for control and elimination.

Lebu S, Kibone W, Muoghalu CC, Ochaya S, Salzberg A, Bongomin F, Manga M.

10-08-2023

Researchers have raised the possibility that soil-transmitted helminth (STH) infections might modify the host's immune response against other systemic infections. STH infections can alter the immune response towards type 2 immunity that could then affect the likelihood and severity of other illnesses. However, the importance of co-infections is not completely understood, and the impact and direction of their effects vary considerably by infection. This review synthesizes evidence regarding the relevance of STH co-infections, the potential mechanisms that explain their effects, and how they might affect control and elimination efforts. According to the literature reviewed, there are both positive and negative effects associated with STH infections on other diseases such as malaria, human immunodeficiency virus (HIV), tuberculosis, gestational anemia, pediatric anemia, neglected tropical diseases (NTDs) like lymphatic filariasis, onchocerciasis, schistosomiasis, and trachoma, as well as Coronavirus Disease 2019 (COVID-19) and human papillomavirus (HPV). Studies typically describe how STHs can affect the immune system and promote increased susceptibility, survival, and persistence of the infection in the host by causing a TH2-dominated immune response. The co-infection of STH with other diseases has important implications for the development of treatment and control strategies. Eliminating parasites from a human host can be more challenging because the TH2-dominated immune response induced by STH infection can suppress the TH1 immune response required to control other infections, resulting in an increased pathogen load and more severe disease. Preventive chemotherapy and treatment are currently the most common approaches used for the control of STH infections, but these approaches alone may not be adequate to achieve elimination goals. Based on the conclusions drawn from this review, integrated approaches that combine drug administration with water, sanitation and hygiene (WASH) interventions, hygiene education, community engagement, and vaccines are most likely to succeed in interrupting the transmission of STH co-infections. Gaining a better understanding of the behavior and relevance of STH co-infections in the context of elimination efforts is an important intermediate step toward reducing the associated burden of disease.

Gale

Norwegian Scabies in a 70-Year-Old Renal Transplant Recipient: A Case Report.

Eslahi AV, Sheikhdavoodi N, Badri M.

Avr-Juin 2023

Iran J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37583641/>

Deep learning for AI-based diagnosis of skin-related neglected tropical diseases: A pilot study.

Yotsu RR, Ding Z, Hamm J, Blanton RE.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578966/>

Background: Deep learning, which is a part of a broader concept of artificial intelligence (AI) and/or machine learning has achieved remarkable success in vision tasks. While there is growing interest in the use of this technology in diagnostic support for skin-related neglected tropical diseases (skin NTDs), there have been limited studies in this area and fewer focused on dark skin. In this study, we aimed to develop deep learning based AI models with clinical images we collected for five skin NTDs, namely, Buruli ulcer, leprosy, mycetoma, scabies, and yaws, to understand how diagnostic accuracy can or cannot be improved using different models and training patterns. **Methodology:** This study used photographs collected prospectively in Côte d'Ivoire and Ghana through our ongoing studies with use of digital health tools for clinical data documentation and for tele dermatology. Our dataset included a total of 1,709 images from 506 patients. Two convolutional neural networks, ResNet-50 and VGG-16 models were adopted to examine the performance of different deep learning architectures and validate their feasibility in diagnosis of the targeted skin NTDs. **Principal findings:** The two models were able to correctly predict over 70% of the diagnoses, and there was a consistent performance improvement with more training samples. The ResNet-50 model performed better than the VGG-16 model. A model trained with PCR confirmed cases of Buruli ulcer yielded 1-3% increase in prediction accuracy across all diseases, except, for mycetoma, over a model which training sets included unconfirmed cases. **Conclusions:** Our approach was to have the deep learning model distinguish between multiple pathologies simultaneously-which is close to real-world practice. The more images used for training, the more accurate the diagnosis became. The percentages of correct diagnosis increased with PCR-positive cases of Buruli ulcer. This demonstrated that it may be better to input images from the more accurately diagnosed cases in the training models also for achieving better accuracy in the generated AI models. However, the increase was marginal which may be an indication that the accuracy of clinical diagnosis alone is reliable to an extent for Buruli ulcer. Diagnostic tests also have their flaws, and they are not always reliable. One hope for AI is that it will objectively resolve this gap between diagnostic tests and clinical diagnoses with the addition of another tool. While there are still challenges to be overcome, there is a potential for AI to address the unmet needs where access to medical care is limited, like for those affected by skin NTDs.

Burrow Ink Test for Scabies.

Rauwerdink D, Balak D.

17-08-2023

N Engl J Med.

<https://pubmed.ncbi.nlm.nih.gov/37578077/>

Possibilities of Anxiolytic Therapy in the Elimination of Stress Skin Manifestations: A Case Report.

Sydorova N, Vereshchaka V, Kuts T.
2023

Acta Med Litu.

<https://pubmed.ncbi.nlm.nih.gov/37575372/>

The case of a 42-year-old female patient with pronounced itching and exanthema, mainly in the area of the trunk and lower limbs, is presented. Previously, the patient took antihistamines without effect, was treated for scabies, but the itching remained pronounced and led to rash and excoriations. From the anamnesis, it was found that the patient has a high level of stress. According to the Hospital Anxiety and Depression Scale, the anxiety of the patient reached 14 points, and depression 1 point. Functional (psychogenic) itching was suspected. Since the patient refused dermatologist consultation, therapy with the anxiolytic temgicoluril, topical antipruritic agents and nonpharmacological methods of treatment were recommended at the initial stage. The patient felt a significant relief of itching symptoms on the first day of anxiolytic usage, she withdrew topical antipruritic agents after 5 days of anxiolytic treatment, in 15 days she began to reduce the dose of temgicoluril, and at the end of the third week she stopped treatment with anxiolytic due to a significant positive effect. In three weeks, practically all elements of the rash, except for the largest wounds from scratching, disappeared. The peculiarity of the case is that functional itching was completely eliminated during anxiolytic therapy without other systemic medications, which emphasizes the importance of eliminating the component of stress and anxiety in the treatment of such patients.

Superinfected scabies.

Berna-Rico E, Chamorro-Tojeiro S, Pérez-González A, Pérez-García B.

09-08-2023

Med Clin (Barc).

<https://pubmed.ncbi.nlm.nih.gov/37567823/>

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

Comparative study of a broad qPCR panel and centrifugal flotation for detection of gastrointestinal parasites in fecal samples from dogs and cats in the United States.

Leutenegger CM, Lozoya CE, Tereski J, Andrews J, Mitchell KD, Meeks C, Willcox JL, Freeman G, Richmond HL, Savard C, Evason MD.

16-08-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37587483/>

Background: For decades, zinc sulfate centrifugal fecal flotation microscopy (ZCF) has been the mainstay technique for gastrointestinal (GI) parasite screening at

veterinary clinics and laboratories. Elsewhere, PCR has replaced microscopy because of generally increased sensitivity and detection capabilities; however, until recently it has been unavailable commercially. Therefore, the primary aim of this study was to compare the performance of real-time PCR (qPCR) and ZCF for fecal parasite screening. Secondary aims included further characterization of markers for hookworm treatment resistance and *Giardia* spp. assemblages with zoonotic potential and qPCR optimization. **Methods:** A convenience sampling of 931 canine/feline fecal samples submitted to a veterinary reference laboratory for routine ZCF from the Northeast US (11/2022) was subsequently evaluated by a broad qPCR panel following retention release. Detection frequency and agreement (kappa statistics) were evaluated between ZCF and qPCR for seven GI parasites [hookworm/(*Ancylostoma* spp.), roundworm/(*Toxocara* spp.), whipworm/(*Trichuris* spp.), *Giardia* duodenalis, *Cystoisospora* spp., *Toxoplasma gondii*, and *Tritrichomonas blagburni*] and detections per sample. Total detection frequencies were compared using a paired t-test; positive sample and co-infection frequencies were compared using Pearson's chi-squared test ($p \leq 0.05$ significant) and qPCR frequency for hookworm benzimidazole (BZ) resistance (F167Y) and zoonotic *Giardia* spp. assemblage markers calculated. Confirmatory testing, characterization, and qPCR optimization were carried out with Sanger sequencing. **Results:** qPCR detected a significantly higher overall parasite frequency ($n = 679$) compared to ZCF ($n = 437$) [$p = < 0.0001$, $t = 14.38$, degrees-of-freedom (df) = 930] and $2.6 \times$ the co-infections [qPCR ($n = 172$) vs. ZCF ($n = 66$)], which was also significant ($p = < 0.0001$, $X^2 = 279.49$; $df = 1$). While overall agreement of parasite detection was substantial [kappa = 0.74; (0.69-0.78)], ZCF-undetected parasites reduced agreement for individual and co-infected samples. qPCR detected markers for *Ancylostoma caninum* BZ resistance ($n = 5$, 16.1%) and *Giardia* with zoonotic potential ($n = 22$, 9.1%) as well as two parasites undetected by ZCF (*T. gondii*/*T. blagburni*). Sanger sequencing detected novel roundworm species, and qPCR optimization provided detection beyond ZCF. **Conclusions:** These results demonstrate the statistically significant detection frequency advantage offered by qPCR compared to routine ZCF for both single and co-infections. While overall agreement was excellent, this rapid, commercially available qPCR panel offers benefits beyond ZCF with detection of markers for *Giardia* assemblages with zoonotic potential and hookworm (*A. caninum*) BZ resistance.

Prevalence of gastrointestinal parasites in domestic cats (*Felis catus*) diagnosed by different coproparasitological techniques in the municipality of Seropédica, Rio de Janeiro.

Silva YHD, Campos DR, Lima GAC, Quintal JP, Guimarães BG, Rêgo GMM, Avelar BR, Intrieri JM, Correia TR, Scott FB.

11-08-2023

Rev Bras Parasitol Vet.

<https://pubmed.ncbi.nlm.nih.gov/37585954/>

Cytokine Gene Expression Profiles during HIV and Helminth Coinfection in Underprivileged Peri-Urban South African Adults.

Mpaka-Mbatha MN, Naidoo P, Bhengu KN, Islam MM, Singh R, Nembe-Mafa N, Mkhize-Kwitshana ZL.

25-07-2023

Diagnostics (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37568838/>

Background: Intestinal helminth parasites are potent stimulators of T helper type 2 (Th2) and regulatory Th3 anti-inflammatory immune responses, while human immunodeficiency virus (HIV) infections are activators of predominantly T helper type 1(Th1) pro-inflammatory responses. Studies investigating the immune profiles of individuals coinfecting with helminths and HIV are scarce. Although it is well known that helminths cause a type 2 immune response during the chronic stage of infection that is characterised by Th2 cell differentiation, eosinophil recruitment, and alternative macrophage activation, the immune mechanisms that regulate tissue damage at the time of parasite invasion are poorly understood. **Aim:** The aim of the study was to determine the cytokine gene expression profiles during HIV and helminth coinfection in underprivileged South African adults living in a peri-urban area with poor sanitary conditions and a lack of clean water supply. **Method:** Study participants ($n = 164$) were subdivided into uninfected controls, HIV-infected, helminth-infected, and HIV and helminth-coinfected groups. The Kato-Katz and Mini Parasep techniques and *Ascaris lumbricoides*-specific Immunoglobulin E (IgE) and Immunoglobulin G4 (IgG4) levels were used to detect helminth infections. Participants' HIV status was determined using two HIV1/2 antibody test kits. RNA was isolated from white blood cells for cytokine (Th1-, Th2-, and Th17-related) and transcription factor gene expression profiling using real-time PCR. **Results:** Multivariate regression data were adjusted for age, gender, BMI, antiretroviral treatment (ART), and nutritional supplement intake. The HIV and helminth-coinfected group had significantly higher tumour necrosis factor alpha (*TNF- α*) (adjusted $\beta = 0.53$, $p = 0.036$), interleukin 2 (*IL-2*) (adjusted $\beta = 6.48$, $p = 0.008$), and interleukin 17 (*IL-17*) (adjusted $\beta = 1.16$, $p = 0.001$) levels and lower GATA binding protein 3 (*GATA3*) levels (adjusted $\beta = -0.77$, $p = 0.018$) compared to the uninfected controls. No statistical significance was noted for Th2-related cytokines. **Conclusion:** The coinfecting group had higher proinflammatory Th1- and Th17-related cytokine gene expression profiles compared to the uninfected controls. The findings suggest that pro-inflammatory responses are elevated during coinfection, which supports the hypothesis that helminths have a deleterious effect on HIV immune responses.

Leishmaniose

Discovery of the vector of visceral leishmaniasis, *Phlebotomus (Artemievus) alexandri* Sinton, 1928, in

Kenya suggests complex transmission dynamics.

Kiplagat S, Villinger J, Kigen CK, Kidambasi KO, Muema JM, Mwangi SM, Wangari M, Matoke-Muhia D, Masiga DK, Bargul JL.

28-07-2023

Curr Res Parasitol Vector Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37593661/>

A byproduct from the Valles Calchaquies vineyards (Argentina) rich in phenolic compounds: a tool against endemic Leishmania dissemination.

Salazar PB, Fanzone M, Zabala BA, Rodriguez Vaquero MJ, Cilli E, Barroso PA, Minahk C, Acuña L.

17-08-2023

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/37592068/>

Vineyard-derived pomace is a byproduct of the wine industry that can have a negative impact on the environment if it is only disposed of or used as a fertilizer. Owing to its polyphenol content, grape pomace is an alternative to biocontrol undesirable microorganisms. In the present study, we characterized the phenolic composition of red and white grape pomace from Valles Calchaquies, Argentina, and explored its activity against *Leishmania* (*Leishmania*) *amazonensis*, an etiological agent of American tegumentary leishmaniasis, a neglected endemic disease in northern Argentina. Red and white pomace extracts similarly reduced *Leishmania* viability after a 48-h treatment, with the fractions containing a higher proportion of phenolic compounds being more active. Both extracts stimulated ATPase activity on the parasite plasma membranes, with white grape pomace having a stronger effect than red grape pomace. In addition, the extracts displayed fairly good anticholinesterase activity, which may have contributed to their anti-*Leishmania* activity. These results reinforce the potential applicability of grape pomace as an antimicrobial agent for the development of biopesticides.

Thymoquinone Effect on Leishmania tropica/infantum and Leishmania-Infected Macrophages.

KarimiPourSaryazdi A, Jafari MM, Pirestani M, Sadeghi SH, Moghadamizad Z.

17-08-2023

Acta Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37589882/>

Introduction: *Leishmania* is a parasitic protozoan that tries to enter and amplify within macrophages. Macrophage cells are also immune defense cells that phagocytose many microbes like bacteria, fungi, as well as parasites like *Leishmania* spp. However, they are unable to kill this parasite that resides in the phagosomes of contaminated macrophages and multiplies in these macrophages, leading to the destruction of contaminated macrophages and the emerging of *Leishmania* wounds. A large number of current therapies for *Leishmania* cure have adverse effects, or parasites have developed resistance to some of

these therapies, so a better therapy for the cure of Leishmania is required. Thymoquinone is one of the *Nigella Sativa* ingredients with numerous biological effects, such as antioxidant as well as antimicrobial effects on a variety of microbes, namely fungi, bacteria, as well as parasites like *Leishmania* spp. The impacts of Thymoquinone on *Leishmania tropica* and *Leishmania infantum*, as well as *Leishmania*-infected macrophages, were examined in this study. **Methods:** The impact of various Thymoquinone dosages on *L. tropica* and *L. infantum* promastigotes and amastigotes was examined in vitro. Flow cytometry, as well as MTT, was also applied to examine the cytotoxic activity of Thymoquinone on promastigotes of *L. tropica* and *L. infantum*, as well as the incidence of apoptosis. The amastigote assay is also utilized to calculate the % of contaminated macrophages as well as the number of the present parasites in each macrophage. **Results:** The percentage of macrophages contaminated with *L. tropica* and *L. infantum* amastigotes after medicating with 20 μ M of Thymoquinone was 23% and 19%, respectively. Also, after medicating with 10 μ M of Thymoquinone, these percentages were 32% and 31%, respectively. Flow cytometry indicated that Thymoquinone caused 33.9% and 31.4% apoptosis in *L. tropica* and *L. infantum*, respectively. As determined by the promastigote assay, the inhibitory concentration (IC50) of Thymoquinone for *L. tropica* and *L. infantum* was 9.49 μ M and 12.66 μ M, respectively. The results of the promastigote and amastigote assay show that with an increase in Thymoquinone doses, its ability to kill *Leishmania* parasites increases, too. **Conclusion:** According to the results of the study, Thymoquinone has a potentially lethal impact on *L. tropica* and *L. infantum* promastigotes as well as amastigotes (within *leishmania* contaminated macrophages).

Detection and activity of MMP-2 and MMP-9 in *Leishmania amazonensis* and *Leishmania braziliensis* promastigotes.

Costa BF, de Queiroz Filho TN, da Cruz Carneiro AL, Falcão ASC, da Silva Kataoka MS, Pinheiro JJV, Rodrigues APD.

16-08-2023

BMC Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37587436/>

The Association of Human Leucocyte Antigen (HLA) Class I and II Genes with Cutaneous and Visceral Leishmaniasis in Iranian Patients: A Preliminary Case-Control Study.

Eimanzadeh M, Mohebbali M, Zarrabi M, Foroushani AR, Kazemi M, Hajjarian H, Zarei Z, Kakooei Z, Akhoundi B.

Avr-Juin 2023

Iran J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37583643/>

Background: Leishmaniasis is currently considered a re-emerging or emerging infection based on the geographic region. The outcome of leishmaniasis vastly depends on *Leishmania*-host interaction. This preliminary study aimed to show the association of human leukocyte antigen (HLA)

class I and II genes with healed and non-healed cutaneous leishmaniasis (CL), and symptomatic and asymptomatic visceral leishmaniasis (VL) compared with control groups in Iran. **Methods:** Ninety-five people, including 31 patients versus 64 individuals in the control group, were enrolled. Among them, 20 patients had confirmed CL based on amastigote observation, 10 had improved CL and 10 non-healed CL. Eleven patients were suffering from confirmed VL based on direct agglutination test (Five asymptomatic and six symptomatic VL cases). Besides, they were residents in an endemic area of VL in the northwest of Iran. To select a control group, it was ensured that they had no history of leishmaniasis. Peripheral blood samples were collected from each patient. After DNA extraction, HLA typing was conducted using polymerase chain reaction - sequence-specific priming (PCR-SSP). Subsequently, data were statistically analyzed by SPSS. **Results:** There was a statistical relationship between the presence of HLA-A26 and CL, healed CL and the existence of the B38 allele, C1 allele and symptomatic VL, as well as B1.4 allele and asymptomatic VL ($P < 0.05$). **Conclusion:** This primary finding indicates that several HLA genes have a potential role in the susceptibility of Iranian people to CL and VL.

Molecular Identification of Cutaneous Leishmaniasis Species in the Northcentral Iranian Province of Alborz: Is There a New Focus on Cutaneous Leishmaniasis in the Province?

Sheikhi S, Heidari A, Mohebbali M, Keshavarz H, Heidari A, Sezavar M, Akhoundi B, Bairami A.

Avr-Juin 2023

Iran J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37583638/>

High-resolution melting (HRM)-based detection of polymorphisms in the malic enzyme and glucose-6-phosphate isomerase genes for *Leishmania infantum* genotyping.

Buffi G, Ceccarelli M, Diotallevi A, Abruzzese M, Bruno F, Castelli G, Vitale F, Andreoni F, Bencardino D, Magnani M, Galluzzi L.

14-08-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37580789/>

Thiadiazine-thiones as inhibitors of leishmania pteridine reductase (PTR1) target: investigations and in silico approach.

Shtaiwi A.

14-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37578348/>

Leishmania infection alters macrophage and dendritic cell migration in a three-dimensional environment.

Luz Y, Rebouças A, Bernardes CPOS, Rossi EA, Machado TS, Souza BSF, Brodskyn CI, Veras PST, Dos Santos WLC, de Menezes JPB.

28-07-2023

Front Cell Dev Biol.

<https://pubmed.ncbi.nlm.nih.gov/37576604/>

Background: Leishmaniasis results in a wide spectrum of clinical manifestations, ranging from skin lesions at the site of infection to disseminated lesions in internal organs, such as the spleen and liver. While the ability of *Leishmania*-infected host cells to migrate may be important to lesion distribution and parasite dissemination, the underlying mechanisms and the accompanying role of host cells remain poorly understood. Previously published work has shown that *Leishmania* infection inhibits macrophage migration in a 2-dimensional (2D) environment by altering actin dynamics and impairing the expression of proteins involved in plasma membrane-extracellular matrix interactions. Although it was shown that *L. infantum* induces the 2D migration of dendritic cells, *in vivo* cell migration primarily occurs in 3-dimensional (3D) environments. The present study aimed to investigate the migration of macrophages and dendritic cells infected by *Leishmania* using a 3-dimensional environment, as well as shed light on the mechanisms involved in this process. **Methods:** Following the infection of murine bone marrow-derived macrophages (BMDM), human macrophages and human dendritic cells by *L. amazonensis*, *L. braziliensis*, or *L. infantum*, cellular migration, the formation of adhesion complexes and actin polymerization were evaluated. **Results:** Our results indicate that *Leishmania* infection inhibited 3D migration in both BMDM and human macrophages. Reduced expression of proteins involved in adhesion complex formation and alterations in actin dynamics were also observed in *Leishmania*-infected macrophages. By contrast, increased human dendritic cell migration in a 3D environment was found to be associated with enhanced adhesion complex formation and increased actin dynamics. **Conclusion:** Taken together, our results show that *Leishmania* infection inhibits macrophage 3D migration, while enhancing dendritic 3D migration by altering actin dynamics and the expression of proteins involved in plasma membrane extracellular matrix interactions, suggesting a potential association between dendritic cells and disease visceralization.

Clinical and immunological spectra of human cutaneous leishmaniasis in North Africa and French Guiana.

Saidi N, Blaizot R, Prévot G, Aoun K, Demar M, Cazenave PA, Bouratbine A, Pied S.

27-07-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37575260/>

Cutaneous leishmaniasis (CL) caused by infection with the parasite *Leishmania* exhibits a large spectrum of clinical manifestations ranging from single healing to severe chronic lesions with the manifestation of resistance or not to treatment. Depending on the specie and multiple environmental parameters, the evolution of lesions is determined by a complex interaction between parasite

factors and the early immune responses triggered, including innate and adaptive mechanisms. Moreover, lesion resolution requires parasite control as well as modulation of the pathologic local inflammation responses and the initiation of wound healing responses. Here, we have summarized recent advances in understanding the *in situ* immune response to cutaneous leishmaniasis: *i)* in North Africa caused by *Leishmania* (*L.*) *major*, *L. tropica*, and *L. infantum*, which caused in most cases localized autoresolutive forms, and *ii)* in French Guiana resulting from *L. guyanensis* and *L. braziliensis*, two of the most prevalent strains that may induce potentially mucosal forms of the disease. This review will allow a better understanding of local immune parameters, including cellular and cytokines release in the lesion, that controls infection and/or protect against the pathogenesis in new world compared to old world CL

Design, synthesis and antitrypanosomatid activity of 2-nitroimidazole-3,5-disubstituted isoxazole compounds based on benzimidazole.

Carvalho DB, Costa PAN, Portapilla GB, das Neves AR, Shigemoto CYK, Pelizaro BI, Silva F, Piranda EM, Arruda CCP, Gaspari PDM, Cardoso IA, Luccas PH, Nonato MC, Lopes NP, de Albuquerque S, Baroni ACM.

05-05-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37573209/>

Unfolded protein response pathway in leishmaniasis: A review.

Edirisinghe NM, Manamperi NH, Wanasinghe VS, Karunaweera N

11-08-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37571855/>

Alteration in the physiological state of the endoplasmic reticulum (ER) leads to the specific response known as unfolded protein response (UPR) or ER stress response. The UPR is driven by three sensor proteins, namely: Inositol-Requiring Enzyme 1, Protein Kinase RNA-like ER kinase and Activating Transcription Factor 6 to restore ER homeostasis. Pathogenic infection can initiate UPR activation; some pathogens can subvert the UPR to promote their survival and replication. Many intracellular pathogens, including *Leishmania*, can interact and hijack ER for their survival and replication, triggering ER stress and subsequently ER stress response. This review aims to provide a comprehensive overview of the ER stress response in infections with the *Leishmania* species.

Exploring Novel Drug Combinations: The Therapeutic Potential of Selanyl Derivatives for Leishmania Treatment.

Henriquez-Figueroa A, Moreno E, Sanmartin C, Plano D.

03-08-2023

Molecules.

<https://pubmed.ncbi.nlm.nih.gov/37570815/>

Anti-Candida and Anti-Leishmanial Activities of Encapsulated Cinnamomum verum Essential Oil in Chitosan Nanoparticles.

Essid R, Ayed A, Djebali K, Saad H, Srasra M, Othmani Y, Fares N, Jallouli S, Abid I, Alothman MR, Limam F, Tabbene O.

27-07-2023

Molecules.

<https://pubmed.ncbi.nlm.nih.gov/37570651/>

Detection of Leishmania spp. in Cats: Analysis of Nasal, Oral and Conjunctival Swabs by PCR and HRM.

Alves-Martin MF, Bertozzo TV, Aires IN, Manzini S, Paixão-Marques MDS, Guiraldi LM, Dos Santos WJ, Sánchez GP, Curci VCLM, Richini-Pereira VB, Lucheis SB.

31-07-2023

Animals (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37570277/>

A Tailored Approach to Leishmaniases Vaccination: Comparative Evaluation of the Efficacy and Cross-Protection Capacity of DNA vs. Peptide-Based Vaccines in a Murine Model.

Mas A, Hurtado-Morillas C, Martínez-Rodrigo A, Orden JA, de la Fuente R, Domínguez-Bernal G, Carrión J.

02-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37569710/>

Zoonotic leishmaniases are a worldwide public health problem for which the development of effective vaccines remains a challenge. A vaccine against leishmaniases must be safe and affordable and should induce cross-protection against the different disease-causing species. In this context, the DNA vaccine pHisAK70 has been demonstrated to induce, in a murine model, a resistant phenotype against *L. major*, *L. infantum*, and *L. amazonensis*. Moreover, a chimeric multiepitope peptide, HisDTC, has been obtained by in silico analysis from the histone proteins encoded in the DNA vaccine and has showed its ability to activate a potent CD4⁺ and CD8⁺ T-cell protective immune response in mice against *L. infantum* infection. In the present study, we evaluated the plasmid DNA vaccine pHisAK70 in comparison with the peptide HisDTC (with and without saponin) against *L. major* and *L. infantum* infection. Our preliminary results showed that both formulations were able to induce a potent cellular response leading to a decrease in parasite load against *L. infantum*. In addition, the DNA candidate was able to induce better lesion control in mice against *L. major*. These preliminary results indicate that both strategies are potentially effective candidates for leishmaniases control. Furthermore, it is important to carry out such comparative studies to elucidate which vaccine candidates are the most appropriate for further development.

Novel chemical scaffold as potential drug against Leishmania donovani:

Integrated computational and experimental approaches.

Ranjan P, Dubey VK.

11-08-2023

J Cell Biochem.

<https://pubmed.ncbi.nlm.nih.gov/37566640/>

Anti-Leishmania activity of the Mayan medicinal plant Thouinia paucidentata Radlk extracts.

Uc-Cachón AH, Chan-Bacab MJ, Lezama-Dávila CM, Isaac-Márquez AP, González-Sánchez AA, Dzúl-Beh AJ, Molina-Salinas GM.

11-08-2023

Nat Prod Res.

<https://pubmed.ncbi.nlm.nih.gov/37565472/>

Mexico's Yucatan Peninsula is an endemic area of cutaneous leishmaniasis, locally known as the chiclero's ulcer, and Mayan traditional medicine which refers to the use of *Thouinia paucidentata* Radlk, known as k'an chuunup. Aqueous and organic leaves extracts were evaluated against promastigotes and amastigotes of *Leishmania mexicana*. Toxicity tests of extracts were performed using Vero and J774A.1 macrophage cell lines. The composition of the most active extracts was analysed by GC-MS. The *n*-hexane and ethyl acetate extracts showed potent anti-*Leishmania* activity against the promastigote form, and remarkably, *n*-hexane extract exhibited potent activity against the amastigote form. Both extracts showed low toxicity on Vero both not on J774A.1 cells. Analysis of both bioactive extracts identified as more abundant compounds, germacrene D-4-ol and thunbergen in *n*-hexane, and thunbergol in ethyl acetate extracts. Our study presents *T. paucidentata* as anti-*Leishmania* phytochemistry supporting its medicinal use and contributes to the understanding of its phytochemical composition.

Oral immunization with heat-inactivated Mycobacterium bovis reduces local parasite dissemination and hepatic granuloma development in mice infected with Leishmania amazonensis.

Ferreras-Colino E, Moreno I, Gortázar C, Sevilla I, Agulló-Ros I, Domínguez L, Juste R, Rialde MA, Domínguez M.

Sept-2023

Res Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37517297/>

Aiming to explore whether oral immunization with heat-inactivated *Mycobacterium bovis* (HIMB) protects mice against Leishmania infection, 18 female BALB/c mice were randomly assigned to the immunized group, that received oral HIMB, or the control group, and were infected by inoculation of 10,000 *Leishmania amazonensis* promastigotes in the footpad. Spleen culture was positive in 55.55% of immunized mice and in 100% of control mice ($p = 0.082$). The number of immunolabeled amastigotes number in the popliteal lymph node was lower in the immunized group ($p = 0.009$). The immunized group presented fewer mature granulomas in the liver ($p =$

0.005) and more Lys + macrophages ($p = 0.002$) and fewer CD3+ T lymphocytes ($p < 0.001$) per hepatic granuloma. We conclude that immunization with HIMB via the oral route limited local parasite dissemination and hepatic granuloma development in mice challenged with *Leishmania amazonensis* through stimulation of macrophages, which is compatible with trained immunity.

Development of chimeric protein as a multivalent vaccine for human Kinetoplastid infections: Chagas disease and leishmaniasis.

Clímaco MC, de Figueiredo LA, Lucas RC, Pinheiro GRG, Dias Magalhães LM, Oliveira ALG, Almeida RM, Barbosa FS, Castanheira Bartholomeu D, Bueno LL, Mendes TA, Zhan B, Jones KM, Hotez P, Bottazzi ME, Oliveira FMS, Fujiwara RT.

23-08-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37479612/>

Dogs with canine visceral leishmaniasis have a boost of extracellular vesicles and miR-21-5p up-expression.

da Cruz AB, Carneiro FM, Maia MM, Pereira IS, Taniwaki NN, Namiyama GM, Gava R, Hiramoto RM, Pereira-Chioccia VL.

Sept-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37475490/>

Blood meal analysis and molecular detection of mammalian *Leishmania* DNA in wild-caught *Sergentomyia* spp. from Tunisia and Saudi Arabia.

Remadi L, Farjallah D, Chargui N, Belgacem S, Baba H, Zrieq R, Alzain MA, Babba H, Haouas N.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37449994/>

Phlebotomine sand flies (Diptera: Phlebotominae) belonging to the genus *Phlebotomus* are vectors of pathogens such as arboviruses, bacteria, and parasites (*Leishmania*). Species of the genus *Sergentomyia* (Se.) transmit *Sauroleishmania* (Reptile *Leishmania*) and feed on cold-blooded vertebrates; recently, they have been incriminated in mammalian *Leishmania* transmission. In addition, they have been reported to feed on warm-blooded vertebrates. This study aimed to (i) screen wild-caught *Sergentomyia* species for the detection of mammalian *Leishmania* and (ii) identify the blood meal origin of engorged females. The sand flies were collected using centers for disease control and prevention (CDC) traps, mounted and identified morphologically. Only females of the genus *Sergentomyia* were screened for *Leishmania* infection using PCR targeting the 18S ribosomal DNA locus. For positive specimens, *Leishmania* parasites were typed using nested PCR targeting ribosomal internal transcribed spacer 1 followed by digestion with *HaeIII*. The PCR-RFLP results were confirmed through sequencing. Blood meal identification was performed

through PCR amplification of the vertebrate cytochrome b gene using degenerate primers followed by sequencing. In total, 6026 sand fly specimens were collected between 2009 and 2018. Among these, 511 belonged to five species of *Sergentomyia* genus: *Se. minuta* (58.51%), *Se. fallax* (18.01%), *Se. clydei* (14.68%), *Se. dreyfussi* (6.26%), and *Se. antennata* (2.54%). A total of 256 female *Sergentomyia* sp. specimens were screened for *Leishmania* infection. Seventeen (17) were positive (6.64%). Two *Leishmania* species were identified. *Leishmania major* DNA was detected in five specimens; this included three *Se. fallax*, one *Se. minuta*, and one *Se. dreyfussi* collected from Tunisia. *Leishmania infantum*/*L. donovani* complex was detected in four *Se. minuta* and three *Se. dreyfussi* specimens collected from Tunisia. In addition, we identified the blood meal origin of five engorged *Se. minuta* specimens collected from Tunisia. Sequencing results revealed two blood sources: humans ($n = 4$) and reptiles ($n = 1$) indicating possible role of *Sergentomyia* species in the transmission of human *Leishmania*. In addition, these species could be involved in the life cycle of *L. infantum*/*L. donovani* complex and *L. major*. The results of the blood meal origin showed that *Sergentomyia* fed on both cold- and warm-blooded vertebrates. These findings enable a better understanding of the behavior of this sand fly genus. Further studies should focus on the role of *Sergentomyia* in human *Leishmania* transmission and possible control of this disease.

Same parasite, different outcomes: unraveling the epidemiology of *Leishmania infantum* infection in Brazil and Spain.

de Freitas Milagres T, López-de-Felipe M, da Silva WJ, Martín-Martín I, Gálvez R, da Silva OS.

Sept-2023

Trends Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37442747/>

Structure-Property Optimization of a Series of Imidazopyridines for Visceral Leishmaniasis.

Dichiara M, Simpson QJ, Quotadamo A, Jalani HB, Huang AX, Millard CC, Klug DM, Tse EG, Todd MH, Silva DG, da Silva Emery F, Carlson JE, Zheng SL, Vleminkx M, Matheeußen A, Caljon G, Pollastri MP, Sjö P, Perry B, Ferrins L.

11-08-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37417544/>

Leishmaniasis is a collection of diseases caused by more than 20 *Leishmania* parasite species that manifest as either visceral, cutaneous, or mucocutaneous leishmaniasis. Despite the significant mortality and morbidity associated with leishmaniasis, it remains a neglected tropical disease. Existing treatments have variable efficacy, significant toxicity, rising resistance, and limited oral bioavailability, which necessitates the development of novel and affordable therapeutics. Here, we report on the continued optimization of a series of imidazopyridines for visceral leishmaniasis and a scaffold

hop to a series of substituted 2-(pyridin-2-yl)-6,7-dihydro-5H-pyrrolo[1,2-a]imidazoles with improved absorption, distribution, metabolism, and elimination properties.

Accuracy of serological tests in diagnosing mucosal leishmaniasis.

Oliveira D, Lopes KF, de Avelar DM, Cota G, Oliveira E.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37391643/>

In this serum panel-based study, we evaluated the accuracy of serological tests originally developed for visceral leishmaniasis (VL), for diagnosis of mucosal leishmaniasis (ML). A total of five tests were evaluated, four of which are registered at the National Agency of Sanitary Surveillance (Agência Nacional de Vigilância Sanitária-ANVISA) (RIDASCREEN® Leishmania Ab from R-Biopharm AG., Leishmania ELISA IgG + IgM from Vircell S.L., IFI Leishmaniose Humana-BioManguinhos, and IT-LEISH® from Bio-Rad Laboratories, Inc.), and the other a direct agglutination test (DAT-LPC) prototype kit developed at Fiocruz. The panel was composed of 40 serum samples from patients with confirmed ML and 20 from patients with mucosal involvement and negative parasitological/molecular tests for leishmaniasis and confirmation of another etiology. All cases were treated from 2009 to 2016 in a referral center for leishmaniasis in Belo Horizonte, Minas Gerais, Brazil (Instituto René Rachou, Fiocruz). Diagnostic accuracy, based on the cut-off point for VL diagnosis, was 86.2% with RIDASCREEN® Leishmania Ab, 73.3% with Leishmania ELISA IgG + IgM, and 66.7% with IFI Leishmaniose Humana, while IT-LEISH® and DAT-LPC had the lowest accuracy (38.3%), despite high specificity (100% and 95%, respectively). New cut-off points defined with sera from ML patients improved accuracy from 86.2 to 89% ($p = 0.64$) and 73.3 to 88% ($p = 0.04$) for RIDASCREEN® Leishmania Ab and Leishmania ELISA IgG + IgM, respectively. Moreover, these tests presented greater sensitivity and immunoreactivity in patients with moderate/severe clinical ML forms. The data of this study suggest that ELISA assays can contribute to laboratory diagnosis, especially for patients with moderate or severe mucosal involvement.

IL-18 is required for the T_H1 -adaptation of T_{REG} cells and the selective suppression of T_H17 responses in acute and chronic infections.

Alvarez F, Istomine R, Da Silva Lira Filho A, Al-Aubodah TA, Huang D, Okde R, Olivier M, Fritz JH, Piccirillo CA.

Août-2023

Mucosal Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37182738/>

Transgenic overexpression of heat shock protein (HSP83) enhances protein kinase A activity, disrupts GP63 surface protease expression and alters promastigote morphology in *Leishmania amazonensis*.

Nation CS, Stephany-Brassesso I, Kelly BL, Pizarro JC.

Sept-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37150327/>

Synthesis, antileishmanial activity and molecular modeling of new 1-aryl/alkyl-3-benzoyl/cyclopropanoyl thiourea derivatives.

Mohammadi-Ghalehbin B, Shiran JA, Gholizadeh N, Razzaghi-Asl N.

Août-2023

Mol Divers.

<https://pubmed.ncbi.nlm.nih.gov/36001225/>

Lèpre

A user-centred implementation strategy for tuberculosis contact investigation in Uganda: protocol for a stepped-wedge, cluster-randomised trial.

Katamba A, Gupta AJ, Turimumahoro P, Ochom E, Ggita JM, Nakasendwa S, Nanziri L, Musinguzi J, Hennein R, Sekadde M, Hanrahan C, Byaruhanga R, Yoeli E, Turyahabwe S, Cattamanchi A, Dowdy DW, Haberer JE, Armstrong-Hough M, Kiwanuka N, Davis JL.

17-08-2023

BMC Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37592314/>

Background: Tuberculosis (TB) is among the leading causes of infectious death worldwide. Contact investigation is an evidence-based, World Health Organisation-endorsed intervention for timely TB diagnosis, treatment, and prevention but has not been widely and effectively implemented. **Methods:** We are conducting a stepped-wedge, cluster-randomised, hybrid Type III implementation-effectiveness trial comparing a user-centred to a standard strategy for implementing TB contact investigation in 12 healthcare facilities in Uganda. The user-centred strategy consists of several client-focused components including (1) a TB-education booklet, (2) a contact-identification algorithm, (3) an instructional sputum-collection video, and (4) a community-health-rider service to transport clients, CHWs, and sputum samples, along with several healthcare-worker-focused components, including (1) collaborative improvement meetings, (2) regular audit-and-feedback reports, and (3) a digital group-chat application designed to develop a community of practice. Sites will cross-over from the standard to the user-centred strategy in six, eight-week transition steps following a randomly determined site-pairing scheme and timeline. The primary implementation outcome is the proportion of symptomatic close contacts completing TB evaluation within 60 days of TB treatment initiation by the index person with TB. The primary clinical effectiveness outcomes are the proportion of contacts diagnosed with and initiating active TB disease treatment and the proportion initiating TB preventative therapy within 60 days. We will assess outcomes from routine source documents using intention-to-treat analyses. We will also conduct nested mixed-methods studies of implementation fidelity and context and perform cost-

effectiveness and impact modelling. The Makerere School of Public Health IRB(#554), the Uganda National Council for Science and Technology(#HS1720ES), and the Yale Institutional Review Board(#2000023199) approved the study and waived informed consent for the main trial implementation-effectiveness outcomes. We will submit results for publication in peer-reviewed journals and disseminate findings to local policymakers and representatives of affected communities. **Discussion:** This pragmatic, quasi-experimental implementation trial will inform efforts to find and prevent undiagnosed persons with TB in high-burden settings using contact investigation. It will also help assess the suitability of human-centred design and communities of practice for tailoring implementation strategies and sustaining evidence-based interventions in low-and-middle-income countries.

Erythema ab igne: a cutaneous marker of prolonged thermal exposure.

Chandra A, Sil A, Das S, Chakraborty U.

17-08-2023

BMJ Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37591625/>

Evaluation of Xpert MTB/XDR test for susceptibility testing of Mycobacterium tuberculosis to first and second-line drugs in Uganda.

Katamba A, Ssengooba W, Sserubiri J, Semugenze D, Kasule GW, Nyombi A, Byaruhanga R, Turyahabwe S, Joloba ML.

17-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37590288/>

Background: Drug-Resistant Tuberculosis (DR-TB) is one of the major challenges to TB control.

Design and methods: This was a blinded, laboratory-based cross-sectional study using sputum samples or culture isolates. Samples were from patients with rifampicin-resistant-TB and/or with high risk for isoniazid (INH) resistance and/or 2nd line fluoroquinolones (FQ) and injectable agents (IAs). The diagnostic accuracy of the Xpert® MTB/XDR test was compared to MGIT960 and the Hain Genotype® MTBDRplus and MDRsl assays (LPA) as reference DST methods. Factors for laboratory uptake of the Xpert® MTB/XDR test were also evaluated. **Results:** Of the 100 stored sputum samples included in this study, 65/99 (65.6%) were resistant to INH, 5/100 (5.0%) were resistant to FQ and none were resistant to IAs using MGIT960. The sensitivity and specificity, n (%; 95% Confidence Interval, CI) of Xpert® MTB/XDR test for; INH was 58 (89.2; 79.1-95.5) and 30 (88.2; 72.5-96.6) and for FQ; 4 (80.0; 28.3-99.4) and 95 (100; 96.2-100), respectively. Using LPA as a reference standard, a total of 52/98 (53.1%) were resistant to INH, 3/100 (3.0%) to FQ, and none to IA. The sensitivity and specificity, n (%; 95%CI) of Xpert® MTB/XDR test compared to LPA for; INH was 50 (96.1; 86.7-99.5) and 34 (74.0; 58.8-85.7) for FQ 3 (100; 29.2-100) and 96 (99.0; 94.3-99.9) respectively. The factors for laboratory uptake and roll-out of the Xpert®

MTB/XDR test included: no training needed for technicians with, and one day for those without, previous Xpert-ultra experience, recording and reporting needs were not different from those of Xpert-ultra, the error rate was 4/100 (4%), one (1%) indeterminate rate and test turn-around-time were 1hr/45 minutes. **Conclusion:** There is high sensitivity and specificity of Xpert® MTB/XDR test for isoniazid and fluoroquinolones. There are acceptable Xpert® MTB/XDR test attributes for the test uptake and roll-out.

Immune dysregulation and inflammation causing hypopigmentation in post kala-azar dermal leishmaniasis: partners in crime?

Sengupta R, Roy M, Dey NS, Kaye PM, Chatterjee M.

15-08-2023

Trends Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37586987/>

Post kala-azar dermal leishmaniasis (PKDL), a heterogeneous dermal sequela of visceral leishmaniasis (VL), is challenging in terms of its etiopathogenesis. Hypopigmentation is a consistent clinical feature in PKDL, but mechanisms contributing to the loss of melanocytes remains poorly defined. Like other hypopigmentary dermatoses - for example, vitiligo, psoriasis, and leprosy - the destruction of melanocytes is likely a multifactorial phenomenon, key players being immune dysregulation and inflammation. This review focuses on immunological mechanisms responsible for the 'murder' of melanocytes, prime suspects at the lesional sites being CD8⁺ T cells and keratinocytes and their criminal tools being proinflammatory cytokines, for example, IFN- γ , IL-6, and TNF- α . Collectively, these may cause decreased secretion of melanocyte growth factors, loss/attenuation of cell adhesion molecules and inflammasome activation, culminating in melanocyte death.

Rifapentine in Household Contacts of Patients with Leprosy. Reply.

Wang L, Xiong J, Wang H.

17-08-2023

N Engl J Med.

<https://pubmed.ncbi.nlm.nih.gov/37585642/>

Rifapentine in Household Contacts of Patients with Leprosy.

Yotsu RR, Bedimo R.

17-08-2023

N Engl J Med.

<https://pubmed.ncbi.nlm.nih.gov/37585641/>

Mounting Evidence Suggests Leprosy Is Endemic in Florida.

Harris E.

16-08-2023

JAMA.

<https://pubmed.ncbi.nlm.nih.gov/37585214/>

Cultural adaption and validation of the Explanatory Model Interview Catalogue-Community Stigma Scale in the assessment of public stigma related to schistosomiasis in lakeshore areas of Mwanza region, Tanzania.

Klinker L, Boeckler A, Kreibich S, Mazigo H.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578967/>

Background: Previous qualitative studies on attitudes towards schistosomiasis demonstrated inconclusive results on the extent of stigma towards schistosomiasis in endemic communities around the world. The Explanatory Model Interview Catalogue-Community Stigma Scale (EMIC-CSS) has been used and validated for the assessment of public stigma across numerous countries in various health conditions. This study tested the performance of the scale in the context of stigma related to schistosomiasis in twelve communities in the three districts of Magu, Nyamagana and Illemela in Mwanza region, Tanzania. **Methodology/principal findings:** The 15-item-version of the EMC-CSS was first translated to Kiswahili language. The translation was discussed within the research team to retain the meaning of the items and implement cultural adaptations. Validation of the adapted EMIC-CSS scale was conducted following the framework of Herdman and Fox- Rushby. A pilot study with 41 participants from two communities provided the basis for testing the performance of each item and assessing the semantic and operational equivalence of the scales. In addition, eight qualitative focus group discussions (FGDs) were conducted to evaluate the conceptional equivalence of the EMIC-CSS. Finally, the performance of the adjusted scale was tested on 200 participants with a 50:50 male-female ratio from ten communities. The mean score of the EMIC-CSS $M = 8.35$ ($SD = 6.63$) shows clear indications for public stigma towards schistosomiasis. The EMIC-CSS demonstrated a good internal consistency with Cronbach's alpha $\alpha = .857$ and no floor and ceiling effects.

Conclusion/significance: The results demonstrate that the EMIC-CSS is a useful instrument in assessing public stigma towards schistosomiasis and allow a clear recommendation of the EMIC-CSS for schistosomiasis in the Tanzanian culture. However, future studies are additionally recommended to address specific aspects and forms of the disease and how they contribute to the development of stigma towards schistosomiasis.

Deep learning for AI-based diagnosis of skin-related neglected tropical diseases: A pilot study.

Yotsu RR, Ding Z, Hamm J, Blanton RE.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578966/>

Non-healing trophic ulcer in leprosy: a case of failure at all levels of prevention.

Reddy H, Joshi A.

22-05-2023

Pan Afr Med J.

<https://pubmed.ncbi.nlm.nih.gov/37575517/>

Slit-skin smear in post kala-azar dermal leishmaniasis and leprosy: How a negative report for Leishman-Donovan bodies in Giemsa stain may indicate leprosy.

Chatterjee K, Yadav VS, Ramesh V.

27-06-2023

JAAD Int.

<https://pubmed.ncbi.nlm.nih.gov/37575515/>

My journey in the last mile of elimination of leprosy among the Penan community.

Utap MS.

28-07-2023

Malays Fam Physician.

<https://pubmed.ncbi.nlm.nih.gov/37575357/>

Recurrent choriocarcinoma complicated with leprosy during chemotherapy: A case report and literature review.

Hu S, Lin X, Yin R, Wang W, Li Q.

11-08-2023

Medicine (Baltimore).

<https://pubmed.ncbi.nlm.nih.gov/37565881/>

Rationale: The global prevalence of leprosy has decreased substantially, and cases of leprosy infection are extremely rare in China. In this report, we present a case of recurrent choriocarcinoma complicated by leprosy infection during chemotherapy. **Patient concerns:** A 24-year-old Chinese woman (gravida 3, para 2) presented to a local hospital with vaginal bleeding. Her medical history included a previous diagnosis of hydatidiform mole. **Diagnoses, interventions and outcomes:** The patient was diagnosed with choriocarcinoma and received chemotherapy in 6 cycles. Shortly after the initial treatment was completed, the disease recurred twice with resistance to multiple chemotherapeutic agents. In her second recurrence of choriocarcinoma, she was diagnosed with leprosy with many cutaneous nodules throughout her entire body. The patient was administered chemical treatment for leprosy with the multidrug therapy regimen after being diagnosed. To prevent exacerbating the infection, no immunotherapy was utilized to treat cancer, and the infection was well-controlled at the conclusion of anticancer therapy. **Lessons:** Because of immunological reduction, cancer patients are susceptible to a variety of infections. For patients with cancer, prevention and early detection of rare infectious diseases should receive special attention. Immunotherapy must be used with caution when treating patients with cancer and infections.

Analysis of misdiagnosed or delayed-diagnosed Leprosy bacillus infection from 1990 to 2020 with a prophet time

series prediction in Hubei Province, China.

Chen L, Zheng W, Dong X, Zheng Y, Shi W, Zhang W.

11-08-2023

Medicine (Baltimore).

<https://pubmed.ncbi.nlm.nih.gov/37565877/>

Elimination of tuberculosis requires prior control of silicosis including sub-radiological silicosis.

Singh D, Sarkar B, Sarkar K.

Jul-2023

Indian J Tuberc.

<https://pubmed.ncbi.nlm.nih.gov/37562900/>

India is committed to the elimination of tuberculosis by 2025. But its achievement appears to be difficult as India has a huge burden of silicosis as well as sub-radiological silicosis, which was never given its required attention. Silicotic subjects are highly vulnerable to pulmonary tuberculosis due to the progressive decline of lung immunity. A study among vulnerable glass factory workers in Firozabad, Uttar Pradesh, revealed that silicotic workers were 7.5 times more at risk of pulmonary tuberculosis compared to non-silicotic subjects. Since India has a huge burden of silicosis and sub-radiological silicosis, the elimination of tuberculosis needs prior attention on silicosis. This article may be viewed as an eye-opener for understanding the necessity of dual control of both silicosis as well as tuberculosis by integrating both together.

COVID-19 vaccination and leprosy-A UK hospital-based retrospective cohort study.

de Barros B, Pierce R, Sprenger C, Ong ELH, Walker SL.

04-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37540711/>

Background: Individuals with leprosy are at risk of leprosy reactions, T-cell mediated immunological complications, which lead to nerve function impairment. Leprosy reactions require systemic immunosuppression which is a risk factor for severe COVID-19. Vaccination for SARS-CoV-2 infection is recommended in the UK and became widely available in 2021 with individuals at increased risk of severe disease, including the immunosuppressed, prioritised. Vaccines for SARS-CoV-2 may provoke a T cell response. The latter poses a theoretical risk of provoking an immunological response to latent *Mycobacterium leprae* infection leading to clinical disease or in those with clinical disease triggering a leprosy reaction. BCG vaccination is associated with the development of leprosy in a small proportion of healthy contacts of people with leprosy within twelve weeks of administration. BCG causes a Th1 immune response. **Methodology/principal findings:** We performed a retrospective cohort study to determine the SARS-CoV-2 vaccination status of individuals diagnosed with leprosy attending the Leprosy Clinic in 2021 and whether any had developed leprosy or experienced a new leprosy reaction within twelve weeks

of receiving a dose of a SARS-CoV-2 vaccine. The electronic patient records were used to retrieve data. Fifty-two individuals with leprosy attended the clinic in 2021 of which five people were newly diagnosed with leprosy. Thirty-seven (71%) were male and the median age was 48.5 years old (Range 27-85 years). Eight (15.4%) individuals were taking multi-drug therapy (MDT) and eight (15.4%) had completed MDT within three years of the study. Twenty-two (41.5%) individuals were prescribed a systemic immunosuppressant drug during 2021. Ten (18.9%) individuals have one or more risk factors for severe COVID-19. The SARS-CoV-2 vaccination status of fifty (96%) were recorded of which forty-nine were vaccinated (98%). One individual had declined vaccination. One individual was diagnosed with borderline tuberculoid (BT) leprosy having developed red skin lesions with reduced sensation (which increased in size and number) and thickened peripheral nerves one week after a second dose of BNT162b2 vaccine. Another individual who had completed MDT more than three years earlier developed red plaques and tender thickened nerves consistent with a leprosy Type 1 reaction eight weeks after a single dose of BNT162b2 vaccine (having received two doses of CoronaVac vaccine three months earlier). **Conclusions/significance:** The development of BT leprosy and a Type 1 reaction in another individual shortly after a dose of BNT162b2 vaccine may be associated with vaccine mediated T cell responses. The benefits of vaccination to reduce the risk of severe COVID-19 outweigh these unwanted events but data from leprosy endemic countries may provide further information about potential adverse effects of augmented T cell responses in individuals with leprosy or latent *M. leprae* infection.

Polyunsaturated Fatty Acid-Derived Lipid Mediators as Potential Biomarkers for Leprosy Among Individuals with Asymptomatic *Mycobacterium leprae* Infection.

Silva CAM, Graham BG, Webb K, Islam MN, Harton M, de Mello Marques MA, Marques de Carvalho F, Pinheiro RO, Spencer J, Sarno EN, Batista Pereira GM, Vidal Pessolani MC, Santos de Macedo C, Belisle JT.

11-08-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37428112/>

Morsures de serpent

First report of envenomation symptoms caused by the Eastern Montpellier snake, *Malpolon insignitus* (St.-Hilaire, 1827).

Dibiasi W, Lüddecke T.

15-08-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37591328/>

Snakebite is a global health problem with disastrous consequences. Accordingly, venoms plus their function and clinical aspects were intensively studied for several snakes, primarily with proteroglyphous and solenoglyphous dentition. Much less is known about the

venoms from most opisthoglyphous (rear-fanged) snakes and it is often questionable which symptoms they may cause. Here, we provide the first description of the envenomation symptoms caused by a bite of the Eastern Montpellier snake *Malpolon insignitus* from Croatia. The clinical manifestations elicited by the bite were only local, and included bleeding, pulsatility and paresthesia, followed by sweating and signs of inflammation. The observed features subsided quickly, and the patient recovered fully with no long-term illness. Therefore, we conclude that *M. insignitus* does not represent a substantial (i.e. life threatening or morbidity-causing) threat. However, as related species in the *Malpolon* genus are known to be capable to deliver neurotoxic envenoming, we recommend to nevertheless carefully interact with *M. insignitus* and recommend that future studies should unveil its venom composition.

Comparing cost of F(ab')₂AV vs FabAV in the treatment of copperhead envenomation-One center's experience.

Hack JB, Brewer KL, Meggs WJ.

08-08-2023

Am J Emerg Med.

<https://pubmed.ncbi.nlm.nih.gov/37573662/>

The definitive treatment of North American crotalid snakebites is antivenin. In 2000, an FabAV antivenom (CroFab®) was introduced and in 2022, F(ab')₂AV (Anavip®) was approved for treatment of copperhead bites. Our center that sees primarily copperhead snake bites added the recently approved treatment as a second option for the 2022 snake bite season. This brief report we describe our initial experience with the two antivenins via retrospective chart review: the cost, charge, laboratory differences, response to therapy, complications and duration of hospitalization of admitted patients with copperhead envenomation. Using three independent reviewers in this IRB exempt report we found 31 patients with copperhead bites (7 exclusions) leaving 19 adults and 7 children for analysis. We found there was no difference in age, sex, presence of lab abnormalities, total vials administered, or length of stay. There was significant differences in hospital costs and charges to the patient. Future research should include multi-center experiences comparing the two antivenins.

Structural capacity and continuum of snakebite care in the primary health care system in India: a cross-sectional assessment.

Bhaumik S, Norton R, Jagnoor J.

11-08-2023

BMC Prim Care.

<https://pubmed.ncbi.nlm.nih.gov/37563556/>

Non-standard nature. Venoms, serum and serpentariums in the uneven fabrication of global health.

Quet M.

Sept-2023

Soc Sci Med.

<https://pubmed.ncbi.nlm.nih.gov/37499481/>

Bothrops asper bite and post-traumatic stress disorder in Costa Rica: Report of two cases.

Millán-González R, Monge-Morales LF, De La Cruz-Villalobos N, Bonilla-Murillo F, Gutiérrez JM.

01-08-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37328114/>

Snakebite envenoming (SBE) is a public health problem of high impact worldwide. The psychiatric consequences of SBE have been poorly documented. Here we present in detail the phenomenology of two clinical cases of *Bothrops asper* snakebite post-traumatic stress disorder (SBPTSD) in Costa Rica. We suggest that there is a characteristic presentation of SBPTSD and hypothesize that main contributors to the development of this disorder are: the systemic inflammatory response, the repetition of events that put the patient's life at risk and the human innate fear of snakes. Protocols for the prevention, detection and treatment of PTSD in patients who suffer a SBE should be implemented, with at least one mental health care consultation during hospitalization and a 3-5 months follow-up after the discharge.

Identifying the geographic distribution pattern of venomous snakes and regions of high snakebite risk in Iran.

Kazemi SM, Hosseinzadeh MS, Weinstein SA.

01-08-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37321410/>

Epidemiology and clinical features of *Hypnale nepa* (hump-nosed pit viper) envenoming in Sri Lanka.

Rathnayaka RMMKN, Nishanthi Ranathunga PEA, Kularatne SAM.

01-08-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37321409/>

Production and evaluation of monovalent anti-snake immunoglobulins from chicken egg yolk using Ghanaian puff adder (*Bitis arietans*) Venom: Isolation, purification, and neutralization efficacy.

Gyawu VB, Firempong CK, Hamidu JA, Tetteh AY, Ti-Baliana Martha NJ, Yingshu F, Yi Z.

01-08-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37290727/>

Mycétome

First report on mycetoma in Turkana County-North-western Kenya.

Colom MF, Ferrer C, Ekai JL, Ferrández D, Ramírez L, Gómez-Sánchez N, Leting S, Hernández C.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578968/>

Mycetoma is one of the six Neglected Tropical Diseases that are prevalent in Turkana County (northwest Kenya). The aim of the study was to estimate the prevalence of mycetoma in the county, as well as to describe the main causative agents involved in the disease using methods affordable locally. Based on the data collected by the team of cooperative medicine Cirugia en Turkana (Surgery in Turkana), a specific study for mycetoma was started during the 16th humanitarian medicine campaign in February 2019. Patients with suspected mycetoma were studied at the Lodwar County Referral Hospital (LCRH). After informing the patient and getting their consent, the lesions were examined and sampled (mainly by biopsy) and clinical data were recorded. Samples were washed in sterile saline solution and cut in fragments. Some of these were inoculated on Sabouraud Dextrose Agar, Malt Extract Agar, and diluted Nutrient Agar plates. One fragment of each sample was used for DNA extraction. The DNA and the rest of the fragments of samples were kept at -20°C. All cultures were incubated at room temperature at the LCRH laboratory. The DNA obtained from clinical samples was submitted to PCR amplification of the ITS-5.8S and the V4-V5 16S rRNA gene region, for the detection and identification of fungi and bacteria respectively. From February 2019 till February 2022, 60 patients were studied. Most of them were men (43, 74,1%) between 13 and 78 y.o. (mean age 37). Half of the patients were herdsman but, among women 40% (6) were housewives and 26.7% (4) charcoal burners. Lesions were mainly located at the feet (87.9%) and most of the patients (54; 93.1%) reported discharge of grains in the exudate, being 27 (46.6%) yellow or pale colored and 19 (32.8%) of them dark grains. Culture of clinical samples yielded 35 fungal and bacterial putative causative agents. Culture and molecular methods allowed the identification of a total of 21 causative agents of mycetoma (39.6% of cases studied). Most of them (17) corresponded to fungi causing eumycetoma (80.9%) being the most prevalent the genus *Madurella* (7; 41.2%), with two species involved (*M. mycetomatis* and *M. fahalii*), followed by *Aspergillus* (2; 11.8%). Other minority genera detected were *Cladosporium*, *Fusarium*, *Acremonium*, *Penicillium*, and *Trichophyton* (5.9% each of them). Actinobacteria were detected in 19.1% of samples, but only *Streptomyces somaliensis* was identified as a known agent of mycetoma, the rest being actinobacteria not previously described as causative agents of the disease, such as *Cellulosimicrobium cellulans* detected in two of the patients. Although Kenya is geographically located in the mycetoma belt, to our knowledge this is the first report on mycetoma in this country from 1973, and the first one for Turkana County.

Deep learning for AI-based diagnosis of skin-related neglected tropical diseases: A pilot study.

Yotsu RR, Ding Z, Hamm J, Blanton RE.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578966/>

Background: Deep learning, which is a part of a broader concept of artificial intelligence (AI) and/or machine learning has achieved remarkable success in vision tasks. While there is growing interest in the use of this technology in diagnostic support for skin-related neglected tropical diseases (skin NTDs), there have been limited studies in this area and fewer focused on dark skin. In this study, we aimed to develop deep learning based AI models with clinical images we collected for five skin NTDs, namely, Buruli ulcer, leprosy, mycetoma, scabies, and yaws, to understand how diagnostic accuracy can or cannot be improved using different models and training patterns. **Methodology:** This study used photographs collected prospectively in Côte d'Ivoire and Ghana through our ongoing studies with use of digital health tools for clinical data documentation and for tele dermatology. Our dataset included a total of 1,709 images from 506 patients. Two convolutional neural networks, ResNet-50 and VGG-16 models were adopted to examine the performance of different deep learning architectures and validate their feasibility in diagnosis of the targeted skin NTDs. **Principal findings:** The two models were able to correctly predict over 70% of the diagnoses, and there was a consistent performance improvement with more training samples. The ResNet-50 model performed better than the VGG-16 model. A model trained with PCR confirmed cases of Buruli ulcer yielded 1-3% increase in prediction accuracy across all diseases, except, for mycetoma, over a model which training sets included unconfirmed cases. **Conclusions:** Our approach was to have the deep learning model distinguish between multiple pathologies simultaneously-which is close to real-world practice. The more images used for training, the more accurate the diagnosis became. The percentages of correct diagnosis increased with PCR-positive cases of Buruli ulcer. This demonstrated that it may be better to input images from the more accurately diagnosed cases in the training models also for achieving better accuracy in the generated AI models. However, the increase was marginal which may be an indication that the accuracy of clinical diagnosis alone is reliable to an extent for Buruli ulcer. Diagnostic tests also have their flaws, and they are not always reliable. One hope for AI is that it will objectively resolve this gap between diagnostic tests and clinical diagnoses with the addition of another tool. While there are still challenges to be overcome, there is a potential for AI to address the unmet needs where access to medical care is limited, like for those affected by skin NTDs.

Onchocercose

The onchocerciasis hypothesis of nodding syndrome.

Colebunders R, Hadermann A, Siewe Fodjo JN.

17-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37590176/>

Prevalence of epilepsy in the onchocerciasis endemic middle belt of Ghana after 27 years of mass drug administration with ivermectin.

Otabil KB, Ankras B, Bart-Plange EJ, Donkoh ES, Avarikame FA, Ofori-Appiah FO, Babae TN, Kudzordzi PC, Darko VA, Ameyaw J, Bamfo JG, Sakibu RA, Antwi-Berko D, Fodjo JNS, Basáñez MG, Schallig HDFH, Colebunders R.

17-08-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/37587500/>

Epilepsy and nodding syndrome in association with an *Onchocerca volvulus* infection drive distinct immune profile patterns.

Arndts K, Kegele J, Massarani AS, Ritter M, Wagner T, Pfarr K, Lämmer C, Dörmann P, Peisker H, Menche D, Al-Bahra M, Prazeres da Costa C, Schmutzhard E, Matuja W, Hoerauf A, Layland-Heni LE, Winkler AS.

03-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37535695/>

Previous studies have described the association of onchocerciasis (caused by *Onchocerca volvulus*) with epilepsy, including nodding syndrome, although a clear etiological link is still missing. Cases are found in different African countries (Tanzania, South Sudan, Uganda, Democratic Republic of the Congo, Central African Republic and Cameroon). In our study we investigated immunological parameters (cytokine, chemokine, immunoglobulin levels) in individuals from the Mahenge area, Tanzania, presenting with either epilepsy or nodding syndrome with or without *O. volvulus* infection and compared them to *O. volvulus* negative individuals from the same endemic area lacking neurological disorders. Additionally, cell differentiation was performed using blood smears and systemic levels of neurodegeneration markers, leiomodin-1 and N-acetyltyramine-O, β -glucuronide (NATOG) were determined. Our findings revealed that cytokines, most chemokines and neurodegeneration markers were comparable between both groups presenting with epilepsy or nodding syndrome. However, we observed elevated eosinophil percentages within the *O. volvulus* positive epilepsy/nodding syndrome patients accompanied with increased eosinophilic cationic protein (ECP) and antigen-specific IgG levels in comparison to those without an *O. volvulus* infection. Furthermore, highest levels of NATOG were found in *O. volvulus* positive nodding syndrome patients. These findings highlight that the detection of distinct biomarkers might be useful for a differential diagnosis of epilepsy and nodding syndrome in *O. volvulus* endemic areas. Trial-registration: NCT03653975.

Pian

Deep learning for AI-based diagnosis of skin-related neglected tropical diseases: A pilot study.

Yotsu RR, Ding Z, Hamm J, Blanton RE.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578966/>

Rage

Self-immolative nanocapsules precisely regulate depressive neuronal microenvironment for synergistic antidepressant therapy.

Liu Z, Chen B, Xiang S, Hu S.

17-08-2023

J Nanobiotechnology.

<https://pubmed.ncbi.nlm.nih.gov/37592281/>

Background: Pharmacotherapy constitutes the first-line treatment for depression. However, its clinical use is hindered by several limitations, such as time lag, side effects, and narrow therapeutic windows. Nanotechnology can be employed to shorten the onset time by ensuring permeation across the blood brain barrier (BBB) to precisely deliver more therapeutic agents; unfortunately, formidable challenges owing to the intrinsic shortcomings of commercial drugs remain. **Results:** Based on the extraordinary capability of monoamines to regulate the neuronal environment, we engineer a network nanocapsule for delivering serotonin (5-hydroxytryptamine, 5-HT) and catalase (CAT) to the brain parenchyma for synergistic antidepressant therapy. The nanoantidepressants are fabricated by the formation of 5-HT polymerization and simultaneous payload CAT, following by surface modifications using human serum albumin and rabies virus glycoprotein. The virus-inspired nanocapsules benefit from the surface-modifying strategies and exhibit pronounced BBB penetration. Once nanocapsules reach the brain parenchyma, the mildly acidic conditions trigger the release of 5-HT from the sacrificial nanocapsule. Releasing 5-HT further positively regulate moods, relieving depressive symptoms. Meanwhile, cargo CAT alleviates neuroinflammation and enhances therapeutic efficacy of 5-HT. **Conclusion:** Altogether, the results offer detailed information encouraging the rational designing of nanoantidepressants and highlighting the potential of nanotechnology in mental health disorder therapies.

Development of a novel bispecific antibody GR1801 for rabies.

Long C, Wang W, Hao X, Yu C, Feng Y, Tu C, Sun S, Bian L, Liu Z, Wang L.

August-2023

J Med Virol.

<https://pubmed.ncbi.nlm.nih.gov/37587669/>

Engram stability and maturation during systems consolidation.

Refaeli R, Kreisel T, Groysman M, Adamsky A, Goshen I.

10-08-2023

Curr Biol.

<https://pubmed.ncbi.nlm.nih.gov/37586373/>

Identification of 3, 4-dihydroxy complexes as potential antiviral via DFT, molecular docking, molecular dynamics and MM/PBSA against rabies and dengue receptors.

Sinha P, Yadav AK.

14-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37580968/>

The occurrence and extent of anxiety and distress among Dutch travellers after encountering an animal associated injury.

Warmerdam AMT, Luppino FS, Visser LG.

15-08-2023

Trop Dis Travel Med Vaccines.

<https://pubmed.ncbi.nlm.nih.gov/37580813/>

Background: Prompt administration of post-exposure prophylaxis (PEP) is crucial to prevent a fatal rabies infection after an animal associated injury (AAI), preferably within 24 h. PEP, especially in case of a type III injury for which rabies immune globulin (RIG) is needed, is difficult to obtain abroad. This, along with the fear of potentially having contracted a lethal disease, might be an important source for anxiety and distress. We investigated the occurrence and extent of self-reported anxiety and distress at different timepoints among Dutch travellers after encountering an AAI, and the involved factors.

Methods: A retrospective quantitative observational study was conducted including insured Dutch travellers who actively contacted Eurocross Assistance after encountering an AAI abroad. An online questionnaire was designed to measure anxiety and distress levels, using the HADS (Hospital Anxiety and Depression Scale) and distress thermometer at three time points: departure from home (T1), post-AAI (T2), and treatment administration (T3). Statistical analyses included T-tests, Chi-square tests, and ANCOVA analyses. **Results:** We showed a significant increase in mean anxiety and distress scores at T2, and a significant decrease at T3. Women were more often anxious and distressed. Between T1 and T2, PrEP, and being aware of the risks were positively associated with anxiety levels, and PrEP and WHO region Africa with distress levels. Between T2 and T3, anxiety levels remained higher for monkey-induced injury, thoracic injuries, and WHO region Southeast Asia. PEP-delay between 24-48 h resulted in decreased distress levels at this time period, while type II injury elevated distress levels. **Conclusions:** This study showed significant anxiety and distress levels after an AAI among the vast majority of travellers, which is detrimental to their health-related quality of life (HR-QOL). This highlights the importance of proper pre-travel information. In the context of rabies prevention, these

results suggest that pre-travel advice and policy makers should also take aspects of HR-QOL into consideration.

Demographic, environmental and physiological predictors of gastrointestinal parasites in urban raccoons.

Wait LF, Johnson SR, Nelson KM, Chipman RB, Pogmore FE, Dobson AP, Graham AL.

27-04-2023

Int J Parasitol Parasites Wildl.

<https://pubmed.ncbi.nlm.nih.gov/37575663/>

Epidemiological pattern and management of dog bite injuries in Karachi, Pakistan: A cross-sectional study.

Khan UR, Soomar SM, Ghazi SM, Naeem R, Kerai S, Jamali S.

August-2023

Injury.

<https://pubmed.ncbi.nlm.nih.gov/37573070/>

Superior antibody immunogenicity of a viral-vectored RH5 blood-stage malaria vaccine in Tanzanian infants as compared to adults.

Silk SE, Kalinga WF, Mtaka IM, Lililime NS, Mpina M, Milando F, Ahmed S, Diouf A, Mkwepu F, Simon B, Athumani T, Rashid M, Mohammed L, Lweno O, Ali AM, Nyaulingo G, Mwalimu B, Mswata S, Mwamlima TG, Barrett JR, Wang LT, Themistocleous Y, King LDW, Hodgson SH, Payne RO, Nielsen CM, Lawrie AM, Nugent FL, Cho JS, Long CA, Miura K, Draper SJ, Minassian AM, Olotu AI.

07-08-2023

Med.

<https://pubmed.ncbi.nlm.nih.gov/37572659/>

Background: RH5 is a leading blood-stage candidate antigen for a *Plasmodium falciparum* vaccine; however, its safety and immunogenicity in malaria-endemic populations are unknown. **Methods:** A phase 1b, single-center, dose-escalation, age-de-escalation, double-blind, randomized, controlled trial was conducted in Bagamoyo, Tanzania ([NCT03435874](https://clinicaltrials.gov/ct2/show/study/NCT03435874)). Between 12th April and 25th October 2018, 63 healthy adults (18-35 years), young children (1-6 years), and infants (6-11 months) received a priming dose of viral-vectored ChAd63 RH5 or rabies control vaccine. Sixty participants were boosted with modified vaccinia virus Ankara (MVA) RH5 or rabies control vaccine 8 weeks later and completed 6 months of follow-up post priming. Primary outcomes were the number of solicited and unsolicited adverse events post vaccination and the number of serious adverse events over the study period. Secondary outcomes included measures of the anti-RH5 immune response. **Findings:** Vaccinations were well tolerated, with profiles comparable across groups. No serious adverse events were reported. Vaccination induced RH5-specific cellular and humoral responses. Higher anti-RH5 serum immunoglobulin G (IgG) responses were observed post

boost in young children and infants compared to adults. Vaccine-induced antibodies showed growth inhibition activity (GIA) in vitro against *P. falciparum* blood-stage parasites; their highest levels were observed in infants.

Conclusions: The ChAd63-MVA RH5 vaccine shows acceptable safety and reactogenicity and encouraging immunogenicity in children and infants residing in a malaria-endemic area. The levels of functional GIA observed in RH5-vaccinated infants are the highest reported to date following human vaccination. These data support onward clinical development of RH5-based blood-stage vaccines to protect against clinical malaria in young African infants. **Funding:** Medical Research Council, London, UK.

Epidemiologic Aspects of Animal Bite, Rabies, and Predictors of Delay in Post-exposure Prophylaxis: A National Registry-based Study in Iran.

Khazaei S, Shirzadi MR, Amiri B, Pourmozafari J, Ayubi E. Juin-2023

J Res Health Sci.

<https://pubmed.ncbi.nlm.nih.gov/37571954/>

Background: The increasing trend in animal bites and rabies in recent years makes the disease a public health concern in Iran. The objectives of the current study were to investigate the epidemiologic aspects of the animal bite and determine the associated risk factors of the delay in initiation of post-exposure prophylaxis (PEP) against rabies in Iran. **Study design:** National registry-based cross-sectional study. **Methods:** This study included all registered cases of animal bites between March 2021 and March 2022 at the Ministry of Health and Medical Education in Iran. We retrieved epidemiologic data on person, time, place, and PEP outcome. **Results:** A total of 260470 animal bite cases (approximately 334 per 100000 populations, and 11 deaths) were registered during the study period. About 77.2% of them were reported in males, 4.3% in children aged less than 5 years, 56.4% occurred in urban areas, 98% in domestic animals, and mostly in north and northeast areas of Iran. Additionally, 2.8% of cases had a delay of more than 48 hours in the initiation of PEP. Significant determinants of the increase in delay were female gender (OR=1.43, 95% CI: 1.36, 1.51, $P<0.001$), foreign nationality (OR=1.19, 95% CI: 1.01, 1.12, $P=0.001$), rural residence (OR=1.07, 95% CI: 1.01, 1.12, $P=0.010$), and the wild animals (OR=1.22, 95% CI: 1.12, 1.34, $P<0.001$). **Conclusion:** The observed frequency of animal bites in a year indicates a serious public health concern and the need for targeted interventions, especially in at-risk areas and vulnerable populations.

Schistosomiasis

Systematic review with meta-analysis: Prevalence, risk factors, and challenges for urinary schistosomiasis in children (USC).

Masdor NA, Kandayah T, Amsah N, Othman R, Hassan MR, Rahim SSSA, Jeffree MS, Awang Lukman K, Hidrus A. 17-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37590252/>

Relationships between Schistosoma mansoni infection intensity and nutritional status and anemia among preschool-aged children in Uganda.

Colt S, Miller CD, Edielu A, Webb EL, Mawa PA, Wu HW, Nakyesige R, Muheki E, Kabatereine N, Bustinduy AL, Friedman JF.

16-08-2023

Clin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37585653/>

In a cross-sectional analysis of 354 Ugandan children (age 12-48 months) infected with *Schistosoma mansoni*, we assessed relationships between infection intensity and nutritional morbidities. Higher intensity was associated with an increased risk for anemia (RR = 1.05, CI 1.01-1.10) yet not associated with risk for underweight, stunting, or wasting.

Urinogenital schistosomiasis knowledge, attitude, practices, and its clinical correlates among communities along water bodies in the Kwahu Afram Plains North District, Ghana.

Essien-Baidoo S, Essuman MA, Adarkwa-Yiadom B, Adarkwa D, Owusu AA, Amponsah SB.

16-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37585379/>

Background: Adequate knowledge and proper practices coupled with knowledge of the burden of disease are necessary for the eradication of *Schistosoma* infection. This study assessed knowledge, attitude, and practice (KAP) as well as health outcomes related to *Schistosoma haematobium* infection at Kwahu Afram Plains North District (KAPND). **Methods:** A cross-sectional survey using a structured questionnaire was carried out among 140 participants from four local communities in KAPND in August 2021. From these participants, 10ml of urine was collected for determination of the presence of *S. haematobium* and urine routine examination. In addition, 4ml of blood was collected and used for haematological examination. Descriptive statistics and logistic regression analysis using IBM SPSS were used to describe and represent the data collected. **Results:** The study reports a gap in knowledge about schistosomiasis in the study area with the majority indicating that they have not heard of schistosomiasis (60.7%), do not know the mode of transmission (49.3%), and do not know how the disease could be spread (51.5%). The overall prevalence of urinary schistosomiasis was 52.9%. This was associated with age, occupation, perceived mode of *Schistosoma* transmission, knowledge of *Schistosoma* prevention, awareness that schistosomiasis can be treated, frequency of visits to water bodies, and water usage patterns. In multivariate analysis, factors that remained significantly associated with *S.*

haematobium infection were age 21-40 (OR = 0.21, 95% CI: 0.06-0.76), 41-60 (OR = 0.01, 95% CI: 0.01-0.52) and ≥ 60 (OR = 0.02, 95% CI: 0.02-0.87), informal employment (OR = 0.01, 95% CI: 0.01-0.69) and awareness of transmission by drinking water from river body (OR = 0.03, 95% CI: 0.03-0.92). In *Schistosoma* infection, reduced haemoglobin, haematocrit, mean corpuscular volume, mean corpuscular haemoglobin, lymphocytes and eosinophils were observed. White blood cells, neutrophils, and monocytes were significantly elevated in infected states. Urine analysis revealed high pus cells and red blood cells counts among *Schistosoma*-positive participants. **Conclusion:** *Schistosoma* infection is endemic among inhabitants in KAPND, and is associated with a gap in knowledge, awareness, and practice possibly due to inadequate education in the area. Poor clinical outcomes associated with *Schistosoma* infection have been demonstrated in the area. A well-structured public education, nutritional intervention, and mass drug administration will be necessary to eradicate this menace.

Eggshell calcified hydrocele sac: a case report.

Molla YD, Mekonnen DC, Gebrehiwot CL, Tadesse AK, Abera SA, Temeche L.
15-08-2023

J Med Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37580791/>

IgG persistence showed weak clinical aspects in chronic schistosomiasis patients.

Xie S, Zhang Y, Li J, Zhou J, Li J, Zhang P, Liu Y, Luo Y, Ming Y.

14-08-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37580417/>

Update on the Geographic Distribution of the Intermediate Host Snails of *Schistosoma mansoni* on St. Lucia: A Step Toward Confirming the Interruption of Transmission of Human Schistosomiasis.

Mukaratirwa S, Laidemitt MR, Hewitt R, Sengupta ME, Marchi S, Polius C, Belmar S, Scholte RGC, Perez F, Stensgaard AS, Vennervald BJ, Willingham AL, Loker ES.
14-08-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37580035/>

To provide information to guide considerations of declaring interruption of transmission of human schistosomiasis due to *Schistosoma mansoni* on St. Lucia, we undertook an island-wide survey in June-July 2022 to determine the presence of *Biomphalaria* snails, the intermediate hosts of *S. mansoni*, and their infection status. Snail surveys were carried out at 58 habitats to determine presence of *Biomphalaria* snails followed by examination of the collected snails for evidence of infection with *S. mansoni*. Furthermore, water samples were collected at the snail habitats and screened for

presence of *S. mansoni* DNA using an eDNA approach. We found *B. glabrata* present in one habitat (Cul de Sac) where it was abundant. Specimens provisionally identified as *Biomphalaria kuhniana* were recovered from 10 habitats. None of the *Biomphalaria* specimens recovered were positive for *S. mansoni*. None of the eDNA water samples screened were positive for *S. mansoni*. Experimental exposures of both field-derived and laboratory-reared St. Lucian *B. glabrata* and *B. kuhniana* to Puerto Rican and Kenyan-derived *S. mansoni* strains revealed *B. glabrata* to be susceptible to both and *B. kuhniana* proved refractory from histological and snail shedding results. We conclude, given the current rarity of *B. glabrata* on the island and lack of evidence for the presence of *S. mansoni*, that transmission is unlikely to be ongoing. Coupled with negative results from recent human serological surveys, and implementation of improved sanitation and provision of safe water supplies, St. Lucia should be considered a candidate for declaration of interruption of human schistosomiasis transmission.

Prevalence of Soil-Transmitted Helminths and *Schistosoma mansoni* among Schoolchildren across Altitudinal Gradients in Amhara National Regional State, Ethiopia.

Abie A, Hailu T, Alemu G, Nibret E, Amor A, Munshea A.
14-08-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37580029/>

A target-based discovery from a parasitic helminth as a novel therapeutic approach for autoimmune diseases.

Ni Y, Xiong R, Zhu Y, Luan N, Yu C, Yang K, Wang H, Xu X, Yang Y, Sun S, Shi L, Padde JR, Chen L, Chen L, Hou M, Xu Z, Lai R, Ji M.

12-08-2023

EBioMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37579625/>

Background: Regulatory T cells (Tregs) can alleviate the development of autoimmune and inflammatory diseases, thereby proposing their role as a new therapeutic strategy. Parasitic helminths have co-evolved with hosts to generate immunological privilege and immune tolerance through inducing Tregs. Thus, constructing a "Tregs-induction"-based discovery pipeline from parasitic helminth is a promising strategy to control autoimmune and inflammatory diseases. **Methods:** The gel filtration chromatography and reverse-phase high-performance liquid chromatography (RP-HPLC) were used to isolate immunomodulatory components from the egg extracts of *Schistosoma japonicum*. The extracted peptides were evaluated for their effects on Tregs suppressive functions using flow cytometry, ELISA and T cell suppression assay. Finally, we carried out colitis and psoriasis models to evaluate the function of Tregs induced by helminth-derived peptide in vivo. **Findings:** Here, based on target-driven discovery strategy, we successfully identified a small 3 kDa peptide (SjDX5-53) from egg extracts of schistosome, which promoted both human and murine

Tregs production. SjDX5-53 presented immunosuppressive function by arresting dendritic cells (DCs) at an immature state and augmenting the proportion and suppressive capacity of Tregs. In mouse models, SjDX5-53 protected mice against autoimmune-related colitis and psoriasis through inducing Tregs and inhibiting inflammatory T-helper (Th) 1 and Th17 responses. **Interpretation:** SjDX5-53 exhibited the promising therapeutic effects in alleviating the phenotype of immune-related colitis and psoriasis. This study displayed a screening and validation pipeline of the inducer of Tregs from helminth eggs, highlighting the discovery of new biologics inspired by co-evolution of hosts and their parasites. **Funding:** This study was supported by the Natural Science Foundation of China (82272368) and Natural Science Foundation of Jiangsu Province (BK20211586).

Seasonal patterns of *Schistosoma mansoni* infection within *Biomphalaria* snails at the Ugandan shorelines of Lake Albert and Lake Victoria.

Andrus PS, Stothard JR, Wade CM.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578945/>

Intestinal schistosomiasis is hyperendemic in many sub-Saharan African countries. In Uganda, it is endemic at both Lake Albert (LA) and Lake Victoria (LV) and caused by *S. mansoni* that uses *Biomphalaria* snails as obligatory intermediate snail hosts. To shed light on local patterns of infection, we utilised two PCR-based methods to detect *S. mansoni* within *Biomphalaria* spp. as collected at the Ugandan shorelines of Lake Albert and Lake Victoria from 2009-2010. Overall, at our Lake Albert sites, the mean infection prevalence was 12.5% (15 of 120 snails), while at our Lake Victoria sites the prevalence was 5% (3 of 60 snails). At our Lake Albert sites, the highest infection prevalence of 13.3% (8 of 60 snails) was at Walukuba, while at our Lake Victoria sites, the highest infection prevalence of 10% (2 of 20 snails) was at Lwanika. Three species of *Biomphalaria*, *B. pfeifferi*, *B. stanleyi* and *B. sudanica*, were identified at our Lake Albert collection sites, while only a single species, *B. choanomphala*, was identified at our Lake Victoria collection sites. *Biomphalaria stanleyi* (2 of 20 snails; 15%) had the highest infection prevalence, followed by *B. sudanica* (5 of 60 snails; 13.3%), *B. pfeifferi* (4 of 40 snails; 10%) and *B. choanomphala* (3 of 60 snails; 5%). Of the *Biomphalaria* species identified, *B. choanomphala* had the highest haplotype (gene) diversity score, followed by *B. stanleyi*, *B. sudanica* and *B. pfeifferi*. Sites with a higher mean prevalence of *S. mansoni* infection had higher intra-species haplotype diversity scores than sites with a lower mean prevalence. The wet seasons (LA: 13.3%; LV: 8.7%) had a consistently higher mean infection prevalence of *S. mansoni* than the dry seasons (LA: 9.5%; LV: 5%) for all species and all sites tested at both Lake Albert (n = 480) and Lake Victoria (n = 320), though the difference was not statistically significant.

Pediatric Spinal Neuroschistosomiasis in Yemen: An Overlooked Dilemma in an Endemic Region.

Aljuma'ai N, Ghabisha SA, Ahmed F, Al-Mwald T, Mayas A, Almaghribi B, Esmail H, Badheeb M.

12-06-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37575694/>

Solution structure of the N-terminal extension domain of a *Schistosoma japonicum* asparaginyl-tRNA synthetase.

Peck Y, Pickering D, Mobli M, Liddell MJ, Wilson DT, Ruscher R, Ryan S, Buitrago G, McHugh C, Love NC, Pinlac T, Haertlein M, Kron MA, Loukas A, Daly NL.

12-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37572327/>

Praziquantel inhibits *Caenorhabditis elegans* development and species-wide differences might be cct-8-dependent.

Wit J, Dilks CM, Zhang G, Guisbert KSK, Zdraljevic S, Guisbert E, Andersen EC.

10-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37561720/>

Anthelmintic drugs are used to treat parasitic roundworm and flatworm infections in humans and other animals. *Caenorhabditis elegans* is an established model to investigate anthelmintics used to treat roundworms. In this study, we use *C. elegans* to examine the mode of action and the mechanisms of resistance against the flatworm anthelmintic drug praziquantel (PZQ), used to treat trematode and cestode infections. We found that PZQ inhibited development and that this developmental delay varies by genetic background. Interestingly, both enantiomers of PZQ are equally effective against *C. elegans*, but the right-handed PZQ (R-PZQ) is most effective against schistosome infections. We conducted a genome-wide association mapping with 74 wild *C. elegans* strains to identify a region on chromosome IV that is correlated with differential PZQ susceptibility. Five candidate genes in this region: *cct-8*, *znf-782*, *Y104H12D.4*, *Y104H12D.2*, and *cox-18*, might underlie this variation. The gene *cct-8*, a subunit of the protein folding complex TRiC, has variation that causes a putative protein coding change (G226V), which is correlated with reduced developmental delay. Gene expression analysis suggests that this variant correlates with slightly increased expression of both *cct-8* and *hsp-70*. Acute exposure to PZQ caused increased expression of *hsp-70*, indicating that altered TRiC function might be involved in PZQ responses. To test if this variant affects development upon exposure to PZQ, we used CRISPR-Cas9 genome editing to introduce the V226 allele into the N2 genetic background (G226) and the G226 allele into the JU775 genetic background (V226). These experiments revealed that this variant was not sufficient to explain the effects of PZQ on development. Nevertheless, this study shows that *C. elegans* can be used to study PZQ mode of action and resistance mechanisms.

Additionally, we show that the TRiC complex requires further evaluation for PZQ responses in *C. elegans*.

Development of CRISPR/Cas13a-based assays for the diagnosis of Schistosomiasis.

MacGregor SR, McManus DP, Sivakumaran H, Egwang TG, Adriko M, Cai P, Gordon CA, Duke MG, French JD, Collinson N, Olveda RM, Hartel G, Graeff-Teixeira C, Jones MK, You H.

Aug-2023

EBioMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37487416/>

Amino acid usage and protein expression levels in the flatworm *Schistosoma mansoni*.

Lamolle G, Iriarte A, Simón D, Musto H.

Sept-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37478919/>

Dimerization, host-parasite communication and expression studies of an *Echinococcus granulosus* 2DBD nuclear receptor.

Blanco V, Mozzo B, Alvite G.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37395819/>

Nuclear receptors (NRs) are ligand-modulated transcription factors that regulate various biological processes, such as metabolism, development and reproduction. Although NRs with two DNA-binding domains (2DBD) were identified in *Schistosoma mansoni* (Platyhelminth, Trematoda) more than fifteen years ago, these proteins have been poorly studied. 2DBD-NRs could become attractive therapeutic targets to combat parasitic diseases such as cystic echinococcosis since this type of protein is absent in vertebrate hosts. Cystic echinococcosis is a worldwide zoonosis caused by the larval stage of the parasitic platyhelminth *Echinococcus granulosus* (Cestoda) that generates an important public health problem and a significant economic loss. Recently, our research group identified four 2DBD-NRs in *E. granulosus*, named Eg2DBD α , Eg2DBD α .1 (an isoform of Eg2DBD α), Eg2DBD β , and Eg2DBD γ . This work demonstrated that Eg2DBD α .1 forms homodimers through the E and F regions, whereas its interaction with EgRXR β a could not be detected. In addition, the stimulation of Eg2DBD α .1 homodimerization by intermediate host serum was shown, suggesting that at least one lipophilic molecule from bovine serum could bind to Eg2DBD α .1. Finally, Eg2DBDs expression studies in the protoscolex larval stage were performed, indicating that Eg2dbd γ is not expressed, whereas Eg2dbd α has the highest expression level followed by Eg2dbd β and Eg2dbd α .1 in decreased order. Overall, these findings provide new insights into the mechanism of action of Eg2DBD α .1 and its potential role in host-parasite communication.

Experimental infection with *Schistosoma mansoni* from Belém, Pará, Brazil: Strains newly isolated vs. laboratory maintained.

Dias IHL, Fonseca ÁLS, Sousa SRM, Goveia CO, Fernandez MA, Enk MJ.

Sept-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37380123/>

Trachome

The 100 most cited articles on trachoma: a bibliometric analysis.

Aquino-Canchari CR, Chavez-Bustamante SG.

17-08-2023

Int Ophthalmol.

<https://pubmed.ncbi.nlm.nih.gov/37592115/>

Objective: Trachoma is the cause of blindness or visual impairment in 1.9 million people. Few bibliometric studies have been carried out, but none explore the characteristics of the 100 most cited articles on trachoma.

Methods: A keyword-based search without time restriction was performed in September 2022 using the Scopus database. Search keywords include the following: "trachoma; trachome; tracoma; trachomatis." Two authors independently screened the literature and extracted data. The search result was obtained to classify the 100 articles according to their number of citations.

Results: The Top 100 articles were published between 1957 and 2015 with a total of 11,102 citations (range 56-689). The country with the most significant contribution was the USA (n = 56). The Lancet was the most active journal (n = 15). Bailey RL was the author with the highest number of publications (n = 30). The Edna McConnell Clark Foundation (n = 26) was the most prominent funding entity. The type of original article was the most published (n = 83), in addition, the most frequent thematic area was prevention (n = 33). The most popular keywords were trachoma (n = 93), chlamydia trachomatis (n = 55), and azithromycin (n = 34). **Conclusions:** The study provides new insight into trachoma research, information that may help healthcare providers, researchers, and stakeholders better understand trends and influential contributions. It highlights under-researched areas that could be the basis for future research.

Prevalence and associated factors of active trachoma among 1-9 years of age children in Andabet district, northwest Ethiopia, 2023: A multi-level mixed-effect analysis.

Asmare ZA, Seifu BL, Mare KU, Asgedom YS, Kase BF, Shibeshi AH, Tebeje TM, Lombebo AA, Sabo KG, Fente BM, Teshale AB, Asebe HA.

17-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37590321/>

Background: Trachoma is the chief cause of preventable blindness worldwide and has been earmarked for

elimination as a public health problem by 2030. Despite the five-year Surgery, Antibiotics, Facial cleanliness, and Environmental improvement (SAFE)-based interventions in the Andabet district, the prevalence of trachomatous follicular (TF) was 37%. With such a high prevalence of TF, the determinant factors were not revealed. Besides, there were no reports on the overall prevalence of active trachoma (i.e. TF and or trachomatous intense (TI)).

Objective: To determine the prevalence and associated factors of active trachoma among 1-9 years of age children in the Andabet district. **Method:** A community-based cross-sectional study was conducted among children aged under nine years from March 1-30, 2023 in Andabet district, Northwest Ethiopia. Multi-stage systematic random sampling was employed to reach 540 children. A multilevel mixed-effect logistic regression analysis was employed to assess factors associated with active trachoma. We fitted both random effect and fixed effect analysis. Finally, variables with $p < 0.05$ in the multivariable multilevel analysis were claimed to be significantly associated with active trachoma. **Result:** In this study, the overall prevalence of active trachoma was 35.37% (95% CI: 31.32%, 39.41%). The prevalence of TF and TI was 31.3% and 4.07% respectively. In the multilevel logistic regression analysis ocular discharge, fly-eye contact, latrine utilization, and source of water were significantly associated with the prevalence of active trachoma. **Conclusion:** In this study, the prevalence of active trachoma was much higher than the World Health Organization (WHO) threshold prevalence. Ocular discharge, fly-eye contact, latrine utilization, and source of water were independent determinants of active trachoma among children (1-9 years). Therefore, paying special attention to these high-risk groups could decrease the prevalence of a neglected hyperendemic disease, active trachoma.

Soil-transmitted helminths: A critical review of the impact of co-infections and implications for control and elimination.

Lebu S, Kibone W, Muoghalu CC, Ochaya S, Salzberg A, Bongomin F, Manga M.

10-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37561673/>

Targeted Mass Azithromycin Distribution for Trachoma: A Community-Randomized Trial (TANA II).

Mahmud H, Haile BA, Tadesse Z, Gebresillasie S, Shiferaw A, Zerihun M, Liu Z, Callahan EK, Cotter SY, Varnado NE, Oldenburg CE, Porco TC, Lietman TM, Keenan JD.

14-08-2023

Clin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37021692/>

Background: Current guidelines recommend annual community-wide mass administration of azithromycin for trachoma. Targeting treatments to those most likely to be infected could reduce the amount of unnecessary

antibiotics distributed. **Methods:** In a cluster-randomized trial conducted from 1 November 2010 through 8 November 2013, 48 Ethiopian communities previously treated with annual mass azithromycin distributions for trachoma were randomized in equal numbers to (1) annual azithromycin distributions targeted to children aged 0-5 years, (2) annual azithromycin distributions targeted to households with a child aged 0-5 years found to have clinically active trachoma, (3) continued annual mass azithromycin distributions to the entire community, or (4) cessation of treatment. The primary outcome was the community prevalence of ocular chlamydia infection among children aged 0-9 years at month 36. Laboratory personnel were masked to treatment allocation. **Results:** The prevalence of ocular chlamydia infection among children aged 0-9 years increased from 4.3% (95% confidence interval [CI], .9%-8.6%) at baseline to 8.7% (95% CI, 4.2%-13.9%) at month 36 in the age-targeted arm, and from 2.8% (95% CI, .8%-5.3%) at baseline to 6.3% (95% CI, 2.9%-10.6%) at month 36 in the household-targeted arm. After adjusting for baseline chlamydia prevalence, the 36-month prevalence of ocular chlamydia was 2.4 percentage points greater in the age-targeted group (95% CI, -4.8% to 9.6%; $P = .50$; prespecified primary analysis). No adverse events were reported. **Conclusions:** Targeting azithromycin treatment to preschool children was no different than targeting azithromycin to households with a child with clinically active trachoma. Neither approach reduced ocular chlamydia over the 3-year study.

Trématodoses d'origine alimentaire (clonorchiose, opisthorchiose, fasciolose et paragonimose)

Multilayer omics reveals the molecular mechanism of early infection of *Clonorchis sinensis* juvenile.

Wu Y, Deng X, Wu Z, Liu D, Fu X, Tang L, He S, Lv J, Wang J, Li Q, Zhan T, Tang Z.

16-08-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37587524/>

Seroprevalence and risk factors of bovine fasciolosis in the municipalities of Colombia.

Bulla-Castañeda DM, Lancheros-Buitrago DJ, García-Corredor DJ, C-Giraldo-Forero J, Pulido-Medellin MO.

Juin-2023

Vet World.

<https://pubmed.ncbi.nlm.nih.gov/37577203/>

Artemisia vulgaris anthelmintic activities to ova and adult stages of Fasciola gigantica in vitro.

Nurlaelasari A, Wulandari AR, Caro TM, Nugroho HA, Sukaryo S, Cahyadi M, Kurniawan W, Hamid PH.

Mai-2023

Vet World.

<https://pubmed.ncbi.nlm.nih.gov/37576776/>

Background and aim: Fasciolosis due to *Fasciola gigantica* is endemic to tropical countries and *Fasciola hepatica* in temperate climates, highly detrimental to livestock and known as foodborne zoonotic diseases. The strategic control of the disease is mainly the use of chemical anthelmintic. This study aimed to evaluate the anthelmintic properties of *Artemisia vulgaris* extract on the ova and adult stages of *F. gigantica*. **Materials and methods:** Samples were collected from the Ampel Abbatoir, Boyolali District, Central Java, Indonesia. The ova from 20-gallbladders of cattle which were naturally infected with *F. gigantica* and 270 living *F. gigantica* worms were used in this study. The ovicidal assay was performed by incubating the ova with *A. vulgaris* in different concentrations, that is, 5%, 2.5%, and 1.25% for 5, 9, 11, 14, and 16 days. The efficacies were evaluated by quantification of ova degeneration during developmental stages in different time points and egg-hatch assay. The flukicidal effects were observed by mortality assay in 5, 10, 20, 40, 80, 160, 320, and 640 min incubations followed by scanning electron microscopy for surface morphology and histology of the fluke's transversal sections. **Results:** The concentration of 5% *A. vulgaris* showed the strongest ovicidal activities. The percentage of hatching ova on day 16 at concentrations of 5%, 2.5%, and 1.25% were 3.33%, 6.67%, and 16.67%. These ova hatch assay showed a significant reduction ($p < 0.001$) compared to untreated control. The flukicidal effect was significant ($p < 0.001$) at a concentration of 20%, with a mortality rate reaching 66.67% in the 40 min of incubation time. The surface properties of the adult worms, including the spine, tegument, acetabulum, intestine, and vitelline follicles, were disintegrated. **Conclusion:** The results showed that *A. vulgaris* has the potential ovicidal and flukicidal properties to *F. gigantica*. The active compounds remained necessary to be elucidated further and its modes of action would be interesting to be predicted by molecular docking modeling.

How do parasitic worms prevent diabetes? An exploration of their influence on macrophage and β -cell crosstalk.

Camaya I, O'Brien B, Donnelly S.

26-07-2023

Front Endocrinol (Lausanne).

<https://pubmed.ncbi.nlm.nih.gov/37564976/>

Diabetes is the fastest growing chronic disease globally, with prevalence increasing at a faster rate than heart disease and cancer. While the disease presents clinically as chronic hyperglycaemia, two distinct subtypes have been recognised. Type 1 diabetes (T1D) is characterised as an autoimmune disease in which the insulin-producing

pancreatic β -cells are destroyed, and type 2 diabetes (T2D) arises due to metabolic insufficiency, in which inadequate amounts of insulin are produced, and/or the actions of insulin are diminished. It is now apparent that pro-inflammatory responses cause a loss of functional β -cell mass, and this is the common underlying mechanism of both T1D and T2D. Macrophages are the central immune cells in the pathogenesis of both diseases and play a major role in the initiation and perpetuation of the proinflammatory responses that compromise β -cell function. Furthermore, it is the crosstalk between macrophages and β -cells that orchestrates the inflammatory response and ensuing β -cell dysfunction/destruction. Conversely, this crosstalk can induce immune tolerance and preservation of β -cell mass and function. Thus, specifically targeting the intercellular communication between macrophages and β -cells offers a unique strategy to prevent/halt the islet inflammatory events underpinning T1D and T2D. Due to their potent ability to regulate mammalian immune responses, parasitic worms (helminths), and their excretory/secretory products, have been examined for their potential as therapeutic agents for both T1D and T2D. This research has yielded positive results in disease prevention, both clinically and in animal models. However, the focus of research has been on the modulation of immune cells and their effectors. This approach has ignored the direct effects of helminths and their products on β -cells, and the modulation of signal exchange between macrophages and β -cells. This review explores how the alterations to macrophages induced by helminths, and their products, influence the crosstalk with β -cells to promote their function and survival. In addition, the evidence that parasite-derived products interact directly with endocrine cells to influence their communication with macrophages to prevent β -cell death and enhance function is discussed. This new paradigm of two-way metabolic conversations between endocrine cells and macrophages opens new avenues for the treatment of immune-mediated metabolic disease.

Paragonimus westermani preadult fluke in a pulmonary necrotizing granulomatous lesion: A case associated with eating soy sauce-marinated raw freshwater crab, "gejang".

Maekawa K, Nagayasu E, Hata Y, Hanamure F, Maruyama H, Yamashita A.

Aug-2023

Pathol Int.

<https://pubmed.ncbi.nlm.nih.gov/37493110/>

Genetic variation and population structure of Fasciola hepatica: an in silico analysis.

Alvi MA, Khalid A, Ali RMA, Saqib M, Qamar W, Li L, Ahmad B, Fu BQ, Yan HB, Jia WZ.

Sept-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37458821/>

Activity of cumin essential oil to control fascioliasis: Efficacy and changes in the tegument of *Fasciola hepatica*.

Brauner de Mello A, Baccega B, Obelar Martins F, Ignês de Santi I, Islabão YW, de Giacometti M, Pereira Soares M, da Rosa Farias NA, Belmonte Oliveira C.

Sept-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37454922/>

Current status and progress in the omics of *Clonorchis sinensis*.

Wang N, Zhang Z, Huang L, Chen T, Yu X, Huang Y.

Sept-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37127222/>

Clonorchis sinensis (*C. sinensis*) is a fish-borne trematode that inhabits the bile duct of mammals including humans, cats, dogs, rats, and so on. In the complex life cycle of *C. sinensis*, the worm develops successively in two intermediate hosts in fresh water and one definitive host. What's more, it undergoes eight developmental stages with a distinct morphology. Clonorchiasis, caused by *C. sinensis* infection, is an important food-borne parasitic disease and one of the most common zoonoses. *C. sinensis* infection could result in hyperplasia of the bile duct epithelium, obstructive jaundice, gall-stones, cholecystitis and cholangitis, even liver cirrhosis and cholangiocarcinoma. Thus, clonorchiasis is a serious public health problem in endemic areas. Integrated strategies should be adopted in the prevention and control of clonorchiasis due to the epidemiological characteristics. The recent advances in high-throughput technologies have made available the profiling of multiple layers of a biological system, genomics, transcriptomics, proteomics, and metabolomics. These data can help us to get more information about the development, physiology, metabolism, and reproduction of the parasite as well as pathogenesis and parasite-host interactions in clonorchiasis. In the present study, we summarized recent progresses in omics studies on *C. sinensis* providing insights into the studies and future directions on treating and preventing *C. sinensis* associated diseases.

Trypanosomes (trypanosomiasis et maladie de Chagas)

Modelling host- *Trypanosoma brucei* gambiense interactions in vitro using human induced pluripotent stem cell-derived cortical brain organoids.

Chandrasegaran P, Nabilla Lestari A, Sinton MC, Gopalakrishnan J, Quintana JF.

28-07-2023

F1000Res.

<https://pubmed.ncbi.nlm.nih.gov/37588058/>

In silico identification of α -bisabolol and letestuanin C as potential inhibitors of *Trypanosoma brucei* trypanothione reductase.

Nketia PB, Gasu EN, Mensah JO, Borquaye LS.

16-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37584491/>

The RNA-binding protein RBP42 regulates cellular energy metabolism in mammalian-infective *Trypanosoma brucei*.

Das A, Liu T, Li H, Husain S.

15-08-2023

mSphere.

<https://pubmed.ncbi.nlm.nih.gov/37581443/>

RNA-binding proteins (RBPs) are key players in coordinated post-transcriptional regulation of functionally related genes, defined as RNA regulons. RNA regulons play particularly critical roles in parasitic trypanosomes, which exhibit unregulated co-transcription of long unrelated gene arrays. In this report, we present a systematic analysis of an essential RBP, RBP42, in the mammalian-infective bloodstream form of African trypanosome and show that RBP42 is a key regulator of parasite's central carbon and energy metabolism. Using individual-nucleotide resolution UV cross-linking and immunoprecipitation to identify genome-wide RBP42-RNA interactions, we show that RBP42 preferentially binds within the coding region of mRNAs encoding core metabolic enzymes. Global quantitative transcriptomic and proteomic analyses reveal that loss of RBP42 reduces the abundance of target mRNA-encoded proteins, but not target mRNA, suggesting a positive translational regulatory role of RBP42. Significant changes in central carbon metabolic intermediates, following loss of RBP42, further support its critical role in cellular energy metabolism. **IMPORTANCE** *Trypanosoma brucei* infection, transmitted through the bite of blood-feeding tsetse flies, causes deadly diseases in humans and livestock. This disease, if left untreated, is almost always fatal. Existing therapies are toxic and difficult to administer. During *T. brucei*'s lifecycle in two different host environments, the parasite progresses through distinctive life stages with major morphological and metabolic changes, requiring precise alteration of parasite gene expression program. In the absence of regulated transcription, post-transcriptional processes mediated by RNA-binding proteins play critical roles in *T. brucei* gene regulation. In this study, we show that the RNA-binding protein RBP42 plays crucial roles in cellular energy metabolic regulation of this important human pathogen. Metabolic dysregulation observed in RBP42 knockdown cells offers a breadth of potential interest to researchers studying parasite biology and can also impact research in general eukaryotic biology.

Navigating drug repurposing for Chagas disease: advances, challenges, and opportunities.

Porta EOJ, Kalesh K, Steel PG.

27-07-2023

Front Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37576826/>

Chagas disease is a vector-borne illness caused by the protozoan parasite *Trypanosoma cruzi* (*T. cruzi*). It poses a significant public health burden, particularly in the poorest regions of Latin America. Currently, there is no available vaccine, and chemotherapy has been the traditional treatment for Chagas disease. However, the treatment options are limited to just two outdated medicines, nifurtimox and benznidazole, which have serious side effects and low efficacy, especially during the chronic phase of the disease. Collectively, this has led the World Health Organization to classify it as a neglected disease. To address this problem, new drug regimens are urgently needed. Drug repurposing, which involves the use of existing drugs already approved for the treatment of other diseases, represents an increasingly important option. This approach offers potential cost reduction in new drug discovery processes and can address pharmaceutical bottlenecks in the development of drugs for Chagas disease. In this review, we discuss the state-of-the-art of drug repurposing approaches, including combination therapy with existing drugs, to overcome the formidable challenges associated with treating Chagas disease. Organized by original therapeutic area, we describe significant recent advances, as well as the challenges in this field. In particular, we identify candidates that exhibit potential for heightened efficacy and reduced toxicity profiles with the ultimate objective of accelerating the development of new, safe, and effective treatments for Chagas disease.

Histopathology and virulence of an in vitro-adapted *Trypanosoma evansi* TEDC 953 strain (Thailand isolate) in mice.

Phongphaew W, Wongsali C, Boonyakong T, Samritwatchasai T, Chimnoi W, Kamyngkird K.

Mai-2023

Vet World.

<https://pubmed.ncbi.nlm.nih.gov/37576763/>

***Trypanosoma cruzi* infection in mammals in Florida: New insight into the transmission of *T. cruzi* in the southeastern United States.**

Torhorst CW, Ledger KJ, White ZS, Milleson MP, Corral CC, Beatty NL, Wisely SM.

25-06-2023

Int J Parasitol Parasites Wildl.

<https://pubmed.ncbi.nlm.nih.gov/37575667/>

Insights into the microRNA landscape of *Rhodnius prolixus*, a vector of Chagas disease.

Santiago PB, da Silva Bentes KL, da Silva WMC, Praça YR, Charneau S, Chaouch S, Grellier P, Dos Santos Silva Ferraz MA, Bastos IMD, de Santana JM, de Araújo CN.

12-08-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37573416/>

The growing interest in microRNAs (miRNAs) over recent years has led to their characterization in numerous organisms. However, there is currently a lack of data available on miRNAs from triatomine bugs (Reduviidae: Triatominae), which are the vectors of the protozoan parasite *Trypanosoma cruzi*, the causative agent of Chagas disease. A comprehensive understanding of the molecular biology of vectors provides new insights into insect-host interactions and insect control approaches, which are key methods to prevent disease incidence in endemic areas. In this work, we describe the miRNome profiles from gut, hemolymph, and salivary gland tissues of the *Rhodnius prolixus* triatomine. Small RNA sequencing data revealed abundant expression of miRNAs, along with tRNA- and rRNA-derived fragments. Fifty-two mature miRNAs, previously reported in Ecdysozoa, were identified, including 39 ubiquitously expressed in the three tissues. Additionally, 112, 73, and 78 novel miRNAs were predicted in the gut, hemolymph, and salivary glands, respectively. In silico prediction showed that the top eight most highly expressed miRNAs from salivary glands potentially target human blood-expressed genes, suggesting that *R. prolixus* may modulate the host's gene expression at the bite site. This study provides the first characterization of miRNAs in a Triatominae species, shedding light on the role of these crucial regulatory molecules.

Tackling Sleeping Sickness: Current and Promising Therapeutics and Treatment Strategies.

Jamabo M, Mahlalela M, Edkins AL, Boshoff A.

07-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37569903/>

Human African trypanosomiasis is a neglected tropical disease caused by the extracellular protozoan parasite *Trypanosoma brucei*, and targeted for eradication by 2030. The COVID-19 pandemic contributed to the lengthening of the proposed time frame for eliminating human African trypanosomiasis as control programs were interrupted. Armed with extensive antigenic variation and the depletion of the B cell population during an infectious cycle, attempts to develop a vaccine have remained unachievable. With the absence of a vaccine, control of the disease has relied heavily on intensive screening measures and the use of drugs. The chemotherapeutics previously available for disease management were plagued by issues such as toxicity, resistance, and difficulty in administration. The approval of the latest and first oral drug, fexinidazole, is a major chemotherapeutic achievement for the treatment of human African trypanosomiasis in the past few decades. Timely and accurate diagnosis is essential for effective treatment, while poor compliance and resistance remain outstanding challenges. Drug discovery is on-going, and herein we review the recent advances in anti-trypanosomal drug discovery, including novel potential drug targets. The numerous challenges associated with disease eradication will also be addressed.

Trypanosoma cruzi Secreted Cyclophilin TcCyP19 as an Early Marker for Trypanocidal Treatment Efficiency.

Perrone AE, Pinillo M, Rial MS, Fernández M, Milduburger N, González C, Bustos PL, Fichera LE, Laucella SA, Albareda MC, Bua J.

25-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37569250/>

A unique mRNA decapping complex in trypanosomes.

Kramer S, Karolak NK, Odenwald J, Gabiatti B, Castañeda Londoño PA, Zavřelová A, Freire ER, Almeida KS, Braune S, Moreira C, Eder A, Goos C, Field M, Carrington M, Holetz F, Górna MW, Zoltner M.

11-08-2023

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/37309887/>

Improved models for the relationship between age and the probability of trypanosome infection in female tsetse, Glossina pallidipes Austen.

Hargrove JW, Van Sickle J.

Août-2023

Bull Entomol Res.

<https://pubmed.ncbi.nlm.nih.gov/37194504/>

Ulcère de Buruli

Deep learning for AI-based diagnosis of skin-related neglected tropical diseases: A pilot study.

Yotsu RR, Ding Z, Hamm J, Blanton RE.

14-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37578966/>