



Veille scientifique Maladies tropicales négligées

Semaine 01
02 au 08 janvier 2023

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Dengue, chikungunya et maladie à virus Zika

Mosquito vector competence for dengue is modulated by insect-specific viruses.

Olmo RP, Todjro YMH, Aguiar ERGR, de Almeida JPP, Ferreira FV, Armache JN, de Faria IJS, Ferreira AGA, Amadou SCG, Silva ATS, de Souza KPR, Vilela APP, Babarit A, Tan CH, Diallo M, Gaye A, Paupy C, Obame-Nkoghe J, Visser TM, Koenraadt CJM, Wongsokarijo MA, Cruz ALC, Prieto MT, Parra MCP, Nogueira ML, Avelino-Silva V, Mota RN, Borges MAZ, Drumond BP, Kroon EG, Recker M, Sedda L, Marois E, Imler JL, Marques JT.

Jan-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36604511/>

Inhibition of Chikungunya virus genome replication by targeting essential RNA structures within the virus genome.

Prosser O, Stonehouse NJ, Tuplin A.

02-01-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/36603772/>

Chikungunya virus (CHIKV) is a pathogenic arbovirus spread by *Aedes* spp. mosquitos. CHIKV has a wide global prevalence and represents a significant health burden in affected populations. Symptoms of CHIKV infection include fever, rashes and debilitating joint and muscle pain, which can persist for several months to years in some patients. To date, there remains no vaccine or specific antiviral therapy against this important human pathogen. Based on our previously published structural and phenotypic analysis of the 5' region of the CHIKV genome, we designed a panel of locked nucleic acid oligonucleotides to bind structured RNA replication elements within the virus genome, which are essential for efficient CHIKV replication. Using electromobility shift assays, we confirmed the relative binding efficiencies of each LNA to target CHIKV genomic RNA. We then went on to demonstrate, using both sub-genomic replicon and infectious virus systems, that targeting individual RNA replication elements inhibits CHIKV genome replication and production of infectious virus. Time course assays demonstrated that LNAs can access the CHIKV replication complex and virus genome, during active virus replication. For the first time, these findings show that functional RNA elements can be specifically targeted during the CHIKV lifecycle and consequently represent potential novel antiviral targets.

Nuclear accumulation of host transcripts during Zika Virus Infection.

Leon KE, Khalid MM, Flynn RA, Fontaine KA, Nguyen TT, Kumar GR, Simoneau CR, Tomar S, Jimenez-Morales D, Dunlap M, Kaye J, Shah PS, Finkbeiner S, Krogan NJ, Bertozzi C, Carette JE, Ott M.

05-01-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/36603024/>

Zika virus (ZIKV) infects fetal neural progenitor cells (NPCs) causing severe neurodevelopmental disorders in utero. Multiple pathways involved in normal brain development are dysfunctional in infected NPCs but how ZIKV centrally reprograms these pathways remains unknown. Here we show that ZIKV infection disrupts subcellular partitioning of host transcripts critical for neurodevelopment in NPCs and functionally link this process to the up-frameshift protein 1 (UPF1). UPF1 is an RNA-binding protein known to regulate decay of cellular and viral RNAs and is less expressed in ZIKV-infected cells. Using infrared crosslinking immunoprecipitation and RNA sequencing (irCLIP-Seq), we show that a subset of mRNAs loses UPF1 binding in ZIKV-infected NPCs, consistent with UPF1's diminished expression. UPF1 target transcripts, however, are not altered in abundance but in subcellular localization, with mRNAs accumulating in the nucleus of infected or UPF1 knockdown cells. This leads to diminished protein expression of FREM2, a protein required for maintenance of NPC identity. Our results newly link UPF1 to the regulation of mRNA transport in NPCs, a process perturbed during ZIKV infection.

Unusual co-infection of severe malaria by *Plasmodium vivax* and dengue virus in Mexico.

Queb-Pech NM, Núñez-Oreza LA, Estrada-Méndez A, Tamay-Segovia P, Colli-Heredia JP, Blum-Domínguez SC.

01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602218/>

Malaria and dengue fever are among the most common mosquito-borne diseases worldwide; however, reports of coinfection are rare. We present a case of severe malaria and dengue coinfection in a 16-year-old female patient presenting with fever, thrombocytopenia, pleural effusion, myopericarditis, and acute respiratory distress syndrome. Dengue infection was confirmed by the presence of immunoglobulin M antibodies and nonstructural protein 1, while malaria was confirmed by the presence of *Plasmodium vivax* in thick and thin blood smears. This is the first report of a dengue/malaria coinfection in Mexico.

Development of a TaqMan minor groove binding probe-based quantitative reverse transcription polymerase chain reaction for the detection and quantification of Zika virus.

Chin KL, Teoh BT, Sam SS, Loong SK, Tan KK, Azizan NS, Lim YK, Khor CS, Nor'e SS, Abd-Jamil J, AbuBakar S.

01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602210/>

Lactic acid bacteria waste infusion as a source of attraction and oviposition stimulation of gravid female *Aedes albopictus* mosquitoes.

Suria MM, Yap PC, Lov VL, AbuBakar S, Lee HY.
01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602207/>

Targeted in vitro gene silencing of E2 and nsP1 genes of chikungunya virus by biocompatible zeolitic imidazolate framework.

Tagore R, Alagarasu K, Patil P, Pyreddy S, Polash SA, Kakade M, Shukla R, Parashar D.

14-12-2023

Front Bioeng Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/36601387/>

Chikungunya fever caused by the mosquito-transmitted chikungunya virus (CHIKV) is a major public health concern in tropical, sub-tropical and temperate climatic regions. The lack of any licensed vaccine or antiviral agents against CHIKV warrants the development of effective antiviral therapies. Small interfering RNA (siRNA) mediated gene silencing of CHIKV structural and non-structural genes serves as a potential antiviral strategy. The therapeutic efficiency of siRNA can be improved by using an efficient delivery system. Metal-organic framework biocomposites have demonstrated an exceptional capability in protecting and efficiently delivering nucleic acids into cells. In the present study, carbonated ZIF called ZIF-C has been utilized to deliver siRNAs targeted against E2 and nsP1 genes of CHIKV to achieve a reduction in viral replication and infectivity. Cellular transfection studies of E2 and nsP1 genes targeting free siRNAs and ZIF-C encapsulated siRNAs in CHIKV infected Vero CCL-81 cells were performed. Our results reveal a significant reduction of infectious virus titre, viral RNA levels and percent of infected cells in cultures transfected with ZIF-C encapsulated siRNA compared to cells transfected with free siRNA. The results suggest that delivery of siRNA through ZIF-C enhances the antiviral activity of CHIKV E2 and nsP1 genes directed siRNAs.

The Serological Confirmation and Outcome of the Pediatric Dengue Patients Presenting to Emergency Department: A Cross-Sectional Study.

Soomar SM, Issani A, Moin G, Dhalla Z, Adnan A, Soomar SM.

26-12-2022

Glob Pediatr Health.

<https://pubmed.ncbi.nlm.nih.gov/36601355/>

Discovering recent selection forces shaping the evolution of dengue viruses based on polymorphism data across geographic scales.

Li NK, Corander J, Grad YH, Chang HH.

29-11-2022

Virus Evol.

<https://pubmed.ncbi.nlm.nih.gov/36601300/>

Incomplete selection makes it challenging to infer selection on genes at short time scales, especially for

microorganisms, due to stronger linkage between loci. However, in many cases, the selective force changes with environment, time, or other factors, and it is of great interest to understand selective forces at this level to answer relevant biological questions. We developed a new method that uses the change in d_N/d_S , instead of the absolute value of d_N/d_S , to infer the dominating selective force based on sequence data across geographical scales. If a gene was under positive selection, d_N/d_S was expected to increase through time, whereas if a gene was under negative selection, d_N/d_S was expected to decrease through time. Assuming that the migration rate decreased and the divergence time between samples increased from between-continent, within-continent different-country, to within-country level, d_N/d_S of a gene dominated by positive selection was expected to increase with increasing geographical scales, and the opposite trend was expected in the case of negative selection. Motivated by the McDonald-Kreitman (MK) test, we developed a pairwise MK test to assess the statistical significance of detected trends in d_N/d_S . Application of the method to a global sample of dengue virus genomes identified multiple significant signatures of selection in both the structural and non-structural proteins. Because this method does not require allele frequency estimates and uses synonymous mutations for comparison, it is less prone to sampling error, providing a way to infer selection forces within species using publicly available genomic data from locations over broad geographical scales.

A systematic review and meta-analysis of the effects of temperature on the development and survival of the Aedes mosquito.

Nik Abdull Halim NMH, Che Dom N, Dapari R, Salim H, Precha N.

19-12-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36600940/>

A cluster-randomized, placebo-controlled trial to evaluate the efficacy of a spatial repellent (Mosquito Shield™) against Aedes-borne virus infection among children ≥ 4-16 years of age in the Gampaha District, Sri Lanka: study protocol (the AEGIS program).

Tissera H, Dheerasinghe DSAF, Malavige N, de Silva HA, Morrison AC, Scott TW, Reiner RC Jr, Grieco JP, Achee NL.

04-01-2023

Trials.

<https://pubmed.ncbi.nlm.nih.gov/36600308/>

Correction: Pandemic-associated mobility restrictions could cause increases in dengue virus transmission.

Cavany SM, España G, Vazquez-Prokopec GM, Scott TW, Perkins TA.

04-01-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36598896/>

Association Between Hydrological Conditions and Dengue Fever Incidence in Coastal Southeastern China From 2013 to 2019.

Li C, Wang Z, Yan Y, Qu Y, Hou L, Li Y, Chu C, Woodward A, Schikowski T, Saldiva PHN, Liu Q, Zhao Q, Ma W.

03-01-2023

JAMA Netw Open.

<https://pubmed.ncbi.nlm.nih.gov/36598784/>

Importance: Dengue fever is a climate-sensitive infectious disease. However, its association with local hydrological conditions and the role of city development remain unclear. **Objective:** To quantify the association between hydrological conditions and dengue fever incidence in China and to explore the modification role of city development in this association. **Design, setting, and participants:** This cross-sectional study collected data between January 1, 2013, and December 31, 2019, from 54 cities in 4 coastal provinces in southeast China. The Standardized Precipitation Evapotranspiration Index (SPEI) was calculated from ambient temperature and precipitation, with SPEI thresholds of 2 for extreme wet conditions and -2 for extreme dry conditions. The SPEI-dengue fever incidence association was examined over a 6-month lag, and the modification roles of 5 city development dimensions were assessed. Data were analyzed in May 2022. **Exposures:** City-level monthly temperature, precipitation, SPEI, and annual city development indicators from 2013 to 2019. **Main outcomes and measures:** The primary outcome was city-level monthly dengue fever incidence. Spatiotemporal bayesian hierarchal models were used to examine the SPEI-dengue fever incidence association over a 6-month lag period. An interaction term between SPEI and each city development indicator was added into the model to assess the modification role of city development. **Results:** Included in the analysis were 70 006 dengue fever cases reported in 54 cities in 4 provinces in China from 2013 to 2019. Overall, a U-shaped cumulative curve was observed, with wet and dry conditions both associated with increased dengue fever risk. The relative risk [RR] peaked at a 1-month lag for extreme wet conditions (1.27; 95% credible interval [CrI], 1.05-1.53) and at a 6-month lag for extreme dry conditions (1.63; 95% CrI, 1.29-2.05). The RRs of extreme wet and dry conditions were greater in areas with limited economic development, health care resources, and income per capita. Extreme dry conditions were higher and prolonged in areas with more green space per capita (RR, 1.84; 95% CrI, 1.37-2.46). Highly urbanized areas had a higher risk of dengue fever after extreme wet conditions (RR, 1.80; 95% CrI, 1.26-2.56), while less urbanized areas had the highest risk of dengue fever in extreme dry conditions (RR, 1.70; 95% CrI, 1.11-2.60). **Conclusions and relevance:** Results of this study showed that extreme hydrological conditions were associated with increased dengue fever incidence within a 6-month lag period, with different dimensions of city development playing various modification roles in this association. These findings may help in developing climate change adaptation strategies and public health interventions against dengue fever.

In Vitro and In Vivo Coinfection and Superinfection Dynamics of Mayaro and Zika Viruses in Mosquito and Vertebrate Backgrounds.

Brustolin M, Pujhari S, Terradas G, Werling K, Asad S, Metz HC, Henderson CA, Kim D, Rasgon JL.

04-01-2023

J Virol.

<https://pubmed.ncbi.nlm.nih.gov/36598200/>

Longitudinal proteomic profiling of the inflammatory response in dengue patients.

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

03-01-2023

PLoS Negl Trop Dis.

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

Human IL-10-producing Th1 cells exhibit a molecular signature distinct from Tr1 cells in malaria.

Edwards CL, Ng SS, de Labastida Rivera F, Corvino D, Engel JA, Montes de Oca M, Bukali L, Frame TC, Bunn PT, Chauhan SB, Singh SS, Wang Y, Na J, Amante FH, Loughland JR, Soon MS, Waddell N, Mukhopadhyay P, Koufariotis LT, Johnston RL, Lee JS, Kuns R, Zhang P, Boyle MJ, Hill GR, McCarthy JS, Kumar R, Engwerda CR.

03-01-2023

J Clin Invest.

<https://pubmed.ncbi.nlm.nih.gov/36594463/>

Control of intracellular parasites responsible for malaria requires host IFN- γ +T-bet+CD4⁺ T cells (Th1 cells) with IL-10 produced by Th1 cells to mitigate the pathology induced by this inflammatory response. However, these IL-10-producing Th1 (induced type 1 regulatory [Tr1]) cells can also promote parasite persistence or impair immunity to reinfection or vaccination. Here, we identified molecular and phenotypic signatures that distinguished IL-10-Th1 cells from IL-10+Tr1 cells in *Plasmodium falciparum*-infected people who participated in controlled human malaria infection studies, as well as C57BL/6 mice with experimental malaria caused by *P. berghei* ANKA. We also identified a conserved Tr1 cell molecular signature shared between patients with malaria, dengue, and graft-versus-host disease. Genetic manipulation of primary human CD4⁺ T cells showed that the transcription factor cMAF played an important role in the induction of IL-10, while BLIMP-1 promoted the development of human CD4⁺ T cells expressing multiple coinhibitory receptors. We also describe heterogeneity of Tr1 cell coinhibitory receptor expression that has implications for targeting these molecules for clinical advantage during infection. Overall, this work provides insights into CD4⁺ T cell development during malaria that offer opportunities for creation of strategies to modulate CD4⁺ T cell functions and improve antiparasitic immunity.

SERTAD3 induces proteasomal degradation of ZIKV capsid protein and represents a therapeutic target.

Sun N, Zhang RR, Song GY, Cai Q, Aliyari SR, Nielsen-Saines K, Jung JU, Yang H, Cheng G, Qin CF.

03-01-2023

J Med Virol.

<https://pubmed.ncbi.nlm.nih.gov/36594413/>

Zika virus (ZIKV) is a mosquito-borne RNA virus that belongs to the Flaviviridae family. While flavivirus replication is known to occur in the cytoplasm, a significant portion of the viral capsid protein localizes to the nucleus during infection. However, the role of nuclear capsid is less clear. Herein, we demonstrated SERTA domain containing 3 (SERTAD3) as an antiviral interferon stimulatory gene product had an antiviral ability to ZIKV but not JEV. Mechanistically, we found that SERTAD3 interacted with the capsid protein of ZIKV in the nucleolus and reduced capsid protein abundance through proteasomal degradation. Furthermore, an eight amino acid peptide of SERTAD3 was identified as the minimum motif that binds with ZIKV capsid protein. Remarkably, the 8 amino acid synthetic peptide from SERTAD3 significantly prevented ZIKV infection in culture and pregnant mouse models. Taken together, these findings not only reveal the function of SERTAD3 in promoting proteasomal degradation of a specific viral protein but also provide a promising host-targeted therapeutic strategy against ZIKV infection. This article is protected by copyright. All rights reserved.

Routine blood parameters of dengue infected children and adults. A meta-analysis.

Low GK, Jiee SF, Masilamani R, Shanmuganathan S, Rai P, Manda M, Omosumwen OF, Kagize J, Gavino AI, Azahar A, Jabbar MA.

02-01-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36593636/>

The World Health Organization (WHO) has revised dengue case classification in 2009 to better reflect the severity of the disease. However, there was no comprehensive meta-analysis of pooled routine blood parameters according to the age or the categories of the 2009 WHO classification. This study aimed to meta-analyze the routine blood parameters of dengue infected children and adults. Electronic search was performed with eligible articles included for review. Meta-analysis was conducted for six blood parameters stratified into children, adults and all ages, which were further grouped into the three 2009 WHO case classifications (dengue without warning signs, DwoWS; dengue with warning signs, DwWS; severe dengue, SD), non-severe dengue (non-SD) and 'All' cases. A total of 55 articles were included in the meta-analysis. Fifteen studies were conducted in the children's age category, 31 studies in the adult category and nine studies in all ages. The four selected pooled blood parameters for children were white blood cell (WBC) ($\times 10^3/L$) with 5.11 (SD), 5.64 (DwoWS), 5.52 (DwoWS) and 4.68 (Non-SD) hematocrit (HCT) (%) with 36.78 (SD), 40.70 (DwoWS), 35.00 (DwoWS) and 29.78 (Non-SD) platelet (PLT)

($\times 10^3/\mu L$) with 78.66 (SD), 108.01 (DwoWS), 153.47 (DwoWS) and 108.29 (non-SD); and aspartate aminotransferase (AST) ($/\mu L$) with 248.88 (SD), 170.83 (DwoWS), 83.24 (DwoWS) and 102.99 (non-SD). For adult, WBC were 4.96 (SD), 6.44 (DwoWS), 7.74 (DwoWS) and 3.61 (non-SD); HCT were 39.50 (SD), 39.00 (DwoWS), 37.45 (DwoWS) and 41.68 (non-SD); PLT were 49.62 (SD), 96.60 (DwoWS), 114.37 (DwoWS) and 71.13 (non-SD); and AST were 399.50 (SD), 141.01 (DwoWS), 96.19 (DwoWS) and 118.13 (non-SD). These blood parameters could not differentiate between each dengue severity according to the WHO 2009 classification, SD, DwoWS, DwWS and non-SD, because the timing of blood drawing was not known and there was an overlapping confidence interval among the clinical classification. Hence, these pooled blood parameter values could not be used to guide clinicians in management and did not correlate with severity as in previous scientific literatures and guidelines.

Therapeutics for flaviviral infections.

Bifani AM, Chan KWK, Borrenberghs D, Tan MJA, Phoo WW, Watanabe S, Goethals O, Vasudevan SG, Choy MM.

31-12-2022

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/36592668/>

Flaviviruses are vector-borne pathogens capable of causing devastating human diseases. The re-emergence of Zika in 2016 notoriously led to a widescale epidemic in the Americas. New daunting evidence suggests that a single mutation in Zika virus genome may increase transmission and pathogenesis, further highlighting the need to be prepared for flavivirus outbreaks. Dengue, in particular infects about 400 million people each year, leading to reoccurring local outbreaks. Public health efforts to mitigate flavivirus transmission is largely dependent on vector control strategies, as only a limited number of flavivirus vaccines have been developed thus far. There are currently no commercially available antivirals for flaviviruses, leaving supportive care as the primary treatment option. In this review, we will briefly paint a broad picture of the flavivirus landscape in terms of therapeutics, with particular focus on viral targets, promising novel compounds entering the drug discovery pipeline, as well as model systems for evaluating drug efficacy.

Estimation of a cut-off value for immature platelet fraction (IPF) in predicting platelet recovery in dengue patients with thrombocytopenia.

Ahmad J, Md Noor S, Mustapha SZ, Idris F.

Dec-2022

Malays J Pathol.

<https://pubmed.ncbi.nlm.nih.gov/36591717/>

Spatial repellents: The current roadmap to global recommendation of spatial repellents for public health use.

Achee NL, Perkins TA, Moore SM, Liu F, Sagara I, Van Hulle S, Ochomo EO, Gimnig JE, Tissera HA, Harvey SA,

Monroe A, Morrison AC, Scott TW, Reiner RC Jr, Grieco JP.

09-12-2022

Curr Res Parasitol Vector Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/36590345/>

Spatial repellent (SR) products are envisioned to complement existing vector control methods through the continual release of volatile active ingredients (AI) providing: (i) protection against day-time and early-evening biting; (ii) protection in enclosed/semi-enclosed and peri-domestic spaces; (iii) various formulations to fit context-specific applications; and (iv) increased coverage over traditional control methods. SR product AIs also have demonstrated effect against insecticide-resistant vectors linked to malaria and *Aedes*-borne virus (ABV) transmission. Over the past two decades, key stakeholders, including World Health Organization (WHO) representatives, have met to discuss the role of SRs in reducing arthropod-borne diseases based on existing evidence. A key focus has been to establish a critical development path for SRs, including scientific, regulatory and social parameters that would constitute an outline for a SR target product profile, i.e. optimum product characteristics. The principal gap is the lack of epidemiological data demonstrating SR public health impact across a range of different ecological and epidemiological settings, to inform a WHO policy recommendation. Here we describe in brief trials that are designed to fulfill evidence needs for WHO assessment and initial projections of SR cost-effectiveness against malaria and dengue.

Dengue outbreaks in South Asia amid Covid-19: Epidemiology, transmission, and mitigation strategies.

Manna S, Satapathy P, Bora I, Padhi BK.

15-12-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36589966/>

A case report of late treatment failure in Plasmodium falciparum malaria in a traveler from the Democratic Republic of the Congo to India.

Sharma S, Ahmed N, Faizi N, Bharti PK, Sharma A, Srivastava B.

16-12-2022

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/36589765/>

A young male returned from the Democratic Republic of the Congo (DRC) to India after four months during his official work. Within a week of his arrival, he developed a high-grade fever with nausea and was hospitalized in a private hospital in New Delhi. He was diagnosed with malaria, treated with an artesunate injection as antimalarial, and discharged on day 5th from the hospital. A week later, he was diagnosed with malaria and dengue positive at ICMR-National Institute of Malaria Research, New Delhi. Artesunate with sulphadoxine and pyrimethamine (AS+SP) was administered following India's

malaria treatment policy. However, high-grade fever, along with the asexual stage of the *P. falciparum* parasite, was observed within 28 days of treatment with AS+SP, signifying late treatment failure (LTF). Further, the molecular analysis from both the days of episodes was analyzed using genomic DNA from dried blood spots, revealing resistance to sulphadoxine-pyrimethamine with mutations at codons *pfdhfr* 51I, *pfdhfr* 59 R, *pfdhfr* 108 N, *pfdhps* 437 A, *pfdhps* 581 G. No functional mutation associated was found in *pfKelch13*, but interestingly the sensitive codons to chloroquine (CQ) (wild type *pfcrk76* and *pfmdrN86*) revealed the probably reversible CQ sensitivity in the sample from DRC.

A perfect storm: acute portal vein thrombosis in a patient with severe dengue and hemorrhagic manifestations-a case report.

Gonzalez CER, Villamizar JDC, León YM, García DFG, Hurtado KTC.

2022

Egypt Liver J.

<https://pubmed.ncbi.nlm.nih.gov/36589635/>

The impact of COVID-19 followed by extreme flooding on vector borne diseases in Pakistan: A mini narrative review.

Rahmat ZS, Sadiq M, Vohra LI, Ullah H, Essar MY.

Jan-2023

New Microbes New Infect.

<https://pubmed.ncbi.nlm.nih.gov/36589270/>

While the Coronavirus pandemic continues to spread havoc across the world, countries like Pakistan are faced with another challenge: the steady rise of vector borne diseases alongside a spike in COVID-19 cases. Moreover, signs and clinical manifestations of multiple arbovirus infections mimic those experienced in COVID-19, causing further complications in management and diagnosis. Without urgent adequate management and testing equipment, the recent surge of COVID-19 along with the steady rise in Vector Borne Diseases (VBDs) could collapse the exhausted Pakistani healthcare system. This article explores the impact of COVID-19 on the management, diagnosis, and treatment of the common arbovirus infections of Pakistan, including dengue (DENV), malaria, chikungunya (CHIKV), and other foreign infections that are on a hazardous rise.

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.

01-01-2023

Phytother Res.

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

Cepharanthine Inhibits Dengue Virus Production and Cytokine Secretion.

Phumesin P, Panaampon J, Kariya R, Limjindaporn T, Yenchitsomanus PT, Okada S.

29-12-2022

Virus Res.

<https://pubmed.ncbi.nlm.nih.gov/36587870/>

Dengue virus (DENV) infection is a public health problem in tropical and subtropical regions. It can cause a spectrum of clinical manifestations ranging from mild dengue fever (DF) to severe dengue haemorrhagic fever (DHF) and potentially life-threatening disease including dengue shock syndrome (DSS). Severe DENV infection is caused by high viral load and cytokine storm in dengue-infected patients. Currently, there is no specific antiviral drug for DENV infection. An anti-DENV agent that demonstrates inhibitory effects on both DENV replication and cytokine secretion is urgently needed. In this study, cepharanthine (CEP), which is an anti-inflammatory, anti-HIV, and anti-tumor compound isolated from *Stephania cepharantha* Hayata, was tested for inhibition of DENV infection. We investigated the efficacy of CEP to inhibit DENV infection, replication, and cytokine production. The inhibitory effect of CEP treatment was studied in DENV-infected human chronic myeloid leukemia (K562) cells. The levels of DENV E protein and DENV production were determined by flow cytometry and FFU assay, respectively. CEP treatment significantly reduced viral E protein and viral production in all DENV-1, 2, 3, 4 serotypes. In addition, CEP treatment reduced the IL-6 proinflammatory cytokine production in DENV-infected A549 cells. Taken together, CEP has inhibitory effects on DENV infection specifically at the initial viral replication states and proinflammatory cytokine secretion, and is a promising candidate for further development as an anti-DENV treatment.

Dengue virus Induced autophagy is mediated by HMGB1 and promotes viral propagation.

Chaudhary N, Srivastava S, Gupta S, Menon MB, Patel AK.

29-12-2022

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/36587643/>

Dengue virus (DENV) exploits various cellular pathways including autophagy to assure enhanced virus propagation. The mechanisms of DENV mediated control of autophagy pathway are largely unknown. Our investigations have revealed a novel role for high-mobility group box1 protein (HMGB1) in regulation of cellular autophagy process in DENV-2 infected A549 cell line. While induction of autophagy by rapamycin treatment resulted in enhanced DENV-2 propagation, the blockade of autophagy flux with bafilomycin A1 suppressed viral replication. Furthermore, siRNA-mediated silencing of HMGB1 significantly abrogated dengue induced autophagy, while LPS induced HMGB1 expression counteracted these effects. Interestingly, silencing of HMGB1 showed reduction of BECN1 and stabilization of BCL-2 protein. On the contrary, LPS induction of HMGB1 resulted in enhanced BECN1 and reduction in BCL-2 levels.

This study shows that the modulation of autophagy by DENV-2 is HMGB1/BECN1 dependent. In addition, glycyrrhizic acid (GA), a potent HMGB1 inhibitor suppressed autophagy as well as DENV-2 replication. Altogether, our data suggests that HMGB1 induces BECN1 dependent autophagy to promote DENV-2 replication.

Mechanism of autophagy induced by activation of the AMPK/ERK/mTOR signaling pathway after TRIM22-mediated DENV-2 infection of HUVECs.

Wu N, Gou X, Hu P, Chen Y, Ji J, Wang Y, Zuo L.

31-12-2022

Virol J.

<https://pubmed.ncbi.nlm.nih.gov/36587218/>

Flavivirus proteases: The viral Achilles heel to prevent future pandemics.

Teramoto T, Choi KH, Padmanabhan R.

29-12-2022

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/36586467/>

Modeling the spread of the Zika virus by sexual and mosquito transmission.

Agudelo S, Ventresca M.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584063/>

Zika Virus (ZIKV) is a flavivirus that is transmitted predominantly by the *Aedes* species of mosquito, but also through sexual contact, blood transfusions, and congenitally from mother to child. Although approximately 80% of ZIKV infections are asymptomatic and typical symptoms are mild, multiple studies have demonstrated a causal link between ZIKV and severe diseases such as Microcephaly and Guillain Barré Syndrome. Two goals of this study are to improve ZIKV models by considering the spread dynamics of ZIKV as both a vector-borne and sexually transmitted disease, and also to approximate the degree of under-reporting. In order to accomplish these objectives, we propose a compartmental model that allows for the analysis of spread dynamics as both a vector-borne and sexually transmitted disease, and fit it to the ZIKV incidence reported to the National System of Public Health Surveillance in 27 municipalities of Colombia between January 1 2015 and December 31 2017. We demonstrate that our model can represent the infection patterns over this time period with high confidence. In addition, we argue that the degree of under-reporting is also well estimated. Using the model we assess potential viability of public health scenarios for mitigating disease spread and find that targeting the sexual pathway alone has negligible impact on overall spread, but if the proportion of risky sexual behavior increases then it may become important. Targeting mosquitoes remains the best approach of those considered. These results may be useful for public health organizations and governments to construct and implement suitable health policies and reduce the impact of the Zika outbreaks.

Using machine learning to understand microgeographic determinants of the Zika vector, *Aedes aegypti*.

Alexander J, Wilke ABB, Mantero A, Vasquez C, Petrie W, Kumar N, Beier JC.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584050/>

There are limited data on why the 2016 Zika outbreak in Miami-Dade County, Florida was confined to certain neighborhoods. In this research, *Aedes aegypti*, the primary vector of Zika virus, are studied to examine neighborhood-level differences in their population dynamics and underlying processes. Weekly mosquito data were acquired from the Miami-Dade County Mosquito Control Division from 2016 to 2020 from 172 traps deployed around Miami-Dade County. Using random forest, a machine learning method, predictive models of spatiotemporal dynamics of *Ae. aegypti* in response to meteorological conditions and neighborhood-specific socio-demographic and physical characteristics, such as land-use and land-cover type and income level, were created. The study area was divided into two groups: areas affected by local transmission of Zika during the 2016 outbreak and unaffected areas. *Ae. aegypti* populations in areas affected by Zika were more strongly influenced by 14- and 21-day lagged weather conditions. In the unaffected areas, mosquito populations were more strongly influenced by land-use and day-of-collection weather conditions. There are neighborhood-scale differences in *Ae. aegypti* population dynamics. These differences in turn influence vector-borne disease diffusion in a region. These results have implications for vector control experts to lead neighborhood-specific vector control strategies and for epidemiologists to guide vector-borne disease risk preparations, especially for containing the spread of vector-borne disease in response to ongoing climate change.

The correlation between serum 25-hydroxy-vitamin D levels and anti-SARS-CoV-2 S-RBD IgG and neutralizing antibody levels among cancer patients receiving COVID-19 vaccines.

Rachman A, Iriani A, Priantono D, Rumondor BB, Betsy R, Juanputra S.

13-12-2022

Front Nutr.

<https://pubmed.ncbi.nlm.nih.gov/36583218/>

Acute acalculous cholecystitis in a patient with dengue fever: A case report.

Gurung S, Karki S, Khadka M, Gurung S, Dhakal S.

17-11-2022

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/36582863/>

The threat of dengue in Europe.

Buchs A, Conde A, Frank A, Gottet C, Hedrich N, Lovey T, Shindleman H, Schlagenhauf P.

30-11-2022

New Microbes New Infect.

<https://pubmed.ncbi.nlm.nih.gov/36582814/>

Chikungunya patient transcriptional signatures faithfully recapitulated in a C57BL/6J mouse model.

Bishop CR, Caten FT, Nakaya HI, Suhrbier A.

12-12-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36578476/>

Structural basis of transition from initiation to elongation in de novo viral RNA-dependent RNA polymerases.

Wu J, Wang X, Liu Q, Lu G, Gong P.

03-01-2023

Proc Natl Acad Sci U S A.

<https://pubmed.ncbi.nlm.nih.gov/36577062/>

De novo viral RNA-dependent RNA polymerases (RdRPs) utilize their priming element (PE) to facilitate accurate initiation. Upon transition to elongation, the PE has to retreat from the active site to give room to the template-product RNA duplex. However, PE conformational change upon this transition and the role of PE at elongation both remain elusive. Here, we report crystal structures of RdRP elongation complex (EC) from dengue virus serotype 2 (DENV2), demonstrating a dramatic refolding of PE that allows establishment of interactions with the RNA duplex backbone approved to be essential for EC stability. Enzymology data from both DENV2 and hepatitis C virus (HCV) RdRPs suggest that critical transition of the refolding likely occurs after synthesis of a 4- to 5-nucleotide (nt) product together providing a key basis in understanding viral RdRP transition from initiation to elongation.

Epidemiology and costs of dengue in Thailand: A systematic literature review.

Thisyakorn U, Saokaew S, Gallagher E, Kastner R, Suamsiri R, Oliver L, Hanley R.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534668/>

A peptide derived from the N-terminal of NS2A for the preparation of ZIKV NS2A recognition polyclonal antibody.

Yu Y, Chen Y, Wang J, Fan X, He Z, Qiao S, Hou S, Zou P.

Jan-2023

J Immunol Methods.

<https://pubmed.ncbi.nlm.nih.gov/36463933/>

Zika virus non-structural protein NS2A participates in viral replication, organization, and budding, as well as escaping host immunity. NS2A also involved in the induction of microcephaly by ZIKV. However, the above studies were mainly performed through NS2A with a tag due to the lack of available antibodies against NS2A. ZIKV NS2A is a multiplex transmembrane protein, which leads to difficulties in the preparation of its recognition antibodies, thus seriously affecting the study of ZIKV NS2A. In this

study, we found that a peptide (GSTDHMDHFSGLGVL) derived from the N-terminal of ZIKV NS2A coupled to KLH induced antibodies recognizing ZIKV NS2A in rabbits. The purified polyclonal antibody recognized ZIKV NS2A in ZIKV-infected cells with high efficiency and specificity, as detected by western blot and immunofluorescence assay. Our study has important implications for the preparation of ZIKV NS2A antibodies and the in-depth study of ZIKV NS2A.

A competition smFRET assay to study ligand-induced conformational changes of the dengue virus protease.

Maus H, Hinze G, Hammerschmidt SJ, Basché T, Schirmeister T.

Jan-2023

Protein Sci.

<https://pubmed.ncbi.nlm.nih.gov/36461913/>

Ligand binding to proteins often is accompanied by conformational transitions. Here, we describe a competition assay based on single molecule Förster resonance energy transfer (smFRET) to investigate the ligand-induced conformational changes of the dengue virus (DENV) NS2B-NS3 protease, which can adopt at least two different conformations. First, a competitive ligand was used to stabilize the closed conformation of the protease. Subsequent addition of the allosteric inhibitor reduced the fraction of the closed conformation and simultaneously increased the fraction of the open conformation, demonstrating that the allosteric inhibitor stabilizes the open conformation. In addition, the proportions of open and closed conformations at different concentrations of the allosteric inhibitor were used to determine its binding affinity to the protease. The K_D value observed is in accordance with the IC_{50} determined in the fluorometric assay. Our novel approach appears to be a valuable tool to study conformational transitions of other proteases and enzymes.

Biologics for dengue prevention: up-to-date.

Waickman AT, Newell K, Endy TP, Thomas SJ.

Jan-2023

Expert Opin Biol Ther.

<https://pubmed.ncbi.nlm.nih.gov/36417290/>

Immunogenicity of a Live Dengue Vaccine (TAK-003).

de Silva A, White L.

28-12-2022

J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36285800/>

Fetal Zika virus infection diagnosed by metagenomic next-generation sequencing of amniotic fluid.

Fourgeaud J, Regnault B, Faury H, Da Rocha N, Jamet A, Stirnemann J, Eloit M, Perot P, Leruez-Ville M, Driessen M; Collaborators.

Jan-2023

Ultrasound Obstet Gynecol.

<https://pubmed.ncbi.nlm.nih.gov/36102858/>

RNA In Situ Hybridization and Immunohistochemistry to Visualize Gene Expression in Peripheral Chemosensory Tissues of Mosquitoes.

Herre M, Greppi C.

03-01-2023

Cold Spring Harb Protoc.

<https://pubmed.ncbi.nlm.nih.gov/35940640/>

Mosquito-borne diseases such as malaria, Zika virus, and dengue virus are a menace to the human population. Although many mosquito species are not attracted to humans and do not feed on blood, human-biting female mosquitoes are strongly attracted to people and use chemosensory cues to identify a suitable host for a blood meal. Mosquitoes need blood components to reproduce, rendering them excellent vectors for blood-borne diseases. The three genera (*Culex*, *Anopheles*, and *Aedes*) responsible for most of these diseases find hosts by using their peripheral sensory organs. These organs include the antennae, maxillary palps, and proboscis. All three contain diverse populations of highly sensitive neurons that express sensory receptors that can detect odorants, temperature, chemicals, and tastants. Although these organs are essential to the host-seeking behavior that results in biting, their small size and thick outer cuticle can hinder typical histochemical analyses. Here, we briefly review the role the peripheral sensory organs play in mosquito behavior. Then, we introduce how to investigate their gene expression profiles using immunohistochemical and RNA in situ approaches for both whole-mount and frozen-section preparations.

Clinical and laboratory characteristics of dengue and COVID-19 coinfecting patients in Dhaka, Bangladesh.

Hannan TB, Hossain Z, Hasan MN, Khan AH, Alam MR, Rahman MM, Arafat SM, Chowdhury FR.

03-01-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/35443278/>

Background: Dengue-COVID-19 coinfection is one of the greatest emerging challenges in dengue-endemic areas during the continuing pandemic. With coinciding clinical and laboratory pictures, early diagnosis becomes burdensome, with management discrepancy. **Methods:** A descriptive study was performed on dengue-COVID-19 coinfecting patients during July-August 2021 for an overview of disease progression, severity and outcome. A total of 11 patients who were positive for dengue NS1 and/or antidengue IgM were included in this study. **Results:** In total, 45.5% patients developed severe COVID-19 disease, 45.5% patients developed group B dengue fever and 9% patients developed group C dengue fever. Concurrent severity of both diseases was seen to be rare, except for in one patient. **Conclusion:** Early diagnosis and compatible management still stand as basic principles to prevent fatality and morbidity.

Effect of mutation of NS2B cofactor residues on Dengue 2 NS2B-NS3 protease complex - an insight to viral replication.

Mohanty AK, Kumar MS.

Feb-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/34871140/>

Immuno-informatics guided designing of a multi-epitope vaccine against Dengue and Zika.

Bhardwaj A, Sharma R, Grover A.

Jan-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/34796791/>

Rage

"SPATIAL PATTERNS AND RISK OF AGGRESSION OF DOGS AND CATS IN A CENTRAL TOWNSHIP OF MEXICO CITY".

Quezada-Nolasco JL, Galarde-López M, Sánchez-Zamorano LM, Serrano-Márquez JM, Arvizu-Tovar LO, Reyna-Sevilla A, Gallardo VMA, Soberanis-Ramos O.

02-01-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36603802/>

Dog and cat aggressions are public health concerns associated with rabies transmission to the human population. The social and environmental conditions of marginalized and urban areas stand a risk due to people's contact with dogs. This study aimed to identify spatial patterns related to dog and cat aggression in a densely populated area in the center of Mexico City, analyzing the risk of aggression at the census unit level in the 2018-2020 triennium. This cross-sectional study was carried out in Coyoacán, in the south-central area of Mexico City's urbanized region. The total number of cases ($n = 1,078$) was obtained from monthly records of aggressions by dogs and cats, from the Control and Prevention of Zoonoses-Rabies Program of the Coyoacán Sanitary Jurisdiction. The information collected was related to the victims and the aggressors. Associations between the occurrence of bites and the characteristics of the victim were evaluated using a geographic information system (GIS), as well as the spatio-temporal distribution of the aggressions to the census unit level. Out of 1,078 cases reported, 977 (90.6%) were caused by dogs and 101 (9.4%) by cats, 55.1% ($n = 587$) occurred within the same household, and 13.7% ($n = 148$) were categorized as severe injuries. Adult men were the most affected group. Attacks on the street had a higher risk of resulting in a severe injury, compared to those that occurred at home (OR 1.63, 95CI 1.15 - 2.31, $p < 0.006$). According to the standardized rate of the triennium, the values ranged between 54.1 and 619 aggressions per 100,000 inhabitants, and summer was the season with a higher probability of occurrence. These results provide a basis for the analytical investigation of

the spatial patterns of dog and cat aggression, highlighting the need to implement efficient surveillance systems and public health strategies.

Rabies Encephalitis and the Use of Optic Nerve Sheath Diameter to Detect Elevated Intracranial Pressure.

Arreaza Kaufman D, Teng E, Biro N.

03-12-2022

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/36601198/>

Rabies is a rare but rapidly progressive and almost universally fatal disease. A previously healthy 59-year-old male presented with rabies encephalitis. We measured his optic nerve sheath diameter (ONSD) daily in both eyes using ultrasonography to indirectly monitor for elevated intracranial pressure (ICP). We performed CT and MRI brain on days when his ONSD changed significantly. An increase in ONSD temporally correlated with radiologic findings of cerebral edema and acute subarachnoid hemorrhage (SAH). ONSD measurement is a fast, inexpensive, and widely-available imaging modality that may serve as a surrogate marker for elevated ICP. It may be especially useful in patients who are difficult to be transported to radiology due to the unstable nature of their disease.

Re-formation of synaptic connectivity in dissociated human stem cell-derived retinal organoid cultures.

Ludwig AL, Mayerl SJ, Gao Y, Banghart M, Bacig C, Fernandez Zepeda MA, Zhao X, Gamm DM.

10-01-2023

Proc Natl Acad Sci U S A.

<https://pubmed.ncbi.nlm.nih.gov/36598946/>

Human pluripotent stem cell (hPSC)-derived retinal organoids (ROs) can efficiently and reproducibly generate retinal neurons that have potential for use in cell replacement strategies [Capowski *et al.*, *Development* 146, dev171686 (2019)]. The ability of these lab-grown retinal neurons to form new synaptic connections after dissociation from ROs is key to building confidence in their capacity to restore visual function. However, direct evidence of reestablishment of retinal neuron connectivity via synaptic tracing has not been reported to date. The present study employs an in vitro, rabies virus-based, monosynaptic retrograde tracing assay [Wickersham *et al.*, *Neuron* 53, 639-647 (2007); Sun *et al.*, *Mol. Neurodegener.* 14, 8 (2019)] to identify de novo synaptic connections among early retinal cell types following RO dissociation. A reproducible, high-throughput approach for labeling and quantifying traced retinal cell types was developed. Photoreceptors and retinal ganglion cells-the primary neurons of interest for retinal cell replacement-were the two major contributing populations among the traced presynaptic cells. This system provides a platform for assessing synaptic connections in cultured retinal neurons and sets the stage for future cell replacement studies aimed at characterizing or enhancing synaptogenesis. Used in this manner, in vitro synaptic tracing is envisioned to complement traditional preclinical

animal model testing, which is limited by evolutionary incompatibilities in synaptic machinery inherent to human xenografts.

Subthalamic neurons interact with nigral dopaminergic neurons to regulate movement in mice.

Fan JP, Zhang X, Han Y, Ji Y, Gu WX, Wu HC, Zhou CY, Xiao C.

04-01-2023

Acta Physiol (Oxf).

<https://pubmed.ncbi.nlm.nih.gov/36598331/>

Backyard chickens - A cross-sectional survey of current and prospective backyard chicken owners in Ontario (2019-2021).

Paphitis K, Metcalf D, Weese JS.

Jan-2023

Can Vet J.

<https://pubmed.ncbi.nlm.nih.gov/36593929/>

Biochemical monitoring throughout all stages of rabies virus-like particles production by Raman spectroscopy using global models.

Guardalini LGO, da Silva Cavalcante PE, Leme J, de Mello RG, Bernardino TC, Astray RM, Barbosa E, da Silveira SR, Ho PL, Tonso A, Jorge SAC, Núñez NGF.

29-12-2022

J Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/36587847/>

An inactivated recombinant rabies virus chimerically expressed RBD induces humoral and cellular immunity against SARS-CoV-2 and RABV.

Zhang H, Jin H, Yan F, Song Y, Dai J, Jiao C, Bai Y, Sun J, Liu D, Wang S, Zhang M, Lu J, Huang J, Huang P, Li Y, Xia X, Wang H.

29-12-2022

Virol Sin.

<https://pubmed.ncbi.nlm.nih.gov/36587795/>

Many studies suggest that severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) can infect various animals and transmit among animals, and even to humans, posing a threat to humans and animals. There is an urgent need to develop inexpensive and efficient animal vaccines to prevent and control coronavirus disease 2019 (COVID-19) in animals. Rabies virus (RABV) is another important zoonotic pathogen that infects almost all warm-blooded animals and poses a great public health threat. The present study constructed two recombinant chimeric viruses expressing the S1 and RBD proteins of the SARS-CoV-2 Wuhan01 strain based on a reverse genetic system of the RABV SRV9 strain and evaluated their immunogenicity in mice, cats and dogs. The results showed that both inactivated recombinant viruses induced durable neutralizing antibodies against SARS-CoV-2 and RABV and a strong cellular immune response in

mice. Notably, inactivated SRV-nCoV-RBD induced earlier antibody production than SRV-nCoV-S1, which was maintained at high levels for longer periods. Inactivated SRV-nCoV-RBD induced neutralizing antibodies against both SARS-CoV-2 and RABV in cats and dogs, with a relatively broad-spectrum cross-neutralization capability against the SARS-CoV-2 pseudoviruses including Alpha, Beta, Gamma, Delta, and Omicron, showing potential to be used as a safe bivalent vaccine candidate against COVID-19 and rabies in animals.

Emerging tick-borne spotted fever group rickettsioses in the Balkans.

Banović P, Díaz-Sánchez AA, Foucault-Simonin A, Mateos-Hernandez L, Wu-Chuang A, Galon C, Simin V, Mijatović D, Bogdan I, Corona-González B, Báez LC, Kulisz J, Woźniak A, Zając Z, Obregón D, Moutailler S, Cabezas-Cruz A.

28-12-2022

Infect Genet Evol.

<https://pubmed.ncbi.nlm.nih.gov/36586459/>

Trachome

Indian traditional medicinal plants in ophthalmic diseases.

Nafees S, Akhtar J, Kaur J.

Nov-Dec 2022

Avicenna J Phytomed.

<https://pubmed.ncbi.nlm.nih.gov/36583172/>

Objective: Traditional herbal plants have been in use since ancient times to treat ophthalmic conditions; so, the aim of this study is to evaluate some potent Indian traditional medicinal plants used in ophthalmic diseases in order to summarize their potential effect in ophthalmology along with their mechanism of action. **Materials and methods:** Databases PubMed, Google Scholar, and Embase were extensively explored. Additionally, relevant textbooks and literatures were consulted to summarize most of the considerable scientific literature for the review. Search term included ophthalmology, glaucoma, cataract, trachoma, conjunctivitis, traditional medicines, Unani drugs, and ayurvedic drugs were used. Around 80 review articles were consulted from the year 1982 to 2021. **Results:** The traditional medicinal plants are easily available, cost-effective and have no associated side effects in comparison to current conventional treatments. Moreover, these drugs in oppose to modern medicine, have an inherent potential to accelerate the body's own immunity to fight against any infection. A large volume of scientific studies has reported the beneficial effects of traditional drugs in ophthalmology. **Conclusion:** This review, therefore, describes the potential benefits and uses of some traditional medicinal plants used in ophthalmic diseases.

Ulcère de Buruli

Prevalence of skin Neglected Tropical Diseases and superficial fungal infections in two peri-urban schools and one rural community setting in Togo.

Saka B, Kassang P, Gnosike P, Head MG, Akakpo AS, Teclessou JN, Elegbede YM, Mouhari-Toure A, Mahamadou G, Tevi K, Katsou K, Kombaté K, Walker SL, Pitché P.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534701/>

Introduction: Skin neglected tropical diseases (NTDs), are endemic and under-diagnosed in many lower-income communities. The objective of this study was to determine the prevalence of skin NTDs and fungal infections in two primary schools and a community setting in rural Togo.

Method: This was a cross-sectional study that took place between June-October 2021. The two primary schools are located on the outskirts of Lomé, the capital city. The community setting was Ndjéi, in north-east Togo. Study sites were purposively selected. Dermatologists examined the skin of study participants. Diagnosis of skin NTDs were made clinically. **Results:** A total of 1401 individuals were examined, 954 (68.1%) from Ndjéi community, and 447 (31.9%) were children in the schools. Cutaneous skin infections were diagnosed in 438 (31.3%) participants, of whom 355 (81%) were in community settings. There were 105 observed skin NTDs (7.5%). Within the school setting, there were 20 individuals with NTDs (4.5% of 447 participants), and 85 NTDs (8.9%) from 954 community participants. Across all settings 68/1020 (6.7%) NTDs were in children, and 37/381 (9.7%) in adults. In addition, there were 333 observed mycoses (23.8% prevalence). The main cutaneous NTDs diagnosed were scabies (n = 86; 6.1%) and suspected yaws (n = 16, 1.1%). The prevalence of scabies in schools was 4.3%, and 7.0% in the rural community. One case of leprosy was diagnosed in each school and the rural community, and one suspected Buruli Ulcer case in the community. In the school setting, five (6%) children with a skin NTD reported being stigmatised, four of whom had refused to attend school because of their dermatosis. In Ndjéi, 44 (4.6%) individuals reported having experienced stigma and 41 (93.2%) of them missed at least one day of school or work. **Conclusion:** This study shows that the burden of scabies and skin infections such as superficial mycoses is high in the school and rural community settings in Togo, with associated presence of stigma. Improved health promotion and education across institutional and community settings may reduce stigma and encourage early reporting of skin infection cases to a health facility.

Pian

Prevalence of skin Neglected Tropical Diseases and superficial fungal infections in two peri-urban schools and one rural community setting in Togo.

Saka B, Kassang P, Gnosike P, Head MG, Akakpo AS, Teclessou JN, Elegbede YM, Mouhari-Toure A, Mahamadou G, Tevi K, Katsou K, Kombaté K, Walker SL, Pitché P.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534701/>

Introduction: Skin neglected tropical diseases (NTDs), are endemic and under-diagnosed in many lower-income communities. The objective of this study was to determine the prevalence of skin NTDs and fungal infections in two primary schools and a community setting in rural Togo.

Method: This was a cross-sectional study that took place between June-October 2021. The two primary schools are located on the outskirts of Lomé, the capital city. The community setting was Ndjéi, in north-east Togo. Study sites were purposively selected. Dermatologists examined the skin of study participants. Diagnosis of skin NTDs were made clinically. **Results:** A total of 1401 individuals were examined, 954 (68.1%) from Ndjéi community, and 447 (31.9%) were children in the schools. Cutaneous skin infections were diagnosed in 438 (31.3%) participants, of whom 355 (81%) were in community settings. There were 105 observed skin NTDs (7.5%). Within the school setting, there were 20 individuals with NTDs (4.5% of 447 participants), and 85 NTDs (8.9%) from 954 community participants. Across all settings 68/1020 (6.7%) NTDs were in children, and 37/381 (9.7%) in adults. In addition, there were 333 observed mycoses (23.8% prevalence). The main cutaneous NTDs diagnosed were scabies (n = 86; 6.1%) and suspected yaws (n = 16, 1.1%). The prevalence of scabies in schools was 4.3%, and 7.0% in the rural community. One case of leprosy was diagnosed in each school and the rural community, and one suspected Buruli Ulcer case in the community. In the school setting, five (6%) children with a skin NTD reported being stigmatised, four of whom had refused to attend school because of their dermatosis. In Ndjéi, 44 (4.6%) individuals reported having experienced stigma and 41 (93.2%) of them missed at least one day of school or work. **Conclusion:** This study shows that the burden of scabies and skin infections such as superficial mycoses is high in the school and rural community settings in Togo, with associated presence of stigma. Improved health promotion and education across institutional and community settings may reduce stigma and encourage early reporting of skin infection cases to a health facility.

Two *Streptococcus pyogenes* emm types and several anaerobic bacterial species are associated with idiopathic cutaneous ulcers in children after community-based mass treatment with azithromycin.

Griesenauer B, Xing Y, Fortney KR, Gao X, González-Beiras C, Nelson DE, Ren J, Mitjà O, Dong Q, Spinola SM.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534698/>

Background: In yaws-endemic areas, two-thirds of exudative cutaneous ulcers (CU) are associated with *Treponema pallidum* subsp. *pertenue* (TP) and

Haemophilus ducreyi (HD); one-third are classified as idiopathic ulcers (IU). A yaws eradication campaign on Lihir Island in Papua New Guinea utilizing mass drug administration (MDA) of azithromycin initially reduced but failed to eradicate yaws; IU rates remained constant throughout the study. Using 16S rRNA gene sequencing, we previously determined that *Streptococcus pyogenes* was associated with some cases of IU. Here, we applied shotgun metagenomics to the same samples we analyzed previously by 16S rRNA sequencing to verify this result, identify additional IU-associated microorganisms, and determine why *S. pyogenes*-associated IU might have persisted after MDA of azithromycin.

Methodology/principal findings: We sequenced DNA extracted from 244 CU specimens separated into four groups based upon microorganism-specific PCR results (HD+, TP+, TP+HD+, and TP-HD- or IU). *S. pyogenes* was enriched in IU (24.71% relative abundance [RA]) specimens compared to other ulcer sub-groups, confirming our prior results. We bioinformatically identified the *emm* (M protein gene) types found in the *S. pyogenes* IU specimens and found matches to *emm156* and *emm166*. Only ~39% of IU specimens contained detectable *S. pyogenes*, suggesting that additional organisms could be associated with IU. In the sub-set of *S. pyogenes*-negative IU specimens, *Criobacterium bergeronii*, a member of the Peptostreptococcaceae, and *Fusobacterium necrophorum* (7.07% versus 0.00% RA and 2.18% versus 0.00% RA, respectively), were enriched compared to the *S. pyogenes*-positive sub-set. Although a broad range of viruses were detected in the CU specimens, none were specifically associated with IU.

Conclusions/significance: Our observations confirm the association of *S. pyogenes* with IU in yaws-endemic areas, and suggest that additional anaerobic bacteria, but not other microorganisms, may be associated with this syndrome. Our results should aid in the design of diagnostic tests and selective therapies for CU.

Lèpre

Long-term presence of autoantibodies in plasma of cured leprosy patients.

Yang X, Dong H, Kuang YQ, Yu XF, Long H, Zhang CY, Wang D, Zhang DF, Li YY.

05-01-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/36604576/>

Autoantibodies have been detected in leprosy patients, indicating that infection with *M. leprae* may lead to autoimmune disorders. However, whether autoimmune response last until patients are cured is unknown. Knowing the autoimmune response in cured leprosy patients is essential to identify whether symptoms are caused by leprosy itself or by other immune-related diseases. This knowledge is essential for the ongoing health management in cured leprosy patients where autoimmune disorders still exist. In our study, we selected six autoantibodies, including anticardiolipin antibody of IgG (ACA), anti-nuclear antibody (ANA), extractable nuclear antigen antibody (ENA), anti-streptolysin O (ASO),

anti-double stranded DNA antibody (dsDNA), and rheumatoid factor (RF), that had been reported in leprosy patients as typical autoantibodies. We tested the six typical autoantibodies combined with LACC1, which encodes a protein associated with autoimmune disease such as Crohn's disease and is also the susceptible gene conferring leprosy risk, in cured leprosy patients through ELISA to assess the cured patient's immune status. We observed high positive rates of autoantibodies in cured leprosy patients, and the average plasma levels of five (ACA, ANA, ENA, ASO, and RF) out of the six autoantibodies were significantly higher in cured leprosy patients than in controls. The positive detection of autoantibodies is independent of the recovery period. Moreover, the level of these autoantibodies showed a strong positive correlation with the level of LACC1 in both controls and cured patients. This study showed that there is long-term autoimmunological activation in leprosy patients, even after decades of recovery. Autoimmune responses may influence the development and prognosis of leprosy. Special care should be given to posttreatment or cured leprosy patients regarding long-term autoimmunological activation.

Whole-transcriptome-based skin virome profiling in typical epidermodysplasia verruciformis reveals α -, β - and γ -HPV infections.

Saeidian AH, Youssefian L, Naji M, Mahmoudi H, Barnada SM, Huang CY, Naghipoor K, Hozhabrpour A, Park JS, Manzo Margiotta F, Vahidnezhad F, Saffarian Z, Kamyab-Hesari K, Tolouei M, Faraji N, Azimi SZ, Namdari G, Mansouri P, Casanova JL, Béziat V, Jouanguy E, Uitto J, Vahidnezhad H.

05-01-2023

JCI Insight.

<https://pubmed.ncbi.nlm.nih.gov/36602881/>

Human papillomaviruses (HPVs), are DNA viruses, including ~450 types, classified into five genera (α -, β -, γ -, μ -, and ν -HPV). The γ - and β -HPVs are present in low-copy numbers in healthy individuals, however, in patients with an inborn error of immunity, certain species of β -HPVs can cause epidermodysplasia verruciformis (EV), manifesting as recalcitrant cutaneous warts and skin cancer. EV presents as either "typical" or "atypical". Manifestations in typical EV are limited to the skin and are caused by abnormal keratinocyte-intrinsic immunity to β -HPVs due to pathogenic sequence variants in TMC6, TMC8, or CIB1. We applied a transcriptome-based computational pipeline, VirPy, on RNA extracted from normal-appearing skin and wart samples of patients with typical EV, to explore the viral and human genetic determinants. In 26 patients, nine distinct biallelic mutations in TMC6 (5), TMC8 (1), and CIB1 (3), seven being previously unreported, were detected. Additionally, 20 different HPV species, including three α -, 16 β -, and one γ -HPVs, were detected, eight of which are being reported for the first time in EV patients (β -HPV-37, -47, -80, -151, -159, α -HPV-2, -57, and γ -HPV-128). This study expands the TMC6, TMC8, and CIB1 sequence variant spectrum and implicates new HPV subtypes in the pathogenesis of typical EV.

Clinico-Epidemiological Profile of Allergic Contact Dermatitis and Its Correlation With Patch Testing in a Tertiary Care Center in Eastern India.

Sahu S, Sethy M, Besra L, Sachan S, Kar HK, Devi BK.

01-12-2022

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/36601177/>

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

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

03-01-2023

PLoS Negl Trop Dis.

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

Background: Adipose derived stromal vascular fraction (SVF) contains a heterogeneous population of mononuclear cells, progenitor cells and about 1-10% are mesenchymal stromal cells. These cells are an ideal candidate for regenerative medicine for peripheral neuropathy. Leprosy is a disabling disorder with neuropathy, usually with consequences of permanent disability of the extremities. We conducted a preliminary study to evaluate the cell yield, its characteristics and clinical outcomes after SVF injections in four leprosy patients. **Methods:** Four post leprosy patients were recruited and evaluated for sensory testing (warm detection, cold detection, vibration, pain and sensation) on the ulnar area of the hand. Liposuction was done and adipose tissue was processed into SVF with a closed system and injected to the ulnar area of the hand at the dorsal and palmar side. Evaluation of sensory testing was done after 3 days, 1 week, 1 month and 3 months following SVF injection. SVF was also characterized using flow cytometry, cell counting, sterility and presence of mycobacteria. **Results:** The results showed that leprosy patients had a low count of mesenchymal cells and a high amount of CD34/CD45 positive cells. One patient was positive for mycobacteria from his adipose tissue and SVF. Sensory examination after SVF injection showed an improvement in temperature and pain sensation in the palmar and superficial branch. Meanwhile, touch sensation improved on the dorsal branch, and there was no improvement for vibration in all patients. **Conclusions:** The results showed that SVF had a potential to improve sensory loss in leprosy patients.

Endoplasmic reticulum stress mediates the myeloid-derived immune suppression associated with cancer and infectious disease.

Lou X, Gao D, Yang L, Wang Y, Hou Y.

02-01-2023

J Transl Med.

<https://pubmed.ncbi.nlm.nih.gov/36593497/>

Myeloid-derived suppressor cells (MDSCs), which are immature heterogeneous bone marrow cells, have been described as potent immune regulators in human and

murine cancer models. The distribution of MDSCs varies across organs and is divided into three subpopulations: granulocytic MDSCs or polymorphonuclear MDSCs (G-MDSCs or PMN-MDSCs), monocytic MDSCs (M-MDSCs), as well as a recently identified early precursor MDSC (eMDSCs) in humans. Activated MDSCs induce the inactivation of NK cells, CD4+, and CD8+ T cells through a variety of mechanisms, thus promoting the formation of tumor immunosuppressive microenvironment. ER stress plays an important protecting role in the survival of MDSC, which aggravates the immunosuppression in tumors. In addition, ferroptosis can promote an anti-tumor immune response by reversing the immunosuppressive microenvironment. This review summarizes immune suppression by MDSCs with a focus on the role of endoplasmic reticulum stress-mediated immune suppression in cancer and infectious disease, in particular leprosy and tuberculosis.

Governing a pandemic: biopower and the COVID-19 response in Zimbabwe.

Mhazo AT, Maponga CC.

Dec-2022

BMJ Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36585029/>

Unidigital clubbing in a patient with ulnar neuropathy due to Hansen's disease.

Evangelista V, Mermelstein SA, Jardim M.

Dec-2022

Arq Neuropsiquiatr.

<https://pubmed.ncbi.nlm.nih.gov/36580969/>

Prevalence of skin Neglected Tropical Diseases and superficial fungal infections in two peri-urban schools and one rural community setting in Togo.

Saka B, Kassang P, Gnossike P, Head MG, Akakpo AS, Teclessou JN, Elegbede YM, Mouhari-Toure A, Mahamadou G, Tevi K, Katsou K, Kombaté K, Walker SL, Pitché P.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534701/>

Introduction: Skin neglected tropical diseases (NTDs), are endemic and under-diagnosed in many lower-income communities. The objective of this study was to determine the prevalence of skin NTDs and fungal infections in two primary schools and a community setting in rural Togo. **Method:** This was a cross-sectional study that took place between June-October 2021. The two primary schools are located on the outskirts of Lomé, the capital city. The community setting was Ndjéi, in north-east Togo. Study sites were purposively selected. Dermatologists examined the skin of study participants. Diagnosis of skin NTDs were made clinically. **Results:** A total of 1401 individuals were examined, 954 (68.1%) from Ndjéi community, and 447 (31.9%) were children in the schools. Cutaneous skin infections were diagnosed in 438 (31.3%) participants, of

whom 355 (81%) were in community settings. There were 105 observed skin NTDs (7.5%). Within the school setting, there were 20 individuals with NTDs (4.5% of 447 participants), and 85 NTDs (8.9%) from 954 community participants. Across all settings 68/1020 (6.7%) NTDs were in children, and 37/381 (9.7%) in adults. In addition, there were 333 observed mycoses (23.8% prevalence). The main cutaneous NTDs diagnosed were scabies (n = 86; 6.1%) and suspected yaws (n = 16, 1.1%). The prevalence of scabies in schools was 4.3%, and 7.0% in the rural community. One case of leprosy was diagnosed in each school and the rural community, and one suspected Buruli Ulcer case in the community. In the school setting, five (6%) children with a skin NTD reported being stigmatised, four of whom had refused to attend school because of their dermatosis. In Ndjéi, 44 (4.6%) individuals reported having experienced stigma and 41 (93.2%) of them missed at least one day of school or work. **Conclusion:** This study shows that the burden of scabies and skin infections such as superficial mycoses is high in the school and rural community settings in Togo, with associated presence of stigma. Improved health promotion and education across institutional and community settings may reduce stigma and encourage early reporting of skin infection cases to a health facility.

From the Alps to the Mediterranean and beyond: genetics, environment, culture and the "impossible beauty" of Italy.

Anagnostou P, Montinaro F, Sazzini M, Di Vincenzo F, Destro Bisol G.

30-12-2022

J Anthropol Sci.

<https://pubmed.ncbi.nlm.nih.gov/36511799/>

Since prehistoric times, Italy has represented a bridge between peoples, genes and cultures. Its peculiar geographical position explains why: it is located in the center of the Mediterranean Sea, flanked by the Balkans and the Hellenic Peninsula to the east, Iberia to the west and surrounded by North Africa to the south and central Europe to the north. This makes Italy of extraordinary interest for the study of some different aspects of human diversity. Here we overview current knowledge regarding the relationships between the structure of the genetic variation of Italian populations and the geographical, ecological and cultural factors that have characterized their evolutionary history. Human presence in Italian territory is deeply rooted in the past. Lithic artifacts produced by the genus Homo and remains of Homo sapiens are among the earliest to have been found on the continent, as shown by the lithic industry of Pirro Nord (between 1.3 and 1.6 Mya) and the dental remains of the "Grotta del Cavallo" (between 45 and 43 Kya). Genetic and genomic studies relating to existing and extinct human groups have shed light on the migrations from Europe, Africa and Asia that created the ancient layers of the genetic structure of today's Italian populations, especially before the Iron Age. The important role of isolation (genetic and cultural) in shaping genetic structure is clearly visible in the patterns of intra- and inter-population diversity observed among Italian ethno-linguistic minorities that settled on the peninsula and on the major

islands until the 19th century. Finally, selective pressures have likely driven the distribution of originally adaptive variants and haplotypes that now confer protection or susceptibility to major diseases such as diabetes and cardiovascular disease (in northern Italy) and tuberculosis and leprosy (in the south). What emerges is a picture where the combined effects of migration, isolation and natural selection generated by the interplay of geography, environment and culture have shaped a complex pattern of human diversity that is unique in Europe and which goes hand in hand with today's rich animal and plant biodiversity. In a nutshell, scientific evidence and cultural heritage paint Italy as a place with extremely diverse environments where distant peoples have met since the deep past, bringing and sharing genes and ideas.

Added value of the measles-rubella supplementary immunization activity in reaching unvaccinated and under-vaccinated children, a cross-sectional study in five Indian districts, 2018-20.

Prosperi C, Thangaraj JWV, Hasan AZ, Kumar MS, Truelove S, Kumar VS, Winter AK, Bansal AK, Chauhan SL, Grover GS, Jain AK, Kulkarni RN, Sharma SK, Soman B, Chaaithanya IK, Kharwal S, Mishra SK, Salvi NR, Sharma NP, Sharma S, Varghese A, Sabarinathan R, Duraiswamy A, Rani DS, Kanagasabai K, Lachyan A, Gawali P, Kapoor M, Chonker SK, Cutts FT, Sangal L, Mehendale SM, Sapkal GN, Gupta N, Hayford K, Moss WJ, Murhekar MV.

09-01-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/36481106/>

Tumor targeted delivery of mycobacterial adjuvant encapsulated chitosan nanoparticles showed potential anti-cancer activity and immune cell activation in tumor microenvironment.

Chakraborty A, Roy G, Swami B, Bhaskar S.

Jan-2023

Int Immunopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36462337/>

Targeting immunotherapeutics inside the tumor microenvironment (TME) with intact biological activity remains a pressing issue. Mycobacterium indicus pranii (MIP), an approved adjuvant therapy for leprosy has exhibited promising results in clinical trials of lung (NSCLC) and bladder cancer. Whole MIP as well as its cell wall fraction have shown tumor growth suppression and enhanced survival in mice model of melanoma, when administered peritumorally. Clinically, peritumoral delivery remains a procedural limitation. In this study, a tumor targeted delivery system was designed, where chitosan nanoparticles loaded with MIP adjuvants, when administered intravenously showed preferential accumulation within the TME, exploiting the principle of enhanced permeability and retention effect. Bio-distribution studies revealed their highest concentration inside the tumor after 6 h of administration. Interestingly, MIP adjuvant nano-formulations significantly reduced the

tumor volume in the treated groups and increased the frequency of activated immune cells inside the TME. For chemioimmunotherapeutics studies, MIP nano-formulation was combined with standard dosage regimen of Paclitaxel. Combined therapy exhibited a further reduction in tumor volume relative to either of the MIP nano formulations. From this study a three-pronged strategy emerged as the underlying mechanism; chitosan and Paclitaxel have shown direct role in tumor cell death and the MIP nano-formulation activates the tumor residing immune cells which ultimately leads to the reduced tumor growth.

Trypanosomes (trypanosomiasis et maladie de Chagas)

First record of *Trypanosoma evansi* DNA in *Dichelacera alcicornis* and *Dichelacera januarii* (Diptera: Tabanidae) flies in South America.

Ramos CJR, de Souza Franco C, da Luz SP, Marques J, de Souza KM, do Nascimento LFN, das Neves GB, Moreira RS, Miletto LC.

Jan-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36604766/>

Phylogenetic evidence for a clade of tick-associated trypanosomes.

Koual R, Buysse M, Grillet J, Binetruy F, Ouass S, Sprong H, Duhayon M, Boulanger N, Jourdain F, Alafaci A, Verdon J, Verheyden H, Rispe C, Plantard O, Duron O.

05-01-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36604731/>

Molecular prevalence, associated risk factors and genetic characterization of *Trypanosoma evansi* in camels.

Alfaleh F, Elhaig MM.

02-01-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/36603695/>

Surra is a major infectious disease of camels being caused by *Trypanosoma evansi* (T. evansi) in developing countries, including Egypt. However, the identification of changes in the T. evansi prevalence in Egypt is important. In this study, the prevalence of T. evansi and its associated risk factors as well as the genetic characterization of the parasite were estimated. Blood samples were collected from 163 camels from two governorates in Lower Egypt. PCR targeting RoTat 1.2VSG was used for the detection of T. evansi and internal transcribed spacer 1 (ITS-1) was used for sequencing analysis and genetic characterization. Overall prevalence was 19.6% using RoTat 1.2VSG. The risk of the infection in females was 4 times higher than in males ($P = 0.0004$, $OR = 4$; 95% $CI = 0.79-8.96$) and in

camels with a history of clinical signs it was 2.3 times higher than camels without clinical signs ($P = 0.04$, $OR = 2.3$, 95% $CI = 1.035-5.15$). Analysis of the ITS-1 sequences of four T. evansi isolates showed little heterogeneity compared to similar sequences in the database. Sequence and phylogenetic analysis, based on the ITS-1 region, confirmed the presence of two distinct genotypes of T. evansi in Egyptian camels with more than 99% similarity with T. evansi isolates from different countries across the ITS-1 region and were closely related to Filipino and Chinese isolates. The results of the study can be used for the observation and prevention of disease and updating the epidemiological data.

Epitopes in the Glycosylphosphatidylinositol Attachment Signal Peptide of *Trypanosoma cruzi* Mucin Proteins Generate Robust But Delayed and Nonprotective CD8+ T Cell Responses.

Bunkofsky ME, Perumal N, White B, Strauch EM, Tarleton R.

04-01-2023

J Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36603035/>

Expression of Inhibitory Receptors TIGIT, TIM-3, and LAG-3 on CD4+ T Cells from Patients with Different Clinical Forms of Chronic Chagas Disease.

Ferragut F, Alcaraz PB, Beati P, Girard MC, Ossowski MS, Chadi R, Fernández M, Hernández-Vásquez Y, Acevedo GR, Gómez KA.

04-01-2023

J Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36602929/>

T cells are central to the adaptive immune response against *Trypanosoma cruzi* infection. In chronic Chagas disease (CCD), circulating parasite-specific memory T cells show reduced functionality and increased expression of inhibitory receptors as a result of persistent antigenic stimulation. This phenotype has been linked to progression of cardiac pathology, whereas the presence of polyfunctional T cells shows association with therapeutic success. In this study, we demonstrate that T. cruzi-specific human CD4+ T cells can be identified by their expression of OX40 and CD25 upon in vitro stimulation. We characterized the expression of the inhibitory receptors T cell immunoreceptor with Ig and ITIM domains (TIGIT), T cell Ig and mucin-domain containing-3 (TIM-3), and lymphocyte activation gene 3 (LAG-3) in CD4+ T cells from CCD patients with and without cardiac alterations. Our results show that, independently of their clinical stage, CCD patients present an increased frequency of CD4+ T cells expressing TIGIT in comparison with non-T. cruzi-infected donors. Exposure to parasite Ags increases the expression of TIM-3 in CD4+ T cells from CCD patients, especially in those with cardiac compromise. Upregulation of LAG-3 was also detected in CCD individuals without cardiac manifestations, predominantly within the subpopulation of cells that did not become activated upon

stimulation. Further differences were found between groups in the coexpression of these receptors. Blockade of each individual receptor did not affect activation or the production of IFN- γ and IL-10 by CD4+ T cells in response to parasite Ags. Our results suggest a role for TIGIT, TIM-3, and LAG-3 in the modulation of inflammatory phenomena thought to ultimately lead to tissue damage and cardiac pathology.

Prevalence and Molecular Analysis of Hellbender (Cryptobranchus alleganiensis) Trypanosomes in Tennessee.

Baker E, Hardman RH, Sutton WB, Reinsch S, Freake M, Holder E, Frost C, Nissen B, Nolan E, Gerhold R, Miller D.
05-01-2023

J Wildl Dis.

<https://pubmed.ncbi.nlm.nih.gov/36602794/>

Editorial: Rising stars in parasite and host 2022.

De Niz M, Gold DA, Kumar S, Mast FD, Richard D, Simões ML.

19-12-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36601303/>

Correction: Clinical profile and mortality in patients with T. cruzi/HIV co-infection from the multicenter data base of the "Network for healthcare and study of Trypanosoma cruzi/HIV co-infection and other immunosuppression conditions".

Shikanai-Yasuda MA, Mediano MFF, Novaes CTG, Sousa AS, Sartori AMC, Santana RC, Correia D, Castro CN, Severo MMD, Hasslocher-Moreno AM, Fernandez ML, Salvador F, Pinazo MJ, Bolella VR, Furtado PC, Corti M, Pinto AYN, Fica A, Molina I, Gascon J, Viñas PA, Cortez-Escalante J, Jr ANR, Almeida EA.

04-01-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36598894/>

Retinal Degeneration Animal Models in Bardet-Biedl Syndrome and Related Ciliopathies.

Delvallée C, Dollfus H.

03-01-2023

Cold Spring Harb Perspect Med.

<https://pubmed.ncbi.nlm.nih.gov/36596648/>

Retinal degeneration due to photoreceptor ciliary-related proteins dysfunction accounts for more than 25% of all inherited retinal dystrophies. The cilium, being an evolutionarily conserved and ubiquitous organelle implied in many cellular functions, can be investigated by way of many models from invertebrate models to nonhuman primates, all these models have massively contributed to the pathogenesis understanding of human ciliopathies. Taking the Bardet-Biedl syndrome (BBS) as an emblematic

example as well as other related syndromic ciliopathies, the contribution of a wide range of models has enabled to characterize the role of the BBS proteins in the archetypical cilium but also at the level of the connecting cilium of the photoreceptors. There are more than 24 BBS genes encoding for proteins that form different complexes such as the BBSome and the chaperone proteins complex. But how they lead to retinal degeneration remains a matter of debate with the possible accumulation of proteins in the inner segment and/or accumulation of unwanted proteins in the outer segment that cannot return in the inner segment machinery. Many BBS proteins (but not the chaperonins for instance) can be modeled in primitive organisms such as *Paramecium*, *Chlamydomonas reinhardtii*, *Trypanosoma brucei*, and *Caenorhabditis elegans*. These models have enabled clarifying the role of a subset of BBS proteins in the primary cilium as well as their relations with other modules such as the intraflagellar transport (IFT) module, the nephronophthisis (NPHP) module, or the Meckel-Gruber syndrome (MKS)/Joubert syndrome (JBTS) module mostly involved with the transition zone of the primary cilia. Assessing the role of the primary cilia structure of the connecting cilium of the photoreceptor cells has been very much studied by way of zebrafish modeling (*Danio rerio*) as well as by a plethora of mouse models. More recently, large animal models have been described for three BBS genes and one nonhuman primate model in rhesus macaque for *BBS7*. In completion to animal models, human cell models can now be used notably thanks to gene editing and the use of induced pluripotent stem cells (iPSCs). All these models are not only important for pathogenesis understanding but also very useful for studying therapeutic avenues, their pros and cons, especially for gene replacement therapy as well as pharmacological triggers.

Exploration of aminoacyl-tRNA synthetases from eukaryotic parasites for drug development.

Gill J, Sharma A.

31-12-2022

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/36596362/>

A qualitative exploration of knowledge of Chagas disease among adolescents in rural Ecuador.

Mora-Criollo P, Carrasco-Tenezaca M, Casapulla S, Bates BR, Grijalva MJ.

Jan-2023

Rural Remote Health.

<https://pubmed.ncbi.nlm.nih.gov/36596293/>

An induced population of Trypanosoma cruzi epimastigotes more resistant to complement lysis promotes a phenotype with greater differentiation, invasiveness, and release of extracellular vesicles.

Rossi IV, Nunes MAF, Sabatke B, Ribas HT, Winnischofer SMB, Ramos ASP, Inal JM, Ramirez MI.

14-12-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36590580/>

New metabolic signature for Chagas disease reveals sex steroid perturbation in humans and mice.

Golizeh M, Nam J, Chatelain E, Jackson Y, Ohlund LB, Rasoolizadeh A, Camargo FV, Mahrouche L, Furtos A, Sleno L, Ndao M.

15-12-2022

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/36590505/>

The causative agent of Chagas disease (CD), *Trypanosoma cruzi*, claims thousands of lives each year. Current diagnostic tools are insufficient to ensure parasitological detection in chronically infected patients has been achieved. A host-derived metabolic signature able to distinguish CD patients from uninfected individuals and assess antiparasitic treatment efficiency is introduced. Serum samples were collected from chronic CD patients, prior to and three years after treatment, and subjected to untargeted metabolomics analysis against demographically matched CD-negative controls. Five metabolites were confirmed by high-resolution tandem mass spectrometry. Several database matches for sex steroids were significantly altered in CD patients. A murine experiment corroborated sex steroid perturbation in *T. cruzi*-infected mice, particularly in male animals. Proteomics analysis also found increased steroidogenesis in the testes of infected mice. Metabolic alterations identified in this study shed light on the pathogenesis and provide the basis for developing novel assays for the diagnosis and screening of CD patients.

Combined use of real-time PCR and serological techniques for improved surveillance of chronic and acute American trypanosomiasis in dogs and their owners from an endemic rural area of Neotropical Mexico.

Chan-Pérez JI, Torres-Acosta JFJ, Ortega-Pacheco A, Hernández-Cortazar IB, Cigarroa-Toledo N, Jiménez-Coello M.

07-02-2022

Curr Res Parasitol Vector Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/36589870/>

In this study, the prevalence of *T. cruzi* infection was estimated in dogs and their owners from a rural community in Mexico using serological techniques for chronic infection cases, qPCR for acute phase cases, and a combination of both techniques to detect chronic and acute infections. Eighty-nine blood samples were collected from owners and their dogs for obtaining serum and parasite DNA. Prevalence was calculated using (i) positive cases detected in a serological test (ELISA and Western blot), (ii) positive cases detected in a qPCR test, and (iii) positive cases detected by both techniques. Sensitivity, specificity, and predictive values were determined individually for serology, qPCR and for both techniques used simultaneously. The prevalence observed varied: for

serology, 25.8% of the dogs and 7.9% of the owners were seropositive, while for qPCR 29.2% of the dogs and 10.1% of the owners were identified as positive. Combination of serological and molecular techniques resulted in a prevalence of 38.2% for dogs and 12.4% for their owners. The sensitivity, specificity and predictive values calculated for both techniques improved when both techniques were used simultaneously (sensitivity of 92.4% and specificity of 100% for infected dogs and sensitivity of 93.4% and specificity of 100% for infected owners). Combined use of serological tests and qPCR allowed identifying a greater number of positive cases in dogs and their owners. This strategy may help implement adequate and timely epidemiological surveillance of American trypanosomiasis in order to prevent the appearance of new cases of *Trypanosoma cruzi* infections in endemic zones.

Diagnostic study of trypanosomiasis of cats in Mosul, Iraq.

Mohammed NH, Moosa DA, Altaliby MA.

Sep-Oct 2022

Open Vet J.

<https://pubmed.ncbi.nlm.nih.gov/36589397/>

Prevalence of pathogenic trypanosome species in naturally infected cattle of three sleeping sickness foci of the south of Chad.

Vourchakbé J, Tiofack AAZ, Kante ST, Barka PA, Simo G.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584086/>

***Trypanosoma cruzi* PARP is enriched in the nucleolus and is present in a thread connecting nuclei during mitosis.**

Kevorkian ML, Vilchez Larrea SC, Fernández Villamil SH.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584038/>

***Trypanosoma brucei* RRP44: a versatile enzyme for processing structured and non-structured RNA substrates.**

Cesaro G, da Soler HT, Guerra-Slomp EP, Haouz A, Legrand P, Zanchin NIT, Guimaraes BG.

30-12-2022

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/36583334/>

Rrp44/Dis3 is a conserved eukaryotic ribonuclease that acts on processing and degradation of nearly all types of RNA. It contains an endo- (PIN) and an exonucleolytic (RNB) domain and, its depletion in model organisms supports its essential function for cell viability. In *Trypanosoma brucei*, depletion of Rrp44 (TbRRP44) blocks maturation of ribosomal RNA, leading to disruption of ribosome synthesis and inhibition of cell proliferation. We have determined the crystal structure of the exoribonucleolytic module of TbRRP44 in an active conformation, revealing novel details of the catalytic

mechanism of the RNB domain. For the first time, the position of the second magnesium involved in the two-metal-ion mechanism was determined for a member of the RNase II family. In vitro, TbRRP44 acts preferentially on non-structured uridine-rich RNA substrates. However, we demonstrated for the first time that both TbRRP44 and its homologue from *Saccharomyces cerevisiae* can also degrade structured substrates without 3'-end overhang, suggesting that Rrp44/Dis3 ribonucleases may be involved in degradation of a wider panel of RNA than has been assumed. Interestingly, deletion of TbRRP44 PIN domain impairs RNA binding to different extents, depending on the type of substrate.

The Role of Flavanones as Scaffolds for the Development of New Treatments against Malaria and African and American Trypanosomiasis.

Boniface PK, Ferreira EI, Fabrice FB.

29-12-2022

Mini Rev Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36582061/>

Parasitic infections are diseases transmitted by parasites usually found in contaminated food, water, or insect bites. Generally classified as neglected tropical diseases, malaria and trypanosomiasis are some of the most prominent parasitic diseases that cause significant loss of life annually. In 2020, an estimated 241 million malaria cases were reported, with 627,000 deaths worldwide. An estimated 6 to 7 million people are infected with *Trypanosoma cruzi* worldwide, whereas an estimated 1000 global cases of African human trypanosomiasis were reported in 2020. Flavanones are a group of compounds that belong to the flavonoid family and are chemically obtained by direct cyclization of chalcones. Recent pharmacological studies have demonstrated the effectiveness of plant flavanones in inhibiting the growth of the parasites responsible for malaria and trypanosomiasis.
Objective: The present work aims to summarize up-to-date and comprehensive literature information on plant flavanones with antimalarial and antitrypanosomal activities. The mechanisms of action of the antiparasitic flavanones are also discussed.
Method: A literature search was performed for naturally occurring flavanones and antimalarial and antitrypanosomal activities by referencing textbooks and scientific databases (SciFinder, Wiley, American Chemical Society, Science Direct, National Library of Medicine, Scientific Electronic Library Online, Web of Science, etc.) from their inception until April 2022.
Results: Based on in vitro experiments, more than sixty flavanones were reported to exhibit antimalarial, anti-*T. cruzi*, and anti-*T. brucei* activities. Previous studies demonstrated that these compounds bind to PGP-like transporters of *P. falciparum* to reverse the parasite's resistance. Other reports pinpointed the direct effect of these compounds on the mitochondria of the malaria parasite. Moreover, flavanones have shown strong docking to several validated *T. cruzi* and *T. brucei* protein targets, including adenosine kinase, pteridine reductase 1, dihydrofolate reductase, and trypanothione reductase, among others.

Conclusion: Flavanones, isolated and characterized from diverse plant parts, were reported to exhibit moderate to high activity against *P. falciparum*, *T. cruzi*, and *T. brucei* in in vitro studies. These potentially active flavanones can be used as scaffolds for the development of new antiparasitic agents. However, more studies on the cytotoxicity, pharmacokinetics, and mechanisms of action of potent flavanones should be performed.

Urban vectors of Chagas disease in the American continent: A systematic review of epidemiological surveys.

Carbajal-de-la-Fuente AL, Sánchez-Casaccia P, Piccinali RV, Provecho Y, Salvá L, Meli S, Cano F, Hernández R, Nattero J.

14-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36516183/>

Leishmaniose

Protease inhibitors as a potential agent against visceral Leishmaniasis: A review to inspire future study.

Sreedharan V, Rao KVB.

02-01-2022

Braz J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36603827/>

Leishmaniasis is transmitted by sandfly which carries the intracellular protozoa in their midgut. Among visceral, cutaneous and mucocutaneous leishmaniasis, visceral type that is caused by *Leishmania donovani* is the most lethal one. Findings of leishmanial structure and species took place in 19th century and was initiated by Donovan. Leishmaniasis is still a major concern of health issues in many endemic countries in Asia, Africa, the Americas, and the Mediterranean region. Worldwide 1.5-2 million new cases of cutaneous leishmaniasis and 500,000 cases of visceral leishmaniasis are reported each year. Leishmaniasis is endemic in nearly 90 countries worldwide and close to 12 million new cases of leishmaniasis are reported worldwide annually. Studies on antileishmanial drug development is of major concern as leishmaniasis are the second largest parasitic killer in the world and the available drugs are either toxic or costly. The major surface GP63 protease, also known as Zinc- metalloproteases present on the surface of leishmanial promastigotes, can be targeted for drug development. Protease inhibitors targeting such surface proteases show promising results. Different protease inhibitors have been isolated from marine actinobacteria against many infectious diseases. Metabolites produced by these actinobacteria may have greater importance for the discovery and development of new antileishmanial drugs. Hence, this review discusses the background, current situation, treatment, and protease inhibitors from marine actinobacteria for drug development against GP63 molecules.

Does infection with *Leishmania* protect against Covid-19?

Saidi N, Jelassi R.

02-01-2023

Immunol Lett.

<https://pubmed.ncbi.nlm.nih.gov/36603800/>

Emerging strategies and challenges of molecular therapeutics in antileishmanial drug development.

Gupta D, Singh PK, Yadav PK, Narender T, Patil UK, Jain SK, Chourasia MK.

03-01-2023

Int Immunopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36603357/>

Cytokine and phenotypic cell profiles in human cutaneous leishmaniasis caused by *Leishmania donovani*.

Wijesooriya H, Samaranyake N, Karunaweera ND.

05-01-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36602989/>

Efficacy of pentamidine-loaded chitosan nanoparticles as a novel drug delivery system for *Leishmania tropica*.

Khan RU, Khan M, Sohail A, Ullah R, Iqbal A, Ahmad B, Khan IU, Tariq A, Ahmad M, Said A, Ullah S, Ali A, Rahman MU, Zaman A, Bilal H.

01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602209/>

The present study compares the in vitro effects of nanoparticles loaded pentamidine drug and conventional pentamidine on *Leishmania tropica*. Herein, pentamidine-loaded chitosan nanoparticles (PTN-CNPs) have been synthesized through an ionic gelation method with sodium tripolyphosphate (TPP). Next, the physical characteristics of PTN-CNPs were determined through the surface texture, zeta potential, in vitro drug release, drug loading content (DLC), and encapsulation efficacy (EE) and compared its efficacy with free pentamidine (PTN) drug against promastigotes and axenic amastigotes forms of *L. tropica* in vitro. The PTN-CNPs displayed a spherical shape having a size of 88 nm, an almost negative surface charge (-3.09 mV), EE for PTN entrapment of 86%, and in vitro drug release of 92% after 36 h. In vitro antileishmanial activity of PTN-CNPs and free PTN was performed against *Leishmania tropica* KWH23 promastigote and axenic amastigote using 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) assay. It was observed that the effect of PTN-CNPs and free PTN on both forms of the parasite was dose and time dependent. Free PTN presented low efficacy even at higher dose (40 µg/ml) with 25.6 ± 1.3 and 26.5 ± 1.4 mean viability rate of the promastigotes and axenic amastigotes, respectively after 72 hrs incubation. While PTN-CNPs showed strong antileishmanial effects on both forms of parasite with 16 ± 0.4 and 19 ± 0.7 mean viability rate at the same higher concentration (40 µg/ml) after 72 hrs incubation. Half maximal inhibitory concentration (IC₅₀) values of PTN-CNPs toward promastigotes and amastigotes were

obtained as 0.1375 µg/ml and 0.1910 µg/ml, respectively. In conclusion, PTN-CNPs effectively inhibited both forms of the *L. tropica*; however, its effect was more salient on promastigotes. This data indicates that the PTN-CNPs act as a target drug delivery system. However, further research is needed to support its efficacy in animal and human CL.

Chemokine receptors on human regulatory T cells during cutaneous leishmaniasis.

de Castro MCAB, Silva RFE, Cavalcante MKA, Silva LLSB, Gomes FODS, Brito MEF, Pereira VRA.

04-01-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36601688/>

Editorial: Rising stars in parasite and host 2022.

De Niz M, Gold DA, Kumar S, Mast FD, Richard D, Simões ML.

19-12-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36601303/>

Exploration of aminoacyl-tRNA synthetases from eukaryotic parasites for drug development.

Gill J, Sharma A.

31-12-2022

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/36596362/>

Parasitic diseases result in considerable human morbidity and mortality. The continuous emergence and spread of new drug-resistant parasite strains is an obstacle to controlling and eliminating many parasitic diseases. Aminoacyl-tRNA synthetases (aaRSs) are ubiquitous enzymes essential for protein synthesis. The design and development of diverse small molecule, drug-like inhibitors against parasite-encoded and expressed aaRSs have validated this enzyme family as druggable. In this work, we have compiled the progress to date towards establishing the druggability of aaRSs in terms of their biochemical characterization, validation as targets, inhibitor development and structural interpretation from parasites responsible for malaria (*Plasmodium*), lymphatic filariasis (*Brugia*), giardiasis (*Giardia*), toxoplasmosis (*Toxoplasma gondii*), leishmaniasis (*Leishmania*), cryptosporidiosis (*Cryptosporidium*) and trypanosomiasis (*Trypanosoma*). This work thus provides a robust framework for the systematic dissection of aaRSs from these pathogens and will facilitate the cross-usage of potential inhibitors to jump-start antiparasitic drug development.

Effect of *Leishmania* RNA virus 2 on virulence factors and cytokines gene expression in a human macrophage infected with *Leishmania major*: A preliminary study.

Rahmanipour M, Mohebbali M, Koosha M, Kazemirad E, Yasami-Khiabani S, Mirjalali H, Hajjaran H.

31-12-2022

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36596336/>

Cutaneous leishmaniasis (CL) is one of the most important infectious parasitic diseases in the world caused by the Leishmania parasite. In recent decades, the presence of a virus from the Totiviridae family has been proven in some Leishmania species. Although the existence of LRV2 in the Old world Leishmania species has been confirmed, almost no studies have been done to determine the potential impact of LRV2 on the immunopathogenicity of the Leishmania parasite. In this preliminary study, we measured the expression of target genes, including Glycoprotein 63 (gp63), Heat Shock Protein 70 (hsp70), Cysteine Protease b (cpb), Interleukin 1 beta (IL-1 β), IL8 and IL-12 in LRV2 positive Leishmania major strain (LRV2⁺L. major) and LRV2 negative L. major strain (LRV2⁻L. major). We exposed THP-1, a human leukemia monocytic cell line, to promastigotes of both strains. After the initial infection, RNA was extracted at different time points, and the relative gene expression was determined using a real-time quantitative reverse transcription-polymerase chain reaction (qRT-PCR). Findings showed that the presence of LRV2 in L. major was able to increase the expression of gp63, hsp70, and cpb genes; also, we observed lower levels of expression in cytokine genes of IL-1 β , IL-8, IL-12 in the presence of LRV2⁺, which are critical factors in the host's immune response against leishmaniasis. These changes could suggest that the presence of LRV2 in L. major parasite may change the outcome of the disease and increase the probability of Leishmania survival; nevertheless, further studies are needed to confirm our results.

A zymographic study of metalloproteinase activities in whole cell extracts and extracellular secretions of Leishmania (L.) , L. major and L. infantum from Iran.

Pourshahid P, Bozorg-Ghalati F, Mohammadpour I, Alishavandi M, Hatam GR.

2022

Ann Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36596277/>

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

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

03-01-2023

Biochemistry.

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

Fumarate hydratase (FH) is a remarkable catalyst that decreases the free energy of the catalyzed reaction by 30 kcal mol⁻¹, much larger than most exceptional enzymes with extraordinary catalytic rates. Two classes of FH are observed in nature: class-I and class-II, which have different folds, yet catalyze the same reversible

hydration/dehydration reaction of the dicarboxylic acids fumarate/malate, with equal efficiencies. Using class-I FH from the hyperthermophilic archaeon *Methanocaldococcus jannaschii* (Mj) as a model along with comparative analysis with the only other available class-I FH structure from *Leishmania major* (Lm), we provide insights into the molecular mechanism of catalysis in this class of enzymes. The structure of MjFH apo-protein has been determined, revealing that large intersubunit rearrangements occur across apo- and holo-protein forms, with a largely preorganized active site for substrate binding. Site-directed mutagenesis of active site residues, kinetic analysis, and computational studies, including density functional theory (DFT) and natural population analysis, together show that residues interacting with the carboxylate group of the substrate play a pivotal role in catalysis. Our study establishes that an electrostatic network at the active site of class-I FH polarizes the substrate fumarate through interactions with its carboxylate groups, thereby permitting an easier addition of a water molecule across the olefinic bond. We propose a mechanism of catalysis in FH that occurs through transition-state stabilization involving the distortion of the electronic structure of the substrate olefinic bond mediated by the charge polarization of the bound substrate at the enzyme active site.

Partial characterization of purified glycoprotein from nutshell of Arachis hypogea L. towards macrophage activation and leishmaniacidal activity.

Srinivasan S, Charan Raja MR, Kar A, Ramasamy A, Jayaraman A, Vadivel V, Kar Mahapatra S.

03-01-2023

Glycoconj J.

<https://pubmed.ncbi.nlm.nih.gov/36595117/>

Arachis hypogea L. protein fraction-2 (AHP-F2) from the Peanut shell was extracted and characterized and its potent immunomodulatory and anti-leishmanial role was determined in this present study. AHP-F2 was found to be a glycoprotein as the presence of carbohydrates were confirmed by the analysis of high-performance liquid chromatography (HPLC) yielded glucose, galactose, mannose, and xylose. AHP-F2 molecular mass was found to be ~28 kDa as indicated in MALDI-TOF and peptide mass fingerprinting analysis followed by Mascot search. The peptide matches revealed the similarity of the mannose/glucose binding lectin with 71.07% in the BLAST analysis. After that, the 3D structure of the AHP-F2 model was designed and validated by the Ramachandran plot. The immunomodulatory role of AHP-F2 was established in murine peritoneal macrophages as induction of nitric oxide (NO), and stimulation of proinflammatory cytokines (IL-12 and IFN- γ) in a dose-dependent manner was observed. Interestingly, it was also found that AHP-F2 has interacted with the innate immune receptor, toll-like receptors (TLRs) as established in molecular docking as well as mRNA expression. The anti-leishmanial potential of AHP-F2 was revealed with a prominent inhibition of amastigote growth within the murine macrophages with prompt induction of nitrite release. Altogether, the isolated AHP-F2 from Arachis hypogea L. has strong

immunomodulatory and anti-leishmanial potential which may disclose a new path to treat leishmaniasis.

PpSP32, the Phlebotomus papatasi immunodominant salivary protein, exerts immunomodulatory effects on human monocytes, macrophages, and lymphocytes.

Souissi C, Marzouki S, Elbini-Dhouib I, Jebali J, Oliveira F, Valenzuela JG, Srairi-Abid N, Kamhawi S, Ben Ahmed M.
02-01-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36593519/>

Exploring the repositioning of the amodiaquine as potential drug against visceral leishmaniasis: The in vitro effect against Leishmania infantum is associated with multiple mechanisms, involving mitochondria dysfunction, oxidative stress and loss of cell cycle control.

Antinarelli LMR, Midlej V, da Silva EDS, Ferraz Coelho EA, David da Silva A, Coimbra ES.
30-12-2022

Chem Biol Interact.

<https://pubmed.ncbi.nlm.nih.gov/36592711/>

In vitro and in silico study of an exclusive insertion in the nicotinamide/nicotinate mononucleotide adenylyltransferase from Leishmania braziliensis.

Ortiz-Joya LJ, Contreras Rodríguez LE, Ochoa R, Ramírez Hernández MH.
09-12-2022

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/36590501/>

Limitations of current chemotherapy and future of nanoformulation-based AmB delivery for visceral leishmaniasis- An updated review.

Kumar P, Kumar P, Singh N, Khajuria S, Patel R, Rajana VK, Mandal D, Velayutham R.
14-12-2022

Front Bioeng Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/36588956/>

Visceral leishmaniasis (VL) is the most lethal of all leishmaniasis diseases and the second most common parasitic disease after malaria and, still, categorized as a neglected tropical disease (NTD). According to the latest WHO study, >20 Leishmania species spread 0.7-1.0 million new cases of leishmaniasis each year. VL is caused by the genus, *Leishmania donovani* (LD), which affects between 50,000 and 90,000 people worldwide each year. Lack of new drug development, increasing drug resistance, toxicity and high cost even with the first line of treatment of Amphotericin B (AmB), demands new formulation for treatment of VL. Further the lack of a

vaccine, allowed the researchers to develop nanoformulation-based AmB for improved delivery. The limitation of AmB is its kidney and liver toxicity which forced the development of costly liposomal AmB (AmBisome) nanoformulation. Success of AmBisome have inspired and attracted a wide range of AmB nanoformulations ranging from polymeric, solid lipid, liposomal/micellar, metallic, macrophage receptor-targeted nanoparticles (NP) and even with sophisticated carbon/quantum dot-based AmB nano delivery systems. Notably, NP-based AmB delivery has shown increased efficacy due to increased uptake, on-target delivery and synergistic impact of NP and AmB. In this review, we have discussed the different forms of leishmaniasis disease and their current treatment options with limitations. The discovery, mechanism of action of AmB, clinical status of AmB and improvement with AmBisome over fungizone (AmB-deoxycholate) for VL treatment was further discussed. At last, the development of various AmB nanoformulation was discussed along with its advantages over traditional chemotherapy-based delivery.

Leishmania Vaccines: the Current Situation with Its Promising Aspect for the Future.

Dinc R.

Dec-2022

Korean J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36588414/>

Assessing the effect of antimony pressure on trypanothione reductase activity in Leishmania (Viannia) braziliensis.

Zabala-Peñañiel A, Dias-Lopes G, Souza-Silva F, Miranda LFC, Conceição-Silva F, Alves CR.
28-12-2022

Biochimie.

<https://pubmed.ncbi.nlm.nih.gov/36586564/>

Leishmania parasites have an oxidative and chemical defense mechanism called trypanothione system ($T[SH]_2$), the most abundant thiol system in trypanosomatids. This system has a central role in processing pentavalent antimony and resistance has been related to a better capacity to metabolize it through the activation of $T[SH]_2$ enzymatic cascade. A biochemical approach was applied to assess the effect of trivalent (Sb^{III}) and pentavalent antimony (Sb^V) on Trypanothione Reductase (TR) activity of two Leishmania (Viannia) braziliensis clinical isolates, which were labeled as responder (R) and non-responder (NR) after patient treatment with Glucantime®. Both isolates were characterized based on in vitro susceptibility to Sb^{III} and Sb^V and trypanothione reductase (TR) activity. Sb^{III} and Sb^V discriminated susceptibility profiles in all parasite forms, since isolate NR had significantly higher EC_{50} values than isolate R. Differences were observed in TR activity between promastigotes, axenic and intracellular amastigotes: R (0.439 ± 0.009 , 0.103 ± 0.01 and 0.185 ± 0.01 nmol min⁻¹. μ g of protein⁻¹) and NR (1.083 ± 0.04 , 0.914 ± 0.04 and 0.343 ± 0.04 nmol min⁻¹. μ g of protein⁻¹), respectively. Incubation with Sb^{III} and Sb^V using each form

EC₅₀ value caused a time-dependent differential effect on TR activity suggesting that oxidative defense is related to the antimony susceptibility phenotype. Data gathered here shows a biochemical approach able to discriminate two *L. (V.) braziliensis* clinical isolates measurements TR activity of promastigotes, axenic and intracellular amastigotes.

Lethal action of Licarin A derivatives in *Leishmania (L.) infantum*: Imbalance of calcium and bioenergetic metabolism.

de Castro Levatti EV, Costa-Silva TA, Morais TR, Fernandes JPS, Lago JHG, Tempone AG.

28-12-2022

Biochimie.

<https://pubmed.ncbi.nlm.nih.gov/36586562/>

Natural metabolites present an extraordinary chemo-diversity and have been used as the inspiration for new drugs. Considering the need for new treatments against the neglected parasitic disease leishmaniasis, three semi-synthetic derivatives of natural neolignane licarin A were prepared: O-acetyl (1a), O-allyl (1b), and 5-allyl (1c). Using an ex vivo assay, compounds 1a, 1b, and 1c showed activity against the intracellular amastigotes of *Leishmania (L.) infantum*, with IC₅₀ values of 9, 13, and 10 μ M, respectively. Despite no induction of hemolytic activity, only compound 1b resulted in mammalian cytotoxicity (CC₅₀ = 64 μ M). The most potent compounds (1a and 1c) resulted in selectivity indexes >18. The mechanism of action of compound 1c was evaluated by fluorescent/luminescent based techniques and MALDI-TOF/MS. After a short incubation period, increased levels of the cytosolic calcium were observed in the parasites, with alkalinization of the acidocalcisomes. Compound 1c also induced mitochondrial hyperpolarization, resulting in decreased levels of ATP without altering the reactive oxygen species (ROS). Neither plasma membrane damages nor DNA fragmentation were observed after the treatment, but a reduction in the cellular proliferation was detected. Using MALDI-TOF/MS, mass spectral alterations of promastigote proteins were observed when compared to untreated and miltefosine-treated groups. This chemically modified neolignan induced lethal alterations of the bioenergetic and protein metabolism of *Leishmania*. Future PKPD and animal efficacy studies are needed to optimize this promising natural-derived compound.

Dataset of dual RNA-seq mapping in visceral leishmaniasis: Inquiry on parasite transcripts in human blood transcriptome upon *Leishmania infantum* infection.

Gomes E, Rogerio LA, Takamiya NT, Torres C, da Silva JS, Almeida RP, Maruyama SR.

08-12-2022

Data Brief.

<https://pubmed.ncbi.nlm.nih.gov/36582994/>

This dataset is related to the article "Insight Into the Long Noncoding RNA and mRNA Coexpression Profile in the Human Blood Transcriptome Upon *Leishmania infantum* Infection" by S.R. Maruyama, C.A. Fuzo, A.E.R. Oliveira, L.A.

Rogerio, N.T. Takamiya, G. Pessenda, E.V. de Melo, A.M. da Silva, A.R. Jesus, V. Carregaro, H.I. Nakaya, R.P. Almeida and J.S. da Silva. *Frontiers in Immunology*, 2022. Through the reuse of raw sequencing data, we generated original dataset by performing a dual RNA-seq mapping procedure to survey the parasite transcripts found in RNA-seq samples from blood of visceral leishmaniasis patients. Diseased patients with active infection displayed the highest number of reads mapped to *L. infantum* genome. Even after six months later of the treatment, when the patients were considered cured, parasite reads were still detected. Parasite reads were also detected in asymptomatic individuals. The original dual RNA-seq alignment read count data provided here can be further explored to evaluate either host or parasite transcripts.

Humoral response in Leishmaniasis.

Conde L, Maciel G, de Assis GM, Freire-de-Lima L, Nico D, Vale A, Freire-de-Lima CG, Morrot A.

12-12-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36579347/>

Leishmaniasis presents different types of clinical manifestations that can be divided into cutaneous leishmaniasis and visceral leishmaniasis. The host's immune system, associated with genetic and nutritional factors, is strongly involved in the evolution of the disease or parasite escape. Humoral immunity is characterized by the production of antibodies capable of promoting neutralization, opsonization, and activation of the complement system. In this scenario, B lymphocytes produce antibodies that play an important role in *Leishmania* infection although neglected for a long time. Thus, relevant aspects in the establishment of *Leishmania* infection will be addressed, highlighting the importance of humoral immunity during the entire process of *Leishmania* infection.

Detection of *Leishmania donovani* using ITS1-RFLP from positive and negative smear samples among clinically reported patients visiting University of Gondar Comprehensive Specialized Hospital.

Usmael UA, Tesema NB, Girma S, Kendie DA, Abas MK.

29-12-2022

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36577945/>

Design and synthesis of novel halogen rich salicylanilides as potential antileishmanial agents.

Lal J, Ramalingam K, Meena R, Ansari SB, Saxena D, Chopra S, Goyal N, Reddy DN.

15-03-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36565533/>

The available therapeutic treatment for leishmaniasis is inadequate and toxic due to side effects, expensive and emergence of drug resistance. Affordable and safe

antileishmanial agents are urgently needed and toward this objective, we synthesized a series of 32 novel halogen rich salicylanilides including niclosamide and oxyclozanide and investigated their antileishmanial activity against amastigotes of *Leishmania donovani*. In vitro data showed fifteen compounds inhibited intracellular amastigotes with an IC_{50} of below 5 μM and selectivity index above 10. Among 15 active compounds, 14 and 24 demonstrated better activity with an IC_{50} of 2.89 μM and 2.09 μM respectively and selectivity index is 18. Compound 24 exhibited significant in vivo antileishmanial efficacy and reduced 65% of the splenic parasite load on day 28th post-treatment in the experimental visceral leishmaniasis golden hamster model. The data suggest that 24 can be a promising lead candidate possessing potential to be developed into a leishmanial drug candidate.

Molecular Modeling, Virtual Screening, and Molecular Dynamics for Leishmania infantum Methionyl-tRNA Synthetase.

Teles HR, Valli M, Ferreira LLG, Andricopulo AD.

29-12-2022

J Phys Chem B.

<https://pubmed.ncbi.nlm.nih.gov/36534784/>

Visceral leishmaniasis is a neglected tropical disease (NTD) caused by *Leishmania infantum* and *L. donovani* that is lethal in cases of nontreatment. The treatments are limited by serious drawbacks involving safety, resistance, stability, and high costs. In this work, we aimed to identify inhibitors of *Leishmania infantum* methionyl-tRNA synthetase (*LiMetRS*), a validated molecular target for leishmaniasis drug discovery, using a combination of strategies. A virtual database of compounds was organized by filtering compounds from the ZINC15 database. Homology modeling was used to obtain the structure of *LiMetRS* based on the crystal coordinates of the enzyme from *Trypanosoma brucei* (*TbMetRS*). A virtual screening using molecular docking identified 10 candidate compounds from among more than 5 million that were included in the initial database. The selected hits were further evaluated using a script created in this work to select only the ligands that interacted with specific amino acids in the catalytic site of the enzyme. Furthermore, suitable pharmacokinetic profiles were predicted for the selected compounds, especially a good balance between aqueous solubility and lipophilic character, no ability to cross the blood-brain barrier, good oral absorption, and no liability toward P-gp efflux for most compounds. Six compounds were then subjected to all-atom molecular dynamics. Two compounds showed good stability when bound to the leishmanial enzyme, which provided a deeper understanding of the structural differences between *TbMetRS* and *LiMetRS* that can guide further drug discovery efforts for visceral leishmaniasis.

Detecting Leishmania in dogs: A hierarchical-modeling approach to investigate the performance of parasitological and qPCR-based diagnostic procedures.

Vital T, Teixeira AIP, Silva DM, de Carvalho BC, Dallago B, Hagström L, Hecht MM, Nitz N, Abad-Franch F.

16-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36525465/>

Synthesis and in vitro antileishmanial activity of alkylene-linked nitrofurantoin-triazole hybrids.

Zuma NH, Aucamp J, Janse van Rensburg HD, N'Da DD.

15-01-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36516584/>

Leishmaniasis is a vector-borne parasitic disease that mostly affects populations in tropical and sub-tropical countries. There is currently no protective anti-leishmanial vaccine and only a paucity of clinical drugs is available to treat this disease albeit their toxicity. Leishmaniasis is curable but its eradication and elimination have been hampered by the emergence of multidrug resistant strains of the causative pathogens. This heightens the necessity for new and effective antileishmanial drugs. In search for such agents, nitrofurantoin, a clinical antibiotic, was appended to triazole scaffold through alkylene linkers of various length, and the resulting hybrids were evaluated for in vitro antileishmanial efficacy against *Leishmania* (L.) parasite of two strains. The hybrid 13, harboring a n-pentylene linker was uncovered as a leishmanicidal hit with micromolar activity against antimonial-resistant *L. donovani*, the causative of deadly visceral Leishmaniasis.

Mode of action of p-quinone derivatives with trypanocidal activity studied by experimental and in silico models.

Ballesteros-Casallas A, Quiroga C, Ortiz C, Benítez D, Denis PA, Figueroa D, Salas CO, Bertrand J, Tapia RA, Sánchez P, Miscione GP, Comini MA, Paulino M.

15-01-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36508970/>

Quinones are attractive pharmacological scaffolds for developing new agents for the treatment of different transmissible and non-transmissible human diseases due to their capacity to alter the cell redox homeostasis. The bioactivity and potential mode of action of 19 p-quinone derivatives fused to different aromatic rings (carbo or heterocycles) and harboring distinct substituents were investigated in infective *Trypanosoma brucei brucei*. All the compounds, except for a furanequinone ($EC_{50}=38 \mu M$), proved to be similarly or even more potent ($EC_{50} = 0.5-5.5 \mu M$) than the clinical drug nifurtimox ($EC_{50} = 5.3 \mu M$). Three furanequinones and one thiazolequinone displayed a higher selectivity than nifurtimox. Two of these selective hits resulted potent inhibitors of *T. cruzi* proliferation ($EC_{50}=0.8-1.1 \mu M$) but proved inactive against *Leishmania infantum* amastigotes. Most of the p-quinones induced a rapid and marked intracellular oxidation in *T. b. brucei*. DFT calculations on the oxidized quinone (Q), semiquinone ($Q^{\bullet-}$) and hydroquinone (QH_2) suggest that all quinones have negative ΔG for the formation of $Q^{\bullet-}$. Qualitative and

quantitative structure-activity relationship analyses in two or three dimensions of different electronic and biophysical descriptors of quinones and their corresponding bioactivities (killing potency and oxidative capacity) were performed. Charge distribution over the quinone ring carbons of Q and Q⁻ and the frontier orbitals energies of SUMO (Q⁻) and LUMO (Q) correlate with their oxidative and trypanocidal activity. QSAR analysis also highlighted that both bromine substitution in the p-quinone ring and a bulky phenyl group attached to the furane and thiazole rings (which generates a negative charge due to the π electron system polarized by the nearby heteroatoms) are favorable for activity. By combining experimental and in silico procedures, this study disclosed important information about p-quinones that may help to rationally tune their electronic properties and biological activities.

Novel approaches to preventing phagosomal infections: timing is key.

Peters NC, Khan N, Mody CH.

Jan-2023

Trends Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36494273/>

Small molecules containing chalcogen elements (S, Se, Te) as new warhead to fight neglected tropical diseases.

Henriquez-Figueroa A, Morán-Serradilla C, Angulo-Elizari E, Sanmartín C, Plano D.

15-01-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36493616/>

Neglected tropical diseases (NTDs) encompass a group of infectious diseases with a protozoan etiology, high incidence, and prevalence in developing countries. As a result, economic factors constitute one of the main obstacles to their management. Endemic countries have high levels of poverty, deprivation and marginalization which affect patients and limit their access to proper medical care. As a matter of fact, statistics remain uncollected in some affected areas due to non-reporting cases. World Health Organization and other organizations proposed a plan for the eradication and control of the vector, although many of these plans were halted by the COVID-19 pandemic. Despite of the available drugs to treat these pathologies, it exists a lack of effectiveness against several parasite strains. Treatment protocols for diseases such as American trypanosomiasis (Chagas disease), leishmaniasis, and human African trypanosomiasis (HAT) have not achieved the desired results. Unfortunately, these drugs present limitations such as side effects, toxicity, teratogenicity, renal, and hepatic impairment, as well as high costs that have hindered the control and eradication of these diseases. This review focuses on the analysis of a collection of scientific shreds of evidence with the aim of identifying novel chalcogen-derived molecules with biological activity against Chagas disease, leishmaniasis and HAT. Compounds illustrated in each figure share the distinction of containing at least one chalcogen element. Sulfur (S), selenium (Se), and tellurium (Te) have been grouped and

analyzed in accordance with their design strategy, chemical synthesis process and biological activity. After an exhaustive revision of the related literature on S, Se, and Te compounds, 183 compounds presenting excellent biological performance were gathered against the different causative agents of CD, leishmaniasis and HAT.

Antileishmania and immunomodulatory potential of cashew nut shell liquid and cardanol.

Ribeiro IMM, de Sousa VC, Melo ECS, Carvalho RCV, Santos MSD, Neto JAON, Melo DS, Teixeira LSA, Citó AMDGL, Moura AKS, Arcanjo DDR, Carvalho FAA, Alves MMM, Mendonça IL.

Mar-2023

Toxicol In Vitro.

<https://pubmed.ncbi.nlm.nih.gov/36435415/>

Conventional treatments for leishmaniasis have caused serious adverse effects, poor tolerance, development of resistant strains. Natural products have been investigated as potential therapeutic alternatives. The cashew nut shell liquid (CNSL) is a natural source of phenolic compounds with several biological activities, where cardanol (CN) is considered one of the most important and promising compounds. This study aimed to evaluate antileishmanial, cytotoxic and immunomodulatory activities of CNSL and CN. Both showed antileishmanial potential, with IC₅₀ for CNSL and CN against *Leishmania infantum*: 148.12 and 56.74 μ g/mL; against *Leishmania braziliensis*: 85.71 and 64.28 μ g/mL; against *Leishmania major*: 153.56 and 122.31 μ g/mL, respectively. The mean cytotoxic concentrations (CC₅₀) of CNSL and CN were 37.51 and 31.44 μ g/mL, respectively. CNSL and CN significantly reduced the percentage of infected macrophages, with a selectivity index (SI) >20 for CN. CNSL and cardanol caused an increase in phagocytic capacity and lysosomal volume. Survival rates of *Zophobas morio* larvae at doses of 3; 30 and 300 mg/kg were: 85%, 75% and 60% in contact with CNSL and 85%, 60% and 40% in contact with CN, respectively. There was a significant difference between the survival curves of larvae when treated with CN, demonstrating a significant acute toxicity for this substance. Additional investigations are needed to evaluate these substances in the in vivo experimental infection model.

Intracellular pathogen *Leishmania* intervenes in iron loading into ferritin by cleaving chaperones in host macrophages as an iron acquisition strategy.

Sen S, Bal SK, Yadav S, Mishra P, G VV, Rastogi R, Mukhopadhyay CK.

Dec-2022

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/36309090/>

Iron (Fe) sequestration is one of the most important strategies of the host to control the growth and survival of invading pathogens. Ferritin (Ft) plays a pivotal role in the sequestration mechanism of mammalian hosts by storing Fe. Recent evidence suggests that poly(rC)-binding

proteins (PCBPs) act as chaperones for loading Fe into Ft. Incidentally, modulation of host PCBPs in respect to storing Fe in Ft during any infection remains unexplored. Among PCBPs, PCBP1 and PCBP2 are present in every cell type and involved in interacting with Ft for Fe loading. *Leishmania donovani* (LD) resides within macrophages during the mammalian stage of infection, causing life-threatening visceral leishmaniasis. Here, we reveal the ability of LD to cleave PCBP1 and PCBP2 in host monocytes/macrophages. LD cleaves PCBP1-FLAG into two fragments and PCBP2-FLAG into multiple fragments, thus affecting their interactions with Ft and resulting in decreased Fe loading into Ft. LD-derived culture supernatant or exosome-enriched fractions are also able to cleave PCBPs, suggesting involvement of a secreted protease of the parasite. Using an immune-depletion experiment and transgenic mutants, we confirmed the involvement of zinc-metalloprotease GP63 in cleaving PCBPs. We further revealed that by cleaving host PCBPs, *Leishmania* could inhibit Fe loading into Ft to accumulate available Fe for higher intracellular growth. This is the first report of a novel strategy adopted by a mammalian pathogen to interfere with Fe sequestration into Ft by cleaving chaperones for its survival advantage within the host.

UVA1 radiation attenuates pro-inflammatory functions in human monocytes.

Peters AF, Kusche Y, Gerdkamp H, Nattkemper E, Vischedyk K, Münck NA, Weishaupt C, Roth J, Barczyk-Kahlert K, Sunderkötter C, Ehrchen JM.

Jan-2023

J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36184911/>

UVA1 therapy is effective in the treatment of inflammatory and autoimmune skin diseases. The mode of action of UVA1 therapy is not completely understood and especially data on cells of the innate immune system like monocytes, which are critically involved in many inflammatory processes, are sparse. We wanted to answer the question whether UVA1 irradiation alters functional properties of human monocytes. We treated human peripheral blood monocytes in vitro with 2 J/cm² UVA1 light, incubated the cells for 48 h and examined both functional properties and alterations in the gene and protein expression profile. While UVA1 did not alter cell viability or susceptibility to apoptosis inducing agents, it decreased the capacity of monocytes for phagocytosis and to eliminate infectious agents like *Leishmania major*. Moreover, we measured a significantly reduced production of interleukin (IL)-1 β mRNA in lipopolysaccharide activated monocytes after UVA1 treatment. Importantly, UVA1-treated monocytes not only produce less IL-1 β , but also upregulate expression of the anti-inflammatory IL-1 β decoy receptor. Our data provide evidence that UVA1 radiation not only interferes with fundamental monocyte properties like phagocytosis, pathogen killing and activation, but could also specifically attenuate pro-inflammatory IL-1 effects. This might constitute a hitherto unknown anti-inflammatory mechanism of UVA1 in human monocytes.

Patterns of cutaneous leishmaniasis during the COVID-19 pandemic in four endemic regions of Iran.

Mazaherifar S, Solhjoo K, Rasti S, Heidarnejadi SM, Abdoli A.

03-01-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36068660/>

Background: Both zoonotic cutaneous leishmaniasis (ZCL) and anthroponotic cutaneous leishmaniasis are endemic in different regions of Iran. It is important to know the type of cutaneous leishmaniasis (CL) for prevention strategies. On the other hand, Iran is one of the countries that was severely affected by the coronavirus 2019 (COVID-19) pandemic. However, little is known about the causative agents of CL during the COVID-19 pandemic in Iran. **Methods:** In this study, a total of 181 samples were isolated from patients with CL lesions in four different endemic cities of Iran (Jahrom, Juyom, Kashan and Shoushtar) during the COVID-19 pandemic (the summer and autumn of 2021). The nested-PCR targeting kinetoplast DNA (kDNA) minicircles was applied for species identification of the parasite and the internal transcribed spacer-1 (ITS-1) gene was applied for sequencing and phylogenetic analysis. **Results:** Molecular detection of kDNA minicircles revealed that all isolates from the four cities were *Leishmania major*, indicating the ZCL pattern. Ten isolates were sequenced by the ITS-1 gene and deposited in GenBank [accession numbers: OL627363-72]. Sequencing and phylogenetic analysis displayed a high similarity rate of the isolates with sequences from other parts of Iran and Iraq. Over half of the patients (53.59%) had a single lesion, while 17.12, 14.92, 2.21 and 12.16% of cases had two, three, four and more than four lesions, respectively. About half of the patients (50.27%) had lesions on their hands, while the rest had lesions on multiple locations (19.34%), legs (16.58%), face (9.94%), ears (1.66%) and waist (2.21%). **Conclusions:** This study revealed the occurrence of ZCL during the COVID-19 pandemic in four endemic regions of Iran. Strategies for prevention and control of the disease should be considered to mitigate the occurrence of ZCL.

An insight into differential protein abundance throughout *Leishmania donovani* promastigote growth and differentiation.

Alcolea PJ, Alonso A, García-Tabares F, Larraga J, Martins LTC, Loayza FJ, Ruiz-García S, Larraga V.

Jan-2023

Int Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/35930160/>

Leishmania donovani causes anthroponotic visceral leishmaniasis, responsible for about 50,000 annual deaths worldwide. Current therapies have considerable side effects. Drug resistance has been reported and no vaccine is available nowadays. The development of undifferentiated promastigotes in the sand fly vector's gut leads to the promastigote form that is highly infective to the mammalian host. Fully differentiated promastigotes play a crucial role in the initial stages of mammalian host

infection before internalization in the host phagocytic cell. Therefore, the study of protein levels in the promastigote stage is relevant for disease control, and proteomics analysis is an ideal source of vaccine candidate discovery. This study aims to get insight into the protein levels during the differentiation process of promastigotes by 2DE-MALDI-TOF/TOF. This partial proteome analysis has led to the identification of 75 proteins increased in at least one of the *L. donovani* promastigote differentiation and growth phases. This study has revealed the differential abundance of said proteins during growth and differentiation. According to previous studies, some are directly involved in parasite survival or are immunostimulatory. The parasite survival-related proteins are ascorbate peroxidase; cystathionine β synthase; an elongation factor 1 β paralog; elongation factor 2; endoribonuclease L-PSP; an iron superoxide dismutase paralog; GDP-mannose pyrophosphorylase; several heat shock proteins-HSP70, HSP83-17, mHSP70-rel, HSP110; methylthioadenosine phosphorylase; two thiol-dependent reductase 1 paralogs; transitional endoplasmic reticulum ATPase; and the AhpC thioredoxin paralog. The confirmed immunostimulatory proteins are the heat shock proteins, enolase, and protein kinase C receptor analog. The potential immunostimulatory molecules according to findings in pathogenic bacteria are fructose-1,6-diphosphate aldolase, dihydrolipoamide acetyltransferase, isocitrate dehydrogenase, pyruvate dehydrogenase E1 α and E1 β subunits, and triosephosphate isomerase. These proteins may become disease control candidates through future intra-vector control methods or vaccines.

Cysticercose

Spirometra mansonii sparganosis identified by mNGS: A Case Report.

Hu D, Jin W, Ding H, Pang Y, Ma S, Yang M, Wu S, Jiang M, Pang L, Luo S, Ning Q.
30-12-2022

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36592686/>

A 30-year-old male patient who had a cyst on the left hip and progressive enlargement for more than 2 months. Combined blood tests, magnetic resonance imaging and pathology findings, cysticercosis infection was suspected. However, the treatment for cysticercosis was ineffective. Then, We conducted a metagenomic next generation sequencing(mNGS) analysis on the FFPE specimen of the patient's surgically excised tissue, and the results suggested *Spirometra mansonii*, mNGS was further confirmed by polymerase chain reaction(PCR) and phylogenetic analysis of cytochrome c oxidase subunit 1 (cox1) gene. Based on these results, we found that mNGS provided a better method in diagnosing parasitic infections.

Diagnosing neurocysticercosis in skeletonized human remains of forensic importance.

Obafunwa JO, Reinhard K.

24-12-2022

J Forensic Leg Med.

<https://pubmed.ncbi.nlm.nih.gov/36584500/>

Diagnostic and therapeutic approach to chronic meningitis in Brazil: a narrative review.

Silva GD, Guedes BF, Junqueira IR, Gomes HR, Vidal JE.

Nov-2022

Arq Neuropsiquiatr.

<https://pubmed.ncbi.nlm.nih.gov/36577417/>

Dracunculose

In vitro scolicidal effect of Calendula officinalis, Artemisia dracunculus, Artemisia absinthium, and Ferula assafoetida extracts against hydatid cyst protoscolices.

Norouzi R, Abedi Maleki R, Siyatpanah A, Fiaid A, El Zowalaty ME.

2022

Ann Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36587611/>

Echinococcus granulosus is the etiologic agent of cystic echinococcosis. Numerous research studies have been conducted on natural scolicidal agents to inactivate protoscolices during surgery. This study was undertaken to compare the in vitro scolicidal effects of hydroalcoholic extracts of *Calendula officinalis*, *Artemisia dracunculus*, *Artemisia absinthium* and *Ferula assafoetida*. The scolicidal activities of the extracts were tested at different concentrations following incubation periods of 10, 30 and 60 min. The chemical composition of the hydroalcoholic extracts were analyzed using Gas Chromatography-Mass Spectrometry (GC-MS). The major chemical components of *C. officinalis*, *A. dracunculus*, *A. absinthium* and *F. assafoetida* were identified as n-Docosane (14.17%), 2H-1-benzopyran-2-one, 7-methoxy (54.96%), n-Docosane (9.72%) and 2-methoxy-3-methyl-butyric acid, methyl ester (13.9%), respectively. The results showed that the hydroalcoholic extracts of *A. absinthium* and *F. assafoetida* at a concentration of 250 mg/ml resulted in killing 100% of the protoscolices at 60 minutes, while the concentration of 250 mg/ml of hydroalcoholic extract of *C. officinalis* and *A. dracunculus* resulted in killing 42.33% and 65.67%, respectively. The findings of the present study showed that *A. absinthium* and *F. assafoetida* have potent scolicidal effects. However, additional in vivo studies are required to confirm the efficacy of these plant-derived extracts against hydatid cyst for their clinical use.

Microbial Population Dynamics in Lemnaceae (Duckweed)-Based Wastewater Treatment System.

Singh P, Jani K, Sharma S, Rale V, Souche Y, Prakash S, Jogdeo P, Patil Y, Dhanorkar MN.

31-12-2022

Curr Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36585971/>

The dynamic microflora associated within, and in the surrounding aquatic environment, has been found to be responsible for the functional properties of many aquatic plants. The aim of the current work was to evaluate the effectiveness of Lemnaceae-based wastewater treatment system under tropical conditions and investigate the changes in the aquatic microflora upon plant growth. A biological wastewater treatment system was designed and investigated using mixed Lemnaceae culture comprising *Lemna minor* and *Spirodela polyrhiza* in a batch mode. A significant reduction in total solids (31.8%), biochemical oxygen demand (93.5%), and chemical oxygen demand (73.2%) was observed after seven days of duckweed growth using a low inoculum. A preliminary study on the change in the microbial population diversity and functionality, in the wastewater before and after treatment, revealed an increase in the denitrifying microflora in wastewater post-Lemnaceae treatment. Dominance of 10 bacterial phyla, contributing for 98.3% of the total bacterial communities, was recorded, and ~ 50.6% loss of diversity post-treatment of wastewater was revealed by the Shannon Index. Among 16 bacterial families showing relative abundance of $\geq 1\%$ in untreated wastewater, Methylobacteriaceae, Pseudomonadaceae, Brucellaceae, Rhodobacteraceae, and Acetobacteraceae prevailed in the water post-treatment by duckweeds. This is a novel work done on the dynamics of aquatic microflora associated with Lemnaceae under tropical Indian conditions. It confirms the application of Lemnaceae-based wastewater treatment system as effective biofilter and calls for further studies on the active involvement of the endophytic and aquatic microflora in the functions of these plant.

Screening of structural and functional alterations in duckweed (*Lemna minor*) induced by per- and polyfluoroalkyl substances (PFASs) with FTIR spectroscopy.

Wu YL, Xiong Q, Wang B, Liu YS, Zhou PL, Hu LX, Liu F, Ying GG.

15-01-2023

Environ Pollut.

<https://pubmed.ncbi.nlm.nih.gov/36436661/>

As a class of common emerging pollutants, per- and polyfluoroalkyl substances (PFASs) and their alternatives have been widely detected in various environmental matrices, exhibiting a great threat to the ecological environment and human health. Nevertheless, changes in biomolecular structure and function of duckweed caused by PFASs and their alternatives remain unknown thus far. Herein, the effects of four PFASs, including two common legacy PFASs (perfluorooctane sulfonic acid (PFOS) and perfluorooctanoic acid (PFOA)) and two PFASs alternatives (perfluorobutane sulfonic acid (PFBS) and 1H,1H,2H, 2H-perfluorooctane sulfonic acid (6:2 FTS)) on duckweed (*Lemna minor*) at biochemical level were investigated with Fourier transform infrared spectroscopy (FTIR). Although no obvious inhibitions were observed in the growth of *L. minor* with PFASs exposure at three levels of $1 \mu\text{g L}^{-1}$, $100 \mu\text{g L}^{-1}$, and 10 mg L^{-1} , significant structural and functional alterations were induced at the biochemical level. In

response to PFASs exposure, lipid peroxidation, proteins aggregation and α -helix to β -sheet transformation of the protein conformation, as well as changes of DNA conformations were detected. Moreover, alterations in lipid, protein, and DNA were proved to be concentration-related and compound-specific. Compared to the two legacy PFASs (PFOS and PFOA), alternative ones exhibited greater effects on the biological macromolecules of *L. minor*. The findings of this study firstly reveal structural and functional alterations in *L. minor* induced by PFASs exposure, providing further understanding of their toxicity effects.

Transcriptome analysis reveals genes expression pattern of *Spirodela polyrhiza* response to heat stress.

Shang S, Zhang Z, Li L, Chen J, Zang Y, Liu X, Wang J, Tang X.

15-01-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/36403776/>

With global warming, high-temperature stress has become an essential abiotic factor affecting plant growth and survival. However, little knowledge was available of the molecular mechanism that aquatic plants respond to this stress. In the present study, we explore the adaptation mechanism of *Spirodela polyrhiza*, a surface-water-grown duckweed species broadly distributed worldwide to high temperatures, and analyze its gene expression pattern of *S. polyrhiza* under heat stress. Three temperature stress treatments, including room temperature group (CK), middle high-temperature group (MTS), and high-temperature group (45°C , HTS) were set. The results showed that the contents of SOD first increased and then decreased, and those of MDA showed an upward trend under elevated high-temperature stress. According to the transcriptome data, 3145, 3487, and 3089 differently expressed genes (DEGs) were identified between MTS and CK, HTS and CK, and HTS and MTS, respectively. The transcription factors (TFs) analysis showed that 14 differentially expressed TFs, including HSF, ERF, WRKY, and GRAS family, were responsive to heat stress, suggesting they might play vital roles in improving resistance to heat stress. In conclusion, *S. polyrhiza* could resist high temperatures by increasing SOD activity and MDA at the physiological level. Several transcription factors, energy accumulation processes, and cell membranes were involved in high-temperature stress at the molecular level. Our findings are helpful in better grasping the adaptation rules of some aquatic plants to high temperatures.

Echinococcosis

Misdiagnosis of hepatic cystic echinococcosis complicated with hepatocellular carcinoma: A case report.

Wang Z, Yang JY, Xia P, Zhu HH, Gai ZG.

23-12-2022

Medicine (Baltimore).

<https://pubmed.ncbi.nlm.nih.gov/36595756/>

Rationale: Hepatic cystic echinococcosis (CE) is a common zoonotic parasitic disease caused by the entry of *Echinococcus granulosus* eggs into human body. Surgical resection is the optimal treatment choice for hepatic CE. However, Coexistence of CE and hepatocellular carcinoma (HCC) have been reported with a rare incidence rate, which led to unsatisfactory prognosis after the operation.

Patient concerns: A 69-year-old male patient was admitted to hospital because of "Upper abdominal pain and discomfort for more than 1 month and an aggravation for 10 days." **Diagnosis:** An elderly male herder who was initially diagnosed as hepatic CE, and none of the preoperative imaging test revealed the existence of HCC. Co-existence of hepatic CE and HCC was confirmed by the postoperative pathological examination. **Interventions:** The patient underwent "combined hepatic segmental resection, portal vein thrombectomy, portal vein repairment, hepatic hydatid internal capsule removal and external subtotal resection, cholecystectomy". **Outcomes:** During follow-up after discharge, the patient did not regularly review and get further treatment and died 8 months after operation. **Lessons:** May improve the clinicians' understanding of CE complicated with HCC, and reduce the misdiagnosis of similar case, as well as provide guidance for clinical treatment.

Imaging Manifestations and Misdiagnosis Analysis of Six Cases of Bone Hydatid Disease.

Sun Y, Yan C, Tian D, Zhang C, Zhang Q.

Dec-2022

Korean J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36588418/>

We retrospectively evaluated the clinical and imaging features of 6 patients with bone hydatid disease confirmed by surgery and pathological examination. Among the 6 patients, 2 were infected with *Echinococcus granulosus* metacestode and 4 were infected with *E. multilocularis* metacestode. The 2 cases with cystic echinococcosis were diagnosed by computed tomographic (CT) examination, and other 4 cases were diagnosed by magnetic resonance (MR) imaging. On the initial evaluation, 1 case each was misdiagnosed as a giant cell tumor or neurogenic tumor, and 2 were misdiagnosed as tuberculosis. The imaging manifestations of bone hydatid disease are complex, but most common findings include expansive osteolytic bone destruction, which may be associated with sclerosing edges or dead bone formation, localized soft tissue masses, and vertebral lesions with wedge-shaped changes and spinal stenosis. Combining imaging findings with the patient's epidemiological history and immunological examinations is of great help in improving the diagnosis and differential diagnosis of bone hydatid disease.

Molecular genotyping of *Echinococcus granulosus sensu stricto* from human *Echinococcal* cysts in Hatay, Türkiye.

Hamamcı B, Açıkgöz G, Çetinkaya Ü, Kılıç E, Koçal S, Karaaslan K, Durgun Yetim T, Yetim İ.

29-12-2022

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36587835/>

Cystic echinococcosis (CE) is one of the zoonotic infections in human, an important global health problem. It was aimed to determine the molecular characterization and phylogenetic analysis of isolates obtained from patients diagnosed with CE in Hatay province, according to the *cox1* gene region. A total of 31 patients, 14 males and 17 females, with a mean age of 35.19 (± 14.28) years were included in the study. 35 cyst materials obtained from patients were studied. DNA isolation was performed from the samples with protoscoleces determined in the cyst fluid. One-way DNA sequencing was performed with the Sanger Sequencing Protocol through the obtained PCR products. In the study, 35 hydatid cysts of human origin were examined and protoscoleces was detected in 11 (31.43%) of them. Twenty of the patients had liver involvement, seven had lung involvement, and four had both liver and lung involvement. All the samples with protoscoleces detected were observed of PCR product with a size of approximately 446 bp. When the sequence results of the isolates were evaluated within themselves, it was seen that there were three different sequences with 99% similarity to each other. As a result, of the phylogenetic analysis, it was determined that the isolates were identified in the *Echinococcus granulosus sensu stricto* (*E. granulosus* s. s.) (G1-G3) complex. This study is thought to contribute to the epidemiology, parasite control, effective diagnosis and treatment techniques, eradication, vaccine and drug development studies of *E. granulosus* s. s in Türkiye.

In vitro scolicidal effect of *Calendula officinalis*, *Artemisia dracunculus*, *Artemisia absinthium*, and *Ferula assafoetida* extracts against hydatid cyst protoscolices.

Norouzi R, Abedi Maleki R, Siyadatpanah A, Fiad A, El Zowalaty ME.

2022

Ann Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36587611/>

Echinococcus granulosus is the etiologic agent of cystic echinococcosis. Numerous research studies have been conducted on natural scolicidal agents to inactivate protoscolices during surgery. This study was undertaken to compare the in vitro scolicidal effects of hydroalcoholic extracts of *Calendula officinalis*, *Artemisia dracunculus*, *Artemisia absinthium* and *Ferula assafoetida*. The scolicidal activities of the extracts were tested at different concentrations following incubation periods of 10, 30 and 60 min. The chemical composition of the hydroalcoholic extracts were analyzed using Gas Chromatography-Mass Spectrometry (GC-MS). The major chemical components of *C. officinalis*, *A. dracunculus*, *A. absinthium* and *F. assafoetida* were identified as n-Docosane (14.17%), 2H-1-benzopyran-2-one, 7-methoxy (54.96%), n-Docosane (9.72%) and 2-methoxy-3-methyl-butyric acid, methyl ester (13.9%), respectively. The results showed that the hydroalcoholic extracts of *A. absinthium* and *F. assafoetida* at a concentration of 250 mg/ml resulted in killing 100% of the protoscolices at 60 minutes, while the concentration

of 250 mg/ml of hydroalcoholic extract of *C. officinalis* and *A. dracunculus* resulted in killing 42.33% and 65.67%, respectively. The findings of the present study showed that *A. absinthium* and *F. assafoetida* have potent scolicidal effects. However, additional in vivo studies are required to confirm the efficacy of these plant-derived extracts against hydatid cyst for their clinical use.

Phylogeny and population structure of *Echinococcus granulosus* (sensu stricto) based on full-length cytb-nad2-atp6 mitochondrial genes - First report from Sialkot District of Pakistan.

Alvi MA, Ali RMA, Li L, Saqib M, Qamar W, Hassan A, Ghafoor M, Rahman SU, Khan MUZ, Fu BQ, Liu Y, Yin H, Yan HB, Jia WZ.

27-12-2022

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36584819/>

Cystic echinococcosis is a zoonotic disease of livestock having serious economic setbacks. The etiological agents of the disease belong to *Echinococcus granulosus sensu lato*. Despite of worldwide distribution of the disease, the molecular studies mainly employ amplification of *cox1*, *nad1* and *nad5* genes. To further strengthen the knowledge about significance of other molecular markers and to investigate the genetic diversity and population structure of *Echinococcus* species in Pakistan, the current study was designed in which full length mitochondrial *cytb*, *atp6* and *nad2* genes were amplified. Based on BLAST searches of the generated *cytb*, *atp6* and *nad2* gene sequences from a total of 18 hydatid cysts collected from cattle, 12 isolates were identified as *E. granulosus* G3 and 6 as *E. granulosus* (G1). The phylogeny inferred by the Bayesian method using nucleotide sequences of *cytb-atp6-nad2* further confirmed their identity. The diversity indices indicated a high haplotype and a low nucleotide diversity. The negative values of Tajima's D and Fu's Fs test demonstrated deviation from neutrality suggesting a recent population expansion. To the best of our knowledge, the present study described the genetic variation of *E. granulosus* population for the first time in Pakistan using full-length *cytb*, *atp6* and *nad2* mitochondrial genes. The findings on the genetic variation of *E. granulosus* in Pakistan will constitute useful baseline information for future studies on the prevalence and population structure of *E. granulosus* based on full-length *cytb*, *atp6* and *nad2*.

A giant isolated primary splenic hydatidosis: A case report.

Sah RK, Sah BK, Dang CTM, Sah VK.

14-11-2022

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/36582909/>

A case of giant primary splenic hydatid cyst: Case report.

Singh S, Kisee S, Amatya S, Singh S, Bista S, Shrestha R, Kumar Chhantel Thapa M.

10-11-2022

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/36582877/>

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

***Fasciola gigantica* vaccine construct: an in silico approach towards identification and design of a multi-epitope subunit vaccine using calcium binding EF-hand proteins.**

Das KC, Konhar R, Biswal DK.

05-01-2023

BMC Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36604615/>

Continuous attempts have been made to pinpoint candidate vaccine molecules and evaluate their effectiveness in order to commercialise such vaccines for the treatment of tropical fascioliasis in livestock. The pathophysiology of fascioliasis can be related to liver damage brought on by immature flukes that migrate and feed, as well as immunological reactions to chemicals produced by the parasites and alarm signals brought on by tissue damage. Future research should, in our opinion, concentrate on the biology of invasive parasites and the resulting immune responses, particularly in the early stages of infection. The goal of the current study was to use the calcium-binding proteins from *F. gigantica* to create a multi-epitope subunit vaccine. The adjuvant, B-cell epitopes, CTL epitopes, and HTL epitopes that make up the vaccine construct are all connected by certain linkers. The antigenicity, allergenicity, and physiochemical properties of the vaccine construct were examined. The vaccine construct was docked with toll-like receptor 2, and simulations of the molecular dynamics of the complex's stability, interaction, and dynamics were run. After performing in silico cloning and immunosimulation, it was discovered that the construct was suitable for further investigation. New vaccination technologies and adjuvant development are advancing our food safety procedures since vaccines are seen as safe and are accepted by the user community. This research is also applicable to the *F. hepatica* system.

Differentiating paramphistome species in cattle using DNA barcoding coupled with high-resolution melting analysis (Bar-HRM).

Buddhachat K, Sriuan S, Nak-On S, Chontanarith T.

05-01-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/36604333/>

Paramphistomosis is caused by paramphistome or amphistome parasites, including *Fischoederius elongatus*, *Gastrothylax crumenifer*, *Orthocoelium parvipapillatum*, and *Paramphistomum epiclitum*. The control and prevention of these parasite outbreaks are difficult because of the wide occurrence of these species. Besides, the clinical manifestations and their egg characteristics are similar to those of other intestinal flukes in the paramphistome group, leading to misdiagnosis. Here, we employed DNA barcoding using NADH dehydrogenase (ubiquinone, alpha 1) (ND1) and cytochrome c oxidase subunit I (COI), coupled with high-resolution melting analysis (Bar-HRM), for species differentiation. As a result, ParND1_3 and ParCOI4 resulted in positive amplification in the paramphistomes and *Fasciola gigantica*, with significantly different melting curves for each species. The melting temperatures of each species obtained clearly differed. Regarding sensitivity, the limit of detection (LoD) for all species of paramphistomes was 1 pg/μl. Our findings suggest that Bar-HRM using ParND1_3 is highly suitable for the differentiation of paramphistome species. This approach can be used in parasite detection and epidemiological studies in cattle.

Intestinal parasitic infections and risk factors among the population in Cambodia.

La N, Leng M, Rattanapitoon K, Pechdee P, Boonsuya A, Arunsan P, Rattanapitoon SK.

01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602213/>

Seasonal dynamics of *Fasciola gigantica* transmission in Prafi district, Manokwari Regency, West Papua, Indonesia.

Purwaningsih P, Palulungan JA, Tethool AN, Noviyanti N, Satrija F, Murtini S.

Nov-2022

Vet World.

<https://pubmed.ncbi.nlm.nih.gov/36590131/>

Background and aim: Indonesia's farming practices are a perfect setting for establishing an infection with *Fasciola gigantica* which can result in economically detrimental. The objectives of the current study were to describe and analyze the transmission dynamics of fasciolosis (*F. gigantica*) in Prafi District, to provide information on effective control strategies and to identify risk factors associated with fasciolosis in cattle. **Materials and methods:** Fecal samples were purposively collected from the rectum of 60 beef cattle in Prafi District, Manokwari Regency, West Papua Province, Indonesia. The samples were collected once a month for 8 months from April 2019 to November 2019. Furthermore, the samples were taken from two rearing system groups: 30 stall cattle and 30 cattle in a palm oil garden. The presence of *F. gigantica* eggs in the fecal samples was examined using a modified Danish Bilharziasis Laboratory technique-sedimentation. Meanwhile, the antigenic diagnosis of *Fasciola* in the fecal samples was analyzed using an enzyme-linked

immunosorbent assay kit to perform an indirect sandwich assay on feces. Snails were collected from an irrigation canal, rice field, and palm oil garden canal around Prafi District. These snails were examined for infection with cercariae larvae of *F. gigantica* by cercarial shedding and crushing techniques. **Results:** The peak occurrence of *F. gigantica* infection was identified in August (65.00%) and the lowest in June (35.00%). The highest prevalence of fasciolosis in cattle was recorded in August and November (90.00%) and the lowest was in May (40.00%). Moreover, the highest prevalence of fasciolosis in cattle exposed to the palm oil garden was recorded in April (53.33%) and the lowest prevalence of *F. gigantica* infection was recorded in June (23.33%). In total, 2046 snails were screened by the cercarial shedding and crushing method; of these, 426 (20.82%) were found to be positive for trematode cercariae. The prevalence of *F. gigantica* infection in *Lymnaea* spp. snails was highest in November (47.46%) and lowest in April (9.28%). **Conclusion:** The current study shows that beef cattle grown in two types of rearing systems in Prafi District were infected with *F. gigantica* during the dry and rainy season. It was revealed that *Lymnaea* spp. are common snails found in and around Prafi District, and can act as intermediate hosts with an infective stage of trematode. The transmission to cattle was highly effective, despite the short activity period, the low infection rate of snails, and the incidental anthelmintic treatment.

Endemic *Paragonimus kellicotti* infections in animals and humans in USA and Canada: Review and personal perspective.

Dubey JP.

09-12-2022

Food Waterborne Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36588917/>

Infections with the lung fluke, *Paragonimus kellicotti*, have been diagnosed in a variety of domestic and wild animals and humans in USA and Canada. Although there are many species of *Paragonimus* in other parts of the world; *P. kellicotti* is the only species definitively diagnosed in USA and Canada. Fresh water snails (several species) and crayfish (mainly *Orconectes* spp.) are its intermediate hosts. Humans and animals become infected with *P. kellicotti* only by ingesting metacercariae encysted in the heart of crayfish. After ingestion, the fluke penetrates intestinal wall, enters peritoneal cavity, and reaches pleural cavity by direct penetration of diaphragm, 2-3 weeks post inoculation (p.i.). Young flukes penetrate lungs and become encysted in pulmonary tissue, often in pairs. Time to maturity is around 4-7 weeks p.i. Eggs are coughed up, swallowed, and are excreted in feces. Although the parasite has been known for more than a century, there has been an upsurge of human infections in the USA. Here, I review *P. kellicotti* infections in naturally infected hosts. Pathogenesis, diagnosis, and treatment in parasite-free cats and dogs experimentally infected *P. kellicotti* are reviewed to shed light on the pathogenesis of human paragonimiasis. Problems and challenges facing diagnosis of paragonimiasis, especially non-pulmonary infections,

are discussed. Fluke stages are deposited in Smithsonian Museum.

Seasonal Prevalence of Helminthic Infections in the Gastrointestinal Tract of Sheep in Mazandaran Province, Northern Iran.

Salehi A, Razavi M, Vahedi Nouri N.

21-12-2022

J Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/36588778/>

Helminthic infection is the major cause of the sheep's reduced productivity. In this study, a total number of 240 fecal samples of sheep from stationary flocks of four different zones of Mazandaran province (Amol, Babol, Sari, and Nowshahr cities) were examined each season, out of which 53.33% of animals were affected by the helminthic infections. The most prevalent infecting parasites were the *Trichostrongylidae* (46.61%), followed by the *Fasciola* (9.96%). In addition, the *Strongyloides* had the lowest proportion with only 2.39%. The other detected parasites included *Chabertia* (5.98%), *Cooperia* (3.19%), *Nematodirus* (3.19%), *Trichuris* (5.58%), *Toxocaridae* (4.78%), *Haemonchus* (4.78%), *Ostertagia* (5.58%), *Oesophagostomum* (4.78%), and *Dicrocoelium* (3.19%). The nematodes had the highest percentage with 86.85%, whereas the trematodes followed them with 13.15%. No significant difference was observed between the infection level in females and males, with 56.9% and 43.94% rates of infection, respectively. Significantly lower infection was observed in winter compared with the other seasons. *Trichostrongylidae* was the dominant genus across all seasons. It was also noted that winter had the lowest percentage of helminthic infection significantly. The eggs per gram of feces was also estimated, and it showed that a significant number of sheep are infected with a moderate number of parasites. In a conclusion, even though livestock farmers have been using antiparasitic drugs in their livestock in recent years, parasitic infection still exists in livestock. Thus, a proper implementation of helminthic infection control programs in this area should be employed as the key element for reducing the high prevalence of livestock helminthic infection.

Prevalence of intestinal parasitic infections and genetic differentiation of *Strongyloides stercoralis* among migrant workers from Myanmar, Lao PDR and Cambodia in northeastern Thailand.

Sangwalee W, Norkaew J, Inthachak S, Janwan P, Rodpai R, Sanpool O, Sadaow L, Boonroumkaew P, Intapan PM, Maleewong W, Thanchomnang T.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584196/>

Intestinal parasitic infections (IPIs) remain a public-health problem worldwide, including in countries of the Lower Mekong subregion. Increases in human migration from neighboring countries might cause reemerging parasitic infections, leading to spread of parasites in the landscape. Here, we conducted a cross-sectional study to identify the

prevalence of IPIs in migrant workers from Myanmar, Lao PDR, and Cambodia who were dwelling in Nakhon Ratchasima Province, northeastern Thailand. The identification of *Strongyloides* species and genetic differentiation of worms from migrant workers with different countries of origin was also assessed. Fresh stool samples were collected from 338 migrant workers and examined for evidence of IPIs using agar plate culture (APC) and the formalin-ethyl acetate concentration technique (FECT). Among those nine samples positive for nematodes by APC, the *Strongyloides* or hookworm species present was confirmed using the polymerase chain reaction (PCR) followed by DNA sequencing. This revealed eight cases of *Strongyloides stercoralis* infection and one of *Necator americanus*. Fifty-one out of 338 individuals (15.09%) were positive for IPIs using FECT and APC. Eggs of *Opisthorchis*-like flukes were the most common parasite (11.83% of samples), followed by *S. stercoralis* (2.37%), *Entamoeba coli* (1.50%), hookworm (0.89%), *Taenia* sp. (0.60%) and *Hymenolepis nana* (0.30%). The genetic differentiation of *S. stercoralis* recovered from migrant workers with different countries of origin was analyzed. Specimens of *S. stercoralis* isolated from workers from Lao PDR, Cambodia and Myanmar were genetically similar to those sequenced from Thailand. However, there were population-genetic differences between *S. stercoralis* from these Southeast Asian countries and other regions of the world. This study demonstrated that IPIs were prevalent in migrant workers in the northeastern region of Thailand. Our findings provided molecular confirmation of the presence of *S. stercoralis* and explored the genetic differentiation of *S. stercoralis* from those infected migrant workers. An effective anti-parasitic drug should be provided for migrant workers and its administration enforced.

New perspectives for fascioliasis in Upper Egypt's new endemic region: Sociodemographic characteristics and phylogenetic analysis of *Fasciola* in humans, animals, and *lymnaeid* vectors.

Ahmad AA, Ramadan HK, Hassan WA, Hakami MA, Huseein EAM, Mohamed SA, Mohamed AA, Elossily NA.

28-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36576925/>

Filariose lymphatique

Pharmacological Profiling of a *Brugia malayi* Muscarinic Acetylcholine Receptor as a Putative Antiparasitic Target.

Gallo KJ, Wheeler NJ, Elmi AM, Ains PM, Zamanian M.

05-01-2023

Antimicrob Agents Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36602350/>

The diversification of anthelmintic targets and mechanisms of action will help ensure the sustainable

control of nematode infections in response to the growing threat of drug resistance. G protein-coupled receptors (GPCRs) are established drug targets in human medicine but remain unexploited as anthelmintic substrates despite their important roles in nematode neuromuscular and physiological processes. Bottlenecks in exploring the druggability of parasitic nematode GPCRs include a limited helminth genetic toolkit and difficulties establishing functional heterologous expression. In an effort to address some of these challenges, we profile the function and pharmacology of muscarinic acetylcholine receptors in the human parasite *Brugia malayi*, an etiological agent of human lymphatic filariasis. While acetylcholine-gated ion channels are intensely studied as targets of existing anthelmintics, comparatively little is known about metabotropic receptor contributions to parasite cholinergic signaling. Using multivariate phenotypic assays in microfilariae and adults, we show that nicotinic and muscarinic compounds disparately affect parasite fitness traits. We identify a putative G protein-linked acetylcholine receptor of *B. malayi* (*Bma-GAR-3*) that is highly expressed across intramammalian life stages and adapt spatial RNA *in situ* hybridization to map receptor transcripts to critical parasite tissues. Tissue-specific expression of *Bma-gar-3* in *Caenorhabditis elegans* (body wall muscle, sensory neurons, and pharynx) enabled receptor deorphanization and pharmacological profiling in a nematode physiological context. Finally, we developed an image-based feeding assay as a reporter of pharyngeal activity to facilitate GPCR screening in parasitized strains. We expect that these receptor characterization approaches and improved knowledge of GARs as putative drug targets will further advance the study of GPCR biology across medically important nematodes

Exploration of aminoacyl-tRNA synthetases from eukaryotic parasites for drug development.

Gill J, Sharma A.

31-12-2022

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/36596362/>

Parasitic diseases result in considerable human morbidity and mortality. The continuous emergence and spread of new drug-resistant parasite strains is an obstacle to controlling and eliminating many parasitic diseases. Aminoacyl-tRNA synthetases (aaRSs) are ubiquitous enzymes essential for protein synthesis. The design and development of diverse small molecule, drug-like inhibitors against parasite-encoded and expressed aaRSs have validated this enzyme family as druggable. In this work, we have compiled the progress to date towards establishing the druggability of aaRSs in terms of their biochemical characterization, validation as targets, inhibitor development and structural interpretation from parasites responsible for malaria (*Plasmodium*), lymphatic filariasis (*Brugia*), giardiasis (*Giardia*), toxoplasmosis (*Toxoplasma gondii*), leishmaniasis (*Leishmania*), cryptosporidiosis (*Cryptosporidium*) and trypanosomiasis (*Trypanosoma*). This work thus provides a robust framework for the systematic dissection of aaRSs from these pathogens and will facilitate the cross-usage of

potential inhibitors to jump-start antiparasitic drug development.

Reverse vaccinology assisted design of a novel multi-epitope vaccine to target *Wuchereria bancrofti* cystatin: An immunoinformatics approach.

Das NC, Gupta PSS, Panda SK, Rana MK, Mukherjee S.

29-12-2022

Int Immunopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36586276/>

Proteases are the critical mediators of immunomodulation exerted by the filarial parasites to bypass and divert host immunity. Cystatin is a small (~15 kDa) immunomodulatory filarial protein and known to contribute in the immunomodulation strategy by inducing anti-inflammatory response through alternative activation of macrophages. Recently, *Wuchereria bancrofti* cystatin has been discovered as a ligand of human toll-like receptor 4 which is key behind the cystatin-induced anti-inflammatory response in major human antigen-presenting cells. Considering the pivotal role of cystatin in the immunobiology of filariasis, cystatin could be an efficacious target for developing vaccine. Herein, we present the design and in-silico analyses of a multi-epitope-based peptide vaccine to target *W. bancrofti* cystatin through immune-informatics approaches. The 262 amino acid long antigen construct comprises 9 MHC-I epitopes and MHC-II epitopes linked together by GPGPG peptide alongside an adjuvant (50S ribosomal protein L7/L12) at N terminus and 6 His tags at C terminus. Molecular docking study reveals that the peptide could trigger TLR4-MD2 to induce protective innate immune responses while the induced adaptive responses were found to be mediated by IgG, IgM and Th1 mediated responses. Notably, the designed vaccine exhibits high stability and no allergenicity in-silico. Furthermore, the multi epitope-vaccine was also predicted for its RNA structure and cloned in pET30ax for further experimental validation. Taken together, this study presents a novel multi-epitope peptide vaccine for triggering efficient innate and adaptive immune responses against *W. bancrofti* to intervene LF through immunotherapy.

Wuchereria Bancrofti Infection in Children Living in a Rubber Plantation Estate in South-South Nigeria.

Ekanem EE, Umoh BD.

29-12-2022

West Afr J Med.

<https://pubmed.ncbi.nlm.nih.gov/36583928/>

Editorial: Host immune response and protective immune responses during filarial infections.

Ritter M, Hübner MP.

13-12-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36582245/>

Mycétome

Burden of Serious Fungal Infections in India.

Ray A, Aayilliath K A, Banerjee S, Chakrabarti A, Denning DW.

26-12-2022

Open Forum Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36589484/>

Background: Fungal disease is frequent in India, but its incidence and prevalence are unclear. This review aims at defining the frequency or burden of various fungal infections in India. **Methods:** A systematic review of the literature on the PubMed, Embase, and Web of Science (WOS) databases was conducted using appropriate search strings. Deterministic modeling determined annual incidence and prevalence estimates for multiple life- and sight-threatening infections with significant morbidity. **Results:** Literature searches yielded >2900 papers; 434 papers with incidence/prevalence/proportion data were analyzed. An estimated 57 251 328 of the 1 393 400 000 people in India (4.1%) suffer from a serious fungal disease. The prevalence (in millions) of recurrent vulvovaginal candidiasis is 24.3, allergic bronchopulmonary aspergillosis is 2.0, tinea capitis in school-age children is 25, severe asthma with fungal sensitization is 1.36, chronic pulmonary aspergillosis is 1.74, and chronic fungal rhinosinusitis is 1.52. The annual incidence rates of *Pneumocystis pneumonia* (58 400), invasive aspergillosis (250 900), mucormycosis (195 000), esophageal candidiasis in HIV (266 600), candidemia (188 000), fungal keratitis (1 017 100), and cryptococcal meningitis (11 500) were also determined. Histoplasmosis, talaromycosis, mycetoma, and chromoblastomycosis were less frequent. **Conclusions:** India's fungal burden is high and underappreciated in clinical practice.

Comparing the performance of the common used eumycetoma diagnostic tests.

Siddig EE, Nyuykonge B, Mhmoud NA, Abdallah OB, El Nour Bahar M, Ahmed ES, Nyaoke B, Zijlstra EE, Verbon A, Bakhiet SM, Fahal AH, van de Sande WWJ.

29-12-2022

Mycoses.

<https://pubmed.ncbi.nlm.nih.gov/36583225/>

Objectives: Mycetoma is a neglected tropical implantation disease caused by 70 different infectious agents. Identifying the causative organism to the species level is essential for appropriate patient management. Ultrasound, histopathology, culture and two species-specific PCRs are most commonly used methods for species identification in endemic regions. The aim of this study was to compare the diagnostic performance of these commonly used assays using sequencing of barcoding genes as the gold standard. **Methods:** This descriptive cross-sectional study was conducted at the Mycetoma Research Centre, University of Khartoum, Sudan. It included 222 patients suspected of fungal mycetoma caused by *Madurella mycetomatis*. **Results:** 154 (69.3%)

were correctly identified by ultrasound, histology, culture and both species-specific PCRs. In 60 patients, at least one of the diagnostic tests failed to identify *M. mycetomatis*. Five patients had no evidence of eumycetoma, and for three, only the ultrasound was indicative of mycetoma. The two species-specific PCRs were the most sensitive and specific methods, followed by culture and histology. Ultrasound was the least specific as it only allowed differentiation between actinomycetoma and eumycetoma. The time to result was 9.38 minutes for ultrasound, 3.76 hours for PCR, 8.5 days for histopathology and 21 days for grain culturing. **Conclusion:** Currently, PCR directly on DNA isolated from grains is the most rapid and reliable diagnostic tool to identify *M. mycetomatis* eumycetoma.

Why the mycetoma patients are still neglected.

Fahal AH, Ahmed KO, Saeed AA, Elkhawad AO, Bakhiet SM.

29-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36580447/>

A scoping review of mycetoma profile in Egypt: revisiting the global endemicity map.

Ahmed SA, El-Sobky TA, de Hoog S, Zaki SM, Taha M.

03-01-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36084235/>

Mycetoma is a chronic infectious disease endemic in sub-Saharan Africa (SSA), India and parts of South and North America. The epidemiologic profile of the disease in Egypt, which neighbours SSA, has not been explored previously. Therefore we conducted a scoping review of the literature on mycetoma in Egypt. We searched the literature comprehensively on MEDLINE and Google Scholar using free-text words and Medical Subject Headings and terms. Both published and non-peer-reviewed (grey literature) articles were included. The initial search identified 133 reports. Of these, only eight were found to be relevant and were included in the study. The total number of mycetoma patients was 59, reported between 1949 and 2015. There was a predilection for eumycetoma (44 of 59) patients (75%), while actinomycetoma constituted 15 patients (25%). Six patients were female, 28 were male and 25 were unreported. Children and adolescents constituted 3 of 59 (5%), 52 (88%) were adults and age was not provided for 4 patients. Only four patients (7%) were non-autochthonous. The incidence of mycetoma in Egypt is higher than previously reported. Egypt is probably a low-endemic country. An accurate estimate of the prevalence and epidemiology of mycetoma necessitates further research collaboration.

Mycetoma management and clinical outcomes: the Mycetoma Research Center experience.

Musa EA, Abdoon IH, Bakhiet SM, Osman B, Abdalla SA, Fahal AH.

03-01-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/35903002/>

Background: Mycetoma is a chronic granulomatous inflammatory disease that affects the cutaneous and subcutaneous tissues, leading to gruesome complications if not treated early. As a neglected disease, it has received scant attention in developing curable drugs. Mycetoma treatment is still based on expert opinions in the absence of guidelines. **Methods:** This descriptive, cross-sectional, hospital-based study aimed to determine and assess the disease treatment outcomes observed at Mycetoma Research Center, Sudan. **Results:** In this study, 75% of patients had eumycetoma, all of whom were treated with itraconazole and 37.4% underwent surgical excision, while 25% of the patients had actinomycetoma, 99.2% of whom were treated with a combination of cotrimoxazole and amoxicillin-clavulanate. The cure rate was 12.7% and 14.3% for patients with eumycetoma and actinomycetoma, respectively. Only 6.1% of eumycetoma patients underwent amputation. Remarkably, no patient with actinomycetoma underwent an amputation. Small lesions (OR=10.09, $p<0.001$) and good follow-up (OR=6.81, $p=0.002$) were positive predictors of complete cure. In terms of amputation, history of surgical recurrence at presentation (OR=3.67, $p=0.020$) and presence of grains (OR=7.13, $p=0.012$) were positive predictors, whereas small lesions were negative predictors (OR=0.06, $p=0.009$). **Conclusions:** Treatment of mycetoma was suboptimal, with a low cure rate despite a long treatment duration. Complete cure has a significant association with small lesions and good follow-up.

Schistosomiasis

Precision mapping of schistosomiasis and soil-transmitted helminthiasis among school age children at the coastal region, Kenya.

Kepha S, Ochol D, Wakesho F, Omondi W, Njenga SM, Njaanake K, Kihara J, Mwatha S, Kanyi C, Oloo JO, Kibati P, Yard E, Appleby LJ, McRae-McKee K, Odiere MR, Matendechero SH.

05-01-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36602986/>

Schistosoma mansoni Infection Is Associated With Increased Monocytes and Fewer Natural Killer T Cells in the Female Genital Tract.

Kingery JR, Chalem A, Mukerebe C, Shigella PS, Miyaye D, Magawa RG, Ward M, Kalluvya SE, McCormick J, Maganga JK, Colombe S, Aristide C, Corstjens PLAM, Lee MH, Chagalucha JM, Downs JA.

07-12-2022

Open Forum Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36601557/>

Schistosoma mansoni infection may impair genital mucosal antiviral immunity, but immune cell populations

have not been well characterized. We characterized mononuclear cells from cervical brushings of women with and without *S. mansoni* infection. We observed lower frequencies of natural killer T cells and higher frequencies of CD14⁺ monocytes in infected women.

Corrigendum: Comparative proteomics analysis of Schistosoma japonicum developed in different Oncomelania snails as intermediate hosts.

Liu G, Miao F, Wang Y, Kou J, Yang K, Li W, Xiong C, Zhang F, Wang X, Yan H, Wei C, Zhao C, Yan G.

16-12-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36594905/>

Molecular detection of Schistosoma species in unusual snail hosts: a note of caution.

Pinto HA.

03-01-2022

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36594275/>

The interaction between snails and species of *Schistosoma* results from an evolutionary process with an intrinsic host-parasite specificity to the snail genus. Faced with this fact, the recent molecular-based report on the potential infection of the thiarid *Melanoides tuberculata* with human schistosome should be cautiously interpreted. The high sensibility of molecular tools can result in false positives, perhaps by amplifying DNA from an external (contaminant) or invasive stage of schistosome found in this non-permissive snail host. Thus, parasitological data are mandatory to extrapolate the importance of the finding for the epidemiology and control of schistosomiasis.

Schistosoma haematobium.

Corsini Campioli C, Sheehy JL, Gomez Urena EO.

22-12-2022

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/36593891/>

Bioactivity of Trigonella foenum (Fenugreek) oil on immunological and biochemical response of Schistosoma mansoni infected mice.

Hassan EM, Osman GY, Mohamed AH, Salem TA.

Jan-202

Egypt J Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36592119/>

The effect of fenugreek oil (FO) on some parasitological, immunological, and biochemical parameters in mice infected with *Schistosoma mansoni* were investigated. Chromatography mass spectrometry (GC/MS) analysis of FO revealed that linoleic acid, (E,E)-4-decadienal, and isopropyl myristate are the major constituents of FO. The results showed that treatment of *S. mansoni*-infected mice with 0.15 ml of FO daily for 10 successive days exhibited a significant reduction in the number of *S.*

mansoni male worms, and coupled worms as compared to an infected control group ($p < 0.05$). Regarding total egg counts and oogram patterns, FO effectively reduced the percentage of hepatic and intestinal egg counts, and elevated immature and dead eggs in ratios closely to praziquantel (PZQ) treated mice. Meanwhile, FO significantly elevated the levels of glutathione and co-enzyme Q-10 (COQ-10) up to 0.33 ± 0.02 ng/ml and 0.28 ± 0.02 ng/ml, respectively. However, when accompanied with PZQ, COQ-10 level was closer to that of the normal control group (0.37 ± 0.021 ng/ml). The result also showed that FO significantly reduced levels of lipid per-oxidation (0.165 ± 0.01 ng/ml) and vascular endothelial growth factor (0.25 ± 0.02 pg/ml) as compared to the PZQ-treated group (0.234 ± 0.02 ng/ml and 0.31 ± 0.008 pg/ml, respectively). Moreover, FO recovered normal values of caspase-7, and when accompanied with PZQ, annexin-V was also significantly reduced. However, treatment of *S. mansoni*-infected mice with PZQ led to a significant increase in the level of annexin-V as compared to *S. mansoni*-infected mice group ($p < 0.05$). It can be concluded that FO may have a potential anti-schistosomal, antioxidant and anti-inflammatory activities. Also, it may have a recovering effect on apoptotic parameters toward the normal values.

Genotypic-specific heat shock response of vector susceptibility to *Schistosoma mansoni*.

Spaan JM, Leavitt N, Shen J, Bundy T, Burrows L, Ingram C, Maehara TR, Ndungu I, Mutuku M, Owino G, Odiere M, Steinauer ML.

Aug-2022

Ecosphere.

<https://pubmed.ncbi.nlm.nih.gov/36590709/>

Living organisms are vulnerable to thermal stress which causes a diversity of physiological outcomes. Previous work has shown that the snail vectors (*Biomphalaria glabrata*) of an important human pathogen, *Schistosoma mansoni*, revert from resistant to susceptible after short exposure to a heat stress as low as 31°C ; however, due to lack of replicability among labs and genetic lines of snails, it has been hypothesized that this effect is genotype dependent. We examined the effects of heat shock on resistance of two species of snail vectors including *B. glabrata* and *B. sudanica*. We used 3 different inbred laboratory snail lines in addition to the F1 generation of field collected snails from Lake Victoria, Kenya, an area with high levels of schistosomiasis transmission. Our results showed marginal effects of heat shock on prevalence of infection in *B. glabrata*, and that this response was genotype specific. We found no evidence of a heat shock effect on prevalence of infection in *B. sudanica* or on intensity of infection (number of infectious stages shed) in either snail species. Such environmentally influenced defense responses stress the importance of considering this unique interaction between snail and parasite genotypes in determining infection dynamics under climate changes.

Assessment of the accuracy of 11 different diagnostic tests for the

detection of *Schistosomiasis mansoni* in individuals from a Brazilian area of low endemicity using latent class analysis.

Mesquita SG, Caldeira RL, Favre TC, Massara CL, Beck LCNH, Simões TC, de Carvalho GBF, Dos Santos Neves FG, de Oliveira G, de Souza Barbosa Lacerda L, de Almeida MA, Dos Santos Carvalho O, Moraes Mourão M, Oliveira E, Silva-Pereira RA, Fonseca CT.

15-12-2022

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36590409/>

Metabolic reprogramming of hepatocytes by *Schistosoma mansoni* eggs.

von Bülow V, Gindner S, Baier A, Hehr L, Buss N, Russ L, Wrobel S, Wirth V, Tabatabai K, Quack T, Haeblerlein S, Kadesch P, Gerbig S, Wiedemann KR, Spengler B, Mehl A, Morlock G, Schramm G, Pons-Kühnemann J, Falcone FH, Wilson RA, Bankov K, Wild P, Grevelding CG, Roeb E, Roderfeld M.

07-11-2022

JHEP Rep.

<https://pubmed.ncbi.nlm.nih.gov/36590323/>

Background & aims: Schistosomiasis is a parasitic infection which affects more than 200 million people globally. *Schistosoma* eggs, but not the adult worms, are mainly responsible for schistosomiasis-specific morbidity in the liver. It is unclear if *S. mansoni* eggs consume host metabolites, and how this compromises the host parenchyma. **Methods:** Metabolic reprogramming was analyzed by matrix-assisted laser desorption/ionization mass spectrometry imaging, liquid chromatography with high-resolution mass spectrometry, metabolite quantification, confocal laser scanning microscopy, live cell imaging, quantitative real-time PCR, western blotting, assessment of DNA damage, and immunohistology in hamster models and functional experiments in human cell lines. Major results were validated in human biopsies. **Results:** The infection with *S. mansoni* provokes hepatic exhaustion of neutral lipids and glycogen. Furthermore, the distribution of distinct lipid species and the regulation of rate-limiting metabolic enzymes is disrupted in the liver of *S. mansoni* infected animals. Notably, eggs mobilize, incorporate, and store host lipids, while the associated metabolic reprogramming causes oxidative stress-induced DNA damage in hepatocytes. Administration of reactive oxygen species scavengers ameliorates these deleterious effects. **Conclusions:** Our findings indicate that *S. mansoni* eggs completely reprogram lipid and carbohydrate metabolism via soluble factors, which results in oxidative stress-induced cell damage in the host parenchyma. **Impact and implications:** The authors demonstrate that soluble egg products of the parasite *S. mansoni* induce hepatocellular reprogramming, causing metabolic exhaustion and a strong redox imbalance. Notably, eggs mobilize, incorporate, and store host lipids, while the metabolic reprogramming causes oxidative stress-induced DNA damage in hepatocytes, independent of the host's immune response. *S. mansoni* eggs take advantage of the host environment through metabolic reprogramming of

hepatocytes and enterocytes. By inducing DNA damage, this neglected tropical disease might promote hepatocellular damage and thus influence international health efforts.

Ectopic Schistosomiasis Involving Axillary Lymph Nodes.

Chen X, He N.

Dec-2022

Korean J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36588417/>

Axillary lymph node schistosomiasis is a form of ectopic schistosomiasis, in which the *Schistosoma* adult worms or eggs are infected in the axillary lymph nodes. A 53-year-old woman visited our hospital with a small mass in the right armpit, which had been present for over 1 month. Histological examination of biopsy samples from the right axillary lymph nodes revealed granulomas containing calcified *Schistosoma* eggs. This is the first authentic case of ectopic schistosomiasis identified in the axillary lymph nodes.

Precision and geographical prevalence mapping of schistosomiasis and soil-transmitted helminthiasis among school-aged children in selected districts of north-western Tanzania.

Mazigo HD, Zinga MM, Kepha S, Yard E, McRee-Mckee K, Kabona G, Ngoma DD, Nshala A.

29-12-2022

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36581956/>

Background: The identification and mapping of at-risk populations at a lower administrative level than the district are prerequisites for the planning, resource allocation and design of impactful control intervention measures. Thus, the objective of the current study was to conduct sub-district precision mapping of soil-transmitted helminthiasis (STH) and schistosomiasis in 29 districts of north-western Tanzania using the current recommended World Health Organization criteria. **Methods:** A cross-sectional survey was conducted in 145 schools between March and May 2021. A urine filtration technique was used for the quantification of *Schistosoma haematobium* eggs, whereas quantification of *Schistosoma mansoni* and STH eggs was done using the Kato-Katz technique. Microhaematuria was examined using a urine dipstick. **Results:** The overall prevalences of any STH and schistosome infections were 9.3% [95% confidence interval (95%CI) 8.6-9.9] and 14.6% (95%CI 13.9-15.4), respectively. The overall prevalence of *S. mansoni* was 8.7% (95%CI 8.1-9.3), and 36.4%, 41.6%, and 21.9% of the children had low, moderate, and heavy infections, respectively. The overall prevalence of *S. haematobium* was 6.1% (95%CI 5.5-6.5), and 71.7% and 28.3% of the infected children had light and heavy intensity infections, respectively. The prevalence of microhaematuria was 7.3% (95%CI 6.7-7.8), with males having the highest prevalence (8.4%, $P < 0.001$). The prevalences of *Trichuris trichiura*, *Ascaris lumbricoides* and hookworm were, respectively, 1.3% (95%CI 0.1-1.5), 2.9% (95%CI 2.5-3.3)

and 6.2% (95%CI 5.7-6.7). Most of the children infected with STH had light to moderate intensities of infection. The overall prevalence of co-infection with STH and schistosomiasis was 19.1%. The prevalence of schistosomiasis ($P < 0.01$) and STH ($P < 0.001$) varied significantly between schools and sub-districts. *Schistosoma mansoni* and *S. haematobium* were observed in 60 and 71 schools, respectively, whereas any STH was observed in 49 schools. In schools where schistosomiasis was observed, prevalence was $< 10\%$ in 90.8% of them, and ranged from $\geq 10\%$ to $< 50\%$ in the other 9.2%. In schools where any STH was observed, the prevalence was $< 10\%$ in 87.7% of them. **Conclusions:** The data reported here show that schistosomiasis and STH are widely distributed around Lake Victoria. In most of the schools where schistosomiasis and STH occurred the transmission thresholds were low. These data are important and need to be taken into consideration when decisions are made on the implementation of the next round of mass chemotherapies for schistosomiasis and STH in Tanzania.

Urogenital schistosomiasis in three different water access in the Senegal river basin: prevalence and monitoring praziquantel efficacy and re-infection levels.

Senghor B, Mathieu-Begn   E, Rey O, Doucour   S, Sow D, Diop B, S  ne M, Boissier J, Sokhna C.

29-12-2022

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36581796/>

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

Intestinal parasitic infections and risk factors among the population in Cambodia.

La N, Leng M, Rattanapitoon K, Pechdee P, Boonsuya A, Arunsan P, Rattanapitoon SK.

01-12-2022

Trop Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36602213/>

Many species of helminths and protozoa caused intestinal parasitic infections (IPIs). It belongs to neglected tropical diseases (NTDs) and remains a major public health problem in several Southeast Asian countries. The present study aimed to investigate the prevalence of IPIs and associated risk factors among the population in Kratie Province in northeastern Cambodia and Phnom Penh is the capital that locates in southern Cambodia. Fecal specimens (n=366) were collected in 10 villages in Kratie Province and Phnom Penh from 2019 to 2021. They were processed using the formalin ethyl-acetate concentration technique (FECT) to investigate parasites at egg and cyst stages and then examined under a light microscope. The

results revealed that the prevalence of IPIs among the population in Kratie Province (n=317) and Phnom Penh (n=49) was 16.12% (n=59); of Kratie Province (n=50, 13.66%) and Phnom Penh (n=9, 2.46%), 12.02% (n=44) were helminths and 4.10% (n=15) were protozoa. The parasitic infection rate was higher in males (9.02%) than in females (7.10%) and more likely to be due to helminths (7.38%) than protozoa (1.64%). Prevalence of *Opisthorchis viverrini* was the highest (5.74%), followed by those of *Entamoeba coli* (4.10%), hookworm (3.83%), *Ascaris lumbricoides* (1.10%), *Hymenolepis nana* (1.09%), *Taenia* spp. (0.54%), *Trichuris trichiura* (0.55%), and *Enterobius vermicularis* (0.27%), respectively. Moreover, *O. viverrini* infection was the most common infection in the <20-year age group in Kratie Province. In addition, the bivariate and multivariate analyses showed that the association between gender. Gender was a significant risk factor positively associated with *O. viverrini* and hookworm infections ($OR_{adj}=0.318$, 95% CI=0.122-0.8270, $P=0.019$ and $OR_{adj}=0.085$, 95% CI=0.017-0.436, $P=0.003$, respectively). In conclusion, the IPIs were highly prevalent, especially *O. viverrini* and hookworm infections, among the population in Cambodia. These IPIs impact the public health burden but can be prevented by education regarding good sanitary practices in this community.

Molecular evidence of hookworms in public environment of Bangladesh.

Nath TC, Eom KS, Choe S, Park H, Lee D.

04-01-2022

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/36599848/>

Soil-transmitted helminthic vaccines: Where are we now?

Wong MTJ, Anuar NS, Noordin R, Tye GJ.

29-12-2022

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36586174/>

It has been tested and proven that vaccination is still the best strategy to combat infectious diseases. However, to date, there are still no vaccines against human soil-transmitted helminthic diseases, despite their high prevalence globally, particularly in developing countries and rural areas with tropical climates and poor sanitation. The development of vaccines against helminths is riddled with obstacles. Helminths have a complex life cycle, multiple stages within the same host with stage-specific antigen expression, and the ability to regulate host immune reactions to evade the immune response. These elements contribute to the main challenge of helminthic vaccines: the identification of effective vaccine candidates. Therefore, this article reviews the current progress and potential future direction of soil-transmitted helminthic vaccines, particularly against *Trichuris trichiura*, *Ascaris lumbricoides*, *Strongyloides stercoralis*, *Necator americanus* and *Ancylostoma duodenale*. The study design employed was a systematic review, using qualitative meta-summary synthesis. Preclinical studies and clinical trials on the development of protein subunit vaccines against the five soil-transmitted helminths were searched on PubMed

and Scopus. Effectiveness was indicated by a reduction in worm burden or larval output, an increase in specific IgG levels, or an increase in cytokine production. Our findings show that only the hookworm vaccine against *N. americanus* is in the clinical trial phase, while the rest is still in exploratory research and pre-clinical development phase

Prevalence of intestinal parasitic infections and genetic differentiation of *Strongyloides stercoralis* among migrant workers from Myanmar, Lao PDR and Cambodia in northeastern Thailand.

Sangwalee W, Norkaew J, Inthachak S, Janwan P, Rodpai R, Sanpool O, Sadaow L, Boonroumkaew P, Intapan PM, Maleewong W, Thanchomnang T.

30-12-2022

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36584196/>

Intestinal parasitic infections (IPIs) remain a public-health problem worldwide, including in countries of the Lower Mekong subregion. Increases in human migration from neighboring countries might cause reemerging parasitic infections, leading to spread of parasites in the landscape. Here, we conducted a cross-sectional study to identify the prevalence of IPIs in migrant workers from Myanmar, Lao PDR, and Cambodia who were dwelling in Nakhon Ratchasima Province, northeastern Thailand. The identification of *Strongyloides* species and genetic differentiation of worms from migrant workers with different countries of origin was also assessed. Fresh stool samples were collected from 338 migrant workers and examined for evidence of IPIs using agar plate culture (APC) and the formalin-ethyl acetate concentration technique (FECT). Among those nine samples positive for nematodes by APC, the *Strongyloides* or hookworm species present was confirmed using the polymerase chain reaction (PCR) followed by DNA sequencing. This revealed eight cases of *Strongyloides stercoralis* infection and one of *Necator americanus*. Fifty-one out of 338 individuals (15.09%) were positive for IPIs using FECT and APC. Eggs of *Opisthorchis*-like flukes were the most common parasite (11.83% of samples), followed by *S. stercoralis* (2.37%), *Entamoeba coli* (1.50%), hookworm (0.89%), *Taenia* sp. (0.60%) and *Hymenolepis nana* (0.30%). The genetic differentiation of *S. stercoralis* recovered from migrant workers with different countries of origin was analyzed. Specimens of *S. stercoralis* isolated from workers from Lao PDR, Cambodia and Myanmar were genetically similar to those sequenced from Thailand. However, there were population-genetic differences between *S. stercoralis* from these Southeast Asian countries and other regions of the world. This study demonstrated that IPIs were prevalent in migrant workers in the northeastern region of Thailand. Our findings provided molecular confirmation of the presence of *S. stercoralis* and explored the genetic differentiation of *S. stercoralis* from those infected migrant workers. An effective anti-parasitic drug should be provided for migrant workers and its administration enforced.

Precision and geographical prevalence mapping of schistosomiasis and soil-transmitted helminthiasis among school-aged children in selected districts of north-western Tanzania.

Mazigo HD, Zinga MM, Kepha S, Yard E, McRee-Mckee K, Kabona G, Ngoma DD, Nshala A.

29-12-2022

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36581956/>

Background: The identification and mapping of at-risk populations at a lower administrative level than the district are prerequisites for the planning, resource allocation and design of impactful control intervention measures. Thus, the objective of the current study was to conduct sub-district precision mapping of soil-transmitted helminthiasis (STH) and schistosomiasis in 29 districts of north-western Tanzania using the current recommended World Health Organization criteria. **Methods:** A cross-sectional survey was conducted in 145 schools between March and May 2021. A urine filtration technique was used for the quantification of *Schistosoma haematobium* eggs, whereas quantification of *Schistosoma mansoni* and STH eggs was done using the Kato-Katz technique. Microhaematuria was examined using a urine dipstick.

Results: The overall prevalences of any STH and schistosome infections were 9.3% [95% confidence interval (95%CI) 8.6-9.9] and 14.6% (95%CI 13.9-15.4), respectively. The overall prevalence of *S. mansoni* was 8.7% (95%CI 8.1-9.3), and 36.4%, 41.6%, and 21.9% of the children had low, moderate, and heavy infections, respectively. The overall prevalence of *S. haematobium* was 6.1% (95%CI 5.5-6.5), and 71.7% and 28.3% of the infected children had light and heavy intensity infections, respectively. The prevalence of microhaematuria was 7.3% (95%CI 6.7-7.8), with males having the highest prevalence (8.4%, $P < 0.001$). The prevalences of *Trichuris trichiura*, *Ascaris lumbricoides* and hookworm were, respectively, 1.3% (95%CI 0.1-1.5), 2.9% (95%CI 2.5-3.3) and 6.2% (95%CI 5.7-6.7). Most of the children infected with STH had light to moderate intensities of infection. The overall prevalence of co-infection with STH and schistosomiasis was 19.1%. The prevalence of schistosomiasis ($P < 0.001$) and STH ($P < 0.001$) varied significantly between schools and sub-districts. *Schistosoma mansoni* and *S. haematobium* were observed in 60 and 71 schools, respectively, whereas any STH was observed in 49 schools. In schools where schistosomiasis was observed, prevalence was $< 10\%$ in 90.8% of them, and ranged from $\geq 10\%$ to $< 50\%$ in the other 9.2%. In schools where any STH was observed, the prevalence was $< 10\%$ in 87.7% of them. **Conclusions:** The data reported here show that schistosomiasis and STH are widely distributed around Lake Victoria. In most of the schools where schistosomiasis and STH occurred the transmission thresholds were low. These data are important and need to be taken into consideration when decisions are made on the implementation of the next round of mass chemotherapies for schistosomiasis and STH in Tanzania.

Gale

Efficacy of a spot-on combination of fluralaner plus moxidectin against naturally acquired *Sarcoptes scabiei* infestation in 10 pet rabbits: Retrospective case series.

d'Ovidio D, Santoro D.

Vet Dermatol. 2023 Feb

<https://pubmed.ncbi.nlm.nih.gov/36062517/>

Prevalence of skin Neglected Tropical Diseases and superficial fungal infections in two peri-urban schools and one rural community setting in Togo.

Saka B, Kassang P, Gnosike P, Head MG, Akakpo AS, Teclessou JN, Elegbede YM, Mouhari-Toure A, Mahamadou G, Tevi K, Katsou K, Kombaté K, Walker SL, Pitché P.

19-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36534701/>

Introduction: Skin neglected tropical diseases (NTDs), are endemic and under-diagnosed in many lower-income communities. The objective of this study was to determine the prevalence of skin NTDs and fungal infections in two primary schools and a community setting in rural Togo.

Method: This was a cross-sectional study that took place between June-October 2021. The two primary schools are located on the outskirts of Lomé, the capital city. The community setting was Ndjéi, in north-east Togo. Study sites were purposively selected. Dermatologists examined the skin of study participants. Diagnosis of skin NTDs were made clinically. **Results:** A total of 1401 individuals were examined, 954 (68.1%) from Ndjéi community, and 447 (31.9%) were children in the schools. Cutaneous skin infections were diagnosed in 438 (31.3%) participants, of whom 355 (81%) were in community settings. There were 105 observed skin NTDs (7.5%). Within the school setting, there were 20 individuals with NTDs (4.5% of 447 participants), and 85 NTDs (8.9%) from 954 community participants. Across all settings 68/1020 (6.7%) NTDs were in children, and 37/381 (9.7%) in adults. In addition, there were 333 observed mycoses (23.8% prevalence). The main cutaneous NTDs diagnosed were scabies ($n = 86$; 6.1%) and suspected yaws ($n = 16$, 1.1%). The prevalence of scabies in schools was 4.3%, and 7.0% in the rural community. One case of leprosy was diagnosed in each school and the rural community, and one suspected Buruli Ulcer case in the community. In the school setting, five (6%) children with a skin NTD reported being stigmatised, four of whom had refused to attend school because of their dermatosis. In Ndjéi, 44 (4.6%) individuals reported having experienced stigma and 41 (93.2%) of them missed at least one day of school or work. **Conclusion:** This study shows that the burden of scabies and skin infections such as superficial mycoses is high in the school and rural community settings in Togo, with associated presence of stigma. Improved health promotion and education across institutional and community settings may reduce stigma

and encourage early reporting of skin infection cases to a health facility.

Two Cases of Mange Mite (*Sarcoptes scabiei*) Infestation in Long-Tailed Goral (*Naemorhedus caudatus*) in Republic of Korea.

Park DS, Choi J, Kim HJ, Kim JY, Kim MH, Lee JY, Moon JC, Park HB, Park K, Yun JH, Oh Y, Choe S, Na KJ, Yoon J.
Korean J Parasitol. 2022 Dec
<https://pubmed.ncbi.nlm.nih.gov/36588420/>

Prevalence of scabies and associated factors among children aged 5-14 years in Meta Robi District, Ethiopia.

Ararsa G, Merdassa E, Shibiru T, Etfa W.
PLOS One. 2023 Jan 3
<https://pubmed.ncbi.nlm.nih.gov/36595503/>

Background: Scabies is a public health problem that affects children and elders predominantly. Its burden is higher in resource-poor settings, and scabies has a significant impact on the long-term health of children. In Ethiopia, there is limited information about scabies in children. Therefore, the purpose of this study was to determine the prevalence of scabies and its associated factors among children aged 5-14 years in Meta Robi District, Ethiopia. **Methods:** A community-based cross-sectional study design using a multistage sampling technique was used to collect data from 457 participants by systematic random sampling. Scabies was diagnosed based on the clinical criteria set by the International Alliance for the Control of Scabies (IACS, 2020). **Findings:** The prevalence of scabies among children aged 5-14 years old was 19.26% (95%CI: 17.20-22.52). In addition, over half (54.6%) of identified cases of scabies were of moderate severity. Factors like families' low income (aOR = 2.72; 95%CI: 1.32-5.59), being a male child (aOR = 1.96, 95%CI: 1.61-4.01), using only water for hand washing (aOR = 2.01, 95%CI: 1.84-4.79), having a contact history of scabies/skin lesions (aOR = 4.15, 95%CI: 2.02-13.67), and sharing sleeping beds (aOR = 6.33, 95%CI: 2.09-19.13) were significantly associated with scabies. **Conclusion:** The study highlights a high prevalence of scabies among children aged 5-14 years in the district. Provision of adequate health education for the community and children about the scabies and delivering mass drug administration to the district is suggested.

Human ectoparasitosis by mites of the genus *Pyemotes* Amerling 1861 (Acarina: Pyemotidae).

Stingeni L, Hansel K, Casciola G, Bianchi L, Tramontana M, Marietti R, Zampetti S, Napoli F, Miñón Llera G, Biancolini F, Romani R, Sevarika M, Masini P.
Ital J Dermatol Venerol. 2023 Jan 4.
<https://pubmed.ncbi.nlm.nih.gov/36598397/>

The mites of the family Pyemotidae Berlese (1897) are a large family of ectoparasitoids arthropods, known as pathogen for humans since the 18th century and responsible for the so-called "straw itch" or "grain itch" in granary and dock workers. The identified species of the

genus *Pyemotes* are divided into two groups: the scolyti group (*P. scolyti*, *P. parviscolyti* and *P. dimorphus*) and the ventricosus group (*P. tritici* and *P. ventricosus*). The first group is characterized by nonvenomous mites usually parasitizing bark beetles; the ventricosus group includes species associated with a large number of hosts (Coleoptera, Lepidoptera, Hymenoptera, Diptera and Rhynchota), parasitizing all host stages, often highly poisonous and responsible for itchy skin lesions for humans. Several species of *Pyemotes* mites can be pathogenic to humans, especially in spring and summer and in indoor environments, where worm-eaten wood or infested foodstuffs are present. The most frequent clinical feature is the "strophulus," characterized by small erythematous, edematous, and papular lesions centered by a tiny vesicle evolving into a small erosion covered by crust, or by a central hemorrhagic punctum. Other less frequently observed clinical features are urticaria-like lesions, erythematous excoriated papular and pustular lesions, and rarely scabies-like eruptions. The parasitological diagnosis together with the environmental disinfection and removing of each substrate infested by insects parasitized by Pyemotidae is mandatory to definitely solve *Pyemotes* dermatitis.

Morsures de serpent

Frequency, clinical characteristics and outcomes of *Tropidolaemus* species bite envenomations in Malaysia.

Ismail AK, Abd Hamid MNH, Ariff NA, Frederic Ng VER, Goh WC, Abdul Samat NS, Osman AMZ, Safferi RS, Mohamed Ismail Z.
04-01-2023
PLOS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/36598885/>

Pit vipers from the genus *Tropidolaemus* are identified as one of the common causes of snake bite from venomous species in Malaysia. All *Tropidolaemus* species bite cases referred to the Remote Envenomation Consultation Services (RECS) between 2015-2021 were included. A total of 4,718 snake-related injuries cases consulted to RECS with 310 (6.6%) involved *Tropidolaemus* species; of these 190 (61.3%) were *T. subannulatus* and 120 (38.7%) *T. wagleri*. All the *T. subannulatus* cases occurred in Sabah and Sarawak while all cases of *T. wagleri* occurred in Peninsular Malaysia. The majority of patients were male (74.8%) and adults between 18-59 years old (61.2%). The upper limb (56.6%) was the most frequent anatomical region involved. Most cases were non-occupationally related (75.4%). Bites from both species caused local pain (77.1%) and swelling (27.2%). Most patients complained of mild pain (48.0%). Paracetamol (40.0%) was the most common analgesic prescribed. Antivenom was not indicated in all cases. Two patients were given antivenom inappropriately before RECS consultation. Most patients (54.7%) needed hospital observation for less than 24 hours. No deaths occurred in the group studied.

Comment on: coagulopathy following Crotaline snakebites in northeast Florida.

Dicker FT, Mullins ME.

01-01-2023

Blood Coagul Fibrinolysis.

<https://pubmed.ncbi.nlm.nih.gov/36598378/>

Clinical study of anti-snake venom blockade in the treatment of local tissue necrosis caused by Chinese cobra (*Naja atra*) bites.

Zeng L, Hou J, Ge C, Li Y, Gao J, Zhang C, Huang P, Du J, Mo Z, Liu Y, Zeng Z.

16-12-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36525460/>

Fatal infective necrotising fasciitis: Complication following *Naja nigricincta nigricincta* bite (western barred spitting cobra/zebra snake).

Saaiman EL, Buys PC.

01-12-2022

S Afr Med J.

<https://pubmed.ncbi.nlm.nih.gov/36525460/>

Wound infections following cytotoxic snakebites are common. Bites from *Naja nigricincta nigricincta* (an African spitting cobra) usually present as severe dermonecrosis spreading within the subdermal fascia layer. Primary infections can follow inoculation of the snake's oral flora during the bite, worsening the dermonecrosis into infective necrotising fasciitis. We report the case of a 2½-year-old boy who presented with infective (*Proteus vulgaris*) necrotising fasciitis after an *N. n. nigricincta* bite, resulting in multiple-organ failure and death. A *P. vulgaris* with the same antibiotic profile was cultured from the mouth of the snake.