



Veille scientifique

Maladies tropicales négligées

Semaine 04
23 au 29 janvier 2023

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Dengue, chikungunya et maladie à virus Zika

Seasonal changes in the diversity, host preferences and infectivity of mosquitoes in two arbovirus-endemic regions of Costa Rica.

Romero-Vega LM, Piche-Ovares M, Soto-Garita C, Barantes Murillo DF, Chaverri LG, Alfaro-Alarcón A, Corrales-Aguilar E, Troyo A.

Parasit Vectors.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36703148/>

Background: Mosquitoes are vectors of various arboviruses belonging to the genera Alphavirus and Flavivirus, and Costa Rica is endemic to several of them. The aim of this study was to describe and analyze the community structure of such vectors in Costa Rica.

Methods: Sampling was performed in two different coastal locations of Costa Rica with evidence of arboviral activity during rainy and dry seasons. Encephalitis vector surveillance traps, CDC female gravid traps and ovitraps were used. Detection of several arboviruses by Pan-Alpha and Pan-Flavi PCR was attempted. Blood meals were also identified. The Normalized Difference Vegetation Index (NDVI) was estimated for each area during the rainy and dry seasons. The Chao2 values for abundance and Shannon index for species diversity were also estimated.

Results: A total of 1802 adult mosquitoes belonging to 55 species were captured, among which *Culex quinquefasciatus* was the most caught species. The differences in NDVI were higher between seasons and between regions, yielding lower Chao-Sørensen similarity index values. Venezuelan equine encephalitis virus, West Nile virus and Madariaga virus were not detected at all, and dengue virus and Zika virus were detected in two separate *Cx. quinquefasciatus* specimens. The primary blood-meal sources were chickens (60%) and humans (27.5%). Both sampled areas were found to have different seasonal dynamics and population turnover, as reflected in the Chao2 species richness estimation values and Shannon diversity index. **Conclusion:** Seasonal patterns in mosquito community dynamics in coastal areas of Costa Rica have strong differences despite a geographical proximity. The NDVI influences mosquito diversity at the regional scale more than at the local scale. However, year-long continuous sampling is required to better understand local dynamics.

Analysis of cross-reactivity among flaviviruses using sera of patients with dengue showed the importance of neutralization tests with paired serum samples for the correct interpretations of serological test results for dengue.

Maeki T, Tajima S, Ando N, Wakimoto Y, Hayakawa K, Kutsuna S, Kato F, Taniguchi S, Nakayama E, Lim CK, Saijo M.

J Infect Chemother.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36702208/>

Delaying the Start Date for Obstetrics and Gynecology Subspecialty Training and Inequity.

Ros ST, Malhotra T, Grobman W, Hughes BL, Gyamfi-Bannerman C.

Obstet Gynecol.

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36701623/>

Impact of randomised wMel Wolbachia deployments on notified dengue cases and insecticide fogging for dengue control in Yogyakarta City.

Indriani C, Tanamas SK, Khasanah U, Ansari MR, Rubangi, Tantowijoyo W, Ahmad RA, Dufault SM, Jewell NP, Utarini A, Simmons CP, Anders KL.

Glob Health Action.

31-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36700745/>

Background: Releases of Wolbachia (wMel)-infected *Aedes aegypti* mosquitoes significantly reduced the incidence of virologically confirmed dengue in a previous cluster randomised trial in Yogyakarta City, Indonesia. Following the trial, wMel releases were extended to the untreated control areas, to achieve city-wide coverage of Wolbachia. **Objective:** In this predefined analysis, we evaluated the impact of the wMel deployments in Yogyakarta on dengue hemorrhagic fever (DHF) case notifications and on the frequency of perifocal insecticide spraying by public health teams. **Methods:** Monthly counts of DHF cases notified to the Yogyakarta District Health Office between January 2006 and May 2022 were modelled as a function of time-varying local wMel treatment status (fully- and partially-treated vs untreated, and by quintile of wMel prevalence). The frequency of insecticide fogging in wMel-treated and untreated areas was analysed using negative binomial regression. **Results:** Notified DHF incidence was 83% lower in fully treated vs untreated periods (IRR 0.17 [95% CI 0.14, 0.20]), and 78% lower in areas with 80-100% wMel prevalence compared to areas with 0-20% wMel (IRR 0.23 [0.17, 0.30]). A similar intervention effect was observed at 60-80% wMel prevalence as at 80-100% prevalence (76% vs 78% efficacy, respectively). Pre-intervention, insecticide fogging occurred at similar frequencies in areas later randomised to wMel-treated and untreated arms of the trial. After wMel deployment, fogging occurred significantly less frequently in treated areas (IRR 0.17 [0.10, 0.30]). **Conclusions:** Deployments of wMel-infected *Aedes aegypti* mosquitoes resulted in an 83% reduction in the application of perifocal insecticide spraying, consistent with lower dengue case notifications in wMel-treated areas. These results show that the Wolbachia intervention effect demonstrated previously in a cluster randomised trial was also measurable from routine surveillance data.

N-Phenylpyridine-3-Carboxamide and 6-Acetyl-1H-Indazole Inhibit the RNA Replication Step of the Dengue Virus Life Cycle.

Sow AA, Pahmeier F, Ayotte Y, Anton A, Mazeaud C, Charpentier T, Angelo L, Woo S, Cerikan B, Falzarano D, Abrahamyan L, Lamarre A, Labonté P, Cortese M, Bartenschlager R, LaPlante SR, Chatel-Chaix L.
Antimicrob Agents Chemother.
26-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36700643/>

Scientometric review of research on Neglected Tropical Diseases: a 31-year perspective from the Journal of the Brazilian Society of Tropical Medicine.

Ferreira AF, Heukelbach J, Costa CHN, Souza EA, Maciel AMS, Correia D, Ramos AN Jr.
Rev Soc Bras Med Trop.
23-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36700606/>

The research progress of Chikungunya fever.

Cai L, Hu X, Liu S, Wang L, Lu H, Tu H, Huang X, Tong Y.
Front Public Health.
09-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36699921/>

Chikungunya fever, an acute infectious disease caused by Chikungunya virus (CHIKV), is transmitted by *Aedes aegypti* mosquitoes, with fever, rash, and joint pain as the main features. 1952, the first outbreak of Chikungunya fever was in Tanzania, Africa, and the virus was isolated in 1953. The epidemic has expanded from Africa to South Asia, the Indian Ocean islands and the Americas, and is now present in more than 100 countries and territories worldwide, causing approximately 1 million infections worldwide each year. In addition, fatal cases have been reported, making CHIKV a relevant public health disease. The evolution of the virus, globalization, and climate change may have contributed to the spread of CHIKV. 2005-2006 saw the most severe outbreak on Reunion Island, affecting nearly 35% of the population. Since 2005, cases of Chikungunya fever have spread mainly in tropical and subtropical regions, eventually reaching the Americas through the Caribbean island. Today, CHIKV is widely spread worldwide and is a global public health problem. In addition, the lack of a preventive vaccine and approved antiviral treatment makes CHIKV a major global health threat. In this review, we discuss the current knowledge on the pathogenesis of CHIKV, focusing on the atypical disease manifestations. We also provide an updated review of the current development of CHIKV vaccines. Overall, these aspects represent some of the most recent advances in our understanding of CHIKV pathogenesis and also provide important insights into the current development of CHIKV and potential CHIKV vaccines for current development and clinical trials.

Diseases spectrum in the field of spatiotemporal patterns mining of infectious diseases epidemics: A bibliometric and content analysis.

Lu W, Ren H.
Front Public Health.
09-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36699887/>

Zika virus cleaves GSDMD to disseminate prognosticable and controllable oncolysis in a human glioblastoma cell model.

Kao YT, Wang HI, Shie CT, Lin CF, Lai MMC, Yu CY.
Mol Ther Oncolytics.
02-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36699618/>

Positive-strand RNA viruses-a Keystone Symposia report.

Cable J, Denison MR, Kielian M, Jackson WT, Bartenschlager R, Ahola T, Mukhopadhyay S, Fremont DH, Kuhn RJ, Shannon A, Frazier MN, Yuen KY, Coyne CB, Wolthers KC, Ming GL, Guenther CS, Moshiri J, Best SM, Schoggins JW, Jurado KA, Ebel GD, Schäfer A, Ng LFP, Kikkert M, Sette A, Harris E, Wing PAC, Eggenberger J, Krishnamurthy SR, Mah MG, Meganck RM, Chung D, Maurer-Stroh S, Andino R, Korber B, Perlman S, Shi PY, Bárcena M, Aicher SM, Vu MN, Kenney DJ, Lindenbach BD, Nishida Y, Rénia L, Williams EP.
Ann N Y Acad Sci.
25-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36697369/>

Identification of mosquito proteins that differentially interact with alphavirus nonstructural protein 3, a determinant of vector specificity.

Byers NM, Burns PL, Stuchlik O, Reed MS, Ledermann JP, Pohl J, Powers AM.
PLoS Negl Trop Dis.
25-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36696390/>

Chikungunya virus (CHIKV) and the closely related onyong-nyong virus (ONNV) are arthritogenic arboviruses that have caused significant, often debilitating, disease in millions of people. However, despite their kinship, they are vectored by different mosquito subfamilies that diverged 180 million years ago (anopheline versus culicine subfamilies). Previous work indicated that the nonstructural protein 3 (nsP3) of these alphaviruses was partially responsible for this vector specificity. To better understand the cellular components controlling alphavirus vector specificity, a cell culture model system of the anopheline restriction of CHIKV was developed along with a protein expression strategy. Mosquito proteins that differentially interacted with CHIKV nsP3 or ONNV nsP3 were identified. Six proteins were identified that specifically bound ONNV nsP3, ten that bound CHIKV nsP3

and eight that interacted with both. In addition to identifying novel factors that may play a role in virus/vector processing, these lists included host proteins that have been previously implicated as contributing to alphavirus replication.

Basic reproduction ratio of a mosquito-borne disease in heterogeneous environment.

Zhao H, Wang K, Wang H.

J Math Biol.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695934/>

Inhibition of PIKFYVE kinase interferes ESCRT pathway to suppress RNA virus replication.

Luo Z, Liang Y, Tian M, Ruan Z, Su R, Shereen MA, Yin J, Wu K, Guo J, Zhang Q, Li Y, Wu J.

J Med Virol.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695658/>

ESCRT (Endosomal sorting complex required for transport) is essential in the functional operation of endosomal transport in envelopment and budding of enveloped RNA viruses. However, in non-enveloped RNA viruses such as enteroviruses of the Picornaviridae family, the precise function of ESCRT pathway in viral replication remains elusive. Here, we initially evaluated that ESCRT pathway is important for viral replication upon EV71 (Enterovirus 71) infection. Furthermore, we discovered that YM201636, a specific inhibitor of PIKFYVE (Phosphoinositide kinase, FYVE finger containing) kinase, significantly suppressed EV71 replication and virus-induced inflammation in vitro and in vivo. Mechanistically, YM201636 inhibits PIKFYVE kinase to block ESCRT pathway and endosomal transport, leading to the disruption of viral entry and replication complex in subcellular components and ultimately repression of intracellular RNA virus replication and virus-induced inflammatory responses. Further studies found that YM201636 broadly represses the replication of other RNA viruses, including CVB3 (Coxsackievirus B3), PV1 (Poliovirus 1), E11 (Echovirus 11), ZIKV (Zika virus), and VSV (Vesicular stomatitis virus), rather than DNA viruses, including ADV3 (Adenovirus 3) and HBV (Hepatitis B virus). Our findings shed light on the mechanism underlying PIKFYVE-modulated ESCRT pathway involved in RNA virus replication, and also provide a prospective antiviral therapy during RNA viruses infections. This article is protected by copyright. All rights reserved.

A concerted mechanism involving ACAT and SREBPs by which oxysterols deplete accessible cholesterol to restrict microbial infection.

Heisler DB, Johnson KA, Ma DH, Ohlson MB, Zhang L, Tran M, Corley CD, Abrams ME, McDonald JG, Schoggins JW, Alto NM, Radhakrishnan A.

Elife.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695568/>

Dengue, chikungunya and Zika virus infections among Dutch travellers to Suriname: a prospective study during the introduction of chikungunya and Zika virus, 2014 to 2017.

Overbosch FW, Schinkel J, Matser A, Koen G, Prange I, Prins M, Sonder GJ.

Euro Surveill.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36695478/>

Prospective study of pyrexia with pregnancy.

Mewada BN, Gandhi D, Diwan F, Panchal PN.

Ann Afr Med.

Jan-Mar 2023

<https://pubmed.ncbi.nlm.nih.gov/36695215/>

Chronic Bilateral Symmetric Anterior Shoulder Dislocation Secondary to Seizures in Chikungunya Encephalitis.

Budhoo E, Mohammed SR, Baiju D, Corbin RE, Deane DR, Kassie P.

Cureus.

21-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36694507/>

Bilateral shoulder dislocations are a rare occurrence and can be categorized as either symmetric (both humeral heads dislocate in the same direction) or asymmetric (wherein the humeral heads dislocate in different directions). Shoulder dislocations may be overlooked if they are the result of systemic injury; if diagnosed >21 days after occurring, they are considered chronic dislocations. We describe the case of a 31-year-old male who presented with an eight-week history of bilateral shoulder pain. His onset of pain coincided with a seizure secondary to Chikungunya encephalitis. Clinical and radiological examination demonstrated bilateral symmetric anterior shoulder dislocation with associated greater tuberosity fractures and extensive callus formation bilaterally. Open surgical management was performed first on the left shoulder via the deltopectoral approach. The callus was removed, the greater tuberosity fragment lifted off, reattached to the original position, and held in place with sutures and proximal humeral locking plates. The right shoulder was reduced six weeks after the left shoulder due to patient preference; the reduction utilized the same approach as with the left shoulder. Post-operatively the patient was immobilized, and physiotherapy commenced. He achieved a satisfactory range of motion four months post-operation. Physicians should be cognizant that shoulder pain after a convulsive seizure may signify shoulder dislocation. Thorough clinical and radiological examinations are warranted in such an instance. There exists no consensus on the treatment of chronic shoulder dislocations, but it is recommended that closed reduction only be attempted up to six weeks post-dislocation due to the high risk of iatrogenic fractures and neurovascular damage beyond this time.

Hyperglycemia exacerbates dengue virus infection by facilitating poly(A)-binding protein-mediated viral translation.

Shen TJ, Chen CL, Tsai TT, Jhan MK, Bai CH, Yen YC, Tsai CW, Tseng PC, Yu CY, Lin CF.

JCI Insight.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36692016/>

Casualties during Australian military operations in New Guinea 1914-1919.

Shanks GD.

Intern Med J.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36693644/>

Varied presentations of congenital dengue infection in neonates.

Bhatter S, Jain J.

Trop Doct.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691681/>

[French research organization on emerging infectious diseases: from REACTing to ANRS Emerging Infectious Diseases].

Delfraissy JF.

Bull Acad Natl Med.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691475/>

Emerging infectious diseases (EIDs) can be responsible for epidemics or even pandemics that disrupt societies and cause national and international crises. In our globalized world, anarchic urbanization, ecosystem disruptions (deforestation, creation of dams...), changes in crop and livestock farming conditions, the increasing availability of air transport, population displacement, and climate change are all factors that favor the occurrence and spread of emerging or re-emerging pathogens such as SARS-CoV, MERS-CoV, Ebola, Zika, influenza, or more recently SARS-CoV-2 and Monkeypox. States, regional and international organizations, health and research agencies, non-governmental organizations and the pharmaceutical industry are today challenged by the repetition of these crises and their consequences on health, social, economic and political balances. For the past fifteen years, we have clearly been in a new regime of infectious emergence and re-emergence. This new regime calls for new responses, to meet in the urgency the challenges of emergency epidemic crises and to better respond to the issues of crisis management in a context of "One Health". Research is an essential pillar in the response to these epidemics with a double challenge: i) to improve knowledge on the disease, its prevention, treatment, diagnosis, impact on society ... and ii) to prepare for and understand future emergencies, "anticipate" ... As epidemics have occurred over the last fifteen years, French research has been organized and has evolved to respond to these crises, from the genesis of

REACTing in 2011, to the creation of the ANRS Emerging Infectious Diseases in 2021.

Evaluation of Aedes aegypti Penetration, Probing, and Feeding Times on Mice.

Martin-Martin I, Williams AE, Calvo E.

Cold Spring Harb Protoc.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36690390/>

Effect of BaltPLA₂, a phospholipase A₂ from Bothrops alternatus snake venom, on the viability of cells infected with dengue virus.

Dias EHV, de Sousa Simamoto BB, da Cunha Pereira DF, Ribeiro MSM, Santiago FM, de Oliveira F, Yokosawa J, Mamede CCN.

Toxicol In Vitro.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36690282/>

A safe replication-defective Zika virus vaccine protects mice from viral infection and vertical transmission.

Li N, Deng CL, Li Q, Chen XL, Zhang B, Ye HQ.

Antiviral Res.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36690159/>

Redox Regulation and Metabolic Dependency of Zika Virus Replication: Inhibition by Nrf2-Antioxidant Response and NAD(H) Antimetabolites.

Sahoo BR, Crook AA, Pattnaik A, Torres-Gerena AD, Khalimonchuk O, Powers R, Franco R, Pattnaik AK.

J Virol.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36688653/>

Effects of constant temperature and daily fluctuating temperature on the transovarial transmission and life cycle of Aedes albopictus infected with Zika virus.

Jian XY, Jiang YT, Wang M, Jia N, Cai T, Xing D, Li CX, Zhao TY, Guo XX, Wu JH.

Front Microbiol.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36687634/>

Zika virus knowledge and vaccine acceptance among undergraduate students in Guayaquil, Ecuador.

Searles M, Jose Ronquillo Mora Y, Carlo L, Heydari N, Takyiwa Y, Borbor-Cordova MJ, Campagna CD.

Vaccine X.

28-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36686399/>

Purpose: Zika virus (ZIKV) was declared a Public Health Emergency of International Concern (PHEIC) in 2016. Concerns surrounding the effects of ZIKV persist today and several vaccine candidates are currently in various stages of development worldwide. There is limited research on ZIKV vaccine acceptability worldwide, and little research specific to Latin American countries. This research aims to identify the general beliefs and acceptance of a potential ZIKV vaccine in the undergraduate population at Escuela Superior Politécnica del Litoral (ESPOL) in Guayaquil, Ecuador. **Methods:** Between January and November 2019, 429 undergraduate students at ESPOL responded anonymously to a ZIKV vaccine survey. Frequencies, percentages, simple correspondence analysis, and bivariate inferential analyses were conducted using Kendall's tau-b test. Tests explored associations between likelihood of receiving a ZIKV vaccine and demographic, ZIKV information seeking, ZIKV psychosocial variables, and ZIKV information source variables. **Results:** Among the eligible participants, 241 (56.2%) were willing to receive a ZIKV vaccine if one was made commercially available. Most students were male (61.5%), age 20-25 (63.3%), and of mixed (Mestizo) race (95.3%). Results provided insight into student's knowledge on ZIKV, revealed television as the most common information source, and found most students were willing to receive a ZIKV vaccine were one to become available. Bivariate results revealed most respondents reported feeling neutral or likely to receive a ZIKV vaccine regardless of their agreeability with ZIKV information seeking behavior and psychosocial variables. **Conclusions:** This study provides insight into ZIKV knowledge among ESPOL university students and reveals most respondents obtained ZIKV related information from television. The most common reason for not wanting to receive a hypothetical ZIKV vaccine was vaccine hesitancy. Likelihood of receiving a ZIKV vaccine was associated with several information seeking behavior and psychosocial variables. Public health campaigns should focus on comprehensive ZIKV education efforts in this population.

Dynamic transcriptome analyses reveal m⁶A regulated immune non-coding RNAs during dengue disease progression.

Zhang Y, Guo J, Gao Y, Li S, Pan T, Xu G, Li X, Li Y, Yang J. *Heliyon*. 04-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36685392/>

In silico and in vitro studies of potential inhibitors against Dengue viral protein NS5 Methyl Transferase from Ginseng and Notoginseng.

Jarerattanachai V, Boonarkart C, Hannongbua S, Auewarakul P, Ardkehan R. *J Tradit Complement Med*. 07-12-2022
<https://pubmed.ncbi.nlm.nih.gov/36685072/>

The perinatal health challenges of emerging and re-emerging infectious diseases: A narrative review.

Malange VNE, Hedermann G, Lausten-Thomsen U, Hoffmann S, Voldstedlund M, Aabakke AJM, Eltvéd AK, Jensen JS, Breindahl M, Krebs L, Christiansen M, Hedley PL. *Front Public Health*. 05-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36684933/>

A methodology framework for bipartite network modeling.

Liew CY, Labadin J, Kok WC, Eze MO. *Appl Netw Sci*. 2023
<https://pubmed.ncbi.nlm.nih.gov/36684825/>

A comparative analysis of Aedes albopictus and Aedes aegypti subjected to diapause-inducing conditions reveals conserved and divergent aspects associated with diapause, as well as novel genes associated with its onset.

Diniz DFA, Romão TP, Helvécio E, de Carvalho-Leandro D, Xavier MDN, Peixoto CA, de Melo Neto OP, Melo-Santos MAV, Ayres CFJ. *Curr Res Insect Sci*. 03-10-2023
<https://pubmed.ncbi.nlm.nih.gov/36683953/>

Prediction of Conformational and Linear B-Cell Epitopes on Envelop Protein of Zika Virus Using Immunoinformatics Approach.

Srivastava K, Srivastava V. *Int J Pept Res Ther*. 2023
<https://pubmed.ncbi.nlm.nih.gov/36683612/>

The current spread of Zika virus infection in India has become a public health issue due to the virus's possible link to birth abnormalities and neurological disorders. There is a need for enhanced vaccines or drugs as a result of its epidemic outbreak and the lack of potential medication. B-cell mediated adaptive immunity is capable of developing pathogen-specific memory that confers immunological protection. Therefore, in this study, the envelope protein of the Zika virus was retrieved from the NCBI protein database. The ABCpred and BepiPred software were used to discover linear B-cell epitopes on envelope protein. Conformational B-cell epitopes on envelope protein were identified using SEPPA 3.0 and Ellipro tools. Predicted B-cell epitopes were evaluated for allergenicity, toxicity, and antigenicity. Two consensus linear B-cell epitopes, envelope₁₆₅₋₁₈₀ (AKVEITPNSPRAEATL) and envelope₂₂₄₋₂₃₈ (PWHAGADTGTPHWNN) were identified using ABCpred and BepiPredtools. SEPPA 3.0 and Elliprotools predicted consensus conformational envelope₉₈₋₁₁₀ (DRGWGNGCGLFGK) and envelope₂₄₈₋₂₅₁ (AHAK) epitopes

and one residue (⁷⁵PRO) within envelope protein as a component of B-cell epitopes. These predicted linear and conformational B-cell epitopes will help in designing peptide vaccines that will activate the humoral response. However, in-vitro and in-vivo laboratory experimental confirmations are still needed to prove the application's feasibility.

Dengue determinants: Necessities and challenges for universal dengue vaccine development.

Hussain Z, Rani S, Ma F, Li W, Shen W, Gao T, Wang J, Pei R.

Rev Med Virol.

22-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683235/>

Pupal productivity of larval habitats of *Aedes aegypti* in Msambweni, Kwale County, Kenya.

Mwakutwaa AS, Ngugi HN, Ndenga BA, Krystosik A, Ngari M, Abubakar LU, Yonge S, Kitron U, LaBeaud AD, Mutuku FM.

Parasitol Res.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683088/>

Rapid Diagnostic Tests for the Detection of the Four Dengue Virus Serotypes in Clinically Relevant Matrices.

Pollak NM, Olsson M, Ahmed M, Tan J, Lim G, Setoh YX, Wong JCC, Lai YL, Hobson-Peters J, Macdonald J, McMillan D.

Microbiol Spectr.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682882/>

The efficient and accurate diagnosis of dengue, a major mosquito-borne disease, is of primary importance for clinical care, surveillance, and outbreak control. The identification of specific dengue virus serotype 1 (DENV-1) to DENV-4 can help in understanding the transmission dynamics and spread of dengue disease. The four rapid low-resource serotype-specific dengue tests use a simple sample preparation reagent followed by reverse transcription-isothermal recombinase polymerase amplification (RT-RPA) combined with lateral flow detection (LFD) technology. Results are obtained directly from clinical sample matrices in 35 min, requiring only a heating block and pipettes for liquid handling. In addition, we demonstrate that the rapid sample preparation step inactivates DENV, improving laboratory safety. Human plasma and serum were spiked with DENV, and DENV was detected with analytical sensitivities of 333 to 22,500 median tissue culture infectious doses (TCID₅₀)/mL. The analytical sensitivities in blood were 94,000 to 333,000 TCID₅₀/mL. Analytical specificity testing confirmed that each test could detect multiple serotype-specific strains but did not respond to strains of other serotypes, closely related flaviviruses, or chikungunya virus. Clinical testing on 80 human serum samples demonstrated test specificities of between 94 and 100%, with a DENV-2 test

sensitivity of 100%, detecting down to 0.004 PFU/μL, similar to the sensitivity of the PCR test; the other DENV tests detected down to 0.03 to 10.9 PFU/μL. Collectively, our data suggest that some of our rapid dengue serotyping tests provide a potential alternative to conventional labor-intensive RT-quantitative PCR (RT-qPCR) detection, which requires expensive thermal cycling instrumentation, technical expertise, and prolonged testing times. Our tests provide performance and speed without compromising specificity in human plasma and serum and could become promising tools for the detection of high DENV loads in resource-limited settings. **IMPORTANCE** The efficient and accurate diagnosis of dengue, a major mosquito-borne disease, is of primary importance for clinical care, surveillance, and outbreak control. This study describes the evaluation of four rapid low-resource serotype-specific dengue tests for the detection of specific DENV serotypes in clinical sample matrices. The tests use a simple sample preparation reagent followed by reverse transcription-isothermal recombinase polymerase amplification (RT-RPA) combined with lateral flow detection (LFD) technology. These tests have several advantages compared to RT-qPCR detection, such as a simple workflow, rapid sample processing and turnaround times (35 min from sample preparation to detection), minimal equipment needs, and improved laboratory safety through the inactivation of the virus during the sample preparation step. The low-resource formats of these rapid dengue serotyping tests have the potential to support effective dengue disease surveillance and enhance the diagnostic testing capacity in resource-limited countries with both endemic dengue and intense coronavirus disease 2019 (COVID-19) transmission.

Chikungunya in returning travellers from Bali - A GeoSentinel case series.

Mayer AB, Consigny PH, Grobusch MP, Camprubí-Ferrer D, Huits R, Rothe C.

Travel Med Infect Dis.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682574/>

The safety and immunogenicity of two Zika virus mRNA vaccine candidates in healthy flavivirus baseline seropositive and seronegative adults: the results of two randomised, placebo-controlled, dose-ranging, phase 1 clinical trials.

Essink B, Chu L, Seger W, Barranco E, Le Cam N, Bennett H, Faughnan V, Pajon R, Paila YD, Bollman B, Wang S, Dooley J, Kalidindi S, Leav B.

Lancet Infect Dis.

19-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682364/>

A randomized phase 3 trial of the immunogenicity and safety of coadministration of a live-attenuated tetravalent dengue vaccine (TAK-003) and an inactivated hepatitis a (HAV)

virus vaccine in a dengue non-endemic country.

Tricou V, Eyre S, Ramjee M, Collini P, Mojares Z, Loeliger E, Mandaric S, Rauscher M, Brose M, Lefevre I, Folschweiller N, Wallace D.

Vaccine.

19-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36681529/>

Background: Vaccination against hepatitis A virus (HAV) is largely recommended for travelers worldwide. Concurrent dengue and HAV vaccination may be desired in parallel for travelers to countries where both diseases are endemic. This randomized, observer-blind, phase 3 trial evaluated coadministration of HAV vaccine with tetravalent dengue vaccine (TAK-003) in healthy adults aged 18-60 years living in the UK. **Methods:** Participants were randomized (1:1:1) to receive HAV vaccine and placebo on Day 1, and placebo on Day 90 (Group 1), TAK-003 and placebo on Day 1, and TAK-003 on Day 90 (Group 2), or TAK-003 and HAV vaccine on Day 1, and TAK-003 on Day 90 (Group 3). The primary objective was non-inferiority of HAV seroprotection rate (anti-HAV ≥ 12.5 mIU/mL) in Group 3 versus Group 1, one month post-first vaccination (Day 30) in HAV-naïve and dengue-naïve participants. Sensitivity analyses were performed on combinations of baseline HAV and dengue serostatus. Secondary objectives included dengue seropositivity one month post-second vaccination (Day 120), HAV geometric mean concentrations (GMCs), and safety. **Results:** 900 participants were randomized. On Day 30, HAV seroprotection rates were non-inferior following coadministration of HAV and TAK-003 (Group 3: 98.7 %) to HAV administration alone (Group 1: 97.1 %; difference: -1.68, 95 % CI: -8.91 to 4.28). Sensitivity analyses including participants who were neither HAV-naïve nor DENV-naïve at baseline supported this finding. Anti-HAV GMCs on Day 30 were 82.1 (95 % CI: 62.9-107.1) mIU/mL in Group 1 and 93.0 (76.1-113.6) mIU/mL in Group 3. By Day 120, 90.9-96.8 % of TAK-003 recipients were seropositive (neutralizing antibody titer > 10) to all four dengue serotypes. Coadministration of HAV vaccine and TAK-003 was well tolerated, with no important safety risks identified. **Conclusion:** Immune responses following coadministration of HAV vaccine and TAK-003 were non-inferior to administration of HAV vaccine alone. The results support the coadministration of HAV vaccine and TAK-003 with no adverse impact on immunogenicity, safety, and reactogenicity of either vaccine.

A Systematic Review of Mathematical Models of Dengue Transmission and Vector Control: 2010-2020.

Ogunlade ST, Meehan MT, Adekunle AI, McBryde ES.

Viruses.

16-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680294/>

Exploring the Expression and Function of cTyro3, a Candidate Zika Virus Receptor, in the Embryonic Chicken Brain and Inner Ear.

Negi V, Kuhn RJ, Fekete DM.

Viruses.

15-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680287/>

Association between Anti-DENV IgM Serum Prevalence and CD11b Expression by Classical Monocytes in Obesity.

Costa KB, Garcia BCC, Costa MLB, Pena YG, Figueiredo EAB, Ottoni MHF, Santos JD, de Oliveira Ottone V, de Oliveira DB, Rocha-Vieira E.

Viruses.

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680274/>

Dengue and obesity are currently highly prevalent conditions worldwide and the association between these two conditions may result in greater risk for DENV infection and disease severity. In this study the association between obesity and recent, inapparent dengue was investigated. Serum DENV IgM and NS1 were evaluated in 49 adult volunteers (15 lean and 34 individuals with obesity, according to body mass index), between September 2017 and June 2018. Adiposity, endocrine, metabolic, and immune data of the participants were also obtained. None of the study participants tested positive for the DENV NS1 antigen. DENV IgM was detected in 33.3% of the lean individuals, and in 44.1% of those with obesity; the presence of DENV IgM was not associated with body mass index (OR = 1.32, 95% CI = 0.59-2.98, $p = 0.48$). However, body fat index was higher in obese individuals who had recent inapparent dengue (14.7 ± 3.1 versus 12.7 ± 2.1 kg/m², $p = 0.04$), as was the expression of CD11b by classical (CD14⁺⁺CD16⁻) monocytes (1103.0 ± 311.3 versus 720.3 ± 281.1 mean fluorescence intensity). Our findings suggest an association between adiposity and recent inapparent dengue and the involvement of classical monocytes in this association.

Maternal Immune Response to ZIKV Triggers High-Inflammatory Profile in Congenital Zika Syndrome.

Fialho EMS, Veras EM, de Jesus CM, Khouri R, Sousa PS, Ribeiro MRC, Costa LC, Gomes LN, Nascimento FRF, Silva AAM, Soeiro-Pereira PV.

Viruses.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680261/>

ZDHHC11 Suppresses Zika Virus Infections by Palmitoylating the Envelope Protein.

Hu D, Zou H, Chen W, Li Y, Luo Z, Wang X, Guo D, Meng Y, Liao F, Wang W, Zhu Y, Wu J, Li G.

Viruses.

02-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680184/>

Differential Susceptibility of Fetal Retinal Pigment Epithelial Cells, hiPSC-Retinal Stem Cells, and Retinal Organoids to Zika Virus Infection.

Contreras D, Garcia G Jr, Jones MK, Martinez LE, Jayakarunakaran A, Gangalapudi V, Tang J, Wu Y, Zhao JJ, Chen Z, Ramaiah A, Tsui I, Kumar A, Nielsen-Saines K, Wang S, Arumugaswami V.

Viruses.

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680182/>

Construction of a Chikungunya Virus, Replicon, and Helper Plasmids for Transfection of Mammalian Cells.

Colunga-Saucedo M, Rubio-Hernandez EI, Coronado-Ipiña MA, Rosales-Mendoza S, Castillo CG, Comas-Garcia M.

Viruses.

31-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680173/>

The genome of Alphaviruses can be modified to produce self-replicating RNAs and virus-like particles, which are useful virological tools. In this work, we generated three plasmids for the transfection of mammalian cells: an infectious clone of Chikungunya virus (CHIKV), one that codes for the structural proteins (helper plasmid), and another one that codes nonstructural proteins (replicon plasmid). All of these plasmids contain a reporter gene (mKate2). The reporter gene in the replicon RNA and the infectious clone are synthesized from subgenomic RNA. Co-transfection with the helper and replicon plasmids has biotechnological/biomedical applications because they allow for the delivery of self-replicating RNA for the transient expression of one or more genes to the target cells.

HLA-A, HSPA5, IGFBP5 and PSMA2 Are Restriction Factors for Zika Virus Growth in Astrocytic Cells.

Sher AA, Lao YT, Coombs KM.

Viruses.

29-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680137/>

Aedes aegypti Strain Subjected to Long-Term Exposure to Bacillus thuringiensis svar. israelensis Larvicides Displays an Altered Transcriptional Response to Zika Virus Infection.

Carvalho KS, Rezende TMT, Romão TP, Rezende AM, Chiñas M, Guedes DRD, Paiva-Cavalcanti M, Silva-Filha MHNL.

Viruses.

27-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680112/>

Understanding the Biology and Immune Pathogenesis of Chikungunya Virus Infection for Diagnostic and Vaccine Development.

Hakim MS, Aman AT.

Viruses.

23-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680088/>

Towards the Laboratory Maintenance of Haemagogus janthinomys (Dyar, 1921), the Major Neotropical Vector of Sylvatic Yellow Fever.

Hendy A, Fé NF, Valério D, Hernandez-Acosta E, Chaves BA, da Silva LFA, Santana RAG, da Costa Paz A, Soares MMM, Assunção FP, Andes JT Jr, Andolina C, Scarpassa VM, de Lacerda MVG, Hanley KA, Vasilakis N.

Viruses.

23-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680085/>

Rapid and Non-Invasive Detection of Aedes aegypti Co-Infected with Zika and Dengue Viruses Using Near Infrared Spectroscopy.

Garcia GA, Lord AR, Santos LMB, Kariyawasam TN, David MR, Couto-Lima D, Tátilla-Ferreira A, Pavan MG, Sikulu-Lord MT, Maciel-de-Freitas R.

Viruses.

20-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680052/>

Genomic Characterization of Dengue Virus Outbreak in 2022 from Pakistan.

Umair M, Haider SA, Rehman Z, Jamal Z, Ali Q, Hakim R, Bibi S, Ikram A, Salman M.

Vaccines (Basel).

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680008/>

Pakistan, a dengue-endemic country, has encountered several outbreaks during the past decade. The current study aimed to explore the serotype and genomic diversity of dengue virus responsible for the 2022 outbreak in Pakistan. From August to October 2022, NS-1 positive blood samples (n = 343) were collected from dengue patients, among which, (85%; n = 293) were positive based on RT-PCR. In terms of gender and age, dengue infection was more prevalent in male patients (63%; n = 184), with more adults (21-30 years; n = 94) being infected. The serotyping results revealed DENV-2 to be the most predominant serotype (62%; n = 183), followed by DENV-1 (37%; n = 109) and DENV-3 (0.32%; n = 1). Moreover, a total of 10 samples (DENV-2; n = 8, DENV-1; n = 2) were subjected to whole-genome sequencing. Among these, four were collected in early 2022, and six were collected between August and October 2022. Phylogenetic analysis of DENV-2 sequenced samples (n = 8) revealed a monophyletic clade of cosmopolitan genotype IVA, which is closely related to sequences from China and Singapore 2018, and DENV-1 samples (n = 2) show genotype III, which is closely related to Pakistan isolates from 2019. We also reported the first whole genome sequence of a coinfection case (DENV1-DENV2) in Pakistan detected through a meta-genome approach. Thus, dengue virus dynamics reported in the current study warrant large-scale genomic surveillance to better respond to future outbreaks.

Identification of NS2B-NS3 Protease Inhibitors for Therapeutic Application in ZIKV Infection: A Pharmacophore-Based High-Throughput Virtual Screening and MD Simulations Approaches.

Rehman HM, Sajjad M, Ali MA, Gul R, Irfan M, Naveed M, Bhinder MA, Ghani MU, Hussain N, Said ASA, Al Haddad AHI, Saleem M.

Vaccines (Basel).

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36679976/>

Effects of Statin Combinations on Zika Virus Infection in Vero Cells.

España E, Kim JK.

Pharmaceutics.

23-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678679/>

Low Transmission of Chikungunya Virus by *Aedes aegypti* from Vientiane Capital, Lao PDR.

Calvez E, Miot EF, Keosenhom S, Vungkyly V, Viengphouthong S, Bounmany P, Brey PT, Marcombe S, Grandadam M.

Pathogens.

25-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678379/>

Serosurvey in Two Dengue Hyperendemic Areas of Costa Rica Evidence Active Circulation of WNV and SLEV in Peri-Domestic and Domestic Animals and in Humans.

Piche-Ovares M, Romero-Vega M, Vargas-González D, Murillo DFB, Soto-Garita C, Francisco-Llamas J, Alfaro-Alarcón A, Jiménez C, Corrales-Aguilar E.

Pathogens.

21-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678356/>

Entomo-Virological *Aedes aegypti* Surveillance Applied for Prediction of Dengue Transmission: A Spatio-Temporal Modeling Study.

Leandro AS, Ayala MJC, Lopes RD, Martins CA, Maciel-de-Freitas R, Villela DAM.

Pathogens.

20-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678352/>

Currently, DENV transmitted primarily by *Aedes aegypti* affects approximately one in three people annually. The spatio-temporal heterogeneity of vector infestation and the intensity of arbovirus transmission require surveillance capable of predicting an outbreak. In this work, we used data from 4 years of reported dengue cases and entomological indicators of adult *Aedes* collected from approximately 3500 traps installed in the city of Foz do

Iguaçu, Brazil, to evaluate the spatial and temporal association between vector infestation and the occurrence of dengue cases. Entomological (TPI, ADI and MII) and entomo-virological (EVI) indexes were generated with the goal to provide local health managers with a transmission risk stratification that allows targeting areas for vector control activities. We observed a dynamic pattern in the evaluation; however, it was a low spatio-temporal correlation of *Ae. aegypti* and incidence of dengue. Independent temporal and spatial effects capture a significant portion of the signal given by human arbovirus cases. The entomo-virological index (EVI) significantly signaled risk in a few areas, whereas entomological indexes were not effective in providing dengue risk alert. Investigating the variation of biotic and abiotic factors between areas with and without correlation should provide more information about the local epidemiology of dengue.

Recent Developments in DNA-Nanotechnology-Powered Biosensors for Zika/Dengue Virus Molecular Diagnostics.

Park G, Park H, Park SC, Jang M, Yoon J, Ahn JH, Lee T.

Nanomaterials (Basel).

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678114/>

The Entrapment and Concentration of SARS-CoV-2 Particles with Graphene Oxide: An In Vitro Assay.

Parra B, Contreras A, Mina JH, Valencia ME, Grande-Tovar CD, Valencia CH, Ramírez C, Bolívar GA.

Nanomaterials (Basel).

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678096/>

Prevalence of Dengue, Chikungunya and Zika Viruses in Blood Donors in the State of Pará, Northern Brazil: 2018-2020.

Lamarão LM, Corrêa ASM, de Castro RBH, de Melo Amaral CE, Monteiro PDJ, Palmeira MK, Lopes LN, Oliveira AN, de Lima MSM, Moreira-Nunes CA, Burbano RR.

Medicina (Kaunas).

31-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36676703/>

Arboviruses have been reported over the years as constant threats to blood transfusion recipients, given the high occurrence of asymptomatic cases and the fact that the presence of viremia precedes the onset of symptoms, making it possible that infected blood from donors act as a source of dissemination. This work aims to identify the prevalence of dengue virus (DENV), Zika virus (ZIKV) and Chikungunya virus (CHIKV) infection in blood donors during epidemic and non-epidemic periods; classify the donor as symptomatic or asymptomatic; and verify the need to include DENV, CHIKV and ZIKV in the nucleic acid test (NAT) platform in northern Brazil. We investigated 36,133 thousand donations in two years of collection in Northern Brazil. One donor was positive for DENV and one

for CHIKV (0.002% prevalence). As the prevalence for arboviruses was low in this study, it would not justify the individual screening of samples from donors in a blood bank. Thus, DENV- and CHIKV-positive samples were simulated in different amounts of sample pools, and both were safely detected by molecular biology even in a pool of 14 samples, which would meet the need to include these three viruses in the routine of blood centers in endemic countries such as Brazil.

Machine Learning-Based Detection of Dengue from Blood Smear Images Utilizing Platelet and Lymphocyte Characteristics.

Mayrose H, Bairy GM, Sampathila N, Belurkar S, Saravu K.

Diagnostics (Basel).

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36673030/>

Potential Protective Effect of Dengue NS1 Human Monoclonal Antibodies against Dengue and Zika Virus Infections.

Sootichote R, Puangmanee W, Benjathummarak S, Kowaboot S, Yamanaka A, Boonnak K, Ampawong S, Chatchen S, Ramasoota P, Pitaksajjakul P.

Biomedicines.

16-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36672734/>

Electrochemical Aptasensor Developed Using Two-Electrode Setup and Three-Electrode Setup: Comprising Their Current Range in Context of Dengue Virus Determination.

Hasan MR, Sharma P, Shaikh S, Singh S, Pilloton R, Narang J.

Biosensors (Basel).

20-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36671836/>

We present, for the very first time, the fabrication and electrochemical characterization of a paper-based experimental platform for dengue virus analysis. The paper-based device incorporates a screen-printing technology with the help of black carbon conductive ink. The paper-based device utilizes two styles of electrode setups, i.e., the two-electrode system and three-electrode system, and both setups effectively detected the dengue virus with an LOD of 0.1 µg/mL; however, these paper electrodes exhibit various current ranges, and the created sensor was encompassed and compared in this research based on current response. It is observed that the three-electrode system has a substantially higher current range, ranging from 55.53 µA to 322.21 µA, as compared to the two-electrode system, which has a current range of 0.85 µA to 4.54 µA. According to this study, the three-electrode system displayed a good range of current amplification that is roughly 50 times higher than the two-electrode system, which had a weak current response. As a result, the three-electrode method has emerged as a viable

option for the very sensitive detection of the dengue virus, as well as for the diagnosis of other diseases.

Quantifying Aedes aegypti Host Odor Preference Using a Two-Port Olfactometer.

Metz HC, Zung JL, McBride CS.

Cold Spring Harb Protoc.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36669857/>

The state of health in Pakistan and its provinces and territories, 1990-2019: a systematic analysis for the Global Burden of Disease Study 2019.

GBD 2019 Pakistan Collaborators.

Lancet Glob Health.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36669807/>

Efficacy Assessment of Autodissemination Using Pyriproxyfen-Treated Ovitrap in the Reduction of Dengue Incidence in Parañaque City, Philippines: A Spatial Analysis.

Ligsay AD, Regencia ZJG, Tambio KJM, Aytona MJM, Generale AJA, Alejandro GJD, Tychuaco JS, De Las Llagas LA, Baja ES, Paul REL.

Trop Med Infect Dis.

16-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668973/>

The Risk of Emerging of Dengue Fever in Romania, in the Context of Global Warming.

Ivanescu LM, Bodale I, Grigore-Hristodorescu S, Martinescu G, Andronic B, Matiu S, Azoicai D, Miron L.

Trop Med Infect Dis.

15-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668972/>

Distinguishing SARS-CoV-2 Infection and Non-SARS-CoV-2 Viral Infections in Adult Patients through Clinical Score Tools.

Sirijatuphat R, Sirianan K, Horthongkham N, Komoltri C, Angkasekwinai N.

Trop Med Infect Dis.

12-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668968/>

Nanobody-Based Blocking of Binding ELISA for the Detection of Anti-NS1 Zika-Virus-Specific Antibodies in Convalescent Patients.

Delfin-Riela T, Rossotti MA, Mattiuzzo G, Echaidés C

Trop Med Infect Dis.

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668962/>

Vitamin D Deficiency (VDD) and Susceptibility towards Severe Dengue Fever-A Prospective Cross-Sectional Study of Hospitalized Dengue Fever Patients from Lahore, Pakistan.

Iqtadar S, Khan A, Mumtaz SU, Livingstone S, Chaudhry MNA, Raza N, Zahra M, Abaidullah S.

Trop Med Infect Dis.

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668950/>

Dengue is a mosquito-borne flaviviral serious febrile illness, most common in the tropical and subtropical regions including Pakistan. Vitamin D is a strong immunomodulator affecting both the innate and adaptive immune responses and plays a pivotal role in pathogen-defense mechanisms. There has been considerable interest in the possible role of vitamin D in dengue viral (DENV) infection. In the present prospective cross-sectional study, we assessed a possible association between serum vitamin D deficiency (VDD) and susceptibility towards severe dengue fever (DF) illness. Serum vitamin D levels were measured at the time of hospitalization in 97 patients diagnosed with dengue fever (DF), dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) at Mayo Hospital, King Edward Medical University, Lahore, PK, from 16 November 2021 to 15 January 2022. In terms of disease severity, 37 (38.1%) patients were DF, 52 (53.6%) were DHF grade 1 and 2, and 8 (8.2%) were DSS. The results revealed that most patients (75 (77.3%)) were vitamin-D-deficient (i.e., serum level \leq 20 ng/mL), including 27 (73.0%) in DF, 41 (78.8%) in DHF grade 1 and 2, and 7 (87.5%) in DSS. The degree of VDD was somewhat higher in DSS patients as compared to DF and DHF grade 1 and 2 patients. Overall, serum vitamin D levels ranged from 4.2 to 109.7 ng/mL, and the median (IQR) was in the VDD range, i.e., 12.2 (9.1, 17.8) ng/mL. Our results suggest that there may be a possible association between VDD and susceptibility towards severe dengue illness. Hence, maintaining sufficient vitamin D levels in the body either through diet or supplementation may help provide adequate immune protection against severe dengue fever illness. Further research is warranted.

Democratizing Public Health: Participatory Policymaking Institutions, Mosquito Control, and Zika in the Americas.

Touchton M, Wampler B.

Trop Med Infect Dis.

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668945/>

Increasing Dengue Burden and Severe Dengue Risk in Bangladesh: An Overview.

Kayesh MEH, Khalil I, Kohara M, Tsukiyama-Kohara K.

Trop Med Infect Dis.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668939/>

Identification of Hazard and Socio-Demographic Patterns of Dengue Infections in a Colombian Subtropical Region from 2015 to 2020: Cox Regression Models and Statistical Analysis.

Ortiz S, Catano-Lopez A, Velasco H, Restrepo JP, Pérez-Coronado A, Laniado H, Leiva V.

Trop Med Infect Dis.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668937/>

Reduction in Anti-Dengue Virus IgG Antibody Levels with the Use of a Larvicide for Vector Control in Rural Lao People's Democratic Republic.

Lamaningao P, Kanda S, Shimono T, Kuroda M, Inthavongsack S, Xaypangna T, Nishiyama T.

Trop Med Infect Dis.

27-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668927/>

The Lao People's Democratic Republic is an endemic area of dengue, with cases reported in urban and rural areas every year. In this study, we indirectly evaluated the efficacy of a larvicide (SumiLar™ 2MR discs) that was used for vector control against *Aedes* mosquitoes. Villages in a rural area of Lao PDR were selected as study areas, non-intervention and intervention villages. At the intervention village, the larvicide was used to treat refillable water containers for 27 months (October 2017 to February 2020), while at the non-intervention villages were no treatment. The serum samples of villagers from both villages were randomized to collect in the pre-intervention and in post-intervention periods. An enzyme-linked immunosorbent assay (ELISA) was used to examine anti-dengue virus (DENV) IgG antibody levels in serum samples. Recombinant DENV serotype 2 non-structural protein1 was used as an antigen for the ELISA, the optical density (OD) values were analyzed for comparison. The results showed that the OD values decreased significantly ($p \leq 0.01$) between the pre-intervention and post-intervention periods at the intervention site. The treatment of water storage containers in rural areas with SumiLar™ 2MR discs may help to protect residents from *Aedes* mosquito bites, and hence, reduce DENV infections.

A Use of 56-kDa Recombinant Protein of Orientia tsutsugamushi Karp Serotype in Serodiagnosis of Scrub Typhus by Enzyme-Linked Immunosorbent Assay in Thais.

Chankate P, Kalambaheti T, Kosoltanapiwat N, Tanganuchitcharnchai A, Blacksell SD, Chantratita N, Leaungwutiwong P.

Trop Med Infect Dis.

23-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668917/>

Diagnostic Specificity of Two Dengue Virus IgG ELISAs after Yellow Fever and

Japanese Encephalitis Virus Vaccination.

Schnabel I, Schneitler S, Schüttoff T, Trawinski H, Lübbert C, Jassoy C.

Trop Med Infect Dis.

22-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668914/>

The Influence of Anthropogenic and Environmental Disturbances on Parameter Estimation of a Dengue Transmission Model.

Catano-Lopez A, Rojas-Diaz D, Vélez CM.

Trop Med Infect Dis.

22-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668912/>

Some deterministic models deal with environmental conditions and use parameter estimations to obtain experimental parameters, but they do not consider anthropogenic or environmental disturbances, e.g., chemical control or climatic conditions. Even more, they usually use theoretical or measured in-lab parameters without worrying about uncertainties in initial conditions, parameters, or changes in control inputs. Thus, in this study, we estimate parameters (including chemical control parameters) and confidence contours under uncertainty conditions using data from the municipality of Bello (Colombia) during 2010-2014, which includes two epidemic outbreaks. Our study shows that introducing non-periodic pulse inputs into the mathematical model allows us to: (i) perform parameter estimation by fitting real data of consecutive dengue outbreaks, (ii) highlight the importance of chemical control as a method of vector control, and (iii) reproduce the endemic behavior of dengue. We described a methodology for parameter and sub-contour box estimation under uncertainties and performed reliable simulations showing the behavior of dengue spread in different scenarios.

Knockdown of the Sodium/Potassium ATPase Subunit Beta 2 Reduces Egg Production in the Dengue Vector, *Aedes aegypti*.

Martinez NP, Pinch M, Kandel Y, Hansen IA.

Insects.

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36661978/>

Spatial Distribution of Pyrethroid Resistance and *kdr* Mutations in *Aedes aegypti* from La Guajira, Colombia.

Maestre-Serrano R, Flórez-Rivadeneira Z, Castro-Camacho JM, Soto-Arenilla E, Gómez-Camargo D, Pareja-Loaiza P, Ponce-García G, Juache-Villagrana AE, Flores AE.

Insects.

29-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36661959/>

Assessment of Various Colors Combined with Insecticides in Devising Ovitrap as Attracting and Killing Tools for Mosquitoes.

Khan A, Ullah M, Khan GZ, Ahmed N, Shami A, El Hadi Mohamed RA, Abd Al Galil FM, Salman M.

Insects.

26-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36661953/>

Dengue virus, transmitted by *Aedes aegypti* mosquitoes, is the most important emerging viral disease, infecting more than 50 million people annually. Currently used sticky traps are useful tools for monitoring and controlling *Ae. aegypti*. Therefore, this study was conducted to evaluate the attraction of *Ae. aegypti* mosquitoes using various colors, materials and insecticides. The laboratory and field assessed the four different colors of ovitraps (blue, green, black and transparent). Among the tested ovitraps, the black ovitraps showed the highest number of eggs (348.8) in the laboratory and maximum eggs (80.0) in field trials. In addition, six different materials (casein, urea, yeast, fish meal, chicken meal and water) were also used to evaluate mosquito's attraction. In our results, the highest number of eggs were collected with fish meal having 0.5% concentration in both laboratory (195.17) and the field (100.7). In laboratory trials, the Deltamethrin treated ovitraps (treated with Deltamethrin) significantly trapped and killed the highest percent of female *Ae. aegypti* (91.5%) compared to untreated (not-treated with Deltamethrin) ovitraps (3.3%). In field trials, the lethality was determined by installing 10 lethal ovitraps in one block and 10 untreated ovitraps in another block. The results indicate a significant reduction in eggs collected from the treated block (727 eggs) as compared to the untreated block (1865 eggs). The data also reveal that the ovitrap positive index (50) and egg density index (24.3) were also low in treated areas than in untreated areas, 83.3 and 37.3, respectively. It is concluded that the lethal ovitraps significantly reduced the *Ae. aegypti* population and thus could be considered an integral part of the integrated vector management (IVM) program.

Assessing the hearing of children exposed to zika virus with an initially normal newborn hearing screen: a longitudinal cohort study.

Prestes R, Pandini VCM, Pereira T, Pomilio MCA, Andrade AN, Mizani RM, Fajardo TCG, Gazeta RE, Bertozzi APAP, Lourenço EA, Passos SD.

Acta Otolaryngol.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36661392/>

Dengue fever ophthalmic manifestations: A review and update.

Lucena-Neto FD, Falcão LFM, Moraes ECDS, David JPF, Vieira-Junior AS, Silva CC, de Sousa JR, Duarte MIS, Vasconcelos PFDC, Quaresma JAS.

Rev Med Virol.

19-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36658757/>

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

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

Arch Virol.

20-01-2023

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

Sinococuline, a bioactive compound of *Cocculus hirsutus* has potent anti-dengue activity.

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

Sci Rep.

19-01-2023

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

Interferon-induced restriction of Chikungunya virus infection.

Suzuki Y.

Antiviral Res.

Feb-2023

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

Chikungunya virus (CHIKV) is an enveloped RNA virus that causes Chikungunya fever (CHIKF), which is transmitted to humans through the bite of infected *Aedes* mosquitos. Although CHIKV had been regarded as an endemic disease in limited regions of Africa and Asia, the recent global reemergence of CHIKV heightened awareness of this infectious disease, and CHIKV infection is currently considered an increasing threat to public health. However, no specific drug or licensed vaccine is available for CHIKV infection. As seen in other RNA virus infections, CHIKV triggers the interferon (IFN) response that plays a central role in host defense against pathogens. Experimental evidence has demonstrated that control of CHIKV replication by the IFN response is achieved by antiviral effector molecules called interferon-stimulated genes (ISGs), whose expressions are upregulated by IFN stimulation. This review details the molecular basis of the IFN-mediated suppression of CHIKV, particularly the ISGs restricting CHIKV replication.

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

Richter O, Nguyen A, Nguyen T.

Math Biosci Eng.

05-09-2022

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

Chikungunya and Lyme vaccines make headway.

[No authors listed]

Nat Biotechnol.

Jan-2023

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

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

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

Phytomedicine.

Feb-2023

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

Structure and neutralization mechanism of a human antibody targeting a complex Epitope on Zika virus.

Adams C, Carbaugh DL, Shu B, Ng TS, Castillo IN, Bhowmik R, Segovia-Chumbez B, Puhl AC, Graham S, Diehl SA, Lazear HM, Lok SM, de Silva AM, Premkumar L.

PLoS Pathog.

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36626401/>

Clinical markers of post-Chikungunya chronic inflammatory joint disease: A Brazilian cohort.

Lázari CDS, Ramundo MS, Ten-Caten F, Bressan CS, de Filippis AMB, Manuli ER, de Moraes I, Pereira GM, Côrtes MF, Candido DDS, Gerber AL, Guimarães AP, Faria NR, Nakaya HI, Vasconcelos ATR, Brasil P, Paranhos-Baccalà G, Sabino EC.

PLoS Negl Trop Dis.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36608155/>

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.

PLoS Pathog.

05-01-2023

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

Therapeutics for flaviviral infections.

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

Antiviral Res.

Feb-2023

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

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

Teramoto T, Choi KH, Padmanabhan R.

Antiviral Res.

Feb-2023

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

Targeting the alphavirus virus replication process for antiviral development.

Tan YB, Law MCY, Luo D.

Antiviral Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36574906/>

Clinical and experimental evidence for transplacental vertical transmission of flaviviruses.

Watanabe S, Vasudevan SG.

Antiviral Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36572192/>

Mouse models of Zika virus transplacental transmission.

Li QH, Kim K, Shrestha S.

Antiviral Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36567026/>

A pan-serotype antiviral to prevent and treat dengue: A journey from discovery to clinical development driven by public-private partnerships.

Goethals O, Voge NV, Kesteleyn B, Chaltin P, Jinks T, De Marez T, Koul A, Draghia-Akli R, Neyts J, Van Loock M.

Antiviral Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36567021/>

While progress has been made in fighting diseases disproportionately affecting underserved populations, unmet medical needs persist for many neglected tropical diseases. The World Health Organization has encouraged strong public-private partnerships to address this issue and several public and private organizations have set an example in the past showing a strong commitment to combat these diseases. Pharmaceutical companies are contributing in different ways to address the imbalance in research efforts. With this review, we exemplify the role of a public-private partnership in research and development by the journey of our dengue antiviral molecule that is now in early clinical development. We detail the different steps of drug development and outline the contribution of each partner to this process. Years of intensive collaboration resulted in the identification of two antiviral compounds, JNJ-A07 and JNJ-1802, the latter of which has advanced to clinical development.

Drug repurposing toward the inhibition of RNA-dependent RNA polymerase of various flaviviruses through computational study.

Murali A, Kumar S, Akshaya S, Singh SK.

J Cell Biochem.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36502494/>

Allosteric quinoxaline-based inhibitors of the flavivirus NS2B/NS3 protease.

Zephyr J, Rao DN, Johnson C, Shaqra AM, Nalivaika EA, Jordan A, Kurt Yilmaz N, Ali A, Schiffer CA.

Bioorg Chem.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36446201/>

Discovery of non-nucleoside oxindole derivatives as potent inhibitors against dengue RNA-dependent RNA polymerase.

Maddipati VC, Mittal L, Kaur J, Rawat Y, Koraboina CP, Bhattacharyya S, Asthana S, Gundla R.

Bioorg Chem.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36444792/>

Studies on the sensory sensilla on the tarsi and external genitalia of the Asian tiger mosquito, *Aedes albopictus* (Skuse).

Yamany AS, Abdel-Gaber R.

Microsc Res Tech.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36398839/>

Offspring affected with in utero Zika virus infection retain molecular footprints in the bone marrow and blood cells.

Udenze D, Trus I, Lipsit S, Napper S, Karniychuk U.

Emerg Microbes Infect.

Dec-2023

<https://pubmed.ncbi.nlm.nih.gov/36369716/>

TSPO expression in a Zika virus murine infection model as an imaging target for acute infection-induced neuroinflammation.

Victorio CBL, Msallam R, Novera W, Ong J, Yang TJ, Ganasarajah A, Low J, Watanabe S, Chacko AM.

Eur J Nucl Med Mol Imaging.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36348095/>

Introduction: Zika virus (ZIKV) is a neurotropic human pathogen that causes neuroinflammation, whose hallmark is elevated translocator protein (TSPO) expression in the brain. This study investigates ZIKV-associated changes in adult brain TSPO expression, evaluates the effectiveness of TSPO radioligands in detecting TSPO expression, and identifies cells that drive brain TSPO expression in a mouse infection model. **Methods:** The interferon-deficient AG129 mouse infected with ZIKV was used as neuroinflammation model. TSPO expression was evaluated by tissue immunostaining. TSPO radioligands, [³H]PK11195 and [¹⁸F]FEPPA, were used for in vitro and ex vivo detection of TSPO in infected brains. [¹⁸F]FEPPA-PET was used for in vivo detection of TSPO expression. Cell subsets that

contribute to TSPO expression were identified by flow cytometry. **Results:** Brain TSPO expression increased with ZIKV disease severity. This increase was contributed by TSPO-positive microglia and infiltrating monocytes; and by influx of TSPO-expressing immune cells into the brain. [³H]PK11195 and [¹⁸F]FEPPA distinguish ZIKV-infected brains from normal controls in vitro and ex vivo. [¹⁸F]FEPPA brain uptake by PET imaging correlated with disease severity and neuroinflammation. However, TSPO expression by immune cells contributed to significant blood pool [¹⁸F]FEPPA activity which could confound [¹⁸F]FEPPA-PET imaging results. **Conclusions:** TSPO is a biologically relevant imaging target for ZIKV neuroinflammation. Brain [¹⁸F]FEPPA uptake can be a surrogate marker for ZIKV disease and may be a potential PET imaging marker for ZIKV-induced neuroinflammation. Future TSPO-PET/SPECT studies on viral neuroinflammation and related encephalitis should assess the contribution of immune cells on TSPO expression and employ appropriate image correction methods to subtract blood pool activity.

Dengue Trend During COVID-19 Pandemic in Malaysia.

Ahmad Zaki R, Xin NZ.

Asia Pac J Public Health.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36341513/>

Influence of epidemics and pandemics on paediatric ED use: a systematic review.

Roland D, Gardiner A, Razzaq D, Rose K, Bressan S, Honeyford K, Buonsenso D, Da Dalt L, De T, Farrugia R, Parri N, Oostenbrink R, Maconochie IK, Bogner Z, Moll HA, Titomanlio L, Nijman RGG; in association with the REPEM network (Research in European Paediatric Emergency Medicine) as part of the EPISODES Study.

Arch Dis Child.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36162959/>

Pathogenesis of Zika Virus Infection.

Giraldo MI, Gonzalez-Orozco M, Rajsbaum R.

Annu Rev Pathol.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36151059/>

Effect of delayed mating on reproductive performance and life-history parameters of dengue vector *Aedes aegypti*.

Gunathilaka RAKM, Jayatunga DPW, Ganehiarachchi GASM.

Bull Entomol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36065760/>

Predation risk effects on larval development and adult life of *Aedes aegypti* mosquito.

Cozzer GD, Rezende RS, Lara TS, Machado GH, Dal Magro J, Albeny-Simões D.

Bull Entomol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/35718943/>

Biological control is one of the methods available for control of *Aedes aegypti* populations. We used experimental microcosms to evaluate the effects of actual predation and predation risk by dragonfly larvae (Odonata) on larval development, adult longevity, and adult size of *Ae. aegypti*. We used six treatments: control, removal, variable density cues (Cues VD), fixed density cues (Cues FD), variable density predator (Predator VD), and fixed density predator (Predator FD) ($n = 5$ each). Predator treatments received one dragonfly larva. Cue treatments were composed of crushed *Ae. aegypti* larvae released into the microcosm. For the FD treatments, we maintained a larval density of 200 individuals. The average mortality of *Ae. aegypti* larvae in the Predator VD treatment was used as the standard mortality for the other treatments. Mosquitoes from the Predator VD and Cues VD treatments developed faster, and adults were larger and had greater longevity compared to all other treatments, likely due to the higher food availability from larval density reduction. High larval density negatively affected larval developmental time, adult size, and longevity. Males were less sensitive to density-dependent effects. Results from this study suggest that the presence of predators may lead to the emergence of adult mosquitoes with greater fitness, causing an overall positive effect on *Ae. aegypti* population growth rates.

Myopic Shift in a Patient with Dengue Fever.

Mi Fang H, Ng OT, Agrawal R.

Ocul Immunol Inflamm.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/34648404/>

Rage

Assessment of community perceptions and risk to common zoonotic diseases among communities living at the human-livestock-wildlife interface in Nakuru West, Kenya: A participatory epidemiology approach.

Owiny MO, Ngare BK, Mugo BC, Rotich J, Mutembei A, Chepkorir K, Sitawa R, Obonyo M, Onono JO.

PLoS Negl Trop Dis.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36701376/>

Real-time multiplex PCR for human echinococcosis and differential diagnosis.

Knapp J, Lallemand S, Monnien F, Felix S, Courquet S, Umhang G, Millon L.

Parasite.

2023

<https://pubmed.ncbi.nlm.nih.gov/36700708/>

Molecular identification of rare human infectious pathogens appears to be one of the most relevant current methods for rapid diagnosis and management of patients. PCR techniques, in particular real-time quantitative PCR, are best suited for the detection of DNA from the pathogens, even at low concentrations. Echinococcosis infections are due to helminths of the *Echinococcus* genus, with closely related species involved in parasitic lesions affecting animals and, accidentally, humans. We developed a multiplex qPCR (MLX qPCR) assay allowing for the detection of four *Echinococcus* species involved in Europe in alveolar echinococcosis (AE) and cystic echinococcosis (CE) (*Echinococcus multilocularis*, *E. granulosus sensu stricto*, *E. ortleppi*, and *E. canadensis*), based on short mitochondrial targets. A collection of 81 fresh and formalin-fixed paraffin-embedded tissues (FFPE) of AE and CE lesions was assembled. The qPCR assays were performed in triplex for *Echinococcus* spp. detection, associated with a qPCR inhibitor control. A duplex qPCR was also designed to enable diagnosis of two other dead-end helminthiasis (cysticercosis (*Taenia solium*), and toxocarosis (*Toxocara cati* and *T. canis*)). The sensitivity of the qPCR was assessed and ranged from 1 to 5×10^{-4} ng/μL (seven PCR assays positive), corresponding to 37-42 cycles for quantifiable DNA. The specificity was 100% for all the targets. This multiplex qPCR, adapted to low amounts of DNA can be implemented in the laboratory for the rapid molecular diagnosis of Echinococcosis species.

Rabies.

Jin J.

JAMA.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36692559/>

[Viruses to rescue health: Vaccination].

Tangy F, Tournier JN.

Med Sci (Paris).

Dec-2022

<https://pubmed.ncbi.nlm.nih.gov/36692265/>

Age estimation of puppies based on the radiographically assessed development of ossification centres in the carpal and metacarpal regions.

Van den Broeck M, Chen Y, Cornillie P.

Vet Rec.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691858/>

Identification and Evaluation of Cryptosporidium Species from New York City Cases of Cryptosporidiosis (2015 to 2018): a Watershed Perspective.

Alderisio KA, Mergen K, Moessner H, Madison-Antenucci S.

Microbiol Spectr.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36688660/>

A global analysis of One Health Networks and the proliferation of One Health collaborations.

Mwatondo A, Rahman-Shepherd A, Hollmann L, Chiossi S, Maina J, Kurup KK, Hassan OA, Coates B, Khan M, Spencer J, Mutono N, Thumbi SM, Muturi M, Mutunga M, Arruda LB, Akhbari M, Ettehad D, Ntoumi F, Scott TP, Nel LH, Ellis-Iversen J, Sönksen UW, Onyango D, Ismail Z, Simachew K, Wolking D, Kazwala R, Sijali Z, Bett B, Heymann D, Kock R, Zumla A, Dar O.

Lancet.

19-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682370/>

There has been a renewed focus on threats to the human-animal-environment interface as a result of the COVID-19 pandemic, and investments in One Health collaborations are expected to increase. Efforts to monitor the development of One Health Networks (OHNs) are essential to avoid duplication or misalignment of investments. This Series paper shows the global distribution of existing OHNs and assesses their collective characteristics to identify potential deficits in the ways OHNs have formed and to help increase the effectiveness of investments. We searched PubMed, Google, Google Scholar, and relevant conference websites for potential OHNs and identified 184 worldwide for further analysis. We developed four case studies to show important findings from our research and exemplify best practices in One Health operationalisation. Our findings show that, although more OHNs were formed in the past 10 years than in the preceding decade, investment in OHNs has not been equitably distributed; more OHNs are formed and headquartered in Europe than in any other region, and emerging infections and novel pathogens were the priority focus area for most OHNs, with fewer OHNs focusing on other important hazards and pressing threats to health security. We found substantial deficits in the OHNs collaboration model regarding the diversity of stakeholder and sector representation, which we argue impedes effective and equitable OHN formation and contributes to other imbalances in OHN distribution and priorities. These findings are supported by previous evidence that shows the skewed investment in One Health thus far. The increased attention to One Health after the COVID-19 pandemic is an opportunity to focus efforts and resources to areas that need them most. Analyses, such as this Series paper, should be used to establish databases and repositories of OHNs worldwide. Increased attention should then be given to understanding existing resource allocation and distribution patterns, establish more egalitarian networks that encompass the breadth of One Health issues, and serve communities most affected by emerging, re-emerging, or endemic threats at the human-animal-environment interface.

Factors Associated with Dog Rabies Immunization in Changsha, China: Results of a Cross-Sectional Cluster Survey, 2015-2021.

Ji C, Feng J, Li S, Yang H, Wang H, Geng X, Wang H, Liu Z, Zhang T, He Y, Liu W.

Viruses.

31-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680178/>

Susceptibilities of CNS Cells towards Rabies Virus Infection Is Linked to Cellular Innate Immune Responses.

Feige L, Kozaki T, Dias de Melo G, Guillemot V, Larrous F, Ginhoux F, Bourhy H.

Viruses.

29-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36680128/>

A Cost-Effectiveness Analysis of Pre-Exposure Prophylaxis to Avert Rabies Deaths in School-Aged Children in India.

Royal A, John D, Bharti O, Tanwar R, Bhagat DK, Padmawati RS, Chaudhary V, Umapathi R, Bhadola P, Utarini A.

Vaccines (Basel).

30-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36679933/>

Children contribute to one-half of the total painful rabies mortalities in India. The state-of-the-art rabies mortality averting strategies need exploration for the effective implementation of pre-exposure prophylaxis (PrEP) in India. This study reports on the economic evaluation of various PrEP and post-exposure prophylaxis (PEP) strategies to avert rabies mortalities in school-aged children in India. A decision tree model has been developed for children in the age group of 5-15 years to evaluate various PrEP + PEP and PEP only regimens. The 2-site intradermal regimen administered on day zero and seven was chosen as the intervention [PrEP (I)]. ICER was calculated from the quasi-societal and quasi-health systems' perspectives for the base case analysis, along with one-way sensitivity, and scenario analyses for each regimen. The incremental DALYs averted per million population with the implementation of PrEP (I) ranged between 451 and 85,069 in 2020. The ICER was reported in the range of USD 384-352/DALY averted (non-dominant) in comparison to PEP regimens from a quasi-societal perspective. PrEP (I) is reported to be 'very cost effective' in comparison with PEP regimens from the quasi-societal and quasi-health systems' perspectives and reduce deaths by up to 89.9%. This study concludes that the PrEP (I) regimen is a cost-effective and life-saving strategy to avert painful mortalities due to rabies in school-aged children in India.

Performance Comparison of Recombinant Baculovirus and Rabies Virus-like Particles production Using Two Culture Platforms.

Guardalini LGO, Cavalcante PEDS, Leme J, Mello RG, Bernardino TC, Jared SGS, Antoniazzi MM, Astray RM, Tonso A, Fernández Núñez EG, Jorge SAC.

Vaccines (Basel).

24-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36679884/>

Exogenous Players in Mitochondria-Related CNS Disorders: Viral Pathogens and Unbalanced Microbiota in the Gut-Brain Axis.

Righetto I, Gasparotto M, Casalino L, Vacca M, Filippini F.

Biomolecules.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36671555/>

Adaptive Evolution of the OAS Gene Family Provides New Insights into the Antiviral Ability of Laurasiatherian Mammals.

Liu G, Wu X, Shang Y, Wang X, Zhou S, Zhang H.

Animals (Basel).

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36670749/>

Many mammals risk damage from virus invasion due to frequent environmental changes. The oligoadenylate synthesis (OAS) gene family, which is an important component of the immune system, provides an essential response to the antiviral activities of interferons by regulating immune signal pathways. However, little is known about the evolutionary characteristics of OASs in Laurasiatherian mammals. Here, we examined the evolution of the OAS genes in 64 mammals to explore the accompanying molecular mechanisms of the antiviral ability of Laurasiatherian mammals living in different environments. We found that *OAS2* and *OAS3* were found to be pseudogenes in *Odontoceti* species. This may be related to the fact that they live in water. Some *Antilocaprinae*, *Caprinae*, and *Cervidae* species lacked the *OASL* gene, which may be related to their habitats being at higher altitudes. The OASs had a high number of positive selection sites in *Cetartiodactyla*, which drove the expression of strong antiviral ability. The OAS gene family evolved in Laurasiatherian mammals at different rates and was highly correlated with the species' antiviral ability. The gene evolution rate in *Cetartiodactyla* was significantly higher than that in the other orders. Compared to other species of the *Carnivora* family, the higher selection pressure on the OAS gene and the absence of positive selection sites in *Canidae* may be responsible for its weak resistance to rabies virus. The OAS gene family was relatively conserved during evolution. Conserved genes are able to provide better maintenance of gene function. The rate of gene evolution and the number of positively selected sites combine to influence the resistance of a species to viruses. The positive selection sites demonstrate the adaptive evolution of the OAS gene family to the environment. Adaptive evolution combined with conserved gene function improves resistance to viruses. Our findings offer insights into the molecular and functional evolution of the antiviral ability of Laurasian mammals.

Rabies in Bats (Chiroptera, Mammalia) in Brazil: Prevalence and Potential Risk Factors Based on Twenty Years of

Research in the Northwestern Region of São Paulo, Brazil.

Garcia AB, de Carvalho C, Casagrande D, Picinato MAC, Pedro WA, Marinho M, Queiroz LH.

Vet Sci.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36669035/>

Proteomic analysis of canine vaccines.

Franco J, Aryal UK, HogenEsch H, Moore GE.

Am J Vet Res.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36662608/>

Making dog control more effective.

[No authors listed]

Vet Rec.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36661146/>

Trachome

Epidemiology and control of trachoma in the state of Ceará, Northeast Brazil, 2007-2021.

Maciel AMS, Ramos AN Jr, Gomes VDS, Ferreira AF, Almeida NMGS, Gómez DVF, Favacho JDFR, Maciel MMS, Delerino AL, Pires Neto RDJ.

Rev Soc Bras Med Trop.

23-01-2032

<https://pubmed.ncbi.nlm.nih.gov/36700599/>

Mapping the FtsQBL divisome components in bacterial NTD pathogens as potential drug targets.

Kaur H, Lynn AM.

Front Genet.

04-01-0223

<https://pubmed.ncbi.nlm.nih.gov/36685953/>

Cytokinesis is an essential process in bacterial cell division, and it involves more than 25 essential/non-essential cell division proteins that form a protein complex known as a divisome. Central to the divisome are the proteins FtsB and FtsL binding to FtsQ to form a complex FtsQBL, which helps link the early proteins with late proteins. The FtsQBL complex is highly conserved as a component across bacteria. Pathogens like *Vibrio cholerae*, *Mycobacterium ulcerans*, *Mycobacterium leprae*, and *Chlamydia trachomatis* are the causative agents of the bacterial Neglected Tropical Diseases Cholera, Buruli ulcer, Leprosy, and Trachoma, respectively, some of which seemingly lack known homologs for some of the FtsQBL complex proteins. In the absence of experimental characterization, either due to insufficient resources or the massive increase in novel sequences generated from genomics, functional annotation is traditionally inferred by sequence similarity to a known homolog. With the advent of accurate protein structure prediction methods, features both at the fold level and at the protein interaction level

can be used to identify orthologs that cannot be unambiguously identified using sequence similarity methods. Using the FtsQBL complex proteins as a case study, we report potential remote homologs using Profile Hidden Markov models and structures predicted using AlphaFold. Predicted ortholog structures show conformational similarity with corresponding *E. coli* proteins irrespective of their level of sequence similarity. AlphaFold multimer was used to characterize remote homologs as FtsB or FtsL, when they were not sufficiently distinguishable at both the sequence or structure level, as their interactions with FtsQ and FtsW play a crucial role in their function. The structures were then analyzed to identify functionally critical regions of the proteins consistent with their homologs and delineate regions potentially useful for inhibitor discovery.

Ulcère de Buruli

Mapping the FtsQBL divisome components in bacterial NTD pathogens as potential drug targets.

Kaur H, Lynn AM.

Front Genet.

04-01-0223

<https://pubmed.ncbi.nlm.nih.gov/36685953/>

Cytokinesis is an essential process in bacterial cell division, and it involves more than 25 essential/non-essential cell division proteins that form a protein complex known as a divisome. Central to the divisome are the proteins FtsB and FtsL binding to FtsQ to form a complex FtsQBL, which helps link the early proteins with late proteins. The FtsQBL complex is highly conserved as a component across bacteria. Pathogens like *Vibrio cholerae*, *Mycobacterium ulcerans*, *Mycobacterium leprae*, and *Chlamydia trachomatis* are the causative agents of the bacterial Neglected Tropical Diseases Cholera, Buruli ulcer, Leprosy, and Trachoma, respectively, some of which seemingly lack known homologs for some of the FtsQBL complex proteins. In the absence of experimental characterization, either due to insufficient resources or the massive increase in novel sequences generated from genomics, functional annotation is traditionally inferred by sequence similarity to a known homolog. With the advent of accurate protein structure prediction methods, features both at the fold level and at the protein interaction level can be used to identify orthologs that cannot be unambiguously identified using sequence similarity methods. Using the FtsQBL complex proteins as a case study, we report potential remote homologs using Profile Hidden Markov models and structures predicted using AlphaFold. Predicted ortholog structures show conformational similarity with corresponding *E. coli* proteins irrespective of their level of sequence similarity. AlphaFold multimer was used to characterize remote homologs as FtsB or FtsL, when they were not sufficiently distinguishable at both the sequence or structure level, as their interactions with FtsQ and FtsW play a crucial role in their function. The structures were then analyzed to identify functionally critical regions of the proteins

consistent with their homologs and delineate regions potentially useful for inhibitor discovery.

Completion of 6-mo isoniazid preventive treatment among eligible under six children: A cross-sectional study, Lagos, Nigeria.

Adepoju VA, Adelekan A, Agbaje A, Quaitey F, Ademola-Kay T, Udoekpo AU, Sokoya OD.

World J Clin Cases.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36687175/>

Pian

No evidence for yaws infection in a small-scale cross-sectional serosurvey in Ghanaian monkeys.

Adade E, Roos C, Chuma IS, Sylverken AA, Knauf S.

Vet Med Sci.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36480449/>

Background: *Treponema pallidum* (TP) is a spirochaete bacterium with subspecies that in humans cause syphilis (subsp. *pallidum*), bejel (subsp. *endemicum*) and yaws (subsp. *pertenue*; TPE). The latter is target for eradication which requires detailed information on yaws epidemiology. It has been shown that African nonhuman primates (NHPs) are infected with TPE strains that are closely related to the human infecting yaws bacterium. While human yaws infection is known to be endemic in Ghana, there is a paucity of information regarding TPE infection of Ghana's native NHPs. **Objectives:** The objective was to perform a small-scale cross-sectional serological screening for antibodies against TPE in Ghanaian monkeys. Due to the reports of TPE-infected NHPs from neighbouring Côte d'Ivoire, we hypothesised that monkeys in Ghana are infected with TPE and, therefore, are seropositive for antibodies against *Treponema*. **Methods:** We sampled blood from 37 NHPs representing four species: *Erythrocebus patas* (16/37) 43.2%, *Papio anubis* (15/37) 40.5%, *Chlorocebus sabaeus* (3/37) 8.1% and *Cercopithecus mona* (3/37) 8.1%. Samples were tested using the NHP validated treponemal test ESPLINE TP. **Results:** All 37 animals were seronegative for yaws infection. **Conclusions:** We cannot exclude yaws infection in NHPs in Ghana at this point. Our study, in combination with the absence of reports of clinically infected NHPs in a yaws endemic country is, however, supportive for the current thinking that interspecies infection with TPE is extremely rare. This is an important finding for the current ongoing yaws eradication campaign

Lèpre

Scientometric review of research on Neglected Tropical Diseases: a 31-year perspective from the Journal of the Brazilian Society of Tropical Medicine.

Ferreira AF, Heukelbach J, Costa CHN, Souza EA, Maciel AMS, Correia D, Ramos AN Jr.

Rev Soc Bras Med Trop.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36700606/>

Background: To analyze the temporal evolution of research on Neglected Tropical Diseases (NTDs) published by the Journal of the Brazilian Society of Tropical Medicine (JBSTM). **Methods:** We performed an analysis of the scientific production in JBSTM on NTDs using an advanced search, which included authors' descriptors, title, and abstract, and by combining specific terms for each NTDs from 1991 to 2021. Data related to authors, countries of origin, institutions, and descriptors, were evaluated and analyzed over time. Bibliographic networks were constructed using VOSviewer 1.6.16. **Results:** The JBSTM published 4,268 scientific papers during this period. Of these 1,849 (43.3%) were related to NTDs. The number of publications on NTDs increased by approximately 2.4-fold, from 352 (total 724) during 1991-2000 to 841 (total 2,128) during 2011-2021, despite the proportional reduction (48.6% versus 39.5%). The most common singular NTDs subject of publications included Chagas disease (31.4%; 581/1,849), leishmaniasis (25.5%; 411/1,849), dengue (9.4%; 174/1,849), schistosomiasis (9.0%; 166/1,849), and leprosy (6.5%; 120/1,849), with authorship mostly from Brazil's South and Southeast regions. **Conclusions:** Despite the proportional reduction in publications, JBSTM remains an important vehicle for disseminating research on NTDs during this period. There is a need to strengthen the research and subsequent publications on specific NTDs. Institutions working and publishing on NTDs in the country were concentrated in the South and Southeast regions, requiring additional investments in institutions in other regions of the country.

Assessment of key regulatory genes and identification of possible drug targets for Leprosy (Hansen's disease) using network-based approach.

Khan M, Khan S, Lohani M, Ahmed MM, Sharma D, Ishrat R, Ahmad S, Sherwani S, Haque S, Bhagwath SS.

Biotechnol Genet Eng Rev. 2023 Jan 25:

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36696368/>

Miliaria crystallina.

Palaniappan V, Sadhasivamohan A, Sankarapandian J, Karthikeyan K.

Clin Exp Dermatol.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36692206/>

Correction: Gender differences among patients with drug resistant tuberculosis and HIV co-infection in Uganda: a countrywide retrospective cohort study.

Baluku JB, Mukasa D, Bongomin F, Stadelman AM, Nuwagira E, Haller S, Ntabadde K, Turyahabwe S.

BMC Infect Dis.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36690968/>

Resistance to anti-leprosy drugs: A cross-sectional study from a tertiary care hospital in Puducherry.

Manjula B, Gopinath H, Karthikeyan K.

Indian J Dermatol Venereol Leprol.

07-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36688897/>

Serum lipocalin-2 levels are decreased in patients with leprosy.

Bazid HAS, Shoeib MA, Shoeib MM, Sharaf REA, Mosatafa MI, Abd El Gayed EM.

Indian J Dermatol Venereol Leprol.

08-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36688897/>

Background Leprosy is an infectious disease caused by *Mycobacterium leprae* affecting the skin, peripheral nerves and mucosae. Lipocalin-2 is a key component of the immune system's antimicrobial defence - it prevents iron uptake by binding and sequestering iron-scavenging siderophores and thus inhibits bacterial growth. Aim We evaluated serum lipocalin-2 levels in leprosy patients and its relationship to the pathogenesis and prognosis of the disease. Materials and methods In this case-control study, serum lipocalin-2 levels were measured by ELISA in 20 patients with leprosy and 20 healthy controls. Results Serum levels of lipocalin-2 were significantly reduced ($P < 0.001$) in leprosy patients as compared to controls. The levels were significantly higher ($P < 0.014$) in patients with multibacillary leprosy than in those with paucibacillary leprosy. Although the levels of lipocalin-2 were higher in patients with multiple nerve involvement as compared to those with involvement of 1 or 2 nerves, the results were not statistically significant. Limitation of the study The small sample size and the lack of different ethnic groups in the study were the major limitations of this study. Conclusion The lower lipocalin-2 concentrations in leprosy patients point to the importance of the protective functions of lipocalin-2. The elevated levels of lipocalin-2 observed in leprosy patients with neural involvement may be related to the reported neurodegenerative role of lipocalin-2.

The efficacy of topical adipose mesenchymal stem cell-conditioned medium versus framycetin gauze dressing in chronic plantar ulcer of leprosy: A randomized controlled trial.

Alinda MD, Christopher PM, Listiawan MY, Endaryanto A, Suroto H, Rantam FA, Hendradi E, Notobroto HB, Prakoeswa CRS.

Indian J Dermatol Venereol Leprol.

07-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36688887/>

Artificial intelligence: Its role in dermatopathology.

Jartarkar SR.

Indian J Dermatol Venereol Leprol.

13-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36688886/>

Mucocutaneous manifestations of COVID-19-associated mucormycosis: A retrospective cross-sectional study.

Sachan S, Suvirya S, Yadav K, Gupta P, Saraswat A, Verma P, Chandra U, Singh BP, Chaudhary SC, Dwivedi DK, Garg RK, Singhai A, Malhotra KP, Parihar A, Kumar S.

Indian J Dermatol Venereol Leprol.

13-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36688884/>

Background Cutaneous mucormycosis has shown a significant upsurge during the COVID-19 pandemic. Due to the rapid progression and high mortality of cutaneous mucormycosis in this context, it is important to identify it early. However, very few studies report detailed clinical descriptions of cutaneous mucormycosis in COVID-19 patients. Objectives To describe mucocutaneous lesions of COVID-19-associated mucormycosis based on clinical morphology and attempt to correlate them with radiological changes. Methods A retrospective cross-sectional study was conducted at a tertiary care centre from 1st April to 31st July 2021. Eligibility criteria included hospitalised adult patients of COVID-19-associated mucormycosis with mucocutaneous lesions. Results All subjects were recently recovering COVID-19 patients diagnosed with cutaneous mucormycosis. One of fifty-three (2%) patients had primary cutaneous mucormycosis, and all of the rest had secondary cutaneous mucormycosis. Secondary cutaneous mucormycosis lesions presented as cutaneous-abscess in 25/52 (48%), nodulo-pustular lesions in 1/52 (2%), necrotic eschar in 1/52 (2%) and ulcero-necrotic in 1/52 (2%). Mucosal lesions were of three broad sub-types: ulcero-necrotic in 1/52 (2%), pustular in 2/52 (4%) and plaques in 1/52 (2%). Twenty out of fifty-two patients (38%) presented with simultaneous mucosal and cutaneous lesions belonging to the above categories. Magnetic resonance imaging of the face showed variable features of cutaneous and subcutaneous tissue involvement, viz. peripherally enhancing collection in the abscess group, "dot in circle sign" and heterogeneous contrast enhancement in the nodulo-pustular group; and fat stranding with infiltration of subcutaneous tissue in cases with necrotic eschar and ulcero-necrotic lesions. Limitations The morphological variety of cutaneous mucormycosis patients in a single-centre study like ours might not be very precise. Thus, there is a need to conduct multi-centric prospective studies with larger sample sizes in the future to substantiate our morphological and radiological findings. Conclusions COVID-19-associated mucormycosis patients in our study presented with a few specific types of mucocutaneous manifestations, with distinct magnetic resonance imaging findings. If corroborated by larger studies, these observations would be helpful in the early diagnosis of this serious illness.

Point counting-serial image index: A new scoring system for melasma.

Dubey S, Chethana SG, Kanthraj GR, Betkerur JB.
Indian J Dermatol Venereol Leprol.
15-12-2022
<https://pubmed.ncbi.nlm.nih.gov/36688879/>

Modified tarsorrhaphy versus gold weight implant technique for paralytic lagophthalmos treatment in patients with leprosy: One-year observation of a randomized controlled trial study.

Irawati Y, Natalia MER, Gondhowiardjo TD, Dachlan I, Soebono H.
Front Med (Lausanne).
04-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36687442/>

Completion of 6-mo isoniazid preventive treatment among eligible under six children: A cross-sectional study, Lagos, Nigeria.

Adepoju VA, Adelekan A, Agbaje A, Quaitey F, Ademola-Kay T, Udoekpo AU, Sokoya OD.
World J Clin Cases.
06-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36687175/>

Background: Nigeria is one of the thirty high burden countries with significant contribution to the global childhood tuberculosis epidemic. Tuberculosis annual risk for children could be as high as 4% particularly in high tuberculosis (TB) prevalent communities. Isoniazid (INH) Preventive Therapy has been shown to prevent TB incidence but data on its implementation among children are scarce. **Aim:** To determine the completion of INH among under six children that were exposed to adults with smear positive pulmonary TB in Lagos, Nigeria. **Methods:** This was a hospital-based retrospective cross-sectional review of 265 medical records of eligible children < 6 years old enrolled for INH across 32 private hospitals in Lagos, Nigeria. The study took place between July and September 2020. Data was collected on independent variables (age, gender, type of facility, TB screening, dose and weight) and outcome variables (INH outcome and proportion lost to follow up across months 1-6 of INH treatment). **Results:** About 53.8% of the participants were female, 95.4% were screened for TB and none was diagnosed of having TB. The participants' age ranged from 1 to 72 mo with a mean of 36.01 ± 19.67 mo, and 40.2% were between the ages of 1-24 mo. Only 155 (59.2%) of the 262 participants initiated on INH completed the six-month treatment. Cumulatively, 107 (41.0%) children were lost to follow-up at the end of the sixth month. Of the cumulative 107 loss to follow-up while on INH, largest drop-offs were reported at the end of month 2, 52 (49%) followed by 20 (19%), 17 (16%), 11 (10.2%) and 7 (6.5%) at months 3, 4, 5 and 6 respectively. The analysis showed that there was no significant association between age, gender, type of facility and completion of INH treatment ($P > 0.005$). **Conclusion:** This study demonstrated suboptimal INH completion rate among children with only 6 out of 10 children initiated on INH who completed a 6-mo treatment in Lagos, Nigeria. The huge drop-offs in the first 2 mo of INH calls for

innovative strategies such as the use of 60-d INH calendar that would facilitate reminder and early engagement of children on INH and their caregivers in care and across the entire period of treatment.

Mapping the FtsQBL divisome components in bacterial NTD pathogens as potential drug targets.

Kaur H, Lynn AM.
Front Genet.
04-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36685953/>

Intra-cranial involvement of trigeminal nerve in a patient with borderline tuberculoid leprosy in type 1 lepra reaction.

Sharma A, Narang T, Mehta H, Mahajan R, Takkar A, Prakash M, Dogra S.
Australas J Dermatol.
22-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36683361/>

Hyperfunction variant rs708035 of interleukin 1 receptor-associated kinases 2 gene involved in the predisposition of leprosy infection.

Saleem S, Zia M, Siddiqui F, Ghouri M, Kulsoom U, Kawal S, Fatima S, Zehra S.
J Gene Med.
20-01-2023
<https://pubmed.ncbi.nlm.nih.gov/36670053/>

Multicomponent strategy with decentralised molecular testing for tuberculosis in Uganda: a cost and cost-effectiveness analysis.

Thompson RR, Nalugwa T, Oyuku D, Tucker A, Nantale M, Nakaweesa A, Musinguzi J, Reza TF, Zimmer AJ, Ferguson O, Turyahabwe S, Joloba M, Cattamanchi A, Katamba A, Dowdy DW, Sohn H.
Lancet Glob Health.
Feb-2023
<https://pubmed.ncbi.nlm.nih.gov/36669808/>

Background: Decentralised molecular testing for tuberculosis could reduce missed diagnoses and losses to follow-up in high-burden settings. The aim of this study was to evaluate the cost and cost-effectiveness of the Xpert Performance Evaluation for Linkage to Tuberculosis Care (XPEL-TB) study strategy, a multicomponent strategy including decentralised molecular testing for tuberculosis, in Uganda. **Methods:** We conducted a costing and cost-effectiveness analysis nested in a pragmatic cluster-randomised trial of onsite (decentralised) versus hub-and-spoke (centralised) testing for tuberculosis with Xpert MTB/RIF Ultra (Xpert) in 20 community health centres in Uganda. We collected empirical data on the cost of the XPEL-TB strategy (decentralised Xpert testing, workflow redesign, and performance feedback) and routine tuberculosis testing (onsite smear microscopy with

specimen transport for centralised Xpert testing) from the health system perspective. Time-and-motion studies were performed to estimate activity-based service costs. Cost-effectiveness was assessed as the incremental cost (2019 US\$) per tuberculosis diagnosis and per 14-day treatment initiation. **Findings:** The XPEL-TB study ran from Oct 22, 2018, to March 1, 2020. Effectiveness and cost-effectiveness outcomes were assessed from Dec 1, 2018, to Nov 30, 2019 and included 4867 women and 3139 men. On a per-test basis, the cost of decentralised (\$20-46, range \$17-85-25-72) and centralised (\$18-20, range \$16-58-24-25) Xpert testing was similar. However, decentralised testing resulted in more patients receiving appropriate Xpert testing, so the per-patient cost of decentralised testing was higher: \$20-28 (range \$17-68-25-48) versus \$9-59 (range \$7-62-14-34). The XPEL-TB strategy was estimated to cost \$1332 (95% uncertainty range \$763-5558) per incremental tuberculosis diagnosis and \$687 (\$501-1207) per incremental patient initiating tuberculosis treatment within 14 days. Cost-effectiveness was reduced in sites performing fewer than 150-250 tests annually. **Interpretation:** The XPEL-TB strategy facilitated higher rates of Xpert testing for tuberculosis at a similar per-test cost and modest incremental cost per tuberculosis diagnosis and treatment initiation. Decentralised Xpert testing, with appropriate implementation supports, should be scaled up to clinics with sufficient testing volume to support a single-module device. **Funding:** The National Heart, Lung, and Blood Institute.

Reactive Eccrine Syringofibroadenoma (ESFA) in Association With a Merkel Cell Carcinoma Excision Scar.

Salah HT, Czelusta AJ, Sanchez RL.

Am J Dermatopathol.

01-02-2023

<https://pubmed.ncbi.nlm.nih.gov/36669080/>

Transcription Factor HES-1: How Is the Expression of This Transcriptional Factor in Paucibacillary Leprosy Patients?

Serrano-Coll H, Ospina-Gómez JP, Salamanca C, Restrepo L, Berbeo K, Olarte G, Cardona-Castro N.

Am J Dermatopathol.

01-02-2023

<https://pubmed.ncbi.nlm.nih.gov/36669073/>

Introduction: Leprosy is an ancient and chronic infectious disease caused by 2 mycobacteria (*Mycobacterium leprae* and *Mycobacterium lepromatosis*). Recently, our research group observed that HES-1, an innate cellular component of the Notch signaling pathway, is related to the pathogenesis of leprosy. Therefore, it could be helpful in its detection. **Objective:** To determine the expression of HES-1 in the skin of patients with paucibacillary (PB) leprosy. **Methods:** A cross-sectional, descriptive, observational study was conducted. Forty-five skin samples from patients with leprosy were evaluated (30 samples from MB leprosy and 15 from PB leprosy) using immunohistochemistry of HES-1 and S-100. **Results:** PB

leprosy biopsies revealed a reduction of HES-1 in 66.7% of the epidermis, 80% of the eccrine glands, and 62.5% of the hair follicles of these patients, with statistical differences in the control group ($P < 0.0001$). Besides, HES-1 showed similar utility to S-100 immunostaining in detecting the MB and PB leprosy. **Conclusions:** HES-1 is a transcriptional factor also reduced in PB patients' epidermis and skin appendages. Finally, our data show that HES-1 could be a biomarker in diagnosing PB and MB leprosy.

Meaningful Engagement of Persons Affected by Leprosy in Research: An Exploration of Its Interpretation, Barriers, and Opportunities.

de Groot L, van 't Noordende AT, Duck M, Oraga J, Rai SS, Peters RMH, Veldhuijzen N.

Trop Med Infect Dis.

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668959/>

Nanoscale Topical Pharmacotherapy in Management of Psoriasis: Contemporary Research and Scope.

Ahmad MZ, Mohammed AA, Algahtani MS, Mishra A, Ahmad J.

J Funct Biomater.

29-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36662067/>

Identification of potential inhibitor molecule against MabA protein of *Mycobacterium leprae* by integrated in silico approach.

Khan S, Punnoose K, Bishara NZA, Ali R, Khan S, Ahmad S, Marouf HA, Mirza S, Ishrat R, Haque S.

J Biomol Struct Dyn.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36661253/>

Changes in plasma levels of endocrine hormones in lepromatous leprosy patients.

Dabi YT, Degechisa ST, Bobosha K, Wassie L.

IJID Reg.

10-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36660103/>

Background: Leprosy affects various endocrine glands and causes disorders in internal organs in addition to the skin and peripheral nerves. These disorders are often silent and remain undiagnosed or underreported. In particular, patterns of hormone changes during leprosy, especially in lepromatous leprosy (LL) patients, are often associated with dysregulation of different endocrine and sex hormones. The aim of this study was to assess changes in four endocrine hormones - namely cortisol, dehydroepiandrosterone (DHEA), growth hormone (GH), and leptin - among LL patients compared with apparently healthy controls.

Method: In total, 80 plasma samples were systematically retrieved from a biorepository at the Armauer Hansen Research Institute (AHRI), based on quality, adequacy of sample volume, and appropriateness of linked clinical and sociodemographic data. Forty of the samples were obtained from LL patients (cases) and the remaining 40 from apparently healthy controls. Enzyme-linked immunosorbent assay (ELISA) was used to quantify levels of DHEA, cortisol, GH, and leptin hormones in the plasma samples. Data were analyzed using non-parametric statistics and the Mann-Whitney U-test (GraphPad Prism version 7.01). A p -value < 0.05 was considered statistically significant.

Results: Plasma levels of cortisol concentration were significantly higher in LL cases (median = 111.4 ng/ml, range = 20.54-525.7) compared with healthy controls (median = 51.98 ng/ml, range = 3.805-328.4) ($p = 0.003$). Levels of GH and leptin were significantly lower in LL cases compared with healthy controls (median values for GH = 1.01 μ U/ml, range = 0.4625-86.82 and 2 μ U/ml, range = 0.5838-63.36, respectively ($p = 0.022$); median values for leptin = 891 pg/ml, range = 728.4-21816 and 5147 pg/ml, range = 730.4-52747, respectively ($p < 0.0001$)). There was an apparent reduction in the plasma levels of DHEA among LL cases compared with healthy controls ($p = 0.297$), although this difference was not statistically significant.

Conclusion: Alterations in levels of endocrine hormones seen in LL patients reflect clinical and immunological conditions during lepromatous leprosy. However, large-scale studies are warranted to determine how leprosy causes such alterations in hormones and the interplay between endocrine hormones and the immune system during leprosy disease.

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

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

PLoS One.

01-01-2023 Jan 1

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

A-waves are associated with neuropathic pain in leprosy.

Garbino JA, Kirchner DR, França MC Jr.

Muscle Nerve.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36420641/>

Trypanosomes (trypanosomiasis et maladie de Chagas)

Genomic surveillance: a potential shortcut for effective Chagas disease management.

de Azevedo SLC, Catanho M, Guimarães ACR, Galvão TC.
Mem Inst Oswaldo Cruz.

30-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36700581/>

Chagas disease is an enduring public health issue in many Latin American countries, receiving insufficient investment in research and development. Strategies for disease control and management currently lack efficient pharmaceuticals, commercial diagnostic kits with improved sensitivity, and vaccines. Genetic heterogeneity of *Trypanosoma cruzi* is a key aspect for novel drug design since pharmacological technologies rely on the degree of conservation of parasite target proteins. Therefore, there is a need to expand the knowledge regarding parasite genetics which, if fulfilled, could leverage Chagas disease research and development, and improve disease control strategies. The growing capacity of whole-genome sequencing technology and its adoption as disease surveillance routine may be key for solving this long-lasting problem.

Chemical Optimization of CBL0137 for Human African Trypanosomiasis Lead Drug Discovery.

Singh B, Sharma A, Gunaganti N, Rivers M, Gadekar PK, Greene B, Chichioco M, Sanz-Rodriguez CE, Fu C, LeBlanc C, Burchfield E, Sharif N, Hoffman B, Kumar G, Purmal A, Mensa-Wilmot K, Pollastri MP.

J Med Chem.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695630/>

Delayed Activation of T Cells at the Site of Infection Facilitates the Establishment of *Trypanosoma cruzi* in Both Naive and Immune Hosts.

Padilla AM, Rosenberg C, Cook P, Sanchez-Valdez F, McElhannon C, Tarleton RL.

mSphere.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695605/>

Effectiveness of fluralaner treatment regimens for the control of canine Chagas disease: A mathematical modeling study.

Fiatsonu E, Busselman RE, Hamer GL, Hamer SA, Ndeffo-Mbah ML.

PLoS Negl Trop Dis.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36693084/>

Background: Canine Chagas disease is caused by the protozoan parasite *Trypanosoma cruzi* and transmitted by insect triatomine vectors known as kissing bugs. The agent can cause cardiac damage and long-term heart disease and death in humans, dogs, and other mammals. In laboratory settings, treatment of dogs with systemic insecticides has been shown to be highly efficacious at killing triatomines that feed on treated dogs. **Method:** We developed compartmental vector-host models of *T. cruzi* transmission between the triatomine and dog population accounting for the impact of seasonality and triatomine migration on disease transmission dynamics. We considered a single vector-host model without seasonality, and model with seasonality, and a spatially coupled model. We used the models to evaluate the effectiveness of the insecticide fluralaner with different durations of treatment regimens for reducing *T. cruzi* infection in different transmission settings. **Results:** In low and medium transmission settings, our model showed a marginal difference between the 3-month and 6-month regimens for reducing *T. cruzi* infection among dogs. The difference increases in the presence of seasonality and triatomine migration from a sylvatic transmission setting. In high transmission settings, the 3-month regimen was substantially more effective in reducing *T. cruzi* infections in dogs than the other regimens. Our model showed that increased migration rate reduces fluralaner effectiveness in all treatment regimens, but the relative reduction in effectiveness is minimal during the first years of treatment. However, if an additional 10% or more of triatomines killed by dog treatment were eaten by dogs, treatment could increase *T. cruzi* infections in the dog population at least during the first year of treatment. **Conclusion:** Our analysis shows that treating all peridomestic dogs every three to six months for at least five years could be an effective measure to reduce *T. cruzi* infections in dogs and triatomines in peridomestic transmission settings. However, further studies at the local scale are needed to better understand the potential impact of routine use of fluralaner treatment on increasing dogs' consumption of dead triatomines.

Investigating the lack of translation from cruzain inhibition to *Trypanosoma cruzi* activity with machine learning and chemical space analyses.

Lameiro RF, Montanari CA.

ChemMedChem.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36692246/>

"Mi Casa, Tu Casa": the coati nest as a hub of *Trypanosoma cruzi* transmission in the southern Pantanal biome revealed by molecular blood meal source identification in triatomines.

Pessanha TS, Herrera HM, Jansen AM, Iñiguez AM.

Parasit Vectors.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691054/>

Background: The study of the ecology of *Trypanosoma cruzi* is challenging due to its extreme adaptive plasticity, resulting in the parasitism of hundreds of mammal species and dozens of triatomine species. The genetic analysis of blood meal sources (BMS) from the triatomine vector is an accurate and practical approach for gathering information on which wild mammal species participate in a local transmission network. South American coatis, *Nasua nasua*, act as important reservoir host species of *T. cruzi* in the Pantanal biome because of their high rate of infection and elevated parasitemia, with the main discrete typing unit (DTU) lineages (TcI and TcII). Moreover, the carnivore coati is the only mammal species to build high arboreal nests for breeding and resting that can be shared by various vertebrate and invertebrate species. Herein, we applied the sensitive and specific methodology of DNA barcoding and molecular cloning to study triatomines found in a coati nest to access the diversity of mammal species that explore this structure, and therefore, may be involved in the parasite transmission network. **Methods:** Twenty-three *Triatoma sordida* were collected in one coati's nest in the subregion of Nhecolândia, Pantanal. The DNA isolated from the gut of insects was subjected to BMS detection by PCR using universal primers that flank variable regions of the cytochrome b (cytb) and 12S rDNA mitochondrial genes from vertebrates. The *Trypanosoma* spp. diagnosis and DTU genotyping were based on an 18S rDNA molecular marker and also using new cytb gene primers designed in this study. Phylogenetic analyses and chord diagrams were constructed to visualize BMS haplotypes, DTU lineages detected on vectors, and their interconnections. **Results:** Twenty of 23 triatomines analyzed were PCR-positive (86.95%) showing lineages *T. cruzi* DTU TcI (n = 2), TcII (n = 6), and a predominance of TcI/TcII (n = 12) mixed infection. Intra-DTU diversity was observed mainly from different TcI haplotypes. Genetic analyses revealed that the southern anteater, *Tamandua tetradactyla*, was the unique species detected as the BMS of triatomines collected from the coati's nest. At least three different individuals of *T. tetradactyla* served as BMS of 21/23 bugs studied, as indicated by the cytb and 12S rDNA haplotypes identified. **Conclusions:** The identification of multiple BMS, and importantly, different individuals of the same species, was achieved by the methodology applied. The study demonstrated that the southern anteaters can occupy the South American coati's nest, serving as the BMS of *T. sordida* specimens. Since anteaters have an individualist nonsocial behavior, the three individuals detected as BMS stayed at the coati's nest at different times, which added a temporal character to BMS detection. The TcI and TcII infection, and significantly, a predominance of TcI/TcII mixed infection profile with different TcI and TcII haplotypes was observed, due to the discriminatory capacity of the methodology applied. *Tamandua tetradactyla*, a host which has been little studied, may have an important role in the *T. cruzi* transmission in that Pantanal subregion. The data from the present study indicate the sharing of coatis' nests by other mammal species, expanding the possibilities for *T. cruzi* transmission in the canopy strata. We propose that coatis' nests can act as the true hubs of the *T. cruzi* transmission web in Pantanal, instead of the coatis themselves, as previously suggested.

In silico investigation of cytochrome bc1 molecular inhibition mechanism against *Trypanosoma cruzi*.

Muscat S, Grasso G, Scapozza L, Danani A.

PLoS Negl Trop Dis.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36689459/>

Chagas' disease is a neglected tropical disease caused by the kinetoplastid protozoan *Trypanosoma cruzi*. The only therapies are the nitroheterocyclic chemicals nifurtimox and benznidazole that cause various adverse effects. The need to create safe and effective medications to improve medical care remains critical. The lack of verified *T. cruzi* therapeutic targets hinders medication research for Chagas' disease. In this respect, cytochrome bc1 has been identified as a promising therapeutic target candidate for antibacterial medicines of medical and agricultural interest. Cytochrome bc1 belongs to the mitochondrial electron transport chain and transfers electrons from ubiquinol to cytochrome c1 by the action of two catalytic sites named Qi and Qo. The two binding sites are highly selective, and specific inhibitors exist for each site. Recent studies identified the Qi site of the cytochrome bc1 as a promising drug target against *T. cruzi*. However, a lack of knowledge of the drug mechanism of action unfortunately hinders the development of new therapies. In this context, knowing the cause of binding site selectivity and the mechanism of action of inhibitors and substrates is crucial for drug discovery and optimization processes. In this paper, we provide a detailed computational investigation of the Qi site of *T. cruzi* cytochrome b to shed light on the molecular mechanism of action of known inhibitors and substrates. Our study emphasizes the action of inhibitors at the Qi site on a highly unstructured portion of cytochrome b that could be related to the biological function of the electron transport chain complex.

Home-based exercise program in the indeterminate form of Chagas disease (PEDI-CHAGAS study): A study protocol for a randomized clinical trial.

Mediano MFF, Ribeiro LG, Silva RS, Xavier IGG, Vieira MC, Gonçalves TR, Paravidino VB, Borges JP, Rodrigues Junior LF, Costa HS, Reis MS, Liporagi-Lopes LC, Martinez-Amezcu P, Silva PS, Sperandio Da Silva GM, Sousa AS, Holanda MT, Veloso HH, Carneiro FM, Mazzoli-Rocha F, Costa AR, Saraiva RM, Mendes FSNS, Sengen LHC, Hasslocher-Moreno AM.

Front Med (Lausanne).

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36687410/>

African animal trypanocide resistance: A systematic review and meta-analysis.

Kasozi KI, MacLeod ET, Welburn SC.

Front Vet Sci.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36686196/>

Background: African animal trypanocide resistance (AATr) continues to undermine global efforts to eliminate the

transmission of African trypanosomiasis in endemic communities. The continued lack of new trypanocides has precipitated drug misuse and overuse, thus contributing to the development of the AATr phenotype. In this study, we investigated the threat associated with AATr by using the major globally available chemotherapeutic agents. **Methods:** A total of seven electronic databases were screened for an article on trypanocide resistance in AATr by using keywords on preclinical and clinical trials with the number of animals with treatment relapse, days taken to relapse, and resistant gene markers using the PRISMA checklist. Data were cleaned using the SR deduplicator and covidence and analyzed using Cochrane RevMan®. Dichotomous outputs were presented using risk ratio (RR), while continuous data were presented using the standardized mean difference (SMD) at a 95% confidence interval. **Results:** A total of eight publications in which diminazene aceturate (DA), isometamidium chloride (ISM), and homidium chloride/bromide (HB) were identified as the major trypanocides were used. In all preclinical studies, the development of resistance was in the order of HB > ISM > DA. DA vs. ISM (SMD = 0.15, 95% CI: -0.54, 0.83; $I^2 = 46\%$, $P = 0.05$), DA vs. HB (SMD = 0.96, 95% CI: 0.47, 1.45; $I^2 = 0\%$, $P = 0.86$), and HB vs. ISM (SMD = -0.41, 95% CI: -0.96, 0.14; $I^2 = 5\%$, $P = 0.38$) showed multiple cross-resistance. Clinical studies also showed evidence of multi-drug resistance on DA and ISM (RR = 1.01, 95% CI: 0.71-1.43; $I^2 = 46\%$, $P = 0.16$). To address resistance, most preclinical studies increased the dosage and the treatment time, and this failed to improve the patient's prognosis. Major markers of resistance explored include *TbAT1*, P1/P2 transporters, folate transporters, such as F-I, F-II, F-III, and polyamine biosynthesis inhibitors. In addition, immunosuppressed hosts favor the development of AATr. **Conclusion:** AATr is a threat that requires a shift in the current disease control strategies in most developing nations due to inter-species transmission. Multi-drug cross-resistance against the only accessible trypanocides is a major public health risk, justifying the need to revise the policy in developing countries to promote control of African trypanosomiasis

Trypanosoma cruzi-specific CD8+ T cells and other immunological hallmarks in chronic Chagas cardiomyopathy: Two decades of research.

Puerta CJ, Cuellar A, Lasso P, Mateus J, Gonzalez JM.

Front Cell Infect Microbiol.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683674/>

Solid-state properties of Nifurtimox. Preparation, analytical characterization, and stability of an amorphous phase.

Moroni AB, Perez Mayoral E, Lionello DF, Vega DR, Kaufman TS, Calvo NL.

Eur J Pharm Biopharm.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36681284/>

Identification of Aryl Polyamines Derivatives as Anti-*Trypanosoma cruzi*

Agents Targeting Iron Superoxide Dismutase.

Martín-Escolano R, Molina-Carreño D, Martín-Escolano J, Clares MP, Galiana-Roselló C, González-García J, Cirauqui N, Llinares JM, Rosales MJ, García-España E, Marín C.

Pharmaceutics.

31-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678771/>

Chagas disease (CD) is a tropical and potentially fatal infection caused by *Trypanosoma cruzi*. Although CD was limited to Latin America as a silent disease, CD has become widespread as a result of globalization. Currently, 6-8 million people are infected worldwide, and no effective treatment is available. Here, we identify new effective agents against *T. cruzi*. In short, 16 aryl polyamines were screened in vitro against different *T. cruzi* strains, and lead compounds were evaluated in vivo after oral administration in both the acute and chronic infections. The mode of action was also evaluated at the energetic level, and its high activity profile could be ascribed to a mitochondria-dependent bioenergetic collapse and redox stress by inhibition of the Fe-SOD enzyme. We present compound **15** as a potential compound that provides a step forward for the development of new agents to combat CD.

Preclinical Studies and Drug Combination of Low-Cost Molecules for Chagas Disease.

Aguilera E, Sánchez C, Cruces ME, Dávila B, Minini L, Mosquillo F, Pérez-Díaz L, Serna E, Torres S, Schini A, Sanabria L, Vera de Bilbao NI, Yaluff G, Zolessi FR, Ceilas LF, Cerecetto H, Alvarez G.

Pharmaceuticals (Basel).

23-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678516/>

Role of a 49 kDa Trypanosoma cruzi Mucin-Associated Surface Protein (MASP49) during the Infection Process and Identification of a Mammalian Cell Surface Receptor.

Espinoza B, Martínez I, Martínez-Velasco ML, Rodríguez-Sosa M, González-Canto A, Vázquez-Mendoza A, Terrazas LI.

Pathogens.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678452/>

New Insights into the Role of the Trypanosoma cruzi Aldo-Keto Reductase TcAKR.

Díaz-Viraqué F, Chiribao ML, Paes-Vieira L, Machado MR, Faral-Tello P, Tomasina R, Trochine A, Robello C.

Pathogens.

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678433/>

Old Methods, New Insights: Reviewing Concepts on the Ecology of Trypanosomatids and Bodo sp. by Improving Conventional Diagnostic Tools.

Alves FM, Lisboa CV, Dario MA, Novaes RLM, Tiepolo LM, Moratelli R, Jansen AM.

Pathogens.

02-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678419/>

Evaluation of the Chagas VirClia® and Chagas TESA VirClia® for the Diagnosis of Trypanosoma cruzi Infection.

García-Bermejo I, Arana DM, Zaragoza Vargas G, Carrasco Fernández B, García E, Nieto J, Flores-Chávez MD.

Pathogens.

28-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678398/>

Modulation of Virulence Factors during Trypanosoma cruzi Differentiation.

Oliveira C, Holetz FB, Alves LR, Ávila AR.

Pathogens.

25-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678380/>

The Activity of Red Nigerian Propolis and Some of Its Components against Trypanosoma brucei and Trypanosoma congolense.

Alenezi SS, Alenezi ND, Ebiloma GU, Natto MJ, Ungogo MA, Igoli JO, Ferro VA, Gray AI, Fearnley J, Koning HP, Watson DG.

Molecules.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677679/>

Propolis is a resin that is gathered by bees from exudates produced by various plants. Its exact chemical composition depends on the plants available near the hive. Bees use propolis to coat the surfaces of the hive, where it acts as an anti-infective. Regardless of the chemical composition of propolis, it is always anti-protozoal, probably because protozoan parasites, particularly *Lotmarium passim*, are widespread in bee populations. The protozoa *Trypanosoma brucei* and *T. congolense* cause disease in humans and/or animals. The existing drugs for treating these diseases are old and resistance is an increasingly severe problem. The many types of propolis present a rich source of anti-trypanosomal compounds-from a material gathered by bees in an environmentally friendly way. In the current work, red Nigerian propolis from Rivers State, Nigeria was tested against *T. brucei* and *T. congolense* and found to be highly active (EC₅₀ 1.66 and 4.00 µg/mL, respectively). Four isoflavonoids, vestitol, neovestitol, 7-methylvestitol and medicarpin, were isolated from the propolis. The isolated compounds were also tested against *T. brucei* and *T. congolense*, and vestitol displayed the highest activity at

3.86 and 4.36 µg/mL, respectively. Activities against drug-resistant forms of *T. brucei* and *T. congolense* were similar to those against wild type.

First Phytochemical Profiling and In-Vitro Antiprotozoal Activity of Essential Oil and Extract of *Plagiochila porelloides*.

Pannequin A, Quetin-Leclercq J, Costa J, Tintaru A, Muselli A.

Molecules.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677674/>

A Questionnaire Integrated with the Digital Medical Record Improved the Coverage of a Control Program for Congenital Chagas Disease in Tuscany, Italy.

Barbiero A, Mazzi M, Mantella A, Trotta M, Rossolini GM, Antonelli A, Bordonaro P, Colao MG, Speciale AR, Di Benedetto T, Di Tommaso M, Mantengoli E, Petraglia F, Galli L, Pezzati M, Dani C, Caldes Pinilla MJ, Berni C, Dannaoui B, Albajar Viñas P, Bartoloni A, Zammarchi L.

Microorganisms.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677446/>

Antiparasitic Activity of *Hippeastrum* Species and Synergistic Interaction between Montanine and Benznidazole against *Trypanosoma cruzi*.

Piñeiro M, Ortiz JE, Spina Zapata RM, Barrera PA, Sosa MA, Roitman G, Bastida J, Feresin GE.

Microorganisms.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677436/>

Background: *Hippeastrum* species have a wide range of biological properties. In Argentina, this genus comprises ten widely distributed species. **Purpose:** To evaluate the antiparasitic and anticholinesterase activities and chemical profiles of seven Argentinean *Hippeastrum* species and determine the synergism between the major isolated alkaloid-montanine and benznidazole in anti-*Trypanosoma cruzi* activity. **Methods:** The antiparasitic activity was evaluated through antiproliferative and viability assays against *T. cruzi* epimastigotes. Synergism assays were performed using the Chou-Talalay method. AChE and BuChE inhibitory activities were also assessed. The alkaloid composition was obtained using GC-MS analysis. **Results:** All extracts showed strong growth inhibition of *T. cruzi* epimastigote proliferation. The extracts from *H. aglaiae*, *H. aulicum*, and *H. hybrid* stand out for their potent and total growth inhibition, which was comparable to benznidazole. The *H. reticulatum* extract showed strong Acetylcholinesterase (AChE) inhibitory activities, while five species showed moderate Butyrylcholinesterase (BuChE) inhibition. Fifteen alkaloids were identified by means of GC-MS. Regarding the synergism assessment, the highest synergistic effect was obtained from the combination of montanine and

benznidazole. **Conclusion:** *Hippeastrum* species bulb extracts from Argentina were shown to be a good source of antiparasitic alkaloids and cholinesterase inhibitors. The synergism between montanine and benznidazole emerges as a potential combination for future studies to treat Chagas disease.

Identification of Potential Leishmania N-Myristoyltransferase Inhibitors from *Withania somnifera* (L.) Dunal: A Molecular Docking and Molecular Dynamics Investigation.

Orabi MAA, Alshahrani MM, Sayed AM, Abouelela ME, Shaaban KA, Abdel-Sattar ES.

Metabolites.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677018/>

Antimicrobial Spectrum of Activity and Mechanism of Action of Linear Alpha-Helical Peptides Inspired by Shrimp Anti-Lipopolysaccharide Factors.

Matos GM, Garcia-Teodoro B, Martins CP, Schmitt P, Guzmán F, de Freitas ACO, Stoco PH, Ferreira FA, Stadnik MJ, Robl D, Perazzolo LM, Rosa RD.

Biomolecules.

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36671535/>

Antiparasitic Activities of Compounds Isolated from *Aspergillus fumigatus* Strain Discovered in Northcentral Nigeria.

Diyaolu OA, Preet G, Fagbemi AA, Annang F, Pérez-Moreno G, Bosch-Navarrete C, Adebisi OO, Oluwabusola ET, Milne BF, Jaspars M, Ebel R.

Antibiotics (Basel).

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36671310/>

A Four-Year Survey of Hemoparasites from Nocturnal Raptors (Strigiformes) Confirms a Relation between Leucocytozoon and Low Hematocrit and Body Condition Scores of Parasitized Birds.

Martín-Maldonado B, Mencía-Gutiérrez A, Andreu-Vázquez C, Fernández R, Pastor-Tiburón N, Alvarado A, Carrero A, Fernández-Novo A, Esperón F, González F.

Vet Sci.

12-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36669055/>

Most hemoparasites hosted by wild birds appear to be harmless, but most of the blood parasite studies in avian wildlife are mainly focused on passerines or migratory species. This study aimed to assess the occurrence of blood parasites in nocturnal raptors (Strigiformes order) and their effect on hematological parameters. A total of

134 blood samples were collected during a four-year period for hematological analysis and hemoparasite detection and quantification by microscopical examination of the samples. Overall, the occurrence of hemoparasites was 35.1%, with *Leucocytozoon* being the most frequently detected (32.1%), followed by *Haemoproteus* (11.2%), *Trypanosoma* and *Plasmodium* (2.2% each). Among the different bird species, the Eurasian eagle-owl (*Bubo bubo*) showed the highest blood parasite positivity (94.7%). In barn owls, the positive birds displayed a lower hematocrit measurement and body condition score than the non-parasitized ones ($p = 0.007$ and $p = 0.005$, respectively), especially those parasitized by *Leucocytozoon*. Moreover, the analysis of the magnitude of this association revealed that the presence of hemoparasites is five times more frequent in barn owls with a 2/5 body condition score. Despite the host-parasite coevolution in Strigiformes, our results show a correlation between the presence of hemoparasites and some health parameters, including blood parameters.

Chagas Disease: Seroprevalence and Associated Factors in Indigenous Communities of the Southern Limit of Argentine Chaco.

Colussi C, Nepote M, Chiaraviglio R, Mendicino D.

Trop Med Infect Dis.

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668971/>

Macrophages Mediate Healing Properties of Fenofibrate in Experimental Chagasic Cardiomyopathy.

Cevey ÁC, Pieralisi AV, Donato M, Rada J, Gelpi RJ, Mirkin GA, Goren NB, Penas FN.

ACS Infect Dis.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36661566/>

Green microalgae as a potential source of trypanocide compounds.

Júnior JNDS, da Silva AC, Oliveira KKDS, Moreira LR, Caires SFFDS, da Silva AJ, Moura YAS, Marques DAV, Bezerra RP, de Lorena VMB, Porto ALF.

Nat Prod Res.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36661179/>

Molecular and phylogenetic analysis of a type K1 strain *Trypanosoma evansi* isolate from Nigerian cattle: An evaluation of the therapeutic effects of compounds from *Brassica oleracea* on the histopathology of infected wistar rats.

Moh KO, Luka SA, Ndams IS, Lawal IA, Sani D, Obeta SS, Oderinde GP, Dingwoke EJ, Adamude FA, Ubhenin AE, Umar S.

Biochem Biophys Rep.

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36660764/>

Background: Understanding the pathogenesis of animal trypanosomiasis can be improved by studying the genetics of bovine trypanosomes. Pathogenic animal trypanosomes are a major impediment to livestock production, with negative economic consequences spreading beyond Sub-Saharan Africa to subtropical regions of Northern Africa, Southeast Asia, and Central and South America. An atypical K1 strain of *Trypanosoma evansi* (*T. evansi*) isolates from infected cattle in Nigeria was analyzed. The therapeutic effect of phenolic-rich compounds on the histopathology of wistar rats infected with the K1 strain was studied. **Methods:** The K1 strain *T. evansi* was analyzed molecularly using PCR and sequence analysis of the Spacer-1 ribosomal RNA gene. To assess the evolutionary relationship, this was phylogenetically compared to other species studied in different parts of the world. Thirty adult male wistar rats were divided into six groups of five each. Animals in group A served as the standard control (not infected). Group B animals were infected but not treated. Group C animals were infected and given 3.5 mg/kg body weight of the standard drug diminazene aceturate. Animals in groups D, E, and F were infected and treated with phenolic-rich compounds isolated from *Brassica oleracea* (*B. oleracea*) at concentrations of 100, 200, and 400 mg/kg body weight, respectively. The phytochemicals were extracted using standard analytical procedures, and GCMS analysis revealed the presence of phenolic-rich compounds. The animals were given 0.2 mg/ml trypanosome intraperitoneally, diluted with normal saline. The vital organs of the animals were harvested and histologically examined. **Results:** The nested PCR amplification of the trypanosome's ITS-1 region revealed a DNA amplicon of 627 base pairs. The rRNA nucleotide sequence was deposited in GenBank under the accession number MN462960. Basic Local Alignment search of the obtained ITS-1 rRNA sequences revealed that the K1 strain trypanosome and other strains from different regions have an evolutionary relationship. The phenolic-rich compounds had protective effects on the organs of infected animals, resulting in a decrease in parasitemia levels. They have anti-trypanosome activities at the minimum and maximum effective doses of 200 and 400 mg/kg body weight, respectively. **Conclusions:** The K1 strain *T. evansi* was isolated from naturally infected cattle in this study. The results indicate that phenolic-rich compounds have anti trypanosoma activities capable of healing organ damage caused by trypanosomiasis.

The Pathogenesis of African Trypanosomiasis.

Pays E, Radwanska M, Magez S.

Annu Rev Pathol.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36055769/>

Leishmaniose

Intracellular IFN- γ and IL-4 levels of CD4 + and CD8 + T cells in the peripheral

blood of naturally infected (*Leishmania infantum*) symptomatic dogs before and following a 4-week treatment with miltefosine and allopurinol: a double-blinded, controlled and cross-sectional study.

Matralis DT, Koutinas AF, Papadogiannaki IE, Papadopoulos EG, Papadogiannakis EI.

Acta Vet Scand.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36703227/>

Background: Canine leishmaniosis (CanL) is a systemic disease caused by the protozoan parasite *Leishmania infantum* with a wide spectrum of clinical signs, with cutaneous, ocular, renal and lymphoreactive conditions prevailing in the clinical setting. The immune system plays a pivotal role in the evolution of *Leishmania* infection and its response to antileishmanial treatment. Cytokines are important immune response mediators that are released by activated lymphocytes and less so by other immunocytes. In dogs with leishmaniosis, IFN- γ and IL-4 have been recognized as the main activators of cellular and humoral immunity, respectively. The objective of this study was to investigate intracellular IL-4 and IFN- γ expression by CD4 + and CD8 + lymphocytes in the peripheral blood of symptomatic dogs before and after combined antileishmanial treatment with miltefosine and allopurinol.

Results: Postantileishmanial treatment CD4 + IL-4 + and CD8 + IL-4 + cell counts were significantly decreased, although no similar changes were observed in the comparisons made between the pre- and posttreatment CD4 + IFN- γ + and CD8 + IFN- γ + counts and ratios.

Conclusion: The findings indicate that IL-4 production by T cells may facilitate the symptomatic phase of CanL, whereas IFN- γ production by CD4 + and CD8 + cells may indicate its negligible role in the evolution of natural CanL and perhaps the equivocal positive influence of antileishmanial treatment.

***Leishmania tarentolae*: a vaccine platform to target dendritic cells and a surrogate pathogen for next generation vaccine research in leishmaniasis and viral infections.**

Bandi C, Mendoza-Roldan JA, Otranto D, Alvaro A, Louzada-Flores VN, Pajoro M, Varotto-Bocazzi I, Brilli M, Manenti A, Montomoli E, Zuccotti G, Epis S.

Parasit Vectors.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36703216/>

Parasites of the genus *Leishmania* are unusual unicellular microorganisms in that they are characterized by the capability to subvert in their favor the immune response of mammalian phagocytes, including dendritic cells. Thus, in overt leishmaniasis, dendritic cells and macrophages are converted into a niche for *Leishmania* spp. in which the parasite, rather than being inactivated and disassembled, survives and replicates. In addition, *Leishmania* parasites hitchhike onto phagocytic cells, exploiting them as a mode

of transport to lymphoid tissues where other phagocytic cells are potentially amenable to parasite colonization. This propensity of *Leishmania* spp. to target dendritic cells has led some researchers to consider the possibility that the non-pathogenic, reptile-associated *Leishmania tarentolae* could be exploited as a vaccine platform and vehicle for the production of antigens from different viruses and for the delivery of the antigens to dendritic cells and lymph nodes. In addition, as *L. tarentolae* can also be regarded as a surrogate of pathogenic *Leishmania* parasites, this parasite of reptiles could possibly be developed into a vaccine against human and canine leishmaniasis, exploiting its immunological cross-reactivity with other *Leishmania* species, or, after its engineering, for the expression of antigens from pathogenic species. In this article we review published studies on the use of *L. tarentolae* as a vaccine platform and vehicle, mainly in the areas of leishmaniasis and viral infections. In addition, a short summary of available knowledge on the biology of *L. tarentolae* is presented, together with information on the use of this microorganism as a micro-factory to produce antigens suitable for the serodiagnosis of viral and parasitic infections.

Andrographolide-Soya-L- α -Phosphatidyl Choline Complex Augmented Solubility and Drug Delivery in *Leishmania donovani*, a Causative Agent for Cutaneous and Visceral Leishmaniasis.

Pingle P, Mourya A, Namdeo M, Babu KC, Veerabomma H, Maurya R, Singh PK, Mehra NK, Srivastava S, Madan J.

AAPS PharmSciTech.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36702974/>

Unraveling the role of natural killer cells in leishmaniasis.

Alizadeh Z, Omidnia P, Altalbawy FMA, Gabr GA, Obaid RF, Rostami N, Aslani S, Heidari A, Mohammadi H.

Int Immunopharmacol.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36700775/>

NK cells are known as frontline responders that are efficient in combating several maladies as well as leishmaniasis caused by *Leishmania* spp. As such they are being investigated to be used for adoptive transfer therapy and vaccine. In spite of the lack of antigen-specific receptors at their surface, NK cells can selectively recognize pathogens, accomplished by the activation of the receptors on the NK cell surface and also as the result of their effector functions. Activation of NK cells can occur through interaction between TLR-2 expressed on NK cells and LPG of *Leishmania* parasites. In addition, NK cell activation can occur by cytokines (e.g., IFN- γ and IL-12) that also lead to producing cytokines and chemokines and lysis of target cells. This review summarizes several evidences that support NK cells activation for controlling leishmaniasis and the potentially lucrative roles of NK cells

during leishmaniasis. Furthermore, we discuss strategies of *Leishmania* parasites in inhibiting NK cell functions. *Leishmania* LPG can utilize TLR2 to evade host-immune responses. Also, *Leishmania* GP63 can directly bind to NK cells and modulates NK cell phenotype. Finally, this review analyzes the potentialities to harness NK cells effectiveness in therapy regimens and vaccinations.

Bioinformatics evaluation of anticancer properties of GP63 protein-derived peptides on MMP2 protein of melanoma cancer.

Sharifi F, Sharifi I, Babaei Z, Alahdin S, Afgar A.

J Pathol Inform.

12-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36700237/>

In vitro anti-Leishmania activity of triclabendazole and its synergic effect with amphotericin B.

Borges BS, Bueno GP, Tomiotto-Pellissier F, Figueiredo FB, Soares Medeiros LC.

Front Cell Infect Microbiol.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699729/>

Introduction: Leishmaniasis is a neglected tropical disease, with approximately 1 million new cases and 30,000 deaths reported every year worldwide. Given the lack of adequate medication for treating leishmaniasis, drug repositioning is essential to save time and money when searching for new therapeutic approaches. This is particularly important given leishmaniasis's status as a neglected disease. Available treatments are still far from being fully effective for treating the different clinical forms of the disease. They are also administered parenterally, making it challenging to ensure complete treatment, and they are extremely toxic, in some cases, causing death. Triclabendazole (TCBZ) is a benzimidazole used to treat fasciolosis in adults and children. It presents a lower toxicity profile than amphotericin B (AmpB) and is administered orally, making it an attractive candidate for treating other parasitoses. The mechanism of action for TCBZ is not yet well understood, although microtubules or polyamines could potentially act as a pharmacological target. TCBZ has already shown antiproliferative activity against *T. cruzi*, *T. brucei*, and *L. infantum*. However, further investigations are still necessary to elucidate the mechanisms of action of TCBZ. **Methods:** Cytotoxicity assay was performed by MTT assay. Cell inhibition (CI) values were obtained according to the equation $CI = (O.D \text{ treatment} \times 100 / O.D. \text{ negative control})$. For infection evaluation, fixed cells were stained with Hoechst and read at Operetta High Content Imaging System (Perkin Elmer). For growth curves, cell culture absorbance was measured daily at 600 nm. For the synergism effect, Fractional Inhibitory Concentrations (FICs) were calculated for the IC50 of the drugs alone or combined. Mitochondrial membrane potential (DYm), cell cycle, and cell death analysis were evaluated by flow cytometry. Reactive oxygen species (ROS) and lipid quantification were also determined by

fluorimetry. Treated parasites morphology and ultrastructure were analyzed by electron microscopy.

Results: The selectivity index (SI = CC50/IC50) of TCBZ was comparable with AmpB in promastigotes and amastigotes of *Leishmania amazonensis*. Evaluation of the cell cycle showed an increase of up to 13% of cells concentrated in S and G2, and morphological analysis with scanning electron microscopy showed a high frequency of dividing cells. The ultrastructural analysis demonstrated large cytoplasmic lipid accumulation, which could suggest alterations in lipid metabolism. Combined administration of TCBZ and AmpB demonstrated a synergistic effect *in vitro* against intracellular amastigote forms with cFICs of 0.25. **Conclusions:** Considering that TCBZ has the advantage of being inexpensive and administered orally, our results suggest that TCBZ, combined with AmpB, is a promising candidate for treating leishmaniasis with reduced toxicity.

Activity of the genus Zanthoxylum against diseases caused by protozoa: A systematic review.

Correa-Barbosa J, Sodré DF, Nascimento PHC, Dolabela MF.

Front Pharmacol.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699053/>

Role of antigen-presenting cells in non-ulcerated skin lesions caused by L. (L.) infantum chagasi.

Sandoval Pacheco CM, Araujo Flores GV, Ferreira AF, Matta VLR, Castro Gomes CM, Sosa-Ochoa WH, Zúñiga C, Silveira FT, Corbett CEP, Laurenti MD.

Parasite Immunol.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695719/>

Overexpression of Iron Super Oxide Dismutases A/B Genes Are Associated with Antimony Resistance of Leishmania tropica Clinical Isolates.

Bahrami A, Mohebbi M, Reisi Nafchi H, Raoofian R, Kazemirad E, Hajjarian H.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694571/>

Plant Bioactive Ingredients in Delivery Systems and Nanocarriers for the Treatment of Leishmaniasis: An Evidence-Based Review.

Alanazi AD, Ben Said M.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694570/>

Background: This study was designed considering the challenges of leishmaniasis treatment and the benefits of carriers of drug delivery systems to review plant bioactive

ingredients in delivery systems and nanocarriers for the treatment of leishmaniasis.

Methods: The methodology of this review investigation followed the 06-PRISMA recommendations. The searches were carried out up to January 30, 2022, in the central English databases SCOPUS, WEB OF SCIENCE, EMBASE, PUBMED, and GOOGLE SCHOLAR using the search terms "ç", "leishmaniasis", "herbal medicines", "drug delivery", "nanocarriers", "herbal compounds", and "secondary metabolites". **Results:** Out of 5731 articles, 19 publications, including 12 *in vivo* (63.15%), 3 *in vitro* (15.8%), and 4 *in vitro/in vivo* (21.1%) up to 2022, fulfilled the criteria presence for argument in the current systematic study. Plant bioactive ingredients were curcumin, betulinic acid, artemisinin, 4-nitrobenzaldehyde thiosemicarbazone, andrographolide, pentalinosterol, ursolic acid, amarogentin, carvacrol, 14-deoxy-11-oxo-andrographolide, quercetin, beta-lapachone, cedrol, 2',6'-dihydroxy-4'-methoxychalcone, and oleanolic acid. **Conclusion:** The high potential of plant bioactive ingredients in delivery systems due to the load on the nanocarrier for the treatment of leishmaniasis through some main mechanisms of action, e.g. changes in the fluidity and the structure of the cell wall, creation of reactive oxygen species (ROS) and mitochondrial dysfunction, inhibition of DNA topoisomerase I enzyme, minimal cytotoxicity, stimulation of cell cycle disruption, stimulation of apoptosis, enhancement of the immune system. However, further investigations, especially in the clinical setting, are required to confirm these findings.

PCR-Based Diagnosis of Leishmania Species in Chronic Granulomatous Dermatitis in Mashhad, Iran.

Nahidi Y, Tayyebi Meibodi N, Ghazvini K, Arabi Moghadam HS, Akhlaghi S, Torabian F.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694566/>

Comparison of Sampling Procedures for the Molecular Diagnosis of Leishmaniases.

Andrade Zampieri R, Ide Aoki J, Müller KE, Jon Shaw J, Maria Floeter-Winter L.

Am J Trop Med Hyg.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36689945/>

Correction: Diversity, distribution and natural Leishmania infection of sand flies from communities along the Interoceanic Highway in the Southeastern Peruvian Amazon.

Valdivia HO, Zorrilla VO, Espada LJ, Perez JG, Razuri HR, Vera H, Fernandez R, Tong C, Gherzi BM, Vasquez GM, Burrus RG, Lescano AG, Montgomery JM.

PLoS Negl Trop Dis.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36689363/>

Comparative transcriptomic analysis of long noncoding RNAs in Leishmania-infected human macrophages.

Fernandes JCR, Gonçalves ANA, Floeter-Winter LM, Nakaya HI, Muxel SM.

Front Genet.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36685903/>

It is well established that infection with *Leishmania* alters the host cell's transcriptome. Since mammalian cells have multiple mechanisms to control gene expression, different molecules, such as noncoding RNAs, can be involved in this process. MicroRNAs have been extensively studied upon *Leishmania* infection, but whether long noncoding RNAs (lncRNAs) are also altered in macrophages is still unexplored. We performed RNA-seq from THP-1-derived macrophages infected with *Leishmania amazonensis* (La), *L. braziliensis* (Lb), and *L. infantum* (Li), investigating a previously unappreciated fraction of macrophage transcriptome. We found that more than 24% of the total annotated transcripts and 30% of differentially expressed (DE) RNAs in *Leishmania*-infected macrophage correspond to lncRNAs. lncRNAs and protein coding RNAs with altered expression are similar among macrophages infected with the *Leishmania* species. Still, some species-specific alterations could occur due to distinct pathophysiology in which *Li* infection led to a more significant number of exclusively DE RNAs. The most represented classes among DE lncRNAs were intergenic and antisense lncRNAs. We also found enrichment for immune response-related pathways in the DE protein coding RNAs, as well as putative targets of the lncRNAs. We performed a coexpression analysis to explore potential cis regulation of coding and antisense noncoding transcripts. We identified that antisense lncRNAs are similarly regulated as its neighbor protein coding genes, such as the BAALC/BAALC-AS1, BAALC/BAALC-AS2, HIF1A/HIF1A-AS1, HIF1A/HIF1A-AS3 and IRF1/IRF1-AS1 pairs, which can occur as a species-specific modulation. These findings are a novelty in the field because, to date, no study has focused on analyzing lncRNAs in *Leishmania*-infected macrophage. Our results suggest that lncRNAs may account for a novel mechanism by which *Leishmania* can control macrophage function. Further research must validate putative lncRNA targets and provide additional prospects in lncRNA function during *Leishmania* infection.

Quercetin nano phytosome: as a novel anti-leishmania and anti-malarial natural product.

Hanif H, Abdollahi V, Javani Jouni F, Nikoukar M, Rahimi Esboei B, Shams E, Vazini H.

J Parasit Dis.

12-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36685738/>

A Case of Feline Leishmaniosis with Panniculitis.

Matralis D, Papadogiannaki I, Gkerdidani E, Patsoula E, Tegos N, Papadogiannakis E.

Case Rep Vet Med.

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36685018/>

Membrane-acting biomimetic peptoids against visceral leishmaniasis.

Kumar V, Lin JS, Molchanova N, Fortkort JA, Reckmann C, Bräse S, Jenssen H, Barron AE, Chugh A.

FEBS Open Bio.

22-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683396/>

Visceral leishmaniasis (VL) is among the most neglected tropical diseases in the world. Drug cell permeability is essential for killing the intracellular residing parasites responsible for VL, making cell-permeating peptides a logical choice to address VL. Unfortunately, the limited biological stability of peptides restricts their usage. Sequence-specific oligo-N-substituted glycines ("peptoids") are a class of peptide mimics that offers an excellent alternative to peptides in terms of ease of synthesis and good biostability. We tested peptoids against the parasite *Leishmania donovani* in both forms, i.e., intracellular amastigotes and promastigotes. N-alkyl hydrophobic chain addition (lipidation) and bromination of oligopeptoids yielded compounds with good anti-leishmanial activity against both forms, showing the promise of these antiparasitic peptoids as potential drug candidates to treat VL.

Effectiveness in vivo and in vitro of Polymeric Nanoparticles as a Drug Release System in the Treatment of Leishmaniasis.

de Carvalho Moreira LMC, de Sousa Silva ABA, de Araújo Medeiros K, Oshiro Júnior JA, Casimiro da Silva DT, de Lima Damasceno BPG.

Curr Med Chem.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683370/>

In vitro evaluation of alkaline lignins as antiparasitic agents and their use as an excipient in the release of benznidazole.

da Cruz Filho IJ, Duarte DMFA, da Conceição Alves de Lima D, Marques DSC, Dos Santos FAB, Alves LC, de Lima Aires A, Nogueira F, do Carmo Alves de Lima M.

Int J Biol Macromol.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682648/>

Synthetic hydrazones: In silico studies and in vitro evaluation of the antileishmania potential.

de Sousa VC, de Cássia Viana Carvalho R, Dos Reis Barcelar KG, de Melo DS, Nunes JM, de Araújo Sousa PS, Rocha JA, Lima CC, de Assis Gonsalves A, Araújo CRM, da Costa MP, da Franca Rodrigues KA, de Moraes Alves MM, de Amorim Carvalho FA.

Toxicol In Vitro.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36681287/>

Bioprospecting and synthesis of strategically designed molecules have been used in the search for drugs that can be in leishmaniasis. Hydrazones (HDZ) are promising compounds with extensive biological activities. The objective of this work was to perform in silico studies of hydrazones 1-5 and to evaluate their antileishmanial, cytotoxic and macrophage immunomodulatory potential in vitro. Hydrazones were subjected to prediction and molecular docking studies. Antileishmanial protocols on promastigotes and amastigotes of *Leishmania amazonensis*, cytotoxicity and macrophage immunomodulatory activity were performed. Hydrazones showed a good pharmacokinetic profile and hydrazone 3 and hydrazone 5 were classified as non-carcinogenic. Hydrazone 5 obtained the best conformation with trypanothione reductase. Hydrazone 1 and hydrazone 3 obtained the best mean inhibitory concentration (IC₅₀) values for promastigotes, 4.4-61.96 µM and 8.0-58.75 µM, respectively. It also showed good activity on intramacrophagic amastigotes, with hydrazone 1 being the most active (IC₅₀ = 6.79 µM) with selectivity index of 56. In cytotoxicity to macrophages hydrazone 3 was the most cytotoxic (CC₅₀ = 256.3 ± 0.04 µM), while hydrazone 4 the least (CC₅₀ = 1055.9 ± 0.03 µM). It can be concluded that the hydrazones revealed important pharmacokinetic and toxicological properties, in addition to antileishmania potential in reducing infection and infectivity in parasitized macrophages.

Monitoring of Insecticide Resistance Mutations and Pathogen Circulation in Sand Flies from Emilia-Romagna, a Leishmaniasis Endemic Region of Northern Italy.

Balaska S, Calzolari M, Grisendi A, Scremin M, Dottori M, Mavridis K, Bellini R, Vontas J.

Viruses.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680189/>

Central and Effector Memory Human CD4+ and CD8+ T Cells during Cutaneous Leishmaniasis and after In Vitro Stimulation with *Leishmania* (Viannia) *braziliensis* Epitopes.

de Oliveira BC, da Silva AA, de Andrade Cavalcante MK, de Brito MEF, de Castro MCAB, de Medeiros VLS, de Freitas E Silva R, Pereira VRA.

Vaccines (Basel).

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36680003/>

Cutaneous Leishmaniasis (CL) is a Neglected Tropical Disease characterized by skin ulcers caused by *Leishmania* spp. protozoans and there is no safe and effective vaccine to reduce its negative consequences. In a previous work by our group, we identified T cell epitopes of *Leishmania* (Viannia) *braziliensis* which stimulated patients' T cells in vitro. In the present work, the peptides were tested as two pools for their ability to rescue memory T cells during natural infection by *Leishmania*. We analyzed the

frequency of central memory (TCM, CD45RA-CD62L+) and effector memory (TEM, CD45RA + CD62L-) cells during active CL and post-treatment. In parallel, we investigated cell proliferation levels and the cytokines produced after stimulation. Interestingly, we observed higher frequencies (%) in CD4+ TEM during CL, and CD8+ TEM and CD8+ TCM during CL and post-treatment. Cell proliferation was increased, and a significant difference in expression was observed on T-bet and ROR γ T. Besides that, IFN- γ , IL-2, and IL-10 were detected in patient samples. Collectively, this dataset suggests that during CL there is an increase in the frequency of TCM and TEM, especially in the CD8 compartment. These results indicate a potentially immunogenic profile of the peptide pools, which can support the development of anti-Leishmania formulations.

Vaccination with Formulation of Nanoparticles Loaded with Leishmania amazonensis Antigens Confers Protection against Experimental Visceral Leishmaniasis in Hamster.

González MAC, Gonçalves AAM, Ottino J, Leite JC, Resende LA, Melo-Júnior OA, Silveira P, Cardoso MS, Fujiwara RT, Bueno LL, Santos RL, Carvalho TF, Garcia GM, Paes PRO, Galdino AS, Chávez-Fumagalli MA, Melo MM, Silveira-Lemos D, Martins-Filho OA, Dutra WO, Mosqueira VCF, Giunchetti RC.

Vaccines (Basel).

02-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36679956/>

Amphotericin B Nano-Assemblies Circumvent Intrinsic Toxicity and Ensure Superior Protection in Experimental Visceral Leishmaniasis with Feeble Toxic Manifestation.

Jamal F, Altaf I, Ahmed G, Asad S, Ahmad H, Zia Q, Azhar A, Farheen S, Shafi T, Karim S, Zubair S, Owais M.

Vaccines (Basel).

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36679946/>

Antileishmanial Activity of Clinanthus milagroanthus S. Leiva & Meerow (Amaryllidaceae) Collected in Peru.

Soto-Vásquez MR, Alvarado-García PAA, Osorio EH, Tallini LR, Bastida J.

Plants (Basel).

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36679035/>

Leishmaniasis is a worldwide infectious parasitic disease caused by different species of protozoa of the genus *Leishmania*, which are transmitted to animals and humans through the bite of insects of the Psychodidae family. In the present work, the antileishmanial activity of an alkaloid extract of the bulbs of *Clinanthus milagroanthus* S. Leiva & Meerow (Amaryllidaceae) was evaluated in vitro, in vivo, and in silico against the parasite *Leishmania braziliensis*,

and the chemical profile of the sample was determined by GC-MS analysis. At concentrations of 1, 10, and 100 $\mu\text{g}\cdot\text{mL}^{-1}$, the alkaloid extract presented inhibition percentages of 8.7%, 23.1%, and 98.8%, respectively, against *L. braziliensis* with a $p < 0.05$, and IC_{50} values of $18.5 \pm 0.3 \mu\text{g}\cdot\text{mL}^{-1}$. Furthermore, at a dose of $1.0 \text{ mg}\cdot\text{kg}^{-1}$, a greater decrease in lesion size was observed (90%) for in vivo assays, as well as a decrease in infection (96%), finding no significant differences ($p > 0.05$) in comparison with amphotericin B (92% and 98%, respectively). Eleven alkaloids were identified in *C. milagroanthus* bulbs: galanthamine, vittatine/crinine, 8-*O*-demethylmaritidine, anhydrolycorine, 11,12-dehydroanhydrolycorine, hippamine, lycorine, 2-hydroxyanhydrolycorine, 7-hydroxyclicivonine, 2 α -hydroxyhomolycorine, and 7-hydroxyclicivonine isomer. A molecular model of *Leishmania braziliensis* trypanothione reductase (TRLb) was built using computational experiments to evaluate in silico the potential of the Amaryllidaceae alkaloid identified in *C. milagroanthus* toward this enzyme. The structures galanthamine, 7-hydroxyclicivonine isomer, and crinine showed better estimated free energy of binding than the reference compound, amphotericin B. In conclusion, this is the first in vitro, in vivo, and in silico report about the antileishmanial potential and alkaloid profiling of the extract of *C. milagroanthus* bulbs, which could become an interesting source of bioactive molecules.

In Vivo Safety and Efficacy of Chalcone-Loaded Microparticles with Modified Polymeric Matrix against Cutaneous Leishmaniasis.

Sousa-Batista AJ, Arruda-Costa N, Pacienza-Lima W, Carvalho-Gondim F, Santos RF, Da-Silva SAG, Ré MI, Rossi-Bergmann B.

Pharmaceutics.

24-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678680/>

Selene-Ethylenelacticamides and N-Aryl-Propanamides as Broad-Spectrum Leishmanicidal Agents.

de Sousa NF, da Silva Souza HD, de Menezes RPB, da Silva Alves F, Acevedo CAH, de Lima Nunes TA, Sessions ZL, Scotti L, Muratov EN, Mendonça-Junior FJB, da Franca Rodrigues KA, de Athayde Filho PF, Scotti MT.

Pathogens.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678484/>

The Anti-Leishmania amazonensis and Anti-Leishmania chagasi Action of Copper(II) and Silver(I) 1,10-Phenanthroline-5,6-dione Coordination Compounds.

Oliveira SSC, Santos VS, Devereux M, McCann M, Santos ALS, Branquinho MH.

Pathogens.

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678418/>

Omics Approaches in Drug Development against Leishmaniasis: Current Scenario and Future Prospects.

Rabaan AA, Bakhrebah MA, Mohapatra RK, Farahat RA, Dhawan M, Alwarthan S, Aljeldah M, Al Shammari BR, Al-Najjar AH, Alhusayyen MA, Al-Absi GH, Aldawood Y, Alsaleh AA, Alshamrani SA, Almuthree SA, Alawfi A, Alshengeti A, Alwashmi ASS, Hajissa K, Nassar MS.

Pathogens.

26-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678387/>

Validating Immunomodulatory Responses of r-LdODC Protein and Its Derived HLA-DRB1 Restricted Epitopes against Visceral Leishmaniasis in BALB/c Mice.

Pandey R, Gautam RK, Sharma S, Tedla MG, Mahantesh V, Dikhit MR, Kumar A, Pandey K, Bimal S.

Pathogens.

22-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678364/>

Vaccination is considered the most appropriate way to control visceral leishmaniasis (VL). With this background, the r-LdODC protein as well as its derived HLA-DRB1-restricted synthetic peptides (P1: RLMPSAHAI, P2: LLDQYQIHL, P3: GLYHSFNCI, P4: AVLEVL SAL, and P5: RLPASPAAL) were validated in BALB/c mice against visceral leishmaniasis. The study was initiated by immunization of the r-LdODC protein as well as its derived peptides cocktail with adjuvants (r-CD2 and MPL-A) in different mice groups, separately. Splenocytes isolated from the challenged and differentially immunized mice group exhibited significantly higher IFN- γ secretion, which was evidenced by the increase in the expression profile of intracellular CD4+IFN- γ T cells. However, the IL-10 secretion did not show a significant increase against the protein and peptide cocktail. Subsequently, the study confirmed the ability of peptides as immunoprophylactic agents, as the IE-I/AD-I molecule overexpressed on monocytes and macrophages of the challenged mice group. The parasitic load in macrophages of the protein and peptides cocktail immunized mice groups, and T cell proliferation rate, further established immunoprophylactic efficacy of the r-LdODC protein and peptide cocktail. This study suggests that the r-LdODC protein, as well as its derived HLA-DRB1-restricted synthetic peptides, have immunoprophylactic potential and can activate other immune cells' functions towards protection against visceral leishmaniasis. However, a detailed study in a humanized mice model can explore its potential as a vaccine candidate.

First Phytochemical Profiling and In-Vitro Antiprotozoal Activity of Essential Oil and Extract of *Plagiochila porelloides*.

Pannequin A, Quetin-Leclercq J, Costa J, Tintaru A, Muselli A.

Molecules.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677674/>

Comparative Proteomics and Genome-Wide Druggability Analyses Prioritized Promising Therapeutic Targets against Drug-Resistant *Leishmania tropica*.

Aiman S, Alzahrani AK, Ali F, Abida, Imran M, Kamal M, Usman M, Thabet HK, Li C, Khan A.

Microorganisms.

16-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677520/>

Underestimation of Human Cutaneous Leishmaniasis Caused by *Leishmania infantum* in an Endemic Area of the Mediterranean Basin (Balearic Islands).

Alcover MM, Rocamora V, Ribas A, Fisa R, Riera C.

Microorganisms.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677419/>

Comparative Genomic Analyses of New and Old World Viscerotropic Leishmanine Parasites: Further Insights into the Origins of Visceral Leishmaniasis Agents.

Silveira FT, Sousa Junior EC, Silvestre RVD, Vasconcelos Dos Santos T, Sosa-Ochoa W, Valeriano CZ, Ramos PKS, Casseb SMM, Lima LVDR, Campos MB, da Matta VL, Gomes CM, Flores GVA, Sandoval Pacheco CM, Corbett CE, Laurenti MD.

Microorganisms.

22-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36677318/>

Visceral leishmaniasis (VL), also known as kala-azar, is an anthroponotic disease affecting human populations on five continents. Aetiologic agents belong to the *Leishmania* (*L.*) *donovani* complex. Until the 1990s, three leishmanine parasites comprised this complex: *L. (L.) donovani* Laveran & Mesnil 1903, *L. (L.) infantum* Nicolle 1908, and *L. (L.) chagasi* Lainson & Shaw 1987 (= *L. chagasi* Cunha & Chagas 1937). The VL causal agent in the New World (NW) was previously identified as *L. (L.) chagasi*. After the development of molecular characterization, however, comparisons between *L. (L.) chagasi* and *L. (L.) infantum* showed high similarity, and *L. (L.) chagasi* was then regarded as synonymous with *L. (L.) infantum*. It was, therefore, suggested that *L. (L.) chagasi* was not native to the NW but had been introduced from the Old World by Iberian colonizers. However, in light of ecological evidence from the NW parasite's enzootic cycle involving a wild phlebotomine vector (*Lutzomyia longipalpis*) and a wild mammal reservoir (the fox, *Cerdocyon thous*), we have recently analyzed by molecular clock comparisons of the DNA polymerase alpha subunit gene the whole-genome sequence of *L. (L.) infantum* & *chagasi* of the most prevalent clinical form, atypical dermal leishmaniasis (ADL), from Honduras (Central America) with that of the same parasite from Brazil (South America), as well as those of *L. (L.) donovani* (India) and *L. (L.) infantum* (Europe), which revealed that the Honduran parasite is older

ancestry (382,800 ya) than the parasite from Brazil (143,300 ya), *L. (L.) donovani* (33,776 ya), or *L. (L.) infantum* (13,000 ya). In the present work, we have now amplified the genomic comparisons among these leishmanine parasites, exploring mainly the variations in the genome for each chromosome, and the number of genomic SNPs for each chromosome. Although the results of this new analysis have confirmed a high genomic similarity (~99%) among these parasites [except *L. (L.) donovani*], the Honduran parasite revealed a single structural variation on chromosome 17, and the highest frequency of genomic SNPs (more than twice the number seen in the Brazilian one), which together to its extraordinary ancestry (382,800 ya) represent strong evidence that *L. (L.) chagasi/L. (L.) infantum chagasi* is, in fact, native to the NW, and therefore with valid taxonomic status. Furthermore, the Honduran parasite, the most ancestral viscerotropic leishmanine parasite, showed genomic and clinical taxonomic characteristics compatible with a new *Leishmania* species causing ADL in Central America.

Identification of Potential Leishmania N-Myristoyltransferase Inhibitors from *Withania somnifera* (L.) Dunal: A Molecular Docking and Molecular Dynamics Investigation.

Orabi MAA, Alshahrani MM, Sayed AM, Aboueleta ME, Shaaban KA, Abdel-Sattar ES.

Metabolites.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36677018/>

Leishmania Infection during Ruxolitinib Treatment: The Cytokines-Based Immune Response in the Setting of Immunocompromised Patients.

Duminuco A, Scarso S, Cupri A, Parrinello NL, Villari L, Scuderi G, Giunta G, Leotta S, Milone GA, Giuffrida G, Palumbo GA, Milone G.

J Clin Med.

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36675507/>

Genetic Iron Overload Hampers Development of Cutaneous Leishmaniasis in Mice.

Charlebois E, Li Y, Wagner V, Pantopoulos K, Olivier M.

Int J Mol Sci.

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36675185/>

The survival, growth, and virulence of *Leishmania* spp., a group of protozoan parasites, depends on the proper access and regulation of iron. Macrophages, *Leishmania*'s host cell, may divert iron traffic by reducing uptake or by increasing the efflux of iron via the exporter ferroportin. This parasite has adapted by inhibiting the synthesis and inducing the degradation of ferroportin. To study the role of iron in leishmaniasis, we employed *Hjv*^{-/-} mice, a model of hemochromatosis. The disruption of hemojuvelin (*Hjv*) abrogates the expression of the iron hormone hepcidin.

This allows unrestricted iron entry into the plasma from ferroportin-expressing intestinal epithelial cells and tissue macrophages, resulting in systemic iron overload. Mice were injected with *Leishmania major* in hind footpads or intraperitoneally. Compared with wild-type controls, *Hjv*^{-/-} mice displayed transient delayed growth of *L. major* in hind footpads, with a significant difference in parasite burden 4 weeks post-infection. Following acute intraperitoneal exposure to *L. major*, *Hjv*^{-/-} peritoneal cells manifested increased expression of inflammatory cytokines and chemokines (*Il1b*, *Tnfa*, *Cxcl2*, and *Ccl2*). In response to infection with *L. infantum*, the causative agent of visceral leishmaniasis, *Hjv*^{-/-} and control mice developed similar liver and splenic parasite burden despite vastly different tissue iron content and ferroportin expression. Thus, genetic iron overload due to hemojuvelin deficiency appears to mitigate the early development of only cutaneous leishmaniasis.

Miltefosine and Nifuratel Combination: A Promising Therapy for the Treatment of Leishmania donovani Visceral Leishmaniasis.

Melcon-Fernandez E, Galli G, García-Estrada C, Balaña-Fouce R, Reguera RM, Pérez-Pertejo Y.

Int J Mol Sci.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36675150/>

An RNA Interference (RNAi) Toolkit and Its Utility for Functional Genetic Analysis of Leishmania (Viannia).

Lye LF, Owens KL, Jang S, Marcus JE, Brettmann EA, Beverley SM.

Genes (Basel).

28-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36672832/>

Antiparasitic Activity of Fluorophenyl-Substituted Pyrimido[1,2-a]benzimidazoles.

Nasr ISA, Koko WS, Khan TA, Schobert R, Biersack B.

Biomedicines.

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36672727/>

A series of fourteen pyrimido[1,2-a]benzimidazole compounds was prepared by straightforward heterocyclic chemistry and oxidation methods. The new pyrimidobenzimidazole derivative **2a** with a 3-fluorophenyl substituent was identified as a new antiparasitic compound showing excellent activities against *Leishmania major* parasites. **2a** was highly active against *L. major* promastigotes and amastigotes with EC₅₀ values in the nanomolar concentration range. Compound **3b** was less active than **2a** against *L. major*, but more active against *Toxoplasma gondii* with considerable selectivity. Hence, two promising and selective antiparasitic drug candidates **2a** and **3b** for the treatment of two parasitic diseases were identified, which can be prepared by green chemistry methods using simple one-pot reactions and oxidation procedures, respectively.

Antimicrobial Spectrum of Activity and Mechanism of Action of Linear Alpha-Helical Peptides Inspired by Shrimp Anti-Lipopolysaccharide Factors.

Matos GM, García-Teodoro B, Martins CP, Schmitt P, Guzmán F, de Freitas ACO, Stoco PH, Ferreira FA, Stadnik MJ, Robl D, Perazzolo LM, Rosa RD.

Biomolecules.

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36671535/>

Correction to: Up-regulation of silent information regulator 2 (Sir2) is associated with amphotericin B resistance in clinical isolates of *Leishmania donovani*.

[No authors listed]

J Antimicrob Chemother.

21-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36670472/>

Characterization of Regulatory T Cells in Patients Infected by *Leishmania infantum*.

Peixoto RF, Gois BM, Martins M, Palmeira PHS, Rocha JC, Gomes JAS, Azevedo FLAA, Veras RC, de Medeiros IA, Grisi TC SL, de Araújo DAM, Amaral IPG, Keesen TSL.

Trop Med Infect Dis.

27-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668925/>

High IL-10 levels are pivotal to parasite survival in visceral leishmaniasis (VL). Antigenic stimuli induce IL-10 expression and release of adenosine by CD39/CD73. Due to their intrinsic ability to express IL-10 and produce adenosine from extracellular ATP, we evaluated the IL-10, CD39, and CD73 expression by Regulatory T cells (Treg) correlated with VL pathology. Using flow cytometry, Treg cells were analyzed in peripheral blood samples from VL patients (in the presence and absence of *Leishmania infantum* soluble antigen (SLA)) and healthy individuals (negative endemic control-NEC group), without any treatment. Additionally, IL-10 levels in leukocytes culture supernatant were measured in all groups by ELISA assay. VL patients presented more Treg frequency than NEC group, independently of stimulation. ELISA results demonstrated that SLA induced higher IL-10 expression in the VL group. However, the NEC group had a higher Treg IL-10⁺ compared to the VL group without stimulation and SLA restored the IL-10 in Treg. Additionally, an increase in Treg CD73⁺ in the VL group independently of stimuli compared to that in the NEC group was observed. We suggest that Treg are not the main source of IL-10, while the CD73 pathway may be an attempt to modulate the exacerbation of immune response in VL disease.

Revisiting the diagnosis and treatment of Para Kala-azar Dermal Leishmaniasis in the endemic foci of Bangladesh.

Maruf S, Sagar SK, Rashid MMU, Nath P, Islam MS, Ghosh P, Rashid MU, Mondal D, Abd El Wahed A, Basher A.

PLoS One.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36662825/>

Inhibitory Effects of *Leishmania Mexicana* Infection on MHC-I Expression in Bone Marrow Derived Dendritic Cells.

Rezvan H, Ali SA, Hamoon Navard S.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36660416/>

The Influence of Different Culture Media on the Growth and Recombinant Protein Production of Iranian Lizard *Leishmania* Promastigote.

Abdi Ghavidel A, Aghamiri S, Jajarmi V, Bandehpour M, Kazemi B.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36660414/>

Background: *Leishmania* is a eukaryotic protozoan parasite belonging to the Trypanosomatidae family. The Iranian Lizard *Leishmania* (I.L.L.), which is nonpathogenic to mammals, shows great promise to be used as an expression system for recombinant protein production. Unlike other *Leishmania* strains, the ideal culture medium for I.L.L. has not been established, although it is commonly cultured in the RPMI₁₆₄₀ medium. **Methods:** We investigated the growth rate of the wild and recombinant I.L.L. in BHI, RPMI₁₆₄₀, LB, and M199 media with and without FBS, hemin, or lyophilized rabbit serum. Subsequently, the expression rate of the recombinant protein in these media was compared. **Results:** The growth rate of I.L.L. in RPMI₁₆₄₀ medium and LB broth was similar and supplementation with 10% FBS did not affect the growth rate. The amount of protein expression in the LB medium was higher than in the other three media. **Conclusion:** The LB broth is an appropriate medium for I.L.L. culture and recombinant protein production.

Leishmania: an urgent need for new treatments.

EBioMedicine.

Jan-2023

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

Malnutrition-related parasite dissemination from the skin in visceral leishmaniasis is driven by PGE2-mediated amplification of CCR7-related trafficking of infected inflammatory monocytes.

Osorio EY, Uscanga-Palomeque A, Patterson GT, Cordova E, Travi BL, Soong L, Melby PC.

PLoS Negl Trop Dis.

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36630476/>

People are infected with *Leishmania donovani* when the parasite is deposited in the dermis during the blood meal of the sand fly vector. Most infected people develop a subclinical latent infection, but some develop progressive visceral leishmaniasis. Malnutrition is a risk factor for the development of active VL. We previously demonstrated increased parasite dissemination from the skin to visceral organs in a murine model of malnutrition. Here we investigated the mechanism of early parasite dissemination. After delivery of *L. donovani* to the skin, we found enhanced capture of parasites by inflammatory monocytes and neutrophils in the skin of malnourished mice. However, parasite dissemination in malnourished mice was driven primarily by infected inflammatory monocytes, which showed increased CCR7 expression, greater intrinsic migratory capacity, and increased trafficking from skin to spleen. PGE2 production, which was increased at the site of skin infection, increased monocyte CCR7 expression and promoted CCR7-related monocyte-mediated early parasite dissemination in malnourished mice. Parasite dissemination in monocytes was reduced by inhibition of PGE2, knockdown or silencing of CCR7 in monocytes, and depletion of inflammatory monocytes through administration of diphtheria toxin to CSFR1-DTR transgenic mice that have monocyte-specific DT receptor expression. CCR7-driven trafficking of infected inflammatory monocytes through the lymph node was accompanied by increased expression of its ligands CCL19 and CCL21. These results show that the CCR7/PGE2 axis is responsible for the increased trafficking of *L. donovani*-infected inflammatory monocytes from the skin to the spleen in the malnourished host. Undernutrition and production of PGE2 are potential targets to reduce the risk of people developing VL. Nutritional interventions that target improved immune function and reduced PGE2 synthesis should be studied in people at risk of developing VL.

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

Saidi N, Jelassi R.

Immunol Lett.

Jan-2023

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

Capparis spinosa inhibits *Leishmania* major growth through nitric oxide production in vitro and arginase inhibition in silico.

Darif D, Nait Irahail I, Hammi I, Kihel A, Kachmar MR, Riyad M, Hmimid F, Akarid K.

Exp Parasitol.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36581148/>

Cutaneous leishmaniasis is an infectious disease, considered as a major public health problem in different regions of the world. The current treatments are limited due to their toxicity and treatment failures, which have increased the search for new substances of natural origin

to control this infection. *Capparis spinosa* is an important medicinal plant, rich in biochemical compounds with a broad range of activities including antimicrobial effects. Nevertheless, more investigations are still needed to determine its effect on *Leishmania* parasites. This study aimed to evaluate the effect of *C. spinosa* extracts on *Leishmania* major promastigotes and amastigotes growth as well as on L-arginine metabolic pathways, especially the production of leishmanicidal molecules such as nitric oxide. Our results showed that *C. spinosa* methanolic and aqueous extracts contained polyphenols and flavonoids at different concentrations. The methanolic extract of *C. spinosa*, compared to the aqueous extract, showed significantly higher amounts of total polyphenols (21.23 ± 1.08 mg GAE/g of dw ($P < 0.05$), as well as a higher antioxidant activity evaluated respectively by Reducing Power and DPPH (EC_{50} : 0.31 ± 0.02 and 7.69 ± 1.28 mg/ml. Both extracts significantly inhibited *L. major* promastigotes and intra-macrophagic amastigotes growth in vitro in a dose-dependent manner ($P < 0.001$) and induced NO production not only in *Leishmania*-infected macrophages but also in uninfected macrophages, without showing any cytotoxicity in vitro. Furthermore, in silico docking studies showed that *C. spinosa* compounds identified by RP-HPLC exhibited inhibitory activity against the arginase enzyme. The leishmanicidal effect of *C. spinosa* may be due to its phenolic content and its mechanism of action may be mediated by an increase in NO production and by the inhibition of arginase enzyme in silico. These findings support the hypothesis that *C. spinosa* might be a valuable source of new biomolecules for leishmaniasis treatment.

Mannosylated imiquimod-terbinafine co-loaded transethosomes for cutaneous leishmaniasis; assessment of its anti-leishmanial potential, in vivo safety and immune response modulation.

Jamshaid H, Din FU, Nousheen K, Khan SU, Fatima A, Khan S, Choi HG, Khan GM.

Biomater Adv.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36577194/>

Anti-leishmanial therapy: Caught between drugs and immune targets.

Mahor H, Mukherjee A, Sarkar A, Saha B.

Exp Parasitol.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36572088/>

***Leishmania infantum* (syn. *Leishmania chagasi*) detection in blood donors living in an endemic area.**

Lopes EAO, Florencio-Henschel P, Jordão FT, Sperança MA, Martins LPA, Suzuki RB.

Parasitol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36567398/>

A monoclonal antibody against a *Leishmania mexicana* COX-like

enzymatic activity also recognizes similar proteins in different protozoa of clinical importance.

Hernández-Ramírez VI, Estrada-Figueroa LA, Medina Y, Lizarazo-Taborda MR, Toledo-Leyva A, Osorio-Trujillo C, Morales-Mora D, Talamás-Rohana P.

Parasitol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36562799/>

In *Leishmania mexicana*, the protease gp63 has been documented as the protein responsible for cyclooxygenase (COX) activity. The present work aimed to obtain a monoclonal antibody capable of recognizing this protein without blocking the COX-like enzymatic activity. The antibody produced by the selected hybridoma was named D12 mAb. The antigen recognized by the D12 mAb was characterized by the determination of COX activity associated with immune complexes in the presence of exogenous arachidonic acid (AA) using the commercial Activity Assay Abcam kit. LSM-SMS analysis validated the identity of the antigen associated with the D12 mAb as the *L. mexicana* protease gp63. Confocal microscopy assays with the D12 mAb detected, by cross-recognition, similar proteins in other protozoan parasites. COX-like molecules are located in vesicular structures, homogeneously distributed throughout the cytoplasm in amastigotes (intracellular infectious phase) and promastigotes of *L. mexicana*, and trophozoites of *Entamoeba histolytica*, *Acanthamoeba castellanii*, and *Naegleria fowleri*. However, in *Giardia duodenalis* trophozoites, the distribution of the COX-like molecule was also in perinuclear areas. In comparison, in *Trypanosoma cruzi* trypomastigotes, the distribution was mainly observed in the plasma membrane. Structural analyses of COX-2-like antigens revealed continuous and discontinuous epitopes for B cells, which could be relevant in the cross-reaction of D12 mAb with the analyzed parasites. These results indicate that the D12 mAb against the *L. mexicana* gp63 also recognizes a COX-like molecule in several protozoan parasites, suggesting that this D12 mAb could potentially be used in combined therapies against infectious diseases.

Seroprevalence of canine leishmaniosis in asymptomatic dogs in Kosovo.

Xhekaj B, Stefanovska J, Sherifi K, Rexhepi A, Bizhga B, Rashikj L, Nikolovski M, Kniha E, Cvetkovikj A.

Parasitol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36536229/>

Assessment of pan-Leishmania detection by recombinase polymerase amplification assay.

Louizi C, Khan MAA, Faisal K, Chowdhury R, Ghosh P, Hossain F, Nisansala T, Ranasinghe S, Moreno J, Alvar J, Mondal D, Buhl T, Lüder CGK, Abd El Wahed A.

Diagn Microbiol Infect Dis.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36493571/>

Survey on the presence of *Leishmania* sp. in peridomestic rodents from the Emilia-Romagna Region (North-Eastern Italy).

Magri A, Galuppi R, Fioravanti M, Caffara M.

Vet Res Commun.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/35412180/>

Cysticercose

Real-time multiplex PCR for human echinococcosis and differential diagnosis.

Knapp J, Lallemand S, Monnien F, Felix S, Courquet S, Umhang G, Millon L.

Parasite.

2023

<https://pubmed.ncbi.nlm.nih.gov/36700708/>

Molecular identification of rare human infectious pathogens appears to be one of the most relevant current methods for rapid diagnosis and management of patients. PCR techniques, in particular real-time quantitative PCR, are best suited for the detection of DNA from the pathogens, even at low concentrations. Echinococcosis infections are due to helminths of the *Echinococcus* genus, with closely related species involved in parasitic lesions affecting animals and, accidentally, humans. We developed a multiplex qPCR (MLX qPCR) assay allowing for the detection of four *Echinococcus* species involved in Europe in alveolar echinococcosis (AE) and cystic echinococcosis (CE) (*Echinococcus multilocularis*, *E. granulosus sensu stricto*, *E. ortleppi*, and *E. canadensis*), based on short mitochondrial targets. A collection of 81 fresh and formalin-fixed paraffin-embedded tissues (FFPE) of AE and CE lesions was assembled. The qPCR assays were performed in triplex for *Echinococcus* spp. detection, associated with a qPCR inhibitor control. A duplex qPCR was also designed to enable diagnosis of two other dead-end helminthiases (cysticercosis (*Taenia solium*), and toxocariasis (*Toxocara cati* and *T. canis*)). The sensitivity of the qPCR was assessed and ranged from 1 to 5×10^{-4} ng/ μ L (seven PCR assays positive), corresponding to 37-42 cycles for quantifiable DNA. The specificity was 100% for all the targets. This multiplex qPCR, adapted to low amounts of DNA can be implemented in the laboratory for the rapid molecular diagnosis of Echinococcosis species.

Proteomic analysis of *Taenia solium* cysticercus and adult stages.

Li L, He W, Fan X, Liu M, Luo B, Yang F, Jiang N, Wang L, Zhou B.

Front Vet Sci.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699330/>

Taenia solium (*T. solium*) cysticercosis is a neglected parasitic zoonosis that occurs in developing countries. Since *T. solium* has a complex life cycle that includes eggs, oncospheres, cysticerci, and adults, presumably many proteins are produced that enable them to survive and establish an infection within the host. The objectives of

this study were to perform a comparative proteomic analysis of two ontogenetic stages of *T. solium* (cysticerci and adult) and to analyze their differential expression of proteins. Methods proteins were separated by High Performance Liquid Chromatography (HPLC) fractionation, and protein samples were also digested in liquid and identified by liquid chromatography tandem mass spectrometry (LC-MS/MS); the differentially expressed proteins were then processed by a bioinformatics analysis and verified by parallel reaction monitoring (PRM). Results we identified 2,481 proteins by label-free quantitative proteomics. Then differentially expressed proteins were screened under *P* values < 0.05 and 2 fold change, we found that 293 proteins up-regulated and 265 proteins down-regulated. Discussion through the bioinformatics analysis, we analyzed the differences types and functions of proteins in the *Taenia solium* and cysticercus, the data will provide reference value for studying the pathogenic mechanism of the two stages and the interaction with the host, and also support for further experimental verification.

Genetic Variation of *Taenia Saginata* Cyst Isolates from Iraq Based on Mitochondrial COX1 Sequences.

Mohammed AA.

Helminthologia.

17-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36694824/>

Effects of a Digital Health Literacy Intervention on Porcine Cysticercosis Prevalence and Associated Household Practices in Iringa District, Tanzania.

Kajuna F, Mwang'onde B, Holst C, Ngowi B, Sukums F, Noll J, Winkler AS, Ngowi H.

Pathogens.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678455/>

Digital health is considered an opportunity to engage a wider community in disease control for public health. It has been used in healthcare consultation, in medical treatments and in reporting emergencies. The current study developed digital health literacy content for public health education and assessed its effects on porcine cysticercosis prevalence, pig-keeping style and pig pen and latrine qualities. The intervention was designed and evaluated on the prevention and control of porcine cysticercosis in the Iringa District of southern Tanzania. A quasi-controlled field trial with pre-intervention and post-intervention assessments of porcine cysticercosis, pig-keeping style and pig pen and latrine qualities was conducted. A baseline cross-sectional study was followed immediately by digital health literacy intervention, which comprised educational messages on porcine cysticercosis shown on computer tablets or smartphones. Free internet access supported unsupervised community access. The 25-month post-intervention assessments revealed significantly increased pig confinement (20.1%) (*p* = 0.026) and pig pen quality (16.2%) (*p* = 0.025). However, the quality of household latrines (*p* = 0.453) was not improved,

nor was there any significant effect on the prevalence of porcine cysticercosis (*p* = 0.231). The digital health literacy intervention suggests a strategy for wider and sustainable dissemination of educational messages for *Taenia solium* infection control.

Intraocular and neuro-cysticercosis with diffuse stromal choroiditis.

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

Indian J Pathol Microbiol.

Jan-Mar 2023

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

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

Vishwakarma P, Murthy SI, Joshi V, Mishra DK.

BMJ Case Rep.

17-01-2023

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

Complex neurocysticercosis lesions on imaging: Explained through correlative histomorphology.

Singh P, Paramjit E, Ahuja CK, Modi M, Vyas S, Goyal M, Kumar A, Bhatia V, Prabhakar A, Sharma SK.

Neuroradiol J.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/35538605/>

Objectives: Neurocysticercosis, the commonest neuro-parasite, sometimes presents as complex ring enhancing lesion causing diagnostic dilemma. We aim to establish radio-histo-morphological equivalents of early events in degeneration of the parasite to explain such imaging phenotypes. **Methods:** We compared patterns of degeneration in 23 randomly selected complex NCC on MRI with histo-morphology in 30 cysts obtained from an unrelated post mortem brain. **Results:** The anatomy of the parasite and the degenerative patterns of the scolex (hydropic changes, calcification, evagination, and fragmentation) and the cyst wall (undulation, accessory loculi, and frank disruption) were well demonstrated on both. The intact scolex remarkably resembled head of intestinal *Taenia*. The complex lesions were conglomeration of multiple communicating cysts with a single parent cyst and multiple daughter cysts. The parent cysts contained a solitary variably degenerated scolex, had thicker walls and associated chronic inflammation. The remaining cysts of the lesion complex contained no scolex, had poorly organized walls, turbid contents, and florid perilesional enhancement with leakage of contrast. Three lesions assumed a multi-cystic pseudo-tumorous pattern, of which two resolved into solitary calcific remnants on follow up. **Conclusion:** Complex lesion in NCC result from degeneration of solitary parasite with perilesional gliosis, surrounded by multiple non-larval daughter cysts inciting acute intra and perilesional inflammation due to enhanced

antigenic challenge. Possibly, attempted abortive asexual reproduction by the cellulose cyst as a preterminal event results in a "limited Racemose like transition." Correct interpretation has diagnostic and therapeutic implications as active lesions and their fibrocalcific residue may have greater epileptogenic potential

Dracunculose

Variation in scent amount but not in composition correlates with pollinator visits within populations of deceptive *Arum maculatum* L. (Araceae).

Gfrerer E, Laina D, Gibernau M, Comes HP, Hörger AC, Dötterl S.

Front Plant Sci.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699827/>

Floral scent is vital for pollinator attraction and varies among and within plant species. However, little is known about how inter-individual variation in floral scent affects the abundance and composition of floral visitor assemblages within populations. Moreover, for deceptive plants it is predicted that intra-population variation in scent can be maintained by negative frequency-dependent selection, but empirical evidence is still lacking. To investigate the ecological and evolutionary relations between inter-individual scent variation (i.e., total emission and composition) and floral visitors in deceptive plants, we studied floral scent, visitor assemblages, and fruit set in two populations of fly-pollinated (Psychodidae, Sphaeroceridae; Diptera) and deceptive *Arum maculatum* from Austria (JOS) and northern Italy (DAO). By correlating individual data on floral scent and visitor assemblages, we show that inter-individual variation in floral scent partly explains variation in visitor assemblages. The quantity of floral scent emitted per individual correlated positively with visitor abundance in both populations but explained visitor composition only in DAO, where strongly scented inflorescences attracted more sphaerocerid flies. However, in each population, the composition of floral scent did not correlate with the composition of floral visitors. There was also no evidence of negative frequency-dependent selection on floral scent. Instead, in JOS, more frequent scent phenotypes attracted more pollinators and were more likely to set an infructescence than rarer ones. Our results show that floral scent, despite being key in pollinator attraction in *A. maculatum*, only partly explains variation in pollinator abundance and composition. Overall, this study is the first to shed light on the importance of inter-individual variation in floral scent in explaining floral visitor assemblages at the population level in a deceptive plant species.

Detection of the local adaptive and genome-wide associated loci in southeast Nigerian taro (*Colocasia esculenta* (L.) Schott) populations.

Fufa TW, Menamo TM, Abteu WG, Amadi CO, Oselebe HO.

BMC Genomics.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36694124/>

Melatonin Involved in Protective Effects against Cadmium Stress in *Wolffia arrhiza*.

Chmur M, Bajguz A.

Int J Mol Sci.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36674694/>

Melatonin (MT) is a new plant hormone that protects against adverse environmental conditions. In the present study, the responses of *Wolffia arrhiza* exposed to cadmium (Cd) and MT were analyzed. Quantitative analysis of MT and precursors of its biosynthesis was performed using LC-MS-MS. The photosynthetic pigments and phytochelators (PCs) contents were determined using HPLC, while protein and monosaccharides, stress markers, and antioxidant levels were determined using spectrophotometric methods. Interestingly, the endogenous level of MT and its substrates in *W. arrhiza* exposed to 1-100 μ M Cd was significantly higher compared to the control. Additionally, the application of 25 μ M MT and Cd intensified the biosynthesis of these compounds. The most stimulatory effect on the growth and content of pigments, protein, and sugars was observed in plants treated with 25 μ M MT. In contrast, Cd treatment caused a decrease in plant weight and level of these compounds, while the application of 25 μ M MT mitigated the inhibitory effect of Cd. Additionally, Cd enhanced the level of stress markers; simultaneously, MT reduced their content in duckweed exposed to Cd. In plants treated with Cd, PC levels were increased by Cd treatment and by 25 μ M MT. These results confirmed that MT mitigated the adverse effect of Cd. Furthermore, MT presence was reported for the first time in *W. arrhiza*. In summary, MT is an essential phytohormone for plant growth and development, especially during heavy metal stress.

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

Ko J, Ryu JE, Noh SW, Choi HK.

J Agric Food Chem.

25-01-2023

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

Bioaccumulation and physiological traits qualify *Pistia stratiotes* as a suitable species for phytoremediation and bioindication of iron-contaminated water.

Coelho DG, da Silva VM, Gomes Filho AAP, Oliveira LA, de Araújo HH, Farnese FDS, Araújo WL, de Oliveira JA.

J Hazard Mater.

15-03-2023

<https://pubmed.ncbi.nlm.nih.gov/36603425/>

Evaluation of the composition of konjac glucomannan on the color changes during the deacetylation reaction.

Zhang M, Gu L, Chang C, Li J, Sun Y, Cai Y, Xiong W, Yang Y, Su Y.

Int J Biol Macromol.

15-02-2023

<https://pubmed.ncbi.nlm.nih.gov/36563814/>

As a newly superior konjac variety, the *Amorphophallus bulbifer* (A. bulbifer) has several unique advantages of high reproductive coefficient, short growth cycle, high disease resistance, high konjac glucomannan (KGM) content and climate adaption to hot or humid conditions. However, the gel formed by KGM from the A. bulbifer flour is easily browning during the alkali-induced process and the mechanism underlying them is still unclear. In order to explore the browning mechanisms, the changes of composition and color parameters of KGM were investigated during deacetylation in this research. The L*, h*, total phenols, total flavonoids, reducing sugars, and amino acids decreased along with the increase of deacetylation degree of KGM while a*, ΔE, and browning index increased. The results indicated that the oxidation or polymerization of polyphenols and flavones in alkaline circumstances, and the carbonyl ammonia reaction between reducing sugars and amino acids may be the main reasons for color changes of KGM flour during deacetylation. Hence, this study was expected to provide the theoretical basis for the inhibition of KGM gel browning and further broaden the application range of KGM in food and other industries.

Active Consumption of Konjac and Konjac Products Improves Blood Glucose Control in Patients with Type 2 Diabetes Mellitus.

Ueno H, Haraguchi N, Azuma M, Shiiya T, Noda T, Ebihara E, Uehira Y, Uchida T, Sasaba K, Nakamura M, Uchimura N, Kita E, Umemura A, Nobe T, Sumoto E, Yano Y, Nakazato M.

J Am Nutr Assoc.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/34843410/>

Echinococcosis

Real-time multiplex PCR for human echinococcosis and differential diagnosis.

Knapp J, Lallemand S, Monnien F, Felix S, Courquet S, Umhang G, Millon L.

Parasite.

2023

<https://pubmed.ncbi.nlm.nih.gov/36700708/>

Co-infection of *Echinococcus equinus* and *Echinococcus canadensis* (G6/7) in a gray wolf in Turkey: First report and genetic variability of the isolates.

Kilinc SG, Celik F, Kesik HK, Selcuk MA, Ahmed H, Simsek S.

Int J Parasitol Parasites Wildl.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699504/>

Natural history of *Echinococcus granulosus* microcyst development in long term in vitro culture and molecular and morphological changes induced by insulin and BMP-4.

Derakhshani A, Mousavi SM, Rezaei M, Afgar A, Keyhani AR, Mohammadi MA, Dabiri S, Fasihi Harandi M.

Front Vet Sci.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36699324/>

Introduction: Cystic echinococcosis (CE) caused by the cestode *Echinococcus granulosus* is a disease of worldwide public health and economic importance. The determinants and underlying cellular mechanisms of CE development and fate in intermediate hosts are largely unknown. Hormones and cytokines such as insulin and BMP-4 are the key players in the development, differentiation, and apoptosis. In this study, we evaluated the long term natural history of *E. granulosus* microcysts in an vitro setting and the molecular and morphological changes induced by the growth factors, insulin and BMP4 during the development of metacestode stage of *E. granulosus*. **Methods:** *E. granulosus* protoscoleces were cultivated and the parasite development was followed in the long term mono-phasic culture for 105 days and the morphometric, molecular and immunohistochemical changes were evaluated, including the microcysts number and size, microcysts development and deformation rates as well as the markers of calcification (Alizarin Red staining) and apoptosis (BAX, BCL2, Caspase-3, Caspase-8 and TNF-α expression) in the microcysts. Also the biological, histological and molecular consequences of insulin and BMP-4 treatment on the parasite development were evaluated. **Results:** Insulin and BMP-4 treatment of microcysts resulted in significant increase in microcyst formation, increased size, reduced apoptosis and deformation of the microcysts. Alizarin red staining of the microcysts treated with the insulin and BMP-4 confirmed that calcium deposition is significantly lower than the untreated microcysts. Also Alizarin Red staining and Immunohistochemistry of the microcysts indicates that calcium accumulation in deformed microcysts is higher than the normal ones on day 105. The microcysts began to wrinkle and the germinal layer was partially detached from the laminated layer on day 84. **Conclusion:** Results of the present study suggest that the degenerative changes in hydatid cysts can be slowed down by insulin and BMP-4, indicating that cellular factors and host hormones could contribute to the longevity of hydatid cysts. Significant evidences are provided suggesting that the microcysts cultivated *in vitro* can undergo calcification and apoptotic processes similar to what have been observed in the natural hydatid infection in the intermediate hosts.

Comparison of multiplex copro PCR with coproscopy followed by PCR on

recovered eggs for the detection of *Echinococcus granulosus* and *Taenia* spp. infection in dogs.

Yasur-Landau D, Genad O, Salant H, Dvir E, Mazuz ML, Baneth G.

Vet Parasitol.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36696840/>

Occurrence and Phylogenetic Description of Cystic Echinococcosis Isolate from Egyptian Camel (*Camelus Dromedarius*).

Elshahawy IS, El-Seify MA, Ahamed ZK, Fawaz MM.

Helminthologia.

17-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36694828/>

Cystic echinococcosis is one of the most significant zoonotic diseases of major economic and public health significance worldwide. The current study was carried out to determine the epidemiological profile of cystic echinococcosis as well as to investigate its molecular and phylogenetic status from one-humped camel (*Camelus dromedarius*) in the southern region of Egypt. In the present work, 110 camels freshly slaughtered at Daraw abattoirs, Aswan governorate were inspected for the presence of Hydatid cysts (HCs) visually and manually by palpation and incision, over a period of one year (June, 2018 - May, 2019). Furthermore, fourteen fertile hydatid cyst samples were collected from lungs of slaughtered camels. DNA extraction from two fertile samples was successfully achieved followed by phylogenetic analysis on two mitochondrial genes (*cox1* and *nad1*). Out of 110 camels slaughtered 11 (10 %) were found harboring hydatid cysts. The infection was found to prevail throughout the year, with the highest peak encountered in winter (45.5 %). The lungs were the most frequently infected organs (72.7 %) with liver cysts occurring at a significantly lower rate (27.3 %). The mean value of total protein, glucose, urea, cholesterol, magnesium, potassium, copper and creatinine was higher in cystic fluid from camels as compared to cattle. Blast and phylogenetic analysis on sequenced genes showed the presence of *Echinococcus intermedius*, originally the pig genotype (G7) in camels for the first time in Egypt. To the best of our knowledge, the current research provides a description of the current epidemiological and molecular situation of camel hydatidosis in the southern region of Egypt. Furthermore, the current results may have significant implications for hydatid disease control in the studied region.

Efficacy of Preoperative Albendazole on Protoscoleces Viability in Hydatid Cyst of the Liver.

Vahidirad A, Mansouri M, Shamshirian A, Berenji F, Motie MR.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694569/>

Serological Follow-up of Human Cystic Echinococcosis in the Thrace Region, Turkey.

Eryıldız C, Tarladaçalısır T, Kuyucuklu G, Çakmakçı B, Sakru N.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694561/>

Serological Screening of Patients Diagnosed with Alveolar Echinococcus Disease in Their Home Regions.

Akkas O, Uslu H, Yilmaz I, Aydın Y, Korkut E, Yilmaz A.

Iran J Parasitol.

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36694559/>

Implementing deep learning models for the classification of *Echinococcus multilocularis* infection in human liver tissue.

Sulyok M, Luibrand J, Strohäker J, Karacsonyi P, Frauenfeld L, Makky A, Mattern S, Zhao J, Nadalin S, Fend F, Schürch CM.

Parasit Vectors.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36694210/>

Background: The histological diagnosis of alveolar echinococcosis can be challenging. Decision support models based on deep learning (DL) are increasingly used to aid pathologists, but data on the histology of tissue-invasive parasitic infections are missing. The aim of this study was to implement DL methods to classify *Echinococcus multilocularis* liver lesions and normal liver tissue and assess which regions and structures play the most important role in classification decisions. **Methods:** We extracted 15,756 echinococcus tiles from 28 patients using 59 whole slide images (WSI); 11,602 tiles of normal liver parenchyma from 18 patients using 33 WSI served as a control group. Different pretrained model architectures were used with a 60-20-20% random splitting. We visualized the predictions using probability-thresholded heat maps of WSI. The area-under-the-curve (AUC) value and other performance metrics were calculated. The GradCAM method was used to calculate and visualize important spatial features. **Results:** The models achieved a high validation and test set accuracy. The calculated AUC values were 1.0 in all models. Pericystic fibrosis and necrotic areas, as well as germinative and laminated layers of the metacestodes played an important role in decision tasks according to the superimposed GradCAM heatmaps. **Conclusion:** Deep learning models achieved a high predictive performance in classifying *E. multilocularis* liver lesions. A possible next step could be to validate the model using other datasets and test it against other pathologic entities as well, such as, for example, *Echinococcus granulosus* infection.

A Rare Case Report of Primary Hydatid Disease of the Scapula - an Unforeseen Diagnosis!

Verghese SC, George ST, Duraisamy P, Karthikeyan TM, Kumar SA, Arasu S.

J Orthop Case Rep.

Aug-2022

<https://pubmed.ncbi.nlm.nih.gov/36687497/>

Survey and Molecular Characterization of Echinococcus granulosus sensu stricto from Livestock and Humans in the Altai Region of Xinjiang, China.

Guo B, Zhao L, Zhao L, Mi R, Zhang X, Wang B, Guo G, Ren Y, Qi W, Zhang Z.

Pathogens.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678482/>

Alveolar Echinococcosis in a Patient with Presumed Autoimmune Hepatitis and Primary Sclerosing Cholangitis: An Unexpected Finding after Liver Transplantation.

Fronhoffs F, Dold L, Parčina M, Schneidewind A, Willis M, Barth TFE, Weismüller TJ, Zhou T, Lutz P, Luetkens JA, Gerlach P, Manekeller S, Kalff JC, Vilz TO, Strassburg CP, Kristiansen G.

Pathogens.

30-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678421/>

Primary sclerosing cholangitis is an important reason for liver transplantation. Hepatic alveolar echinococcosis (AE) is caused by *Echinococcus multilocularis* and presents characteristic calcified conglomerates detected by ultrasound or computed tomography scan of the liver. Symptoms of AE only occur after a long period of infection when cholestasis or cholangitis becomes apparent. Here, we report on a patient with presumed autoimmune hepatitis and primary sclerosing cholangitis. After liver transplantation, alveolar echinococcosis was diagnosed in the liver explant.

Assessing Red Fox (*Vulpes vulpes*) Demographics to Monitor Wildlife Diseases: A Spotlight on Echinococcus multilocularis.

Celva R, Crestanello B, Obber F, Dellamaria D, Trevisiol K, Bregoli M, Cenni L, Agreiter A, Danesi P, Hauffe HC, Citterio CV.

Pathogens.

30-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678408/>

Molecular Epidemiology of Cystic Echinococcosis in Rural Baluchistan, Pakistan: A Cross-Sectional Study.

Ullah I, Sattar S, Ali I, Farid A, Ullah A, Eid RA, Samir A Zaki M, Alaa Eldeen M, Ahmed I, Ullah I.

Pathogens.

26-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36678388/>

Muscular hydatid cyst in Iran: A case report.

Agholi M, Heidarian HR, Montaseri Z, Khajeh F.

Int J Surg Case Rep.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36669320/>

Introduction and importance: Hydatid disease, caused by the larval stage of *Echinococcus granulosus*, is a common parasitic infection of humans and herbivores. Although livers and lungs are the most commonly affected organ, hydatid cysts may develop in any body part. Primary muscular hydatid cyst is extremely rare. **Case presentation:** We reported the case of a 40-year-old-woman with the presentation of a soft, mobile, and non-tender lump in the dorsal part of her left upper arm (triceps brachii), which emerged one year ago. Her past medical history was unremarkable. The arm sonography revealed a single uniloculated cystic mass (6.5 cm × 5.5 cm) with a thick wall containing cystic lesions. It suggested the diagnosis of echinococcosis. The patient underwent surgery, and the hydatid cyst was excised. Histopathological examination confirmed hydatidosis. **Clinical discussion:** Hydatid cysts occur rarely (about 4 %) in muscles even in endemic regions. The study is the first case of hydatidosis found in triceps brachii in Fars province, Iran. In endemic regions, considering the hydatid cyst possibility is very important because it presents with many diversities. As it clinically presents a painless slow-growing mass, may be misdiagnosed with benign soft tissue tumors. **Conclusion:** Although muscular hydatidosis is extremely rare, it should be considered a differential diagnosis of any growing subcutaneous or muscular masses or tumors. Imaging modalities and blood tests are highly relevant for diagnosis. Surgical excision, a choice of treatment, should be done with cautions and is combined with anthelmintic therapy to reduce the risk of recurrence.

Echinococcus multilocularis Calreticulin Interferes with C1q-Mediated Complement Activation.

Xian S, Chen L, Yan Y, Chen J, Yu G, Shao Y, Zhan B, Wang Y, Zhao L.

Trop Med Infect Dis.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668954/>

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.

Exp Parasitol.

Feb-2023

<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.

Trématodoses d'origine alimentaire (clonorchiose, opisthorchiase, fasciolase et paragonimose)

A major locus confers triclabendazole resistance in *Fasciola hepatica* and shows dominant inheritance.

Beesley NJ, Cwiklinski K, Allen K, Hoyle RC, Spithill TW, La Course EJ, Williams DJL, Paterson S, Hodgkinson JE.

PLoS Pathog.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36701396/>

Fasciola hepatica infection is responsible for substantial economic losses in livestock worldwide and poses a threat to human health in endemic areas. The mainstay of control in livestock and the only drug licenced for use in humans is triclabendazole (TCBZ). TCBZ resistance has been reported on every continent and threatens effective control of fasciolosis in many parts of the world. To date, understanding the genetic mechanisms underlying TCBZ resistance has been limited to studies of candidate genes, based on assumptions of their role in drug action. Taking an alternative approach, we combined a genetic cross with whole-genome sequencing to localise a ~3.2Mbp locus within the 1.2Gbp *F. hepatica* genome that confers TCBZ resistance. We validated this locus independently using bulk segregant analysis of *F. hepatica* populations and

showed that it is the target of drug selection in the field. We genotyped individual parasites and tracked segregation and reassortment of SNPs to show that TCBZ resistance exhibits Mendelian inheritance and is conferred by a dominant allele. We defined gene content within this locus to pinpoint genes involved in membrane transport, (e.g. ATP-binding cassette family B, ABCB1), transmembrane signalling and signal transduction (e.g. GTP-Ras-adenylyl cyclase and EGF-like protein), DNA/RNA binding and transcriptional regulation (e.g. SANT/Myb-like DNA-binding domain protein) and drug storage and sequestration (e.g. fatty acid binding protein, FABP) as prime candidates for conferring TCBZ resistance. This study constitutes the first experimental cross and genome-wide approach for any heritable trait in *F. hepatica* and is key to understanding the evolution of drug resistance in *Fasciola* spp. to inform deployment of efficacious anthelmintic treatments in the field.

Clonorchis sinensis aggravates biliary fibrosis through promoting IL-6 production via toll-like receptor 2-mediated AKT and p38 signal pathways.

Wang Y, Zhang X, Wang X, Zhang N, Yu Y, Gong P, Zhang X, Ma Y, Li X, Li J.

PLoS Negl Trop Dis.

24-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36693049/>

Clonorchis sinensis is an important food-borne zoonotic parasite which has been linked to biliary fibrosis and cholangiocarcinoma. However, the details of the pathogenesis of *C. sinensis* were unclear. To explore the role and regulatory mechanism of toll-like receptor 2 (TLR2) in *C. sinensis*-induced biliary fibrosis, we established the *C. sinensis*-infected C57BL/6 mouse model with TLR2^{-/-} and wild type (WT) mice. The mortality rate, liver lesions, TLR2 and TGF- β 1 expression, phosphorylation of Smad2/3, AKT, p38, ERK and p65, and cytokine productions were analyzed. Furthermore, similar parameters were examined in mouse biliary epithelial cells (BECs) co-cultured with *C. sinensis* excretory/secretory proteins (ESPs). The results showed that TLR2 expression was enhanced significantly in *C. sinensis*-infected WT mice and mouse BECs. *C. sinensis*-infected TLR2^{-/-} mice exhibited an increased weight and a decreased mortality rate; significantly alleviated liver lesions and biliary fibrosis, reduced numbers of myofibroblasts; decreased expression of TGF- β 1 and phosphorylation level of AKT, p38 and Smad2/3; significantly decreased production of IL-6, TNF- α and IL-4, while increased production of IFN- γ compared with *C. sinensis*-infected WT mice. Furthermore, *C. sinensis* ESPs could activate TLR2-mediated AKT and p38 pathways to increase the production of IL-6 in mouse BECs. In conclusion, these data indicate that *C. sinensis* infection activated TGF- β 1-Smad2/3 through TLR2-mediated AKT and p38 pathways to promote IL-6 production, which resulted in myofibroblast activation and aggravating biliary fibrosis in mice.

Epidemiology of Gastrointestinal Parasites of Cattle in and Around Hosanna Town, Southern Ethiopia.

Tiele D, Sebro E, H/Meskel D, Mathewos M.

Vet Med (Auckl).

17-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691608/>

Effectiveness of public health interventions in reducing the prevalence of *Opisthorchis viverrini*: a protocol for systematic review and network meta-analysis.

Sota P, Alene KA, Andityas M, Tangkawattana S, Sripa B, Clements ACA.

BMJ Open.

08-09-2022

<https://pubmed.ncbi.nlm.nih.gov/36691213/>

Evaluation of bioaccumulation of some heavy metals in liver flukes (*Fasciola hepatica* and *Dicrocoelium dendriticum*) and liver samples of sheep.

Khatemeh S, Imani Baran A.

Vet Res Forum.

2022

<https://pubmed.ncbi.nlm.nih.gov/36686874/>

Different living organisms are used as applicable bioindicators to determine heavy metal pollutions. Recent studies have shown that helminths parasites can be used as efficient environmental sentinels. This study aimed to evaluate *Fasciola hepatica* and *Dicrocoelium dendriticum* as bioaccumulators of lead (Pb), chromium (Cr), cadmium (Cd), copper (Cu). For this work. A total of 50 samples (*F. hepatica*, *D. dendriticum*, and livers from the infected and uninfected sheep, each of 10 samples) were collected from sheep slaughtered in Tabriz abattoir. One gram of each sample was incinerated and analyzed by Flame Atomic Absorption Spectrometry. The analysis of samples showed that Pb, Cr and Cu values in *F. hepatica* were higher than those in *D. dendriticum*, but only the differences of Pb and Cu were significant. The values of heavy metals in *F. hepatica* were significantly higher than those in the infected livers (except for Cd), while in *D. dendriticum*, Cr and Cd were only higher. Based on metal levels in livers, it was found that bioconcentration factors (BCFs) of Cr, Pb and Cu for *F. hepatica* were much more than one, and BCFs of these three metals between two flukes were statistically significant. This study indicated that *F. hepatica* had a higher bioindicator potential than *D. dendriticum* to evaluate environmental pollutants by some metals.

Serum metabolic profiling of rats infected with *Clonorchis sinensis* using LC-MS/MS method.

Han S, Zhang X, Ding J, Li X, Zhang X, Jiang X, Duan S, Sun B, Hu X, Gao Y.

Front Cell Infect Microbiol.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36683702/>

First Molecular Identification of *Fasciola gigantica* in Slaughtered Cattle in Cape Verde: Prevalence, Gross Pathological Lesions, Genetic Identification and Coprological Analysis.

Levy S, Calado M, Mateus TL, Vieira-Pinto M.

Pathogens.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678423/>

A study on fasciolosis prevalence, gross pathological lesions, fluke genetic identification and coprological analysis was carried out in slaughtered cattle from one abattoir in Cape Verde. Of the 131 cattle inspected over two months, 12 (9.0%) presented fasciolosis-compatible lesions (FCL) that resulted in liver condemnation. The genetic characterization of the flukes collected, through restriction fragment length polymorphism analysis of PCR-amplified fragments (PCR-RFLP), confirmed the presence of *Fasciola gigantica*; therefore, being the first identification of this species in cattle from Cape Verde. Animals that released *Fasciola* spp. eggs and, thus, responsible for environment contamination (positive shedders), were identified through coprological analysis (natural sedimentation technique). Of the 12 animals with FCL, samples from 11 were submitted to coprological analysis and 7 (63.6%) were found to be positive shedders. Furthermore, of the 82 animals with non-FCL, randomly selected for coprological analysis, 4 (4.9%) were also found to be positive shedders for *Fasciola* spp. The results of this study, regarding species identification and coprological analysis, are epidemiologically important to update the information regarding fasciolosis in Cape Verde. The new data could help implement effective strategies for disease control and mitigation, consequently reducing economic loss and the level of animal and human infection from the One Health perspective.

microRNAs: Critical Players during Helminth Infections.

Rojas-Pirela M, Andrade-Alviárez D, Quiñones W, Rojas MV, Castillo C, Liempi A, Medina L, Guerrero-Muñoz J, Fernández-Moya A, Ortega YA, Araneda S, Maya JD, Kemmerling U.

Microorganisms.

25-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36677353/>

A Cluster of Paragonimiasis with Delayed Diagnosis Due to Difficulty Distinguishing Symptoms from Post-COVID-19 Respiratory Symptoms: A Report of Five Cases.

Sasaki J, Matsuoka M, Kinoshita T, Horii T, Tsuneyoshi S, Murata D, Takaki R, Tominaga M, Tanaka M, Maruyama H, Kawayama T, Hoshino T.

Medicina (Kaunas).

10-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36676761/>

Prevalence and Associated Risk Factors of Intestinal Parasitic Infections: A Population-Based Study in Phra Lap Sub-District, Mueang Khon Kaen District, Khon Kaen Province, Northeastern Thailand.

Boonjaraspinyo S, Boonmars T, Ekobol N, Artchayasawat A, Sriraj P, Aukkanimart R, Pumhirunroj B, Sripan P, Songsri J, Juasook A, Wonkchalee N.

Trop Med Infect Dis.

27-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668929/>

Intestinal parasitic infections are still a crucial problem among communities in Northeast Thailand. Misuse of antiparasitic drugs and unhealthy food behaviors are known. This study aimed to explore the prevalence, behavioral health factors, and motivation for self-treatment of anti-parasitic drugs in this area. A community-based cross-sectional study was conducted in Phra Lap sub-district, Mu Khon Kaen district, Khon Kaen province, Northeast Thailand, in 2016. A total of 419 participants were recruited to complete a self-administered questionnaire and stool examination. Binary logistic regression was used to assess the association between the risk factor and parasitic infection. Forty-two participants (10%; 95%CI 7.5-13.3) were positive for at least one parasite species. In this community, the most detected intestinal parasite was *Opisthorchis viverrini* (5.3%), followed by *Strongyloides stercoralis* (3.1%). A total of 67.5% of the participants had the experience of anti-parasitic drug treatment within previous 1 year, and "Often eat raw food" was the most common reason for the use of anti-parasitic drugs. On multivariate analysis, parasitic infections were significantly associated with male gender (ORadj. 2.42; 95%CI 1.00-5.85), age ≥ 60 years (ORadj. 7.55; 95%CI 1.60-35.76), and often consuming raw food of at least one type (ORadj. 2.37; 95%CI 1.03-5.44). Given these findings, correction of the dietary habit of eating raw fish/meat, which is the most important measure, and limitation of the use of anthelmintic treatment for individuals with stools positive for ova as well as emphasis on sanitary toilets will be implemented for the prevention and control of parasitic infection in endemic communities.

Successful Treatment of Fasciola hepatica with Metronidazole in a Child: A Case Report.

Ergenc Z, Kepenekli E, Yakut N, Yapici O, Batu U, Tutar E. *Iran J Parasitol.*

Oct-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36660413/>

Filariose lymphatique

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

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

Antimicrob Agents Chemother.

24-01-2023

<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.

Onchocercose

Application of loop mediated isothermal amplification (LAMP) assays for the detection of *Onchocerca volvulus*, *Loa loa* and *Mansonella perstans* in humans and vectors.

Amambo GN, Innocentia N, Abong RA, Fombad FF, Njouendou AJ, Nietcho F, Ekanya R, Kien CA, Ebai R, Lenz B, Ritter M, Esum ME, Deribe K, Cho JF, Beng AA, Enyong PI, Li Z, Hübner MP, Pfarr K, Hoerauf A, Carlow C, Wanji S.

Front Trop Dis.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36684508/>

Onchocerciasis-associated epilepsy: an update and future perspectives.

Hadermann A, Amaral LJ, Van Cutsem G, Siewe Fodjo JN, Colebunders R.

Trends Parasitol.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36528471/>

Direct Proteomic Detection and Prioritization of 19 Onchocerciasis Biomarker Candidates in Humans.

Rosa BA, Curtis K, Erdmann Gilmore P, Martin J, Zhang Q, Sprung R, Weil GJ, Townsend RR, Fischer PU, Mitreva M.

Mol Cell Proteomics.

Jan-2023

<https://pubmed.ncbi.nlm.nih.gov/36435333/>

Schistosomiasis

Correction: "We know about schistosomiasis but we know nothing about FGS": A qualitative assessment of knowledge gaps about female genital schistosomiasis among communities living in Schistosoma haematobium endemic districts of Zanzibar and Northwestern Tanzania.

Mazigo HD, Samson A, Lambert VJ, Kosia AL, Ngoma DD, Murphy R, Matungwa DJ.

PLoS Negl Trop Dis.

26-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36701277/>

Phenotypic Profiling of Macrocyclic Lactones on Parasitic Schistosoma Flatworms.

Ryan KT, Wheeler NJ, Kamara IK, Johnson H, Humphries JE, Zamanian M, Chan JD.

Antimicrob Agents Chemother.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36695583/>

Intestinal Parasitic Infection Among Rural Schoolchildren in Taiz, Yemen: School-based Assessment of The Prevalence and Associated Risk Factors.

Alharazi T.

Helminthologia.

17-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36694831/>

Yemen is an underdeveloped country plagued by poverty, disease, and social conflicts. Furthermore, most of the population lives in rural areas and is vulnerable to intestinal parasite infections (IPI). School-based cross-sectional studies were conducted between 1 February and 31 March 2019 among schoolchildren in rural communities in the Sabir Almadawim and Almadawit districts of Taiz, southwest Yemen. A structured questionnaire collected information regarding sociodemographic characteristics and risk factors. Wet mount and formol-ether concentration techniques were used to detect and identify intestinal parasites in stool specimens. The stool specimens were collected from each study participant using a clean, leak-proof, and adequately labeled stool cup. Statistical analysis of the data was

performed using SPSS version 20. Of the 478 students screened for intestinal parasites, 245 (51.26 %) had at least one parasite. The prevalence of protozoa was higher than helminths (30.3 % versus 20.9 %, respectively). The percentages of single, double, and triple infections were 37.4 %, 4.4 %, and 1.7 %, respectively. *Giardia lamblia* was the most prevalent pathogen (15.5 %), followed by *E. histolytica/dispar* (14.9 %), *Schistosoma mansoni* (13.3 %), *Ascaris lumbricoides* (3.8 %), *Trichuris trichiura* (2.9 %), and *Enterobius vermicularis* (1.3 %). Multivariate analysis confirmed that practicing unwashed hands before eating, open field defecation, unwashed fruits and vegetables, and dirty unclipped fingernails were the most significant predictors of high risk of IPIs ($p < 0.05$). Regarding *Schistosoma mansoni*, multivariate analysis identified the behaviors of practicing swimming in the river/ponds and practicing open defecation, especially near water sources, as independent risk factors for *Schistosoma mansoni* infection among schoolchildren. The current study showed that rural areas in Taiz were significantly infected with IPIs, showing that IPIs remains a significant public health problem in low-income communities. Consequently, prevention efforts should focus on treating and deworming schoolchildren regularly, promoting health education in rural schools, conducting personal hygiene inspections for students, and ensuring that schools have sanitary facilities.

A literature review of schistosomiasis in Ghana: a reference for bridging the research and control gap.

Boateng EM, Dvorak J, Ayi I, Chanova M.

Trans R Soc Trop Med Hyg.

23-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36688317/>

Schistosomiasis is endemic in most sub-Saharan African countries, including Ghana, where the need for effective control involving preventive chemotherapy was indicated by the WHO. Mass drug administration commenced in 2008 and has continued since then in Ghana, but the country remains highly endemic. Here, we review the literature on schistosomiasis to identify research and knowledge gaps potentially affecting disease control. A total of 100 Ghana-related schistosomiasis literature sources were reviewed, showing that most studies were conducted on epidemiology, control of transmission and diagnosis. By contrast, many aspects of this disease remain neglected, including livestock schistosomiasis and its zoonotic potential, recent distribution of disease vectors or widely overlooked genital schistosomiasis. Stratified by region, the highest number of studies focus on Greater Accra, while studies are limited or absent for several other regions. Although this review shows apparent progress in terms of schistosomiasis research and control, a considerable amount of work remains to achieve at least a reduction in the prevalence of the disease, which affects a significant proportion of the population. National epidemiological data based on a nationwide survey, integrated control and improved monitoring and evaluation must be ensured.

Association of schistosome infection with adiposity in Tanzania.

Pham K, PrayGod G, Faurholt-Jepsen D, Olsen MF, Kavishe B, Kitilya B, Corstjens PLAM, de Dood CJ, Friis H, Filteau S, Downs JA, Peck RN.

Front Public Health.

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36684996/>

In vitro evaluation of alkaline lignins as antiparasitic agents and their use as an excipient in the release of benznidazole.

da Cruz Filho IJ, Duarte DMFA, da Conceição Alves de Lima D, Marques DSC, Dos Santos FAB, Alves LC, de Lima Aires A, Nogueira F, do Carmo Alves de Lima M.

Int J Biol Macromol.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36682648/>

The Amazon rainforest is considered the largest tropical timber reserve in the world. The management of native forests in the Amazon is one of the most sensitive geopolitical issues today, given its national and international dimension. In this work, we obtained and characterized physicochemical lignins extracted from branches and leaves of *Protium punctulatum* and *Scleronema micranthum*. In addition, we evaluated in vitro its potential as an antioxidant, cytotoxic agent against animal cells and antiparasitic against promastigotes of *Leishmania amazonensis*, trypomastigotes of *T. cruzi* and against *Plasmodium falciparum* parasites sensitive and resistant to chloroquine. The results showed that the lignins obtained are of the GSH type and have higher levels of guaiacyl units. However, they show structural differences as shown by spectroscopic analysis and radar charts. As for biological activities, they showed antioxidant potential and low cytotoxicity against animal cells. Antileishmanial/trypomastigote assays have shown that lignins can inhibit the growth of promastigotes and trypomastigotes in vitro. The lignins in this study showed low anti-*Plasmodium falciparum* activity against susceptible strains of *Plasmodium falciparum* and were able to inhibit the growth of the chloroquine-resistant strain. And were not able to inhibit the growth of *Schistosoma mansoni* parasites. Finally, lignins proved to be promising excipients in the release of benznidazole. These findings show the potential of these lignins not yet studied to promote different biological activities.

Time series analysis of tegument ultrastructure of in vitro transformed miracidium to mother sporocyst of the human parasite Schistosoma mansoni.

Poteaux P, Gourbal B, Duval D.

Acta Trop.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36681315/>

The transformation of *Schistosoma mansoni* miracidia into mother sporocysts is induced, either in vivo by the penetration of the free-living larval stage, the miracidium, in the snail *Biomphalaria glabrata* or in vitro following the

incubation of the miracidium in Chernin's Balanced Salt Solution (CBSS) or Bge (B. glabrata embryonic cell line) culture medium. The in vitro development of *S. mansoni* miracidium into mother sporocyst was monitored by Scanning Electron Microscopy (SEM) from 2.5 hours to 120 hours in CBSS. The transformation starts when the miracidium ciliate plates detach due to the proliferation of the intercellular ridge associated with the degeneration of mid-body papillae of the miracidium. The loss of ciliated plates causes the appearing of scars, filled across time by the proliferation of a new tegument originating from the interplate ridge. This new tegument covers the entire body of the metamorphosing parasite and differentiates over time, allowing some exchanges (uptakes or secretion/excretion) between the parasite and its host. In contrast to the well-described development of adult and free-living larval stages of *S. mansoni* using SEM, the developmental transformation of intramolluscan stages, especially tegumental changes in the mother sporocyst, has been scarcely documented at the ultrastructural level. In addition, taking into account the latest literature on miracidium electron microscopy and the advances in SEM technologies over the last thirty years, the present study gathers three main objectives: (i) Fill the gap of tegument scanning electron micrographs of in vitro transforming sporocysts; (ii) Update the current bibliographic miracidia and sporocysts image bank due to rapid evolution of SEM technology; (iii) Understand and describe the critical steps and duration of the in vitro miracidium-to-sporocyst transformation process to assist in understanding the interaction between the larval surface and snail immune factors.

Effects of Immunization with Recombinant Schistosoma mansoni Enzymes AK and HGPRT: Murine Infection Control.

Fattori ACM, Montija EA, Fragelli BDL, Correia RO, de Castro CA, Romanello L, Nogueira CT, Allegretti SM, Soares EG, Pereira HD, Anibal FF.

Pathogens.

01-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678417/>

microRNAs: Critical Players during Helminth Infections.

Rojas-Pirela M, Andrade-Alviárez D, Quiñones W, Rojas MV, Castillo C, Liempi A, Medina L, Guerrero-Muñoz J, Fernández-Moya A, Ortega YA, Aráneda S, Maya JD, Kemmerling U.

Microorganisms.

25-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36677353/>

Evaluation of Crude and Recombinant Antigens of Schistosoma japonicum for the Detection of Schistosoma mekongi Human Infection.

Angeles JMM, Wanlop A, Dang-Trinh MA, Kirinoki M, Kawazu SI, Yajima A.

Diagnostics (Basel).

04-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36672994/>

Asian schistosomiasis caused by the blood fluke *Schistosoma mekongi* is endemic in northern Cambodia and Southern Lao People's Democratic Republic. The disease is mainly diagnosed by stool microscopy. However, serodiagnosis such as enzyme-linked immunosorbent assay (ELISA) with soluble egg antigen (SEA), has been shown to have better sensitivity compared to the stool examination, especially in the settings with a low intensity of infection. To date, no recombinant antigen has been assessed using ELISA for the detection of *S. mekongi* infection, due to the lack of genome information for this schistosome species. Thus, the objective of this study is to evaluate several recombinant *S. japonicum* antigens that have been developed in our laboratory for the detection of *S. mekongi* infection. The crude antigen SjSEA and recombinant antigens Sj7TR, SjPCS, SjPRx-4, and SjChi-3 were evaluated in ELISA using serum samples positive for *S. mekongi* infection. The cross-reaction was checked using sera positive for *Ophiorchis viverrini*. ELISA results showed that *S. japonicum* SEA at low concentrations showed better diagnostic performance than the recombinant antigens tested using the archived serum samples from Cambodia. However, further optimization of the recombinant antigens should be conducted in future studies to improve their diagnostic performance for *S. mekongi* detection.

Epidemiology of Gastrointestinal Parasites of Cattle in Three Districts in Central Ethiopia.

Terfa W, Kumsa B, Ayana D, Maurizio A, Tessarin C, Cassini R.

Animals (Basel).

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36670825/>

Population Genetics of Oncomelania hupensis Snails from New-Emerging Snail Habitats in a Currently Schistosoma japonicum Non-Endemic Area.

Cheng YH, Sun MT, Wang N, Gao CZ, Peng HQ, Zhang JY, Gu MM, Lu DB.

Trop Med Infect Dis.

05-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668949/>

Knowledge, Attitude and Practices towards the Prevention of Schistosomiasis Mansoni in an Endemic Area of Alagoas, Northeast Brazil.

Santos AJD, Lima SVM, Sousa AFL, Vasconcelos Dos Santos A, Santos IGA, Bezerra Santos M, Feitosa VLC, Santos ADD, Primão JCM, Andrade D, Silva JRS.

Trop Med Infect Dis.

03-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668941/>

We analyzed the knowledge, attitudes and practices (KAP) of schistosomiasis mansoni prevention in an endemic area of Brazil. This cross-sectional study was conducted between March and May 2021, with 412 participants living in the municipality of Feira Grande, Alagoas, Brazil. Data collection occurred through visits to the Health Center Urbano II and Massapê, through an interview with a structured questionnaire to identify the levels of KAP regarding schistosomiasis prevention. Of all respondents, 70.87% lived in rural areas, 22.66% reported a history of past schistosomiasis and 52.71% never participated in schistosomiasis control program actions. Factors associated with better KAP scores were being part of an older age group, not using rainwater and having no history of past schistosomiasis. Specifically, among the domains, attitude was the highest score and knowledge was the lowest. Participation in a health intervention program, knowing someone who had schistosomiasis and having been informed through a public health program seemed to have an important impact on the population's KAP. Our results contributed to broadening perceptions about schistosomiasis prevention, highlighting the positive impacts that health programs and interventions have on disease control.

Transmission Risk Predicting for Schistosomiasis in Mainland China by Exploring Ensemble Ecological Niche Modeling.

Xue J, Hu X, Hao Y, Gong Y, Wang X, Huang L, Lv S, Xu J, Li S, Xia S.

Trop Med Infect Dis.

28-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668931/>

Helminth species-specific effects on IFN-γ producing T cells during active and latent tuberculosis.

Kiflie A, Bewket G, Tajebe F, Abate E, Schön T, Blomgran R.

PLoS Negl Trop Dis.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36662839/>

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

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

Parasit Vectors.

19-01-2023

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

Schistosomiasis model with treatment, habitat modification and biological control.

Nur W, Trisilowati T, Suryanto A, Kusumawinahyu WM.

Math Biosci Eng.

19-12-2022

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

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

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, Matendecheri SH.

PLoS Negl Trop Dis.

05-01-2023

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

From field to laboratory: isolation, genetic assessment, and parasitological behavior of *Schistosoma mansoni* obtained from naturally infected wild rodent *Holochilus sciureus* (Rodentia, Cricetidae), collected in Northeastern Brazil.

Miranda GS, Rodrigues JGM, Resende SD, Camelo GMA, Silva JKA, Dos Santos JCR, Silva-Souza N, Pereira FB, Furtado LFV, Rabelo ÉML, Negrão-Corrêa D.

Parasitol Res.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36534238/>

Wild rodent species are naturally infected by *Schistosoma mansoni*; however, the genetic characterization of the parasite, its parasitological features, and its role in human schistosomiasis are poorly understood. In this study, we isolated and characterized *Schistosoma* from naturally infected *Holochilus sciureus*, called HS strain, collected from a schistosomiasis endemic region in Maranhão State, Brazil. To isolate the parasite, miracidia obtained from the livers of *H. sciureus* were used to infect *Biomphalaria glabrata* of sympatric (called SB) and allopatric (called BH) strains, and the produced cercariae were subcutaneously inoculated into hamsters and/or BALB/c mice. Parasitological kinetics in experimentally infected hosts were evaluated, and the tRNA^{Cys}-12S (referred to as 16S herein) and cox 1 regions of mtDNA from isolated worms were amplified and sequenced. Only miracidia obtained from infected mice, but not from hamsters, were capable of infecting *B. glabrata*, allowing maintenance of the isolated parasite. Cox1 and 16S mtDNA sequences showed 100% similarity with *S. mansoni*, and phylogenetic analysis showed that the HS strain of *S. mansoni* forms an assemblage with isolates from America and Kenya, confirming the conspecificity. Experimental infection of *B. glabrata* SB with *S. mansoni* HS resulted in two peaks of cercariae shedding at 45 and 70 days post-infection (dpi) and caused higher mortality than in *B. glabrata* BH. The worm recovery rate in mice was approximately 13%, and the peak of egg elimination occurred at the 10th week post-infection. Therefore, *S. mansoni* obtained from *H. sciureus* was successfully isolated, genetically characterized, and maintained in mice, allowing further study of this schistosome strain.

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

Intestinal Parasitic Infection Among Rural Schoolchildren in Taiz, Yemen: School-based Assessment of The Prevalence and Associated Risk Factors.

Alharazi T.

Helminthologia.

17-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36694831/>

Intestinal Parasitic Infections and Associated Risk Factors among Food Handlers of Food and Drinking Establishments in Woldia Town, North-East Ethiopia: A Cross-Sectional Study.

Feleke DG, Bisetegn H, Zewudu G, Alemu Y, Feleke ST.

J Trop Med.

14-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36691674/>

Excretory/Secretory Proteome of Females and Males of the Hookworm *Ancylostoma ceylanicum*.

Uzoechi SC, Rosa BA, Singh KS, Choi YJ, Bracken BK, Brindley PJ, Townsend RR, Sprung R, Zhan B, Bottazzi ME, Hawdon JM, Wong Y, Loukas A, Djuranovic S, Mitreva M.

Pathogens.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36678443/>

The dynamic host-parasite mechanisms underlying hookworm infection establishment and maintenance in mammalian hosts remain poorly understood but are primarily mediated by hookworm's excretory/secretory products (ESPs), which have a wide spectrum of biological functions. We used ultra-high performance mass spectrometry to comprehensively profile and compare female and male ESPs from the zoonotic human hookworm *Ancylostoma ceylanicum*, which is a natural parasite of dogs, cats, and humans. We improved the genome annotation, decreasing the number of protein-coding genes by 49% while improving completeness from 92 to 96%. Compared to the previous genome annotation, we detected 11% and 10% more spectra in female and male ESPs, respectively, using this improved version, identifying a total of 795 ESPs (70% in both sexes, with the remaining sex-specific). Using functional databases (KEGG, GO and Interpro), common and sex-specific enriched functions were identified. Comparisons with the exclusively human-infective hookworm *Necator americanus* identified species-specific and conserved ESPs. This is the first study identifying ESPs from female and male *A. ceylanicum*. The findings provide a deeper understanding of hookworm protein functions that assure long-term host survival and facilitate future engineering of transgenic hookworms and analysis of regulatory elements mediating the high-level expression of ESPs. Furthermore, the findings expand the list of potential vaccine and diagnostic targets and identify biologics that can be explored for anti-inflammatory potential.

Soil-Transmitted Helminth Infections among Antenatal Women in Primary Care Settings in Southern India: Prevalence, Associated Factors and Effect of Anti-Helminthic Treatment.

Ulaganeethi R, Saya GK, Rajkumari N, Kumar SS, Ganapathy K, Dorairajan G.

Trop Med Infect Dis.

07-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668955/>

Mono-Parasitic and Poly-Parasitic Intestinal Infections among Children Aged 36-45 Months in East Nusa Tenggara, Indonesia.

Athiyyah AF, Surono IS, Ranuh RG, Darma A, Basuki S, Rossyanti L, Sudarmo SM, Venema K.

Trop Med Infect Dis.

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668952/>

The prevalence of intestinal parasitic infection remains high in developing countries, especially because of geographic and socio-demographic factors. This study aimed to evaluate intestinal parasitic infection, as well as its risk factors, among children aged 36-45 months in a rural area (North Kodi) and an urban area (Kupang) of East Nusa Tenggara, Indonesia. Anthropometry, socio-demographic factors and personal hygiene practices were assessed. A total of 214 children participated in the study, and 200 stool samples were collected for intestinal parasite examination. Approximately 30.5% (61/200) of the children were infected with one or more intestinal parasites (67.2%; 41/61 being mono-parasitic infections and 32.8%; 20/61 being poly-parasitic infections). A total of 85 intestinal parasites were detected, consisting of 35.3% (30/85) protozoa and 64.7% (55/85) helminths. The predominant protozoa were *Giardia lamblia* (43%; 13/30) and *Blastocystis* spp. (33.3%; 10/30), whereas the predominant helminths were *Trichuris trichiura* (50.9%; 28/55) and *Ascaris lumbricoides* (43.6%; 24/55). Moreover, intestinal parasitic infection was associated with rural area (OR 4.5; 95%CI 2.3-8.6); the absence of treatment with deworming drugs (OR 2.56; 95%CI 1.3-5.0); sanitation facilities without a septic tank (OR 4.3; 95%CI 2.1-8.5); unclean water as a source of drinking water (OR 4.67; 95%CI 2.4-9.4); no handwashing practice after defecation (OR 3.2; 95%CI 1.4-7.3); and stunted children (OR 4.4; 95%CI 2.3-8.3). In conclusion, poly-parasitic infections were common in this study. Poor personal hygiene practice and sanitation factors contributed to the high prevalence of intestinal parasitic infection in 36-45-month-old children in East Nusa Tenggara, Indonesia.

Helminth species-specific effects on IFN- γ producing T cells during active and latent tuberculosis.

Kiflie A, Bewket G, Tajebe F, Abate E, Schön T, Blomgran R.

PLoS Negl Trop Dis.

20-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36662839/>

Ascaris induced acute pancreatitis in paediatric population - a case series.

Afreen M, Mustafa H, Qureshi S, Afreen J, Mansoor A, Shaikh N.

J Pak Med Assoc.

Oct-2022

<https://pubmed.ncbi.nlm.nih.gov/36661004/>

The most common helminthic parasitic infection inhabiting human intestine is *Ascaris lumbricoides* (AL). Being the largest of the helminthic family, it infects almost one billion people worldwide, but any information about local population is unavailable especially in children. When patients present with abdominal pain, having *ascaris* induced pancreatitis never meets the differential diagnosis list even though AL itself is highly prevalent in our part of the world. Infected patients can present with a variety of symptoms depending on the location of parasite. If the biliary tree is inhabited, patients usually

present with symptoms of choledocholithiasis or pancreatitis. We report the case series of 3 patients from paediatric age group, having acute pancreatitis secondary to AL. Patients had upper abdominal pain of varying duration. Ultrasound abdomen showed worm inside the Common Bile Duct (CBD) in all 3 patients. Endoscopic retrograde cholangio-pancreatography (ERCP) showed worms coming out of the ampullary orifice. Two patients received albendazole orally post ERCP and were discharged after complete resolution of symptoms with advice of repeat ERCP after 6 weeks, however one patient was advised Magnetic resonance cholangio-pancreatography (MRCP).

Gale

Erratum: Oral ivermectin to treat scabies: a comparison of two different regimens.

[No authors listed]

Clin Exp Dermatol.

25-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36702579/>

Oral ivermectin to treat scabies: a comparison of two different regimens.

Balestri R, Magnano M, Infusino SD, Girardelli CR, Ioris T, Rech G.

Clin Exp Dermatol.

10-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36702573/>

As *Sarcoptes scabiei* is becoming less sensitive to permethrin, clinicians have started to prescribe oral ivermectin (OI) as a first-line treatment. Guidelines suggest OI 200 µg kg⁻¹ as two doses, 1 week apart. However, the black box of the ivermectin registered in Italy recommends a single dose. To compare these two regimens, we collected 71 cases of scabies and treated them according to this protocol [single-dose group (SDG)]. This population was compared to 68 patients who received two doses 1 week apart [double-dose group (DDG)]. Clearance of the disease was achieved in 98% of DDG patients. In the SDG, treatment was successful in only 58% of patients. This study confirms that the absence of a second intake of OI is one of the main predictors of treatment failure ($P < 0.001$), which may also increase the likelihood of emerging resistance in *S. scabiei*.

A resistant parasitic flare-up amid children in Italy: Comment on "Diagnosis and management of pediatric scabies: Results from a survey on 317 Italian dermatologists".

Herzum A, Gariazzo L, Viglizzo G, Garibeh E, Pastorino C, Occella C.

Travel Med Infect Dis.

18-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36681292/>

Scabicide Potential of Coconut Seed Extract in Rabbits via Downregulating Inflammatory/Immune Cross Talk: A Comprehensive Phytochemical/GC-MS and In Silico Proof.

Zahran EM, Abdel-Maqsood NMR, Tammam OY, Abdel-Rahman IM, Elrehany MA, Bakhsh HT, Altemani FH, Algehainy NA, Alzubaidi MA, Abdelmohsen UR, Elmaidomy AH.

Antibiotics (Basel).

27-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36671243/>

Scabies is an invasive skin condition caused by *Sarcoptes scabiei* mites. The present study investigates the antiscabies potential of coconut seed extract (CSE) in rabbits. GC-MS analysis of the seed oil identified 17 known compounds, while CSE phytochemical investigation afforded 4 known ones. The topical application of seed extract improved all signs of infection, and the improvement started 3 days post application. However, in vitro application of the extract caused 99% mortality of mites 1 day post application. Histopathological examination revealed the absence of inflammatory infiltration and hyperkeratosis of the epidermis, compared with ivermectin-treated groups which revealed less improvement. The mRNA gene expression results revealed a suppression of IL-1 β , IL-6, IL-10, MMP-9, VEGF, and MCP-1, and an upregulation of I-CAM-1, KGF as well as TIMP-1. The docking analysis emphasized a strong binding of gondoic acid with IL-1 β , IL-6, and VEGF with high binding scores of -5.817, -5.291, and -8.362 kcal/mol, respectively, and a high binding affinity of 3''(1'''-O- β -D-glucopyranosyl)-sucrose with GST with -7.24 kcal/mol. Accordingly, and for the first time, our results highlighted the scabicide potential of coconut seed extract, which opens the gate for an efficient, cost-effective as well as herbal-based alternative for the control of scabies in rabbits.

Pruritic papules and nodules as sign of persistent scabies infestation despite treatment according to current guidelines evidence for treatment resistance to ivermectin, benzylbenzoate and permethrin proven by videomicroscopy.

Lehmann P, Kremer A, Assmann T, Mang R.

IDCases.

09-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36660738/>

Scabies infestation is a growing public health issue due to its world wide increase of incidence. The objective of this study was to proof treatment resistance towards treatment, which was applied according to international guidelines. This is a controversial issue since treatment failures were believed to be due to false application of the treatment. Here, we proof for the first time this treatment resistance by videomicroscopic evaluation. Additionally an escalation therapy is described, which led to an effective treatment.

Vaccination with a cocktail vaccine elicits significant protection against *Sarcoptes scabiei* in rabbits, whereas the multi-epitope vaccine offers limited protection.

Shen N, Wei W, Chen Y, Liu S, Xiong L, Xiao J, Gu X, Xie Y, Xu J, Jing B, Peng X, Yang G.

Exp Parasitol.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36509170/>

Morsures de serpent

Factor assay in victims of snake bite: Experience from a tertiary care institute in South India.

Rafi AM, Innah SJ.

Asian J Transfus Sci

Jul-Dec 2022

<https://pubmed.ncbi.nlm.nih.gov/36687535/>

Secretory Phospholipases A₂, from Snakebite Envenoming to a Myriad of Inflammation Associated Human Diseases-What Is the Secret of Their Activity?

Tonello F.

Int J Mol Sci.

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36675102/>

Secreted phospholipases of type A₂ (sPLA₂s) are proteins of 14-16 kDa present in mammals in different forms and at different body sites. They are involved in lipid transformation processes, and consequently in various immune, inflammatory, and metabolic processes. sPLA₂s are also major components of snake venoms, endowed with various toxic and pharmacological properties. The activity of sPLA₂s is not limited to the enzymatic one but, through interaction with different types of molecules, they exert other activities that are still little known and explored, both outside and inside the cells, as they can be endocytosed. The aim of this review is to analyze three features of sPLA₂s, yet under-explored, knowledge of which could be crucial to understanding the activity of these proteins. The first feature is their disulphide bridge pattern, which has always been considered immutable and necessary for their stability, but which might instead be modulable. The second characteristic is their ability to undergo various post-translational modifications that would control their interaction with other molecules. The third feature is their ability to participate in active molecular condensates both on the surface and within the cell. Finally, the implications of these features in the design of anti-inflammatory drugs are discussed.

A global core outcome measurement set for snakebite clinical trials.

Abouyannis M, Esmail H, Hamaluba M, Ngama M, Mwangudzah H, Mumba N, Yeri BK, Mwalukore S, Alphan HJ, Aggarwal D, Alcoba G, Cammack N, Chippaux

JP, Coldiron ME, Gutiérrez JM, Habib AG, Harrison RA, Isbister GK, Lavonas EJ, Martins D, Ribeiro I, Watson JA, Williams DJ, Casewell NR, Walker SA, Lalloo DG; Snakebite Global Core Outcome Set Study Group.

Lancet Glob Health.

Feb-2023

<https://pubmed.ncbi.nlm.nih.gov/36669810/>

Snakebite in South Africa: A retrospective review May 2015-June 2020.

Lerner A, Marks CJ, Kellermann TA.

Toxicon.

17-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36669533/>

Wound Infection of Snakebite from Venomous *Protobothrops mucrosquamatus*, *Viridovipera stejnegeri* and *Naja atra* in Taiwan: Validation of BITE and Cobra BITE Scoring Systems and their Bacteriological Differences in Wound Cultures.

Yeh H, Gao SY, Lin CC.

Toxins (Basel).

15-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668897/>

Patients bitten by *Protobothrops mucrosquamatus*, *Viridovipera stejnegeri*, and *Naja atra* develop different degrees of wound infection. This study validated BITE and Cobra BITE scoring systems that we established previously. Bacteriological studies of patients with wound infection were conducted. The operating characteristic curves and area under the curve (AUC) and wound infection rates were compared between the derivation set (our previous study patient population) and the validation set (new patient cohorts enrolled between June 2017 and May 2021). No significant differences in the AUC for both the BITE (0.84 vs. 0.78, $p = 0.27$) and Cobra BITE (0.88 vs. 0.75, $p = 0.21$) scoring systems were observed between the derivation and validation sets. *Morganella morganii* and *Enterococcus faecalis* were the two most commonly detected bacteria in the microbiological study. More bacterial species were cultured from *N. atra*-infected wounds. Antibiotics such as amoxicillin with clavulanic acid, oxacillin, and ampicillin may not be suitable for treating patients with *P. mucrosquamatus*, *V. stejnegeri*, and *N. atra* bites in Taiwan. Carbapenem, third-generation cephalosporins, and fluoroquinolone may be superior alternatives.

Highly Evolvable: Investigating Interspecific and Intraspecific Venom Variation in Taipans (*Oxyuranus* spp.) and Brown Snakes (*Pseudonaja* spp.).

van Thiel J, Alonso LL, Slagboom J, Dunstan N, Wouters RM, Modahl CM, Vonk FJ, Jackson TNW, Kool J.

Toxins (Basel).

13-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668892/>

In Vitro Efficacy of Antivenom and Varespladib in Neutralising Chinese Russell's Viper (*Daboia siamensis*) Venom Toxicity.

Lay M, Liang Q, Isbister GK, Hodgson WC.

Toxins (Basel).

11-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668882/>

Neuromuscular Weakness and Paralysis Produced by Snakebite Envenoming: Mechanisms and Proposed Standards for Clinical Assessment.

Bickler PE, Abouyannis M, Bhalla A, Lewin MR.

Toxins (Basel).

06-01-2023

<https://pubmed.ncbi.nlm.nih.gov/36668869/>

Respiratory and airway-protective muscle weakness caused by the blockade of neuromuscular transmission is a major cause of early mortality from snakebite envenoming (SBE). Once weakness is manifest, antivenom appears to be of limited effectiveness in improving neuromuscular function. Herein, we review the topic of venom-induced neuromuscular blockade and consider the utility of adopting clinical management methods originally developed for the safe use of neuromuscular blocking agents by anesthesiologists in operating rooms and critical care units. Failure to quantify neuromuscular weakness in SBE is predicted to cause the same significant morbidity that is associated with failure to do so in the context of using a clinical neuromuscular block in surgery and critical care. The quantitative monitoring of a neuromuscular block, and an understanding of its neurophysiological characteristics, enables an objective measurement of weakness that may otherwise be overlooked by traditional clinical examination at the bedside. This is important for the initial assessment and the monitoring of recovery from neurotoxic envenoming. Adopting these methods will also be critical to the conduct of future clinical trials of toxin-inhibiting drugs and antivenoms being tested for the reversal of venom-induced neuromuscular block.

The BRAVO Clinical Study Protocol: Oral Varespladib for Inhibition of Secretory Phospholipase A₂ in the Treatment of Snakebite Envenoming.

Carter RW, Gerardo CJ, Samuel SP, Kumar S, Kotehal SD, Mukherjee PP, Shirazi FM, Akpunonu PD, Bammigatti C, Bhalla A, Manikath N, Platts-Mills TF, Lewin MR; BRAVO Study Group.

Toxins (Basel).

28-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668842/>

Monoclonal-Based Antivenomics Reveals Conserved Neutralizing Epitopes in Type I PLA₂ Molecules from Coral Snakes.

Corrêa-Netto C, Strauch MA, Monteiro-Machado M, Teixeira-Araújo R, Fonseca JG, Leitão-Araújo M, Machado-Alves ML, Sanz L, Calvete JJ, Melo PA, Zingali RB.

Toxins (Basel).

26-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668835/>

Commercial Antivenoms Exert Broad Paraspecific Immunological Binding and In Vitro Inhibition of Medically Important Bothrops Pit Viper Venoms.

Alsolaiss J, Alomran N, Hawkins L, Casewell NR.

Toxins (Basel).

20-12-2022

<https://pubmed.ncbi.nlm.nih.gov/36668821/>

Snakebite envenoming is a life threatening neglected tropical disease that represents a considerable public health concern in the tropics. Viperid snakes of the genus *Bothrops* are among those of greatest medical importance in Latin America, and they frequently cause severe systemic haemotoxicity and local tissue destructive effects in human victims. Although snakebite antivenoms can be effective therapeutics, their efficacy is undermined by venom toxin variation among snake species. In this study we investigated the extent of paraspecific venom cross-reactivity exhibited by three distinct anti-*Bothrops* antivenoms (Soro antibotrópico-crotálico, BothroFav and PoliVal-ICP) against seven different *Bothrops* pit viper venoms from across Latin America. We applied a range of in vitro assays to assess the immunological binding and recognition of venom toxins by the antivenoms and their inhibitory activities against specific venom functionalities. Our findings demonstrated that, despite some variations, the monovalent antivenom BothroFav and the polyvalent antivenoms Soro antibotrópico-crotálico and PoliVap-ICP exhibited extensive immunological recognition of the distinct toxins found in the different *Bothrops* venoms, with Soro antibotrópico-crotálico generally outperformed by the other two products. In vitro functional assays revealed outcomes largely consistent with the immunological binding data, with PoliVap-ICP and BothroFav exhibiting the greatest inhibitory potencies against procoagulant and fibrinogen-depleting venom activities, though Soro antibotrópico-crotálico exhibited potent inhibition of venom metalloproteinase activities. Overall, our findings demonstrate broad levels of antivenom paraspecificity, with in vitro immunological binding and functional inhibition often highly comparable between venoms used to manufacture the antivenoms and those from related species, even in the case of the monovalent antivenom BothroFav. Our findings suggest that the current clinical utility of these antivenoms could possibly be expanded to other parts of Latin America that currently suffer from a lack of specific snakebite therapies.

Ethnobotany, botany, phytochemistry and ethnopharmacology of the genus *Thalictrum* L. (Ranunculaceae): A review.

Singh H, Singh D, Lekhak MM.

J Ethnopharmacol.

Apr-2023

<https://pubmed.ncbi.nlm.nih.gov/36470306/>