



## **Veille scientifique**

# **Maladies tropicales négligées**

**Semaine 24**  
*12 au 18 juin 2023*

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## Cysticercose

### Impaired spatial working memory and reduced hippocampal neuronal density in a rat model of neurocysticercosis.

Baquedano LE, Bernal EG, Carrion DJ, Delgado AD, Gavidia CM, Kirwan DE, Gilman RH, Verastegui MR.

01-06-2023

*Front Cell Neurosci.*

<https://pubmed.ncbi.nlm.nih.gov/37323586/>

### Calcified Neurocysticercosis- Are We Missing Something?: Reply.

Shanmugavel P, Sehgal R.

15-06-2023

*Indian Pediatr.*

<https://pubmed.ncbi.nlm.nih.gov/37293916/>

### Calcified Neurocysticercosis- Are We Missing Something?

Das BK, Khound M.

15-06-2023

*Indian Pediatr.*

<https://pubmed.ncbi.nlm.nih.gov/37293915/>

### Prevalence trend and burden of neglected parasitic diseases in China from 1990 to 2019: findings from global burden of disease study.

Xie Y, Shi D, Wang X, Guan Y, Wu W, Wang Y.

24-05-2023

*Front Public Health.*

<https://pubmed.ncbi.nlm.nih.gov/37293619/>

**Objective:** This study sought to investigate the parasitic diseases of neglected tropical diseases defined by the World Health Organization based on the Global Burden of Disease Study (GBD) database. Importantly, we analyzed the prevalence and burden of these diseases in China from 1990 to 2019 to provide valuable information to formulate more effective measures for their management and prevention. **Methods:** Data on the prevalence and burden of neglected parasitic diseases in China from 1990 to 2019 were extracted from the global health data exchange (GHDx) database, including the absolute number of prevalence, age-standardized prevalence rate, disability-adjusted life year (DALY) and age-standardized DALY rate. Descriptive analysis was used to analyze the prevalence and burden changes, sex and age distribution of various parasitic diseases from 1990 to 2019. A time series model [Auto-Regressive Integrated Moving Average (ARIMA)] was used to predict the DALYs of neglected parasitic diseases in China from 2020 to 2030. **Results:** In 2019, the number of neglected parasitic diseases in China was 152518062, the age-standardized prevalence was 11614.1 (95% uncertainty interval (UI) 8758.5-15244.5), the DALYs were 955722, and the age-standardized DALY rate was 54.9 (95% UI 26.0-101.8). Among these, the age-standardized prevalence of soil-derived helminthiasis was the highest (9370.2/100,000), followed by food-borne

trematodiasis (1502.3/100,000) and schistosomiasis (707.1/100,000). The highest age-standardized DALY rate was for food-borne trematodiasis (36.0/100,000), followed by cysticercosis (7.9/100,000) and soil-derived helminthiasis (5.6/100,000). Higher prevalence and disease burden were observed in men and the upper age group. From 1990 to 2019, the number of neglected parasitic diseases in China decreased by 30.4%, resulting in a decline in DALYs of 27.3%. The age-standardized DALY rates of most diseases were decreased, especially for soil-derived helminthiasis, schistosomiasis and food-borne trematodiasis. The ARIMA prediction model showed that the disease burden of echinococcosis and cysticercosis exhibited an increasing trend, highlighting the need for further prevention and control. **Conclusion:** Although the prevalence and disease burden of neglected parasitic diseases in China have decreased, many issues remain to be addressed. More efforts should be undertaken to improve the prevention and control strategies for different parasitic diseases. The government should prioritize multisectoral integrated control and surveillance measures to prioritize the prevention and control of diseases with a high burden of disease. In addition, the older adult population and men need to pay more attention.

### Low responsiveness of peripheral lymphocytes in extraparenchymal neurocysticercosis.

Romo ML, Osorio R, Toledo A, Carrillo-Mezo R, Valdez R, Romano MC, Sciotto E, Fragoso G, Fleury A.

01-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37262055/>

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## Dengue, chikungunya et maladie à virus Zika

### Case report: Regression of Glioblastoma after flavivirus infection.

Garcez PP, Guasti A, Ventura N, Higa LM, Andreiulo F, de Freitas GPA, Ribeiro LJ, Maia RA, de Lima SMB, de Souza Azevedo A, Schwarcz WD, Caride EC, Chimelli L, Dubois LG, Ferreira Júnior ODC, Tanuri A, Moura-Neto V, Niemeyer P.

01-06-2023

*Front Med (Lausanne).*

<https://pubmed.ncbi.nlm.nih.gov/37324152/>

Glioblastoma is the most frequent and aggressive primary brain cancer. In preclinical studies, Zika virus, a flavivirus that triggers the death of glioblastoma stem-like cells. However, the flavivirus oncolytic activity has not been demonstrated in human patients. Here we report a glioblastoma patient who received the standard of care therapy, including surgical resection, radiotherapy and temozolomide. However, shortly after the tumor mass resection, the patient was clinically diagnosed with a typical arbovirus-like infection, during a Zika virus outbreak in Brazil. Following the infection resolution, the glioblastoma regressed, and no recurrence was observed.

This clinical response continues 6 years after the glioblastoma initial diagnosis.

### Simulations and fractional modeling of dengue transmission in Bangladesh.

Akter S, Jin Z.

27-03-2023

*Math Biosci Eng.*

<https://pubmed.ncbi.nlm.nih.gov/37322916/>

### Incidence and factors associated with chronic chikungunya arthritis following chikungunya virus infection.

Yodtaweepornanan P, Pongsittisak W, Satpanich P.

16-06-2023

*Trop Med Int Health.*

<https://pubmed.ncbi.nlm.nih.gov/37326000/>

**Objectives:** Chikungunya virus infection is a mosquito-borne illness. First-phase symptoms include fever, malaise, rash, and arthritis (self-limiting). Some patients can have chronic-phase symptoms, including chronic tenosynovitis, bursitis, and arthritis. This study aimed to determine the incidence and risk factors of chronic arthritis in patients with chikungunya infection. **Methods:** This retrospective cohort study analysed all adults diagnosed with chikungunya infection between 2015 and 2020 at our centre. Baseline and follow-up symptoms were evaluated in serologically confirmed cases. Chronic chikungunya arthritis was persistent arthritis >3 months after the onset. Patients who had preexisting chronic inflammatory arthritis and were lost to follow-up before 3 months from diagnosis were excluded. **Results:** This study enrolled 120 patients. The median age was 51 (IQR 14) years, and 78% were female. The median number of joints with arthritis was 4 (IQR 8). The initial visual analog scale (VAS) score was 50 mm (IQR 40). Small joints of the hands, wrist, and knee (44.2%, 43.3%, and 42.3%, respectively) were the most affected. The incidence of chronic chikungunya arthritis was 40.4%. From the multivariable logistic regression, the initial number of joints with arthritis, initial VAS scores, and female sex were independently associated with chronic chikungunya arthritis with odds ratios of 1.09 (95% confidence interval [CI] 1.01-1.18), 1.03 (95% CI 1.01-1.06), and 4.17 (95% CI, 1.05-16.67), respectively. **Conclusions:** Chronic chikungunya arthritis is common in patients with chikungunya virus infection. Its predictive factors include the initial number of joints with arthritis, initial VAS scores, and female sex.

### Investigation of Zika virus methyltransferase inhibitors using steered molecular dynamics.

Rabaan AA, AlShehail BM, Halwani MA, Alshengeti A, Najim MA, Garout M, Bajunaid HA, Alshamrani SA, Al Fares MA, Alissa M, Alwashmi ASS.

16-06-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/37325855/>

Zika virus (ZIKV) spread is considered a major public health threat by the World Health Organization (WHO). There are no vaccines or drugs available to control the infection of the Zika virus, therefore a highly effective medicinal molecule is urgently required. In this study, a computationally intensive investigation was performed to identify a potent natural compound that could inhibit the ZIKV NS5 methyltransferase. This research approach is based on target-based drug identification principles where the native inhibitor SAH (S-adenosylhomocysteine) of ZIKV NS5 methyltransferase was selected as a reference. High-throughput virtual screening and tanimoto similarity coefficient were applied to the natural compound library for ranking the potential candidates. The top five compounds were selected for interaction analysis, MD simulation, total binding free energy through MM/GBSA, and steered MD simulation. Among these compounds, Adenosine 5'-monophosphate monohydrate, Tubercidin, and 5-Iodotubercidin showed stable binding to the protein compared to the native compound, SAH. These three compounds also showed less fluctuations in RMSF in contrast to native compound. Additionally, the same interacting residues observed in SAH also made strong interactions with these three compounds. Adenosine 5'-monophosphate monohydrate and 5-Iodotubercidin had greater total binding free energies than the reference ligand. Moreover, the dissociation resistance of all three compounds was equivalent to that of the reference ligand. This study suggested binding properties of three-hit compounds that could be used to develop drugs against Zika virus infections. Communicated by Ramaswamy H. Sarma.

### Predicting potential areas at risk of the Dengue Hemorrhagic Fever in Jakarta, Indonesia-analyzing the accuracy of predictive hot spot analysis in the absence of small geographical area data.

Prasetya V, Vito V, Tanawi IN, Aldila D, Hertono GF.

12-06-2023

*Infect Ecol Epidemiol.*

<https://pubmed.ncbi.nlm.nih.gov/37325468/>

### Dengue and Scrub Typhus Coinfection: A Diagnostic Dilemma.

Chandra A, Hati A, Ray AK, Chakraborty U, Karmakar PS, Dasgupta S.

31-05-2023

*Oman Med J.*

<https://pubmed.ncbi.nlm.nih.gov/37325262/>

### Trends and Pattern of Diseases Under Integrated Disease Surveillance Project in Jodhpur, Rajasthan: A Retrospective Observational Study.

Shekhawat J, Kumar D, Bhardwaj P, Meena DS, Garg MK.

Mars-Avr 2023

*Indian J Community Med.*

<https://pubmed.ncbi.nlm.nih.gov/37323727/>

## **Towards the diagnosis of dengue virus and its serotypes using designed CRISPR/Cas13 gRNAs.**

**Prajapati A, Tandon A, Nain V.**

31-08-2023

*Bioinformation.*

<https://pubmed.ncbi.nlm.nih.gov/37323556/>

## **Crimean-Congo Hemorrhagic Fever Presented in Dengue Epidemic: A Case Report.**

**Salih N, Baig KS, Jan MA, Ihtisham M, Ahmad F, Ghani N, Saeed A, Hussain U.**

14-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37323327/>

In Pakistan, hemorrhagic diseases, including dengue and Crimean-Congo hemorrhagic fever (CCHF), are common. Therefore, an accurate diagnosis is challenging in the early stages of sickness owing to geographic overlap and early clinical similarities between the two disorders. A 35-year-old man who had previously experienced hematemesis and high-grade fever presented to our hospital. Despite receiving supportive care for a preliminary diagnosis of dengue hemorrhagic fever, the patient's condition worsened. The results of the dengue IgM antibody test were negative. On the fourth day of admission, a qualitative polymerase chain reaction test for CCHF virus RNA was performed, and the result returned positive. All medical personnel and attendants who had contact with the patient had to receive ribavirin prophylaxis, which required significant investment in resources. Because CCHF can have long-term financial and health repercussions for contacts, including healthcare personnel in developing nations, it is essential to identify and treat it as soon as possible. It is necessary to keep track of dengue and CCHF cases more closely to develop predictors of disease diagnosis that are reasonably trustworthy, affordable, and quick. These predictors can aid in directing future choices regarding the care of similar situations. Ultimately, such an approach might result in improved cost control in environments with limited resources. Consideration should also be given to patients who receive ribavirin prophylaxis.

## **Magnetic Resonance Imaging Brain Findings in Chikungunya Virus (CHIKV) Infection with Neurological Complication during Epidemic Outbreak.**

**Sethi KS, Aryan AK, Ganeshan PK.**

Mai-Juin 2023

*Neurol India.*

<https://pubmed.ncbi.nlm.nih.gov/37322742/>

**Background and objective:** The Chikungunya virus is an alphavirus RNA of the family *Togaviridae* transmitted by the *Aedes* mosquito. We aim to report magnetic resonance imaging (MRI) brain findings for neurological complications at our institute during epidemic outbreak.

**Materials and methods:** A total of 43 seropositive cases of

Chikungunya infection underwent MRI brain. **Results:** Out of 43 patients, 27 (63%) had discrete and confluent supratentorial T2-weighted (T2W) and fluid-attenuated inversion recovery (FLAIR) hyper-intense white matter foci. A total of 14 patients (33%) showed multiple foci/areas of diffusion restriction, and four of these patients had infra-tentorial T2 & FLAIR hyper-intense foci with restricted diffusion. In three pediatric age group patients including two neonates, the pattern of involvement was diffuse white matter changes with restricted diffusion. In 30% cases, MRI was normal. **Conclusions:** Detection of focal or confluent white matter hyper-intense foci with restricted diffusion on MRI in patients presenting with fever and neurological symptoms has potential to conclude the diagnosis of Chikungunya encephalitis, especially in epidemic settings.

## **Safety and immunogenicity of a single-shot live-attenuated chikungunya vaccine: a double-blind, multicentre, randomised, placebo-controlled, phase 3 trial.**

**Schneider M, Narciso-Abraham M, Hadl S, McMahon R, Toepfer S, Fuchs U, Hochreiter R, Bitzer A, Kosulin K, Larcher-Senn J, Mader R, Dubischar K, Zoihs O, Jaramillo JC, Eder-Lingelbach S, Buerger V, Wressnigg N.**

12-06-2023

*Lancet.*

<https://pubmed.ncbi.nlm.nih.gov/37321235/>

## **Live-attenuated Chikungunya vaccine: a possible new era.**

**Stephenson KE.**

12-06-2023

*Lancet.*

<https://pubmed.ncbi.nlm.nih.gov/37321234/>

## **Dual pattern recognition receptor ligands CL401, CL413, and CL429 as adjuvants for inactivated chikungunya virus.**

**Gosavi M, Kulkarni-Munje A, Patil HP.**

11-06-2023

*Virology.*

<https://pubmed.ncbi.nlm.nih.gov/37321145/>

Chikungunya virus (CHIKV) is responsible for incapacitating joint pains and is a significant health hazard in many countries. Though a definite need for a CHIKV vaccine is felt, long disappearance of CHIKV from circulation in humans has been a concern for vaccine development. Use of two separate pattern recognition receptor ligands has been shown to enhance immune response to the administered antigen. In addition, intradermal delivery of vaccine tends to mimic the natural mode of CHIKV infection. Therefore, in this study, we explored whether intradermal and intramuscular immunization with inactivated CHIKV (I-CHIKV) supplemented with dual pattern-recognition receptor ligands, CL401, CL413, and CL429, is an effective approach to enhancing antibody response to CHIKV. Our in vivo data show that I-CHIKV supplemented with these chimeric PRR ligands induces

enhanced neutralizing antibody response after intradermal delivery, but is less efficient after intramuscular immunization. These results suggest that intradermal delivery of I-CHIKV with chimeric adjuvants is a possible way to elicit a better antibody response.

### **Long non-coding RNAs regulate *Aedes aegypti* vector competence for Zika virus and reproduction.**

**Belavilas-Trovás A, Tastsoglou S, Dong S, Kefi M, Tavadia M, Mathiopoulos KD, Dimopoulos G.**

15-06-2023

*PLoS Pathog.*

<https://pubmed.ncbi.nlm.nih.gov/37319296/>

### **The feasibility of novel point-of-care diagnostics for febrile illnesses at health centres in Southeast Asia: a mixed-methods study.**

**Adella FJ, Vanna M, Adhikari B, Ol S, Tripura R, Davoeung C, Callery JJ, Sovann Y, Chandna A, Bunreth V, Asnong C, von Seidlein L, Dondorp AM, Maude RJ, Lubell Y, Wills B, Lek D, Peto TJ.**

15-06-2023

*Trans R Soc Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/37317948/>

### **Favipiravir Suppresses Zika Virus (ZIKV) through Activity as a Mutagen.**

**Franco EJ, Cella E, Tao X, Hanrahan KC, Azarian T, Brown AN.**

19-05-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317316/>

In a companion paper, we demonstrated that the nucleoside analogue favipiravir (FAV) suppressed Zika virus (ZIKV) replication in three human-derived cell lines-HeLa, SK-N-MC, and HUH-7. Our results revealed that FAV's effect was most pronounced in HeLa cells. In this work, we aimed to explain variation in FAV activity, investigating its mechanism of action and characterizing host cell factors relevant to tissue-specific differences in drug effect. Using viral genome sequencing, we show that FAV therapy was associated with an increase in the number of mutations and promoted the production of defective viral particles in all three cell lines. Our findings demonstrate that defective viral particles made up a larger portion of the viral population released from HeLa cells both at increasing FAV concentrations and at increasing exposure times. Taken together, our companion papers show that FAV acts via lethal mutagenesis against ZIKV and highlight the host cell's influence on the activation and antiviral activity of nucleoside analogues. Furthermore, the information gleaned from these companion papers can be applied to gain a more comprehensive understanding of the activity of nucleoside analogues and the impact of host cell factors against other viral infections for which we currently have no approved antiviral therapies.

### **Molecular Characterization of Dengue Virus Strains from the 2019-2020 Epidemic in Hanoi, Vietnam.**

**Phadungsombat J, Vu HTT, Nguyen QT, Nguyen HTV, Nguyen HTN, Dang BT, Nakayama EE, Ishizaki A, Ichimura H, Shioda T, Pham TN.**

11-05-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317240/>

Dengue virus (DENV), which has circulated in Vietnam for several decades, has multiple serotypes and genotypes. A 2019 dengue outbreak resulted in a larger number of cases than any other outbreak. We conducted a molecular characterization using samples collected in 2019-2020 from dengue patients in Hanoi and nearby cities located in northern Vietnam. The circulating serotypes were DENV-1 (25%,  $n = 22$ ) and DENV-2 (73%,  $n = 64$ ). Phylogenetic analyses revealed that all DENV-1 ( $n = 13$ ) were genotype I and clustered to local strains circulating during the previous outbreak in the 2017, whereas DENV-2 consisted of two genotypes: Asian-I ( $n = 5$ ), related to local strains from 2006-2022, and cosmopolitan ( $n = 18$ ), the predominant genotype in this epidemic. The current cosmopolitan virus was identified as having an Asian-Pacific lineage. The virus was closely related to strains in other recent outbreaks in Southeast Asian countries and China. Multiple introductions occurred in 2016-2017, which were possibly from maritime Southeast Asia (Indonesia, Singapore, and Malaysia), mainland Southeast Asia (Cambodia and Thailand), or China, rather than from an expansion of localized Vietnamese cosmopolitan strains that were previously detected in the 2000s. We also analyzed the genetic relationship between Vietnam's cosmopolitan strain and recent global strains reported from Asia, Oceania, Africa, and South America. This analysis revealed that viruses of Asian-Pacific lineage are not restricted to Asia but have spread to Peru and Brazil in South America.

### **Arbovirus Transmission Predictions Are Affected by Both Temperature Data Source and Modeling Methodologies across Cities in Colombia.**

**Peña-García VH, Luvall JC, Christofferson RC.**

09-05-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317223/>

Weather variables has been described as major drivers of vector proliferation and arbovirus transmission. Among them, temperature has consistently been found to be impactful in transmission dynamics, and models that incorporate temperature have been widely used to evaluate and forecast transmission or arboviruses like dengue, zika, or chikungunya virus. Further, there is growing evidence of the importance of micro-environmental temperatures in driving transmission of *Aedes aegypti*-borne viruses, as these mosquitoes tend to live within domiciles. Yet there is still a considerable gap in our understanding of how accounting for micro-environmental temperatures in models varies from the use of other widely-used, macro-level temperature



measures. This effort combines field-collected data of both indoor and outdoor household associated temperatures and weather station temperature data from three Colombian cities to describe the relationship between the measures representing temperature at the micro- and macro-levels. These data indicate that weather station data may not accurately capture the temperature profiles of indoor micro-environments. However, using these data sources, the basic reproductive number for arboviruses was calculated by means of three modeling efforts to investigate whether temperature measure differences translated to differential transmission predictions. Across all three cities, it was determined that the modeling method was more often impactful rather than the temperature data-source, though no consistent pattern was immediately clear. This suggests that temperature data sources and modeling methods are important for precision in arbovirus transmission predictions, and more studies are needed to parse out this complex interaction.

### Latest Advances in Arbovirus Diagnostics.

**Varghese J, De Silva I, Millar DS.**

28-04-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317133/>

### Favipiravir Inhibits Zika Virus (ZIKV) Replication in HeLa Cells by Altering Viral Infectivity.

**Franco EJ, Hanrahan KC, Brown AN.**

22-04-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317071/>

### Disease mapping for spatially semi-continuous data by estimating equations with application to dengue control.

**Lin PS, Yu YJ, Zhu J.**

14-06-2023

*Stat Med.*

<https://pubmed.ncbi.nlm.nih.gov/37316997/>

Disease mapping is a research field to estimate spatial pattern of disease risks so that areas with elevated risk levels can be identified. The motivation of this article is from a study of dengue fever infection, which causes seasonal epidemics in almost every summer in Taiwan. For analysis of zero-inflated data with spatial correlation and covariates, current methods would either cause a computational burden or miss associations between zero and non-zero responses. In this article, we develop estimating equations for a mixture regression model that accommodates spatial dependence and zero inflation for study of disease propagation. Asymptotic properties for the proposed estimates are established. A simulation study is conducted to evaluate performance of the mixture estimating equations; and a dengue dataset from southern Taiwan is used to illustrate the proposed method.

### Neutralizing antibodies targeting a novel epitope on envelope protein exhibited broad protection against flavivirus without risk of disease enhancement.

**Yen LC, Chen HW, Ho CL, Lin CC, Lin YL, Yang QW, Chiu KC, Lien SP, Lin RJ, Liao CL.**

14-06-2023

*J Biomed Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37316861/>

### Dengue Uveitis - A Major Review.

**Xie Cen A, Ng AWW, Rojas-Carabali W, Cifuentes-González C, de-la-Torre A, Mahendradas P, Agrawal R.**

14-06-2023

*Ocul Immunol Inflamm.*

<https://pubmed.ncbi.nlm.nih.gov/37315302/>

Dengue fever is a significant global public health concern with increasing incidence over the past two decades. The symptoms range from mild to severe, including fever, headache, rash, and joint pain. Ocular complications are prevalent among hospitalized patients, estimated to be between 10% and 40.3%, with varying incidences based on the serotype and severity of dengue. These complications can be hemorrhagic or inflammatory and typically occur after the onset of fever. Modern diagnostic tools such as Optical Coherence Tomography (OCT) and Fundus Fluorescein Angiography (FFA) have enabled physicians to better understand the extent of ocular involvement and guide treatment. This article provides an updated overview of the various manifestations of dengue uveitis, including their diagnosis and treatment.

### Multi-Disease Detection Using a Prism-Based Surface Plasmon Resonance Sensor: A TMM and FEM Approach.

**Rumi RB, Paul AK, Alyami SA, Moni MA.**

14-06-2023

*IEEE Trans Nanobioscience.*

<https://pubmed.ncbi.nlm.nih.gov/37314903/>

This research introduces a surface plasmon resonance (SPR)-based biosensor with multilayered structures for telecommunication wavelength in order to detect multiple diseases. Malaria and chikungunya viruses are taken into account, and the presence of these viruses is determined by examining several blood components in healthy and affected phases. Here, two distinct configurations (Al-BTO-Al-MoS<sub>2</sub> and Cu-BTO-Cu-MoS<sub>2</sub>) are proposed and contrasted for the detection of numerous viruses. The performance characteristics of this work have been analyzed using Transfer Matrix Method (TMM) method and Finite Element Method (FEM) method under the angle interrogation technique. From the TMM and FEM solutions, it is evident that the Al-BTO-Al-MoS<sub>2</sub> structure provides the highest sensitivities of ~270 deg./RIU for malaria and ~262 deg./RIU for chikungunya viruses, with the satisfactory detection accuracy of ~1.10 for malaria, ~1.64 for chikungunya, and quality factor of ~204.40 for malaria, ~208.20 for chikungunya. In addition, the Cu-BTO-Cu MoS<sub>2</sub> structure offers the highest sensitivities of ~310 deg./RIU for malaria and ~298 deg./RIU for chikungunya,

with a satisfactory detection accuracy of ~0.40 for malaria, ~0.58 for chikungunya, and quality factor of ~89.85 for malaria, ~86.38 for chikungunya viruses. Therefore, the performance of the proposed sensors is analyzed using two distinct methods and gives around similar results. In sum, this research could be utilized as a theoretical foundation and the first step in the development of a real sensor.

### **Identification and validation of the first EST-SSR markers based on transcriptome of *Anopheles darlingi*, the primary transmitter of malaria in Brazil.**

**de Souza AT, Batista JS, Guimarães-Marques GM, Cunha-Machado AS, Rafael MS.**

14-06-2023

*Mol Biol Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37314602/>

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

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

14-06-2023

*Pediatr Infect Dis J.*

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

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

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

**Conclusions:** One in every 25 SARS-CoV-2 infections had a dengue coinfection. Continued surveillance is needed to establish the interaction of SARS-CoV-2 and dengue virus, evaluate the impact of COVID-19 and/or dengue

vaccination on coinfection and monitor complications of coinfection.

### **A machine learning model to assess potential misdiagnosed dengue hospitalization.**

**Santos CY, Tuboi S, de Jesus Lopes de Abreu A, Abud DA, Lobao Neto AA, Pereira R, Siqueira JB Jr.**

30-05-2023

*Heliyon.*

<https://pubmed.ncbi.nlm.nih.gov/37313173/>

Dengue, like other arboviruses with broad clinical spectra, can easily be misdiagnosed as other infectious diseases due to the overlap of signs and symptoms. During large outbreaks, severe dengue cases have the potential to overwhelm the health care system and understanding the burden of dengue hospitalizations is therefore important to better allocate medical care and public health resources. A machine learning model that used data from the Brazilian public healthcare system database and the National Institute of Meteorology (INMET) was developed to estimate potential misdiagnosed dengue hospitalizations in Brazil. The data was modeled into a hospitalization level linked dataset. Then, Random Forest, Logistic Regression and Support Vector Machine algorithms were assessed. The algorithms were trained by dividing the dataset in training/test set and performing a cross validation to select the best hyperparameters in each algorithm tested. The evaluation was done based on accuracy, precision, recall, F1 score, sensitivity, and specificity. The best model developed was Random Forest with an accuracy of 85% on the final reviewed test. This model shows that 3.4% (13,608) of all hospitalizations in the public healthcare system from 2014 to 2020 could have been dengue misdiagnosed as other diseases. The model was helpful in finding potentially misdiagnosed dengue and might be a useful tool to help public health decision makers in planning resource allocation.

### **Role of N-acetylcysteine in liver injury due to dengue fever.**

**Gupta M, Gupta S, Sood D, Gupta A, Jesrani G.**

13-06-2023

*Trop Doct.*

<https://pubmed.ncbi.nlm.nih.gov/37312532/>

### **Fogging to combat dengue: factors influencing stakeholders' attitudes in Malaysia.**

**Arham AF, Amin L, Mustapa MAC, Mahadi Z, Yaacob M, Wasli MMP, Rusly NS.**

14-06-2023

*BMC Public Health.*

<https://pubmed.ncbi.nlm.nih.gov/37312081/>

### **The spatio-temporal distribution of acute encephalitis syndrome and its association with climate and landcover in Vietnam.**

Brindle HE, Bastos LS, Christley R, Contamin L, Dang LH, Anh DD, French N, Griffiths M, Nadjm B, van Doorn HR, Thai PQ, Duong TN, Choisy M.

13-06-2023

*BMC Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37312047/>

**Background:** Acute encephalitis syndrome (AES) differs in its spatio-temporal distribution in Vietnam with the highest incidence seen during the summer months in the northern provinces. AES has multiple aetiologies, and the cause remains unknown in many cases. While vector-borne disease such as Japanese encephalitis and dengue virus and non-vector-borne diseases such as influenza and enterovirus show evidence of seasonality, associations with climate variables and the spatio-temporal distribution in Vietnam differs between these. The aim of this study was therefore to understand the spatio-temporal distribution of, and risk factors for AES in Vietnam to help hypothesise the aetiology. **Methods:** The number of monthly cases per province for AES, meningitis and diseases including dengue fever; influenza-like-illness (ILI); hand, foot, and mouth disease (HFMD); and *Streptococcus suis* were obtained from the General Department for Preventive Medicine (GDPM) from 1998-2016. Covariates including climate, normalized difference vegetation index (NDVI), elevation, the number of pigs, socio-demographics, JEV vaccination coverage and the number of hospitals were also collected. Spatio-temporal multivariable mixed-effects negative binomial Bayesian models with an outcome of the number of cases of AES, a combination of the covariates and harmonic terms to determine the magnitude of seasonality were developed. **Results:** The national monthly incidence of AES declined by 63.3% over the study period. However, incidence increased in some provinces, particularly in the Northwest region. In northern Vietnam, the incidence peaked in the summer months in contrast to the southern provinces where incidence remained relatively constant throughout the year. The incidence of meningitis, ILI and *S. suis* infection; temperature, relative humidity with no lag, NDVI at a lag of one month, and the number of pigs per 100,000 population were positively associated with the number of cases of AES in all models in which these covariates were included. **Conclusions:** The positive correlation of AES with temperature and humidity suggest that a number of cases may be due to vector-borne diseases, suggesting a need to focus on vaccination campaigns. However, further surveillance and research are recommended to investigate other possible aetiologies such as *S. suis* or *Orientia tsutsugamushi*.

### Correction to: Comparing the performance of dengue virus IgG and IgG-capture enzyme-linked immunosorbent assays in seroprevalence study.

Tsai JJ, Tsai CY, Lin PC, Chen CH, Tsai WY, Dai YC, Lin YC, Pedroso C, Brites C, Wang WK.

13-06-2023

*BMC Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37312023/>

### Insecticidal and Repellent Properties of Rapid-Acting Fluorine-Containing Compounds against *Aedes aegypti* Mosquitoes.

Zhu X, Valbon W, Qiu M, Hu CT, Yang J, Erriah B, Jankowska M, Dong K, Ward MD, Kahr B.

13-06-2023

*ACS Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37311068/>

### Development of an amplicon-based sequencing approach in response to the global emergence of mpox.

Chen NFG, Chaguza C, Gagne L, Doucette M, Smole S, Buzby E, Hall J, Ash S, Harrington R, Cofsky S, Clancy S, Kapsak CJ, Sevinsky J, Libuit K, Park DJ, Hemarajata P, Garrigues JM, Green NM, Sierra-Patev S, Carpenter-Azevedo K, Huard RC, Pearson C, Incekara K, Nishimura C, Huang JP, Gagnon E, Reeve E, Razeq J, Muyombwe A, Borges V, Ferreira R, Sobral D, Duarte S, Santos D, Vieira L, Gomes JP, Aquino C, Savino IM, Felton K, Bajwa M, Hayward N, Miller H, Naumann A, Allman R, Greer N, Fall A, Mostafa HH, McHugh MP, Maloney DM, Dewar R, Kenicer J, Parker A, Mathers K, Wild J, Cotton S, Templeton KE, Churchwell G, Lee PA, Pedrosa M, McGruder B, Schmedes S, Plumb MR, Wang X, Barcellos RB, Godinho FMS, Salvato RS, Ceniseros A, Breban MI, Grubaugh ND, Gallagher GR, Vogels CBF.

13-06-2023

*PLoS Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37310918/>

### Evaluation of Neutralizing Activity against Omicron Subvariants in BA.5 Breakthrough Infection and Three-Dose Vaccination Using a Novel Chemiluminescence-Based, Virus-Mediated Cytopathic Assay.

Toyoda M, Tan TS, Motozono C, Barabona G, Yonekawa A, Shimono N, Minami R, Nagasaki Y, Miyashita Y, Oshiumi H, Nakamura K, Matsushita S, Kuwata T, Ueno T.

13-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37310218/>

Neutralizing potency of humoral immune responses induced by prior infection or vaccination is vital for protecting of individuals and population against severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2). However, the emergence of viral variants that can evade neutralization by vaccine- or infection-induced immunity is a significant public health threat and requires continuous monitoring. Here, we have developed a novel scalable chemiluminescence-based assay for assessing SARS-CoV-2-induced cytopathic effect to quantify the neutralizing activity of antisera. The assay leverages the correlation between host cell viability and ATP levels in culture to measure the cytopathic effect on target cells induced by clinically isolated, replication-competent, authentic SARS-CoV-2. With this assay, we demonstrate that the recently arisen Omicron subvariants BQ.1.1 and



XBB.1 display a significant decrease in sensitivity to neutralization by antibodies elicited from breakthrough infections with Omicron BA.5 and from receipt of three doses of mRNA vaccines. Thus, this scalable neutralizing assay provides a useful platform to assess the potency of acquired humoral immunity against newly emerging SARS-CoV-2 variants. **IMPORTANCE** The ongoing global pandemic of SARS-CoV-2 has emphasized the importance of neutralizing immunity in protecting individuals and populations against severe respiratory illness. In light of the emergence of viral variants with the potential to evade immunity, continuous monitoring is imperative. A virus plaque reduction neutralization test (PRNT) is a "gold standard" assay for analyzing neutralizing activity for authentic viruses that form plaques, like influenza virus, dengue virus, and SARS-CoV-2. However, this method is labor intensive and is not efficient for performing large-scale neutralization assays on patient specimens. The assay system established in this study allows for the detection of a patient's neutralizing activity by simply adding an ATP detection reagent, providing a simple evaluation system for neutralizing activity of antisera as an alternative to the plaque reduction method. Our extended analysis of the Omicron subvariants highlights their increasing capability to evade neutralization by both vaccine- and infection-induced humoral immunity.

### Combined Therapeutic Plasma Exchange and Continuous Renal Replacement Therapy in Children With Dengue-Associated Acute Liver Failure and Shock Syndrome: Single-Center Cohort From Vietnam.

Vo LT, Do VC, Trinh TH, Vu T, Nguyen TT.

13-06-2023

*Pediatr Crit Care Med.*

<https://pubmed.ncbi.nlm.nih.gov/37310173/>

### Prevalence and predictors of depression, anxiety, and stress among recovered COVID-19 patients in Vietnam.

Trang LTT, Ngoc Le C, Chutipatana N, Shohaimi S, Suwanbamrung C.

2023

*Rocz Panstw Zakl Hig.*

<https://pubmed.ncbi.nlm.nih.gov/37309979/>

**Background:** During the COVID-19 pandemic, a high prevalence of mental health distress has been reported among people who have recovered from the disease.

**Objectives:** To assess the prevalence of depression, anxiety, and stress as well as identify predictors among recovered COVID-19 patients after more than six months of being discharged in Dong Thap Province, Vietnam.

**Material and methods:** The cross-sectional study was conducted among 549 eligible participants recruited by stratified sampling. Data was collected using the depression, anxiety and stress scale - 21 items had Content Validity Index = 0.9, and Cronbach's alpha for depression, anxiety and stress sub-scales were 0.95, 0.81, and 0.86, respectively. Descriptive statistics were used to measure the prevalence levels and distribution of characteristics of

the participant, while factors influencing depression, anxiety, and stress were predicted using binary logistic regression. **Results:** The overall prevalence of depression, anxiety, and stress were 24.8% (95% CI: 21.2-28.6), 41.5% (95% CI: 37.4-45.8), and 25.3% (95% CI: 21.7-29.2), respectively. The predictors of depression were living in urban area (OR = 1.97; 95% CI: 1.27-3.08), holding a bachelor's degree (OR:3.51; 95% CI: 1.13-10.8), having a high monthly income (OR: 2.57; 95% CI: 1.03-6.38), diabetes (OR: 2.21; 95% CI: 1.04-4.68), heart disease (OR: 3.83; 95% CI: 1.79-8.17), respiratory disease (OR: 3.49; 95% CI: 1.24-9.84), and diarrhea (OR: 4.07; 95% CI: 1.06-15.6). Living in the urban area (OR: 1.57; 95% CI: 1.07-2.29), having sleep disturbance (OR: 2.32; 95% CI: 1.56-3.46), and fatigue (OR: 1.57; 95% CI: 1.03-2.39) were predictors for anxiety. Having respiratory disease (OR: 3.75; 95% CI: 1.47-9.60) or diarrhea (OR: 4.34; 95% CI: 1.18-15.9) were predictors of stress. **Conclusion:** People who have recovered from COVID-19 should be assessed for symptoms of depression, anxiety, and stress. Primary healthcare providers should develop interventions to support their recovery.

### Effect of Temperature on Mosquito Olfaction.

Lahondère C, Vinauger C, Liaw JE, Tobin KKS, Joiner JM, Riffell JA.

12-06-2023

*Integr Comp Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37309024/>

Mosquitoes use a wide range of cues to find a host to feed on, eventually leading to the transmission of pathogens. Among them, olfactory cues (e.g., host emitted odors, including CO<sub>2</sub>, and skin volatiles) play a central role in mediating host seeking behaviors. While mosquito olfaction can be impacted by many factors, such as the physiological state of the insect (e.g., age, reproductive state), the impact of environmental temperature on the olfactory system remains unknown. In this study, we quantified the behavioral responses of *Aedes aegypti* mosquitoes, vectors of dengue, yellow fever and Zika viruses, among other pathogens, to host and plant related odors under different environmental temperatures.

### Previous Dengue Infection among Children in Puerto Rico and Implications for Dengue Vaccine Implementation.

Adams LE, Hitchings MDT, Medina FA, Rodriguez DM, Sánchez-González L, Moore H, Whitehead SS, Muñoz-Jordán JL, Rivera-Amill V, Paz-Bailey G.

12-06-2023

*Am J Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/37308104/>

Limited dengue virus (DENV) seroprevalence estimates are available for Puerto Rico, which are needed to inform the potential use and cost-effectiveness of DENV vaccines. The Communities Organized to Prevent Arboviruses (COPA) is a cohort study initiated in 2018 in Ponce, Puerto Rico, to assess arboviral disease risk and provide a platform to evaluate interventions. We recruited participants from households in 38 study clusters, who were interviewed

and provided a serum specimen. Specimens from 713 children aged 1 to 16 years during the first year of COPA were tested for the four DENV serotypes and ZIKV using a focus reduction neutralization assay. We assessed the seroprevalence of DENV and ZIKV by age and developed a catalytic model from seroprevalence and dengue surveillance data to estimate the force of infection for DENV during 2003-2018. Overall, 37% (n = 267) were seropositive for DENV; seroprevalence was 9% (11/128) among children aged 1 to 8 years and 44% (256/585) among children aged 9 to 16 years, exceeding the threshold over which DENV vaccination is deemed cost-effective. A total of 33% were seropositive for ZIKV, including 15% among children aged 0 to 8 years and 37% among children aged 9 to 16 years. The highest force of infection occurred in 2007, 2010, and 2012-2013, with low levels of transmission from 2016 to 2018. A higher proportion of children had evidence of multitypic DENV infection than expected, suggesting high heterogeneity in DENV risk in this setting.

### **Global geotemporal distribution of chikungunya disease, 2011-2022.**

**Grabenstein JD, Tomar AS.**

10-06-2023

*Travel Med Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37307983/>

### **Susceptibility of *Aedes albopictus*, *Ae. aegypti* and human populations to Ross River virus in Kuala Lumpur, Malaysia.**

**Fu JYL, Chua CL, Abu Bakar AS, Vythilingam I, Wan Sulaiman WY, Alphey L, Chan YF, Sam IC.**

12-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37307291/>

### **Zika virus NS3 and NS5 proteins determine strain-dependent differences in dsRNA accumulation in a host cell type-dependent manner.**

**Barnard TR, Landry BN, Wang AB, Sagan SM.**

Juin-2023

*J Gen Virol.*

<https://pubmed.ncbi.nlm.nih.gov/37289497/>

For positive-sense RNA viruses, initiation of viral RNA replication represents a major target of antiviral responses to infection. Despite this, the interplay between viral replication and the innate antiviral response at early steps in the Zika virus (ZIKV) life cycle is not well understood. We have previously identified ZIKV isolates with differing levels of dsRNA accumulation, ZIKV<sup>PR</sup> (high dsRNA per infected cell) and ZIKV<sup>CDN</sup> (low dsRNA per infected cell), and we hypothesized that we could use reverse genetics to investigate how host and viral factors contribute to the establishment of viral RNA replication. We found that both the ZIKV NS3 and NS5 proteins as well as host factors were necessary to determine the dsRNA accumulation phenotype. Additionally, we show that dsRNA correlates with viral negative-strand RNA measured by strand-specific RT-qPCR, suggesting that dsRNA is an accurate

readout of viral RNA replication. Interestingly, although we did not observe NS3- and NS5-dependent differences in cells with defects in interferon (IFN) production, differences in RNA accumulation precede induction of the IFN response, suggesting that RNA sensing pathways or intrinsic restriction factors may differentially restrict ZIKV in an NS3- and NS5-dependent manner. This work expands our understanding of the interplay of early steps of viral RNA replication and the induction of the innate antiviral response to ZIKV infection.

### **High frequency of Voltage-gated sodium channel (VGSC) gene mutations in *Aedes albopictus* (Diptera: Culicidae) suggest rapid insecticide resistance evolution in Shanghai, China.**

**Yuan H, Shan W, Zhang Y, Yan H, Li Y, Zhou Q, Dong H, Tao F, Liu H, Leng P, Peng H, Ma Y.**

02-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37267343/>

### **Different outcomes of neonatal and adult Zika virus infection on startle reflex and prepulse inhibition in mice.**

**Souza INO, Andrade BS, Frost PS, Neris RLS, Gavino-Leopoldino D, Da Poian AT, Assunção-Miranda I, Figueiredo CP, Clarke JR, Neves GA.**

05-08-2023

*Behav Brain Res.*

<https://pubmed.ncbi.nlm.nih.gov/37263423/>

Zika virus (ZIKV) infection causes severe neurological consequences in both gestationally-exposed infants and adults. Sensorial gating deficits strongly correlate to the motor, sensorial and cognitive impairments observed in ZIKV-infected patients. However, no startle response or prepulse inhibition (PPI) assessment has been made in patients or animal models. In this study, we identified different outcomes according to the age of infection and sex in mice: neonatally infected animals presented an increase in PPI and delayed startle latency. However, adult-infected male mice presented lower startle amplitude, while a PPI impairment was observed 14 days after infection in both sexes. Our data further the understanding of the functional impacts of ZIKV on the developing and mature nervous system, which could help explain other behavioral and cognitive alterations caused by the virus. With this study, we support the startle reflex testing in ZIKV-exposed patients, especially infants, allowing for early detection of functional neuromotor damage and early intervention.

### **Expression of recombinant dengue virus type 1 non-structural protein 1 in mammalian cells and preliminary assessment of its suitability to detect human IgG antibodies elicited by viral infection.**

**Malnero CM, Azevedo RC, Bergmann IE, de Meneses MDF, Cavalcanti AC, Ibañez LI, Malirat V.**

Juillet-2023

*J Immunol Methods.*

<https://pubmed.ncbi.nlm.nih.gov/37263391/>

In recent years dengue has become a rapidly growing public health problem worldwide, however, the availability of accurate and affordable diagnostic immunoassays is limited, partly due to the difficulty of producing large quantities of purified antigen. Non-structural protein 1 (NS1) has shown to be a good candidate for inclusion in diagnostic assays and for serosurveys, particularly in endemic countries as a prerequisite for vaccination. In this work the NS1 antigen derived from dengue virus type-1 (DENV1) was expressed in HEK293-T cells and purified by affinity chromatography. The recombinant protein was recovered properly folded as dimers, highly purified and with good yield (1.5 mg/L). It was applied as a serological probe in an indirect ELISA developed in this work to detect human IgG antibodies. Preliminary comparative performance values of 81.1% sensitivity and 83.0% specificity of the developed and preliminary validated iELISA, relative to a commercial kit were obtained, suggesting that the purified recombinant DENV1 NS1 antigen is suitable to detect IgG antibodies, indicative of past DENV infection.

### **An economic evaluation of Wolbachia deployments for dengue control in Vietnam.**

**Turner HC, Quyen DL, Dias R, Huong PT, Simmons CP, Anders KL.**

30-05-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37253037/>

### **Species diversity of phlebotomine sand flies and sympatric occurrence of Leishmania (Mundinia) martiniquensis, Leishmania (Leishmania) donovani complex, and Trypanosoma spp. in the visceral leishmaniasis focus of southern Thailand.**

**Preativatanyou K, Chinwirunsirisup K, Phumee A, Khositharattanakool P, Sunantaraporn S, Depaquit J, Siriyasatien P.**

Août-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37211153/>

Autochthonous leishmaniasis in Thailand has recently been a public health concern due to an increasing number of new clinical cases. Most indigenous cases were diagnosed with *Leishmania (Mundinia) martiniquensis*, and *Leishmania (Mundinia) orientalis*. However, some doubts regarding vector misidentification have arisen and need to be elucidated. Accordingly, we aimed to assess the species composition of sand flies and determine the molecular prevalence of trypanosomatids in the transmission area of leishmaniasis in southern Thailand. In the present study, a total of 569 sand flies were caught from the vicinity of a visceral leishmaniasis patient's house in Na Thawi District, Songkhla Province. Of these, 229 parous and gravid females consisted of *Sergentomyia*

*khawi*, *Se. barraudi*, *Phlebotomus stantoni*, *Grassomyia indica*, and *Se. hivernus*, accounting for 31.4%, 30.6%, 29.7%, 7.9%, and 0.4%, respectively. However, *Se. gemmea*, which has previously been proposed as the most abundant species and putative vector of visceral leishmaniasis, was not found in the present study. Based on ITS1-PCR and sequence analysis, two specimens of *Gr. indica* and *Ph. stantoni* showed positive amplification of *L. martiniquensis* and *L. donovani* complex, respectively, the first one being presumed indigenous and the second one being not. Anuran *Trypanosoma* was also molecularly detected using SSU rRNA-PCR and ubiquitously found in 16 specimens of four dominant sand fly species except for *Se. hivernus*. The obtained sequences could be phylogenetically categorized into the two major amphibian clades (An04/Frog1 and An01+An02/Frog2). The existence of the monophyletic subgroup and distinct lineage suggests them as novel *Trypanosoma* species. The TCS network analysis of these anuran *Trypanosoma* sequences also revealed high haplotype diversity ( $H_d = 0.925 \pm 0.050$ ), but low nucleotide diversity ( $\pi = 0.019 \pm 0.009$ ). Furthermore, the living anuran trypanosomes were microscopically demonstrated in a single specimen of *Gr. indica*, supporting the vectorial capacity. Importantly, our data confirmed the scarcity of *Se. gemmea* and also uncovered, for the first time, the co-circulation of *L. martiniquensis*, *L. donovani* complex, and suspected novel anuran *Trypanosoma* spp. in phlebotomine sand flies, implicating their potential role as vectors of trypanosomatid parasites. Therefore, the novel data from this study would greatly facilitate the comprehension of the complexity of trypanosomatid transmission and the establishment of prevention and control measures for this neglected disease more effectively.

### **A phase 1, randomized, placebo-controlled, dose-ranging study to evaluate the safety and immunogenicity of an mRNA-based chikungunya virus vaccine in healthy adults.**

**Shaw CA, August A, Bart S, Booth PJ, Knightly C, Brasel T, Weaver SC, Zhou H, Panther L.**

13-06-2032

*Vaccine.*

<https://pubmed.ncbi.nlm.nih.gov/37210308/>

### **Limited Effect of Ground Floor Fogging on Mosquito Distribution in High-Rise Condominia.**

**Lee JM, Wasserman RJ, Wilson RF, Cuthbert RN, Rahman S, Yek SH.**

Mar-2023

*Ecohealth.*

<https://pubmed.ncbi.nlm.nih.gov/37129695/>

Fogging with insecticides is one of the main control measures for adult mosquito populations employed in countries that are affected by dengue. In many such countries, urban communities are increasingly characterised by high-density residence in high-rise condominiums. Although fogging is typically applied at the

ground level, its efficacy in three-dimensional urban environments is poorly understood. Here, we investigated the effect of fogging on vector mosquito distribution and abundance in high-rise condominiums by conducting a before-after fogging survey. We showed that although mosquitoes were significantly concentrated at the lower levels in high-rise condominiums, they were found throughout the three-dimensional environments. Fogging did not significantly alter this distribution or abundance pattern across any floor level. Thus, any fogging effect was short-lived as mosquito populations recovered within a few days before the subsequent scheduled treatment. In addition, increasing fogging frequency within practicable limits did not prolong the intended control effect. As urban mosquitoes are increasingly insusceptible to fogging due to insecticide resistance and vertical avoidance, this study demonstrates the need to implement other mosquito control strategies for high-rise condominiums to manage mosquito populations.

### **The role of glial cells in Zika virus-induced neurodegeneration.**

Quincozes-Santos A, Bobermin LD, Costa NLF, Thomaz NK, Almeida RRS, Beys-da-Silva WO, Santi L, Rosa RL, Capra D, Coelho-Aguiar JM, DosSantos MF, Heringer M, Cirne-Lima EO, Guimarães JA, Schuler-Faccini L, Gonçalves CA, Moura-Neto V, Souza DO.

Août-2023

*Glia.*

<https://pubmed.ncbi.nlm.nih.gov/36866453/>

### **Translation and preliminary validation of the Brazilian family resources scale in a sample of parents of children with congenital Zika virus syndrome.**

Barker Ladd S, Williams NA, Villachan-Lyra P, Chaves E, Hollist C, Trefiglio Mendes Gomes R, Barbosa LNF.

2023

*J Pediatr Rehabil Med.*

<https://pubmed.ncbi.nlm.nih.gov/36847025/>

### **Positivity of dengue, chikungunya, and Zika infections in women in Northeast Brazil post-Zika epidemic.**

Frota CC, Correia FGS, Alves Vasconcelos LR, de Sousa PRC, Ferreira MLDS, Saraiva SP, Mota Ferreira R, Romcy KAM, Pinheiro RF, de Oliveira RTG, Pinheiro Júnior FML, Martins AF, Sanhueza-Sanzana C, de Almeida RLF, Kendall C, Coelho ICB, Pires Neto RDJ, Aguiar ÍWO, Kerr LRFS.

Juill-2023

*Pathog Glob Health.*

<https://pubmed.ncbi.nlm.nih.gov/36316985/>

The state of Ceará, in the Northeast Region of Brazil, presents the simultaneous circulation of Zika (ZIKV), dengue (DENV) and chikungunya (CHIKV) viruses. In 2017 there were a high number of cases of these three arboviruses, especially CHIKV. Here, we detected the presence of arboviruses ZIKV, DENV and CHIKV and their coinfections in women in endemic regions of the city of Fortaleza, Ceará in a post-Zika epidemic year.

Sociodemographic and environmental characteristics associated with arbovirus positivity were also analyzed. Women (n = 1289) between 15 and 39 years old were included. RT-qPCR was performed for virus detection and IgM antibody positivity was also analyzed. One hundred and six (8.3%) participants were positive for one or more arboviruses. Mono-infections (76; 5.9%) were distributed between 22 (1.7%) for ZIKV, 39 (3.1%) for DENV and 15 (1.2%) for CHIKV. Co-infections were detected in 30 (2.3%) of the positive participants and one case with triple infection was found. IgM positivity was found in 2.4% of ZIKV RT-qPCR, 9.6% of DENV and 16.3% of CHIKV. RT-qPCR positivity for arboviruses was associated with low socioeconomic class and presence of a water box sealing in the household. A higher positivity to the three viruses occurred in the month with the lowest wind velocity, which was also preceded by the highest peak of rain and humidity. We identified the simultaneous circulation and co-infection of ZIKV, DENV and CHIKV in Fortaleza in a post-Zika epidemic year. We also highlight the need for continuous epidemiological surveillance combined with molecular diagnostic tools.

### **Drug repurposing against the RNA-dependent RNA polymerase domain of dengue serotype 3 by virtual screening and molecular dynamics simulations.**

Gangopadhyay A, Saha A.

Juill-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35642087/>

### **Combined study of docking and molecular dynamics against DENV-3 SN1 protein by bixinoids.**

da Fonseca AM, Soares NB, Meirú MIL, Colares RP, Neto MM, Sobrinho ACN, Dos Santos HS, Marinho ES.

Juill-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35510585/>

Dengue (DENV), Zika virus (ZIKV), and Chikungunya fever (CHIK) are tropical diseases that have caused a lot of problems in general worldwide. Transmitted by mosquitoes of the species *Aedes aegypti* and *albopictus*, they have not been completely eradicated in the country, and their proliferation has only increased in the Northeast region. Within the structure of the virus, it is possible to verify the presence of glycoprotein SN1, which is responsible for its replication. If this macromolecule is inhibited using a specific or complex linker, it can interrupt its replication activity. An alternative to this problem has been using structures derived from natural products that have pharmacological properties. A dynamic and molecular docking combined study used computational simulation in the four isomeric forms of bixin against the SN1 protein. The Z,E-bixin and E,E-bixin isomers, both with affinity energy -6.7 and -6.5 Kcal/mol, presented the best results. Thus, bixin and its isomers, found in annatto seeds, maybe an initial proposal in the search for prototype compounds to study to fight this lethal virus in the future. Communicated by Ramaswamy H. Sarma.



### Identification of neo-andrographolide compound targeting NS1 Lys14: an important residue in NS1 activity driving dengue pathogenesis.

Elumalai E, Suresh Kumar M.

Jul-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35491708/>

### Might Zika virus-associated microcephaly's severity impact deciduous tooth eruption and orofacial structures?

Vaz FFS, da Silva Sobrinho AR, Athayde FRRS, de Vasconcelos Carvalho M, Sette-de-Souza PH, Ferreira SJ.

Jul-2023

*Oral Dis.*

<https://pubmed.ncbi.nlm.nih.gov/35485177/>

### Spatial and temporal analyses of the influences of meteorological and environmental factors on *Aedes albopictus* (Diptera: Culicidae) population dynamics during the peak abundance period at a city scale.

Wang F, Zhu Y, Zhang H, Fan J, Leng P, Zhou J, Yao S, Yang D, Liu Y, Wang J, Yao J, Zhou Y, Zhao T.

10-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37307888/>

*Aedes albopictus* (Diptera: Culicidae) is a major vector of multiple diseases. While vaccines have been developed, preventing these *Aedes*-borne diseases continues to primarily depend on monitoring and controlling the vector population. Despite increasing research on the impacts of various factors on *Ae. albopictus* population dynamics, there is still no consensus on how meteorological or environmental factors affect vector distribution. In this study, the relationships between mosquito abundance and meteorological and environmental indicators were examined at the town level based on data collected from July to September, the peak abundance period of 2019 in Shanghai. In addition to performing Poisson regression, we employed the geographically weighted Poisson regression model to account for spatial dependency and heterogeneity. The result showed that the environmental factors (notably human population density, the Normalized Difference Vegetation Index (NDVI), socioeconomic deprivation, and road density) had more significant impacts than the meteorological variables in accounting for the spatial variation of mosquito abundance at a city scale. The dominant environmental variable differed in urban and rural places. Furthermore, our findings indicated that deprived townships are more susceptible to higher vector densities compared to non-deprived townships. Therefore, it is crucial not only to allocate more resources but also to increase attention towards controlling the vectors responsible for their transmission in these townships.

### Dengue: updates for dermatologists on the world's fastest-growing vector-borne disease.

Braun M, Andersen LK, Norton SA, Coates SJ.

12-06-2023

*Int J Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/37306140/>

Dengue is the world's fastest-growing vector borne disease and has significant epidemic potential in suitable climates. Recent disease models incorporating climate change scenarios predict geographic expansion across the globe, including parts of the United States and Europe. It will be increasingly important in the next decade for dermatologists to become familiar with dengue, as it commonly manifests with rashes, which can be used to aid diagnosis. In this review, we discuss dengue for general dermatologists, specifically focusing on its cutaneous manifestations, epidemiology, diagnosis, treatment, and prevention. As dengue continues to spread in both endemic and new locations, dermatologists may have a larger role in the timely diagnosis and management of this disease.

### Editorial: Trends in dengue evolution, immune pathogenesis, and pathology.

Gowri Sankar S, Alwin Prem Anand A, Chattopadhyay B.

25-05-2023

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/37305420/>

### A comprehensive insight on the challenges for COVID-19 vaccine: A lesson learnt from other viral vaccines.

Singh RS, Singh A, Masih GD, Batra G, Sharma AR, Joshi R, Prakash A, Suroy B, Sarma P, Prajapat M, Kaur H, Bhattacharyya A, Upadhyay S, Medhi B.

09-06-2023

*Heliyon.*

<https://pubmed.ncbi.nlm.nih.gov/37303517/>

### Dengue in Early Pregnancy: A Neglected Problem?

Sinha R, Datta MR.

08-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37303396/>

Introduction Dengue is caused by a virus from the Flaviviridae family. Although the literature on this disease is sparse, some studies have shown the effects of dengue in the first trimester of pregnancy. However, the sample size in these studies is limited. Aims and objective The current study aimed to compare foetomaternal outcomes in pregnant patients with dengue in early (< 24 weeks) and late (> 24 weeks) pregnancy and find the prevalence and predictive factors for abortion in pregnant patients with dengue. Material and methods This retrospective study included all pregnant patients ( $n = 62$ ) admitted to the labour room over a period of six years from April 2016 to February 2022 and who were diagnosed with dengue anytime during pregnancy. Data were collected from their



medical records and analysed. Differences between the two groups were assessed by the Chi-square test, Fisher's exact test, and Mann-Whitney U test. A *p* value of less than 0.05 was considered significant. Results Out of a total of 62 patients, those with dengue at a gestational age of less than 24 weeks (*n* = 15) had more incidence of intrauterine growth restriction (55.6 vs 12.9%) (*p* value = 0.012) and oligohydramnios (66.7 vs 17.9%) (*p* value = 0.007). The incidence of abortion was 33.3%; among the patients at a gestational age of less than 12 weeks, 71.4% had an abortion. When the patients who had abortions were compared with those who did not, the factors predicting abortion were found to be a history of previous abortion (*p* value = 0.004), gestational age of less than 12 weeks (*p* value = 0.003), and decreased platelet count (*p* value = 0.03). Conclusion The effect of dengue infection in early pregnancy includes abortion, intrauterine growth restriction, and oligohydramnios, and these patients should be managed in a tertiary care hospital.

### Organotypic hippocampal culture model reveals differential responses to highly similar Zika virus isolates.

Oliveira MDS, Cassiano LMG, Pioline J, de Carvalho KRA, Salim ACM, Alves PA, Fernandes GDR, Machado AMV, Coimbra RS.

10-06-2023

*J Neuroinflammation.*

<https://pubmed.ncbi.nlm.nih.gov/37301965/>

**Introduction:** Zika virus (ZIKV) caused an outbreak in Brazil, in 2015, being associated to microcephaly. ZIKV has a strong neurotropism leading to death of infected cells in different brain regions, including the hippocampus, a major site for neurogenesis. The neuronal populations of the brain are affected differently by ZIKV from Asian and African ancestral lineages. However, it remains to be investigated whether subtle variations in the ZIKV genome can impact hippocampus infection dynamics and host response. **Objective:** This study evaluated how two Brazilian ZIKV isolates, PE243 and SPH2015, that differ in two specific missense amino acid substitutions, one in the NS1 protein and the other in the NS4A protein, affect the hippocampal phenotype and transcriptome. **Methods:** Organotypic hippocampal cultures (OHC) from infant Wistar rats were infected with PE243 or SPH2015 and analyzed in time series using immunofluorescence, confocal microscopy, RNA-Seq and RT-qPCR. **Results:** Unique patterns of infection and changes in neuronal density in the OHC were observed for PE243 and SPH2015 between 8 and 48 h post infection (p.i.). Phenotypic analysis of microglia indicated that SPH2015 has a greater capacity for immune evasion. Transcriptome analysis of OHC at 16 h p.i. disclosed 32 and 113 differentially expressed genes (DEGs) in response to infection with PE243 and SPH2015, respectively. Functional enrichment analysis suggested that infection with SPH2015 activates mostly astrocytes rather than microglia. PE243 downregulated biological process of proliferation of brain cells and upregulated those associated with neuron death, while SPH2015 downregulated processes related to neuronal development. Both isolates downregulated cognitive and behavioral development processes. Ten

genes were similarly regulated by both isolates. They are putative biomarkers of early hippocampus response to ZIKV infection. At 5, 7, and 10 days p.i., neuronal density of infected OHC remained below controls, and mature neurons of infected OHC showed an increase in the epigenetic mark H3K4me3, which is associated to a transcriptionally active state. This feature is more prominent in response to SPH2015. **Conclusion:** Subtle genetic diversity of the ZIKV affects the dynamics of viral dissemination in the hippocampus and host response in the early stages of infection, which may lead to different long-term effects in neuronal population.

### Assessing the impact of serostatus-dependent immunization on mitigating the spread of dengue virus.

Xue L, Jin X, Zhu H.

11-06-2023

*J Math Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37301798/>

### Highly attenuated poxvirus-based vaccines against emerging viral diseases.

Perdiguerro B, Pérez P, Marcos-Villar L, Albericio G, Astorgano D, Álvarez E, Sin L, Elena Gómez C, García-Arriaza J, Esteban M.

08-06-2023

*J Mol Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37301278/>

Although one member of the poxvirus family, variola virus, has caused one of the most devastating human infections worldwide, smallpox, the knowledge gained over the last 30 years on the molecular, virological and immunological mechanisms of these viruses has allowed the use of members of this family as vectors for the generation of recombinant vaccines against numerous pathogens. In this review, we cover different aspects of the history and biology of poxviruses with emphasis on their application as vaccines, from first- to fourth-generation, against smallpox, monkeypox, emerging viral diseases highlighted by the World Health Organization (COVID-19, Crimean-Congo haemorrhagic fever, Ebola and Marburg virus diseases, Lassa fever, Middle East respiratory syndrome and severe acute respiratory syndrome, Nipah and other henipaviral diseases, Rift Valley fever and Zika), as well as against one of the most concerning prevalent virus, the Human Immunodeficiency Virus, the causative agent of Acquired Immunodeficiency Syndrome. We discuss the implications in human health of the 2022 monkeypox epidemic affecting many countries, and the rapid prophylactic and therapeutic measures adopted to control virus dissemination within the human population. We also describe the preclinical and clinical evaluation of the Modified Vaccinia virus Ankara and New York vaccinia virus poxviral strains expressing heterologous antigens from the viral diseases listed above. Finally, we report different approaches to improve the immunogenicity and efficacy of poxvirus-based vaccine candidates, such as deletion of immunomodulatory genes, insertion of host-range genes and enhanced transcription of foreign genes

through modified viral promoters. Some future prospects are also highlighted.

### **Comparative efficacy trials with alcohol added d-phenothrin formulations against *Aedes aegypti* under open-field condition.**

**Megat Nabil Mohsin S, Ahmad N, Yusof YA.**

10-06-2023

*Pest Manag Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37300851/>

### **Risks of Acute Cholecystitis, Acute Pancreatitis, and Acute Appendicitis in Patients with Dengue Fever: A Population-Based Cohort Study in Taiwan.**

**Shih HI, Chi CY, Wang YP, Chien YW.**

10-06-2023

*Infect Dis Ther.*

<https://pubmed.ncbi.nlm.nih.gov/37300742/>

**Introduction:** Although cases of acute cholecystitis, acute pancreatitis, and acute appendicitis following dengue virus infections have been documented, very few large-scale studies have investigated the postdengue risk of these acute abdominal conditions. **Methods:** This retrospective population-based cohort study included all patients with laboratory-confirmed dengue from 2002 to 2015 in Taiwan and 1:4 nondengue individuals matched by age, sex, area of residence, and symptom onset time. Multivariate Cox proportional hazards regression models were used to investigate the short-term ( $\leq 30$  days), medium-term (31-365 days), and long-term ( $> 1$  year) risks of acute cholecystitis, pancreatitis, and appendicitis after dengue infection, adjusted for age, sex, area of residence, urbanization level, monthly income level, and comorbidities. Bonferroni correction was used for multiple testing; E-values were used to assess the robustness of the results to unmeasured confounding. **Results:** This study included 65,694 individuals with dengue and 262,776 individuals without dengue. Patients with dengue had a significantly increased risk of acute cholecystitis (adjusted hazard ratio (aHR) 60.21; 95% CI 29.11-124.54;  $P < 0.0001$ , E-value = 119.92) and acute pancreatitis (aHR 17.13; 95% CI 7.66-38.29;  $P < 0.0001$ , E-value = 33.75) within the first 30 days postinfection compared to those without dengue, but this increased risk was not present after that. The incidence rates of acute cholecystitis and pancreatitis in the first 30 days were 18.79 and 5.27 per 10,000, respectively. No increased risk of acute appendicitis was observed among patients with acute dengue infection. **Conclusion:** This study was the first large epidemiological study to show a significantly increased risk of acute cholecystitis and pancreatitis among patients with dengue during the acute phase of dengue infection, while no such association was observed for acute appendicitis. Early identification of acute cholecystitis and pancreatitis in patients with dengue is crucial for preventing fatal complications.

### **Mitophagy Activation Targeting PINK1 Is an Effective Treatment to Inhibit Zika Virus Replication.**

**Huang Y, Li Q, Kang L, Li B, Ye H, Duan X, Xie H, Jiang M, Li S, Zhu Y, Tan Q, Chen L.**

10-06-2023

*ACS Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37300493/>

Mitophagy is a selective degradation mechanism that maintains mitochondrial homeostasis by eliminating damaged mitochondria. Many viruses manipulate mitophagy to promote their infection, but its role in Zika virus (ZIKV) is unclear. In this study, we investigated the effect of mitophagy activation on ZIKV replication by the mitochondrial uncoupling agent niclosamide. Our results demonstrate that niclosamide-induced mitophagy inhibits ZIKV replication by eliminating fragmented mitochondria, both *in vitro* and in a mouse model of ZIKV-induced necrosis. Niclosamide induces autophosphorylation of PTEN-induced putative kinase 1 (PINK1), leading to the recruitment of PRKN/Parkin to the outer mitochondrial membrane and subsequent phosphorylation of ubiquitin. Knockdown of PINK1 promotes ZIKV infection and rescues the anti-ZIKV effect of mitophagy activation, confirming the role of ubiquitin-dependent mitophagy in limiting ZIKV replication. These findings demonstrate the role of mitophagy in the host response in limiting ZIKV replication and identify PINK1 as a potential therapeutic target in ZIKV infection.

### **Simulation of Hemorrhage Pathogenesis in Mice through Dual Stimulation with Dengue Envelope Protein Domain III-Coated Nanoparticles and Antiplatelet Antibody.**

**Lien TS, Sun DS, Wu WS, Chang HH.**

25-05-2023

*Int J Mol Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37298220/>

### **Vaccine elicitation and structural basis for antibody protection against alphaviruses.**

**Sutton MS, Pletnev S, Callahan V, Ko S, Tsybovsky Y, Bylund T, Casner RG, Cerutti G, Gardner CL, Guirguis V, Verardi R, Zhang B, Ambrozak D, Beddall M, Lei H, Yang ES, Liu T, Henry AR, Rawi R, Schön A, Schramm CA, Shen CH, Shi W, Stephens T, Yang Y, Florez MB, Ledgerwood JE, Burke CW, Shapiro L, Fox JM, Kwong PD, Roederer M.**

08-06-2023

*Cell.*

<https://pubmed.ncbi.nlm.nih.gov/37295404/>

Alphaviruses are RNA viruses that represent emerging public health threats. To identify protective antibodies, we immunized macaques with a mixture of western, eastern, and Venezuelan equine encephalitis virus-like particles (VLPs), a regimen that protects against aerosol challenge with all three viruses. Single- and triple-virus-specific antibodies were isolated, and we identified 21 unique binding groups. Cryo-EM structures revealed that broad

VLP binding inversely correlated with sequence and conformational variability. One triple-specific antibody, SKT05, bound proximal to the fusion peptide and neutralized all three Env-pseudotyped encephalitic alphaviruses by using different symmetry elements for recognition across VLPs. Neutralization in other assays (e.g., chimeric Sindbis virus) yielded variable results. SKT05 bound backbone atoms of sequence-diverse residues, enabling broad recognition despite sequence variability; accordingly, SKT05 protected mice against Venezuelan equine encephalitis virus, chikungunya virus, and Ross River virus challenges. Thus, a single vaccine-elicited antibody can protect in vivo against a broad range of alphaviruses.

### **Virus infection participates in the occurrence and development of human diseases through monoamine oxidase.**

**Sun Y, Liu W, Luo B.**

09-06-2023

*Rev Med Virol.*

<https://pubmed.ncbi.nlm.nih.gov/37294534/>

Monoamine oxidase (MAO) is a membrane-bound mitochondrial enzyme that maintains the steady state of neurotransmitters and other biogenic amines in biological systems through catalytic oxidation and deamination. MAO dysfunction is closely related to human neurological and psychiatric diseases and cancers. However, little is known about the relationship between MAO and viral infections in humans. This review summarises current research on how viral infections participate in the occurrence and development of human diseases through MAO. The viruses discussed in this review include hepatitis C virus, dengue virus, severe acute respiratory syndrome coronavirus 2, human immunodeficiency virus, Japanese encephalitis virus, Epstein-Barr virus, and human papillomavirus. This review also describes the effects of MAO inhibitors such as phenelzine, clorgyline, selegiline, M-30, and isatin on viral infectious diseases. This information will not only help us to better understand the role of MAO in the pathogenesis of viruses but will also provide new insights into the treatment and diagnosis of these viral diseases.

### **On the systematics of *Phlebotomus betisi* and two new related species from Laos with proposal of the new subgenus *Lewisius*.**

**Vongphayloth K, Randrianambinintsoa FJ, Lakeomany K, Phommavanh N, Mekarnia N, Khadri MS, Kaltenbach ML, Huguenin A, Martinet JP, Depaquit J.**

2023

*Parasite.*

<https://pubmed.ncbi.nlm.nih.gov/37294211/>

### **Global and Local Evolutionary Dynamics of Dengue Virus Serotype 1, 3 and 4.**

**Islam A, Deeba F, Tarai B, Gupta E, Naqvi IH, Abdullah M, Dohare R, Ahmed A, Almajhdi FN, Hussain T, Parveen S.**

09-06-2023

*Epidemiol Infect.*

<https://pubmed.ncbi.nlm.nih.gov/37293986/>

### **Characterizing dengue transmission in rural areas: A systematic review.**

**Man O, Kraay A, Thomas R, Trostle J, Lee GO, Robbins C, Morrison AC, Coloma J, Eisenberg JNS.**

08-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37289678/>

Dengue has historically been considered an urban disease associated with dense human populations and the built environment. Recently, studies suggest increasing dengue virus (DENV) transmission in rural populations. It is unclear whether these reports reflect recent spread into rural areas or ongoing transmission that was previously unnoticed, and what mechanisms are driving this rural transmission. We conducted a systematic review to synthesize research on dengue in rural areas and apply this knowledge to summarize aspects of rurality used in current epidemiological studies of DENV transmission given changing and mixed environments. We described how authors defined rurality and how they defined mechanisms for rural dengue transmission. We systematically searched PubMed, Web of Science, and Embase for articles evaluating dengue prevalence or cumulative incidence in rural areas. A total of 106 articles published between 1958 and 2021 met our inclusion criteria. Overall, 56% (n = 22) of the 48 estimates that compared urban and rural settings reported rural dengue incidence as being as high or higher than in urban locations. In some rural areas, the force of infection appears to be increasing over time, as measured by increasing seroprevalence in children and thus likely decreasing age of first infection, suggesting that rural dengue transmission may be a relatively recent phenomenon. Authors characterized rural locations by many different factors, including population density and size, environmental and land use characteristics, and by comparing their context to urban areas. Hypothesized mechanisms for rural dengue transmission included travel, population size, urban infrastructure, vector and environmental factors, among other mechanisms. Strengthening our understanding of the relationship between rurality and dengue will require a more nuanced definition of rurality from the perspective of DENV transmission. Future studies should focus on characterizing details of study locations based on their environmental features, exposure histories, and movement dynamics to identify characteristics that may influence dengue transmission.

### **Use of unmanned ground vehicle systems in urbanized zones: A study of vector Mosquito surveillance in Kaohsiung.**

**Chen YX, Pan CY, Chen BY, Jeng SW, Chen CH, Huang JJ, Chen CD, Liu WL.**

08-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37289665/>

Dengue fever is a vector-borne disease that has become a serious global public health problem over the past decade. An essential aspect of controlling and preventing mosquito-borne diseases is reduction of mosquito density. Through the process of urbanization, sewers (ditches) have become easy breeding sources of vector mosquitoes. In this study, we, for the first time, used unmanned ground vehicle systems (UGVs) to enter ditches in urban areas to observe vector mosquito ecology. We found traces of vector mosquitoes in ~20.7% of inspected ditches, suggesting that these constitute viable breeding sources of vector mosquitoes in urban areas. We also analyzed the average gravitrap catch of five administrative districts in Kaohsiung city from May to August 2018. The gravitrap indices of Nanzi and Fengshan districts were above the expected average (3.26), indicating that the vector mosquitoes density in these areas is high. Using the UGVs to detect positive ditches within the five districts followed by insecticide application generally yielded good control results. Further improving the high-resolution digital camera and spraying system of the UGVs may be able to effectively and instantly monitor vector mosquitoes and implement spraying controls. This approach may be suitable to solve the complex and difficult task of detecting mosquito breeding sources in urban ditches.

### Notes from the Field: Chikungunya Outbreak - Paraguay, 2022-2023.

Torales M, Beeson A, Grau L, Galeano M, Ojeda A, Martinez B, León N, Cabello A, Rojas F, de Egea V, Galeano R, Ocampos S, Vazquez C, Montoya R, Hills S, Sequera G.

09-06-2023

MMWR Morb Mortal Wkly Rep.

<https://pubmed.ncbi.nlm.nih.gov/37289652/>

## Dracunculose

### Influence of hydrophilic polysaccharide fat replacers on the in vitro digestibility of protein in emulsion-type sausage.

Zeng X, Lv B, Zhu Y, Li Q, Zhang K, Li C, Zhao D, Li C.

Aug-2023

Food Res Int.

<https://pubmed.ncbi.nlm.nih.gov/37316076/>

Hydrophilic polysaccharides have been widely applied as fat replacers in meat products, but their effects on the digestibility of meat proteins has seldom been studied. Replacement of backfat in emulsion-type sausage with konjac gum (KG), sodium alginate (SA) and xanthan gum (XG) were found to reduce the released amino group (-NH<sub>2</sub>) during simulated gastric digestion and initial intestinal digestion. The suppressed gastric digestibility of protein was verified by the denser structures of protein gastric digests and reduced generation of peptides in gastric digestion when a polysaccharide was added. After the whole gastrointestinal digestion, high level of SA and XG resulted in larger digests and a more obvious SDS-PAGE band between 5 and 15 kDa, and KG and SA significantly reduced the total release of -NH<sub>2</sub>. Additional of KG, SA and XG were found to increase the viscosity of the gastric

digests mixture, which could account for the reduced hydrolysis efficiency of pepsin during the gastric digestion, as evidenced in the pepsin activity study (decreased by 12.2-39.1%). This work highlights the influence of polysaccharide fat replacer on the digestibility of meat protein by changing the matrix characteristics.

### Research progress on the bulb expansion and starch enrichment in taro (*Colocasia esculenta* (L.) Schott).

Zhang E, Shen W, Jiang W, Li W, Wan X, Yu X, Xiong F.

08-06-2023

PeerJ.

<https://pubmed.ncbi.nlm.nih.gov/37309370/>

**Background:** Taro is an important potato crop, which can be used as food, vegetable, feed, and industrial raw material. The yield and quality of taro are primarily determined by the expansion degree of taro bulb and the filling condition of starch, whereas the expansion of taro bulb is a complex biological process. However, little information is reviewed on the research progress of bulb expansion and starch enrichment in taro. **Methodology:** PubMed, Web of Science, and the China National Knowledge Infrastructure databases were searched for relevant articles. After removing duplicate articles and articles with little relevance, 73 articles were selected for review. **Results:** This article introduces the formation and development of taro bulb for workers engaged in taro research. The content includes the process of amyloplast formation at the cytological level and changes in bulb expansion and starch enrichment at physiological levels, which involve endogenous hormones and key enzyme genes for starch synthesis. The effects of environment and cultivation methods on taro bulb expansion were also reviewed. **Conclusions:** Future research directions and research focus about the development of taro bulb were proposed. Limited research has been conducted on the physiological mechanism and hormone regulatory pathway of taro growth and development, taro bulb expansion, key gene expression, and starch enrichment. Therefore, the abovementioned research will become the key research direction in the future.

### Assembly and Comparative Analysis of the Complete Mitochondrial Genome of Two Species of Calla Lilies (*Zantedeschia*, Araceae).

Guo Y, Li Z, Jin S, Chen S, Li F, Wu H.

31-05-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37298515/>

In this study, the mitochondrial genomes of two calla species, *Zantedeschia aethiopica* Spreng. and *Zantedeschia odorata* Perry., were assembled and compared for the first time. The *Z. aethiopica* mt genome was assembled into a single circular chromosome, measuring 675,575 bp in length with a 45.85% GC content. In contrast, the *Z. odorata* mt genome consisted of bicyclic chromosomes (chromosomes 1 and 2), measuring 719,764 bp and exhibiting a 45.79% GC content. Both mitogenomes harbored similar gene compositions, with



56 and 58 genes identified in *Z. aethiopica* and *Z. odorata*, respectively. Analyses of codon usage, sequence repeats, gene migration from chloroplast to mitochondrial, and RNA editing were conducted for both *Z. aethiopica* and *Z. odorata* mt genomes. Phylogenetic examination based on the mt genomes of these two species and 30 other taxa provided insights into their evolutionary relationships. Additionally, the core genes in the gynoecium, stamens, and mature pollen grains of the *Z. aethiopica* mt genome were investigated, which revealed maternal mitochondrial inheritance in this species. In summary, this study offers valuable genomic resources for future research on mitogenome evolution and the molecular breeding of calla lily.

### **Pinellia ternata (Thunb.) Breit. attenuates the allergic airway inflammation of cold asthma via inhibiting the activation of TLR4-mediated NF- $\kappa$ B and NLRP3 signaling pathway.**

**Tao X, Li J, He J, Jiang Y, Liu C, Cao W, Wu H.**  
28-10-2023

*J Ethnopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37268256/>

**Ethnopharmacological relevance:** *Pinellia ternata* (Thunb.) Breit. (PT) has been demonstrated to be effective against the allergic airway inflammation (AAI) in clinical practices, especially in cold asthma (CA). Until now, the active ingredients, protective effect, and possible mechanism of PT against CA remain unknown. **Aim of the study:** The aim of this investigation was to examine the therapeutic impact and elucidate the underlying mechanism of PT on the AAI of CA. **Methods:** The compositions of PT water extract were determined via the UPLC-Q-TOF-MS/MS. The ovalbumin (OVA) and cold-water baths were used to induce CA in female mice. Morphological characteristic observations, expectorant effect, bronchial hyperreactivity (BHR), excessive mucus secretion, and inflammatory factors were used to uncover the treatment effect of PT water extract. In addition, the mucin 5AC (MUC5AC) mRNA and protein levels and the aquaporin 5 (AQP5) mRNA and protein levels were detected via qRT-PCR, immunohistochemistry (IHC), and western blotting. Moreover, the protein expressions associated with the TLR4, NF- $\kappa$ B, and NLRP3 signaling pathway were monitored by western blot analysis. **Results:** Thirty-eight compounds were identified from PT water extract. PT showed significant therapeutic effects on mice with cold asthma in terms of expectorant activity, histopathological changes, airway inflammation, mucus secretion, and hyperreactivity. PT exhibited good anti-inflammatory effects in vitro and in vivo. The expression levels of MUC5AC mRNA and protein decreased significantly, while AQP5 expression levels increased significantly in the lung tissues of mice after administration with PT as compared to mice induced by CA. Furthermore, the protein expressions of TLR4, p- $\kappa$ B, p-p65, IL-1 $\beta$ , IL-18, NLRP3, cleaved caspase-1, and ASC were markedly reduced following PT treatment. **Conclusions:** PT attenuated the AAI of CA by modulating Th1- and Th2-type cytokines. PT could inhibit the TLR4-mediated NF- $\kappa$ B signaling pathway

and activate the NLRP3 inflammasome to reduce CA. This study provides an alternative therapeutic agent of the AAI of CA after administration with PT.

### **Effects of environmental parameters on starch and soluble sugars in *Lemna minor*.**

**Van Dyck I, Vanhoudt N, Vives I Batlle J, Horemans N, Van Gompel A, Nauts R, Vangronsveld J.**

Juil-2023

*Plant Physiol Biochem.*

<https://pubmed.ncbi.nlm.nih.gov/37216822/>

### **Mechanism of synergistic stabilization of emulsions by amorphous taro starch and protein and emulsion stability.**

**Fan H, Zhu P, Hui G, Shen Y, Yong Z, Xie Q, Wang M.**  
30-10-2023

*Food Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37209438/>

Amorphous taro starch (TS)/whey protein isolate (WPI) mixtures were prepared using pasting treatment. The TS/WPI mixtures and their stabilized emulsions were characterized to determine the emulsion stability and the mechanism of synergistic stabilization of emulsions. As WPI content increased from 0% to 13%, the paste final viscosity and retrogradation ratio of the TS/WPI mixture gradually decreased from 3683 cP to 2532 cP and from 80.65% to 30.51%, respectively. As the WPI content increased from 0% to 10%, the emulsion droplet size decreased gradually from 96.81  $\mu$ m to 10.32  $\mu$ m, and the storage modulus  $G'$  and stabilities of freeze-thaw, centrifugal, and storage increased gradually. Confocal laser scanning microscopy revealed that WPI and TS were mainly distributed at the oil-water interface and droplet interstice, respectively. Thermal treatment, pH, and ionic strength had little influence on the appearance but had different influences on the droplet size and  $G'$ , and the rates of droplet size and  $G'$  increase under storage varied with different environmental factors.

### **Konjac Glucomannan Aerogels Modified by Hydrophilic Isocyanate and Expandable Graphite with Excellent Hydrolysis Resistance, Mechanical Strength, and Flame Retardancy.**

**Wang L, Lin X, Li J, Yang H, Feng X, Wan C.**  
12-06-2023

*Biomacromolecules.*

<https://pubmed.ncbi.nlm.nih.gov/37141322/>

### **Influence of disaccharide and monosaccharide on the rheological behavior of dry-heated alocasia starch under high pressure assisted treatment.**

**Roy D, Kumar KJ.**

30-06-2023

*Int J Biol Macromol.*

<https://pubmed.ncbi.nlm.nih.gov/37119887/>



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## Echinococcosis

### Echinococcus Species Infections among Wild Canids in Pennsylvania, USA.

Garrett K, Brown J, Grunert RKA, Hunte J, Ruder MG, Van Why K, Yabsley MJ, Cleveland CA.

01-04-2023

*J Wildl Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37036486/>

Echinococcus species are zoonotic tapeworms that can impact the health of wildlife, domestic animals, livestock, and humans. Two species of interest in North America are *Echinococcus multilocularis* and *Echinococcus canadensis* (*Echinococcus granulosus sensu lato*). The primary wildlife definitive hosts for *E. multilocularis* and *E. canadensis* are similar, including red foxes (*Vulpes vulpes*), gray foxes (*Urocyon cinereoargenteus*), coyotes (*Canis latrans*), and wolves (*Canis lupus*). These two *Echinococcus* spp. use different intermediate hosts, including small mammals for *E. multilocularis* and artiodactylids for *E. canadensis*. Although historically absent from much of the eastern US, recent reports in new US states (e.g., Virginia, Vermont, Maine, Missouri) highlight the need for *Echinococcus* spp. surveillance in this region. During 2019-2020, 308 gastrointestinal tracts were collected from wild canids in Pennsylvania and microscopically screened for adult *Echinococcus* species. Two coyotes (2/155) were co-infected with both *E. multilocularis* and *E. canadensis* as determined by molecular confirmation. No red foxes (n=137) or gray foxes (n=16) were positive. These data indicate both *Echinococcus* species are present in Pennsylvanian coyotes, highlighting the need to better understand the ecological and epidemiological consequences for human and animal health.

### Targeted and non-targeted proteomics to characterize the parasite proteins of *Echinococcus multilocularis* metacestodes.

Müller J, Preza M, Kaethner M, Rufener R, Braga S, Uldry AC, Heller M, Lundström-Stadelmann B.

30-05-2023

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/37325510/>

### A rare case of bilateral para-rectal hydatid disease: A case report.

Nasrallah O, ElRifai A, Sidani S, Jamali F.

09-06-2023

*Int J Surg Case Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37315496/>

### Oral Delivery of Anti-Parasitic Agent-Loaded PLGA Nanoparticles: Enhanced Liver Targeting and Improved Therapeutic Effect on Hepatic Alveolar Echinococcosis.

Li J, Yang Y, Han X, Li J, Tian M, Qi W, An H, Wu C, Zhang Y, Han S, Duan L, Wang W, Zhang W.

08-06-2023

*Int J Nanomedicine.*

<https://pubmed.ncbi.nlm.nih.gov/37312930/>

**Background:** Alveolar echinococcosis (AE) is a lethal parasitic disease caused by infection with the metacestode of the dog/fox tapeworm *Echinococcus multilocularis*, which primarily affects the liver. Although continued efforts have been made to find new drugs against this orphan and neglected disease, the current treatment options remain limited, with drug delivery considered a likely barrier for successful treatment.

**Methods:** Nanoparticles (NPs) have gained much attention in the field of drug delivery due to their potential to improve delivery efficiency and targetability. In this study, biocompatible PLGA nanoparticles encapsulating a novel carbazole aminoalcohol anti-AE agent (H1402) were prepared to promote the delivery of the parent drug to liver tissue for treating hepatic AE. **Results:** H1402-loaded nanoparticles (H1402-NPs) had a uniform spherical shape and a mean particle size of 55 nm. Compound H1402 was efficiently encapsulated into PLGA NPs with a maximal encapsulation efficiency of 82.1% and drug loading content of 8.2%. An in vitro uptake assay demonstrated that H1402-NPs rapidly penetrated the in vitro cultured pre-cyst wall and extensively accumulated in the pre-cysts of *E. multilocularis* within only 1 h. The biodistribution profile of H1402-NPs determined through ex vivo fluorescence imaging revealed significantly enhanced liver distribution compared to unencapsulated H1402, which translated to improved therapeutic efficacy and reduced systemic toxicity (especially hepatotoxicity and cytotoxicity) in a hepatic AE murine model. Following a 30-day oral regimen (100 mg/kg/day), H1402-NPs significantly reduced the parasitic burden in both the parasite mass (liver and metacestode total weight, 8.8%) and average metacestode size (89.9%) compared to unmedicated infected mice (both *p*-values < 0.05); the treatment outcome was more effective than those of albendazole- and free H1402-treated individuals.

**Conclusion:** Our findings demonstrate the advantages of encapsulating H1402 into PLGA nanoparticles and highlight the potential of H1402-NPs as a promising liver-targeting therapeutic strategy for hepatic AE.

### In silico Analysis of a 29 kDa *Echinococcus granulosus* Protoscolex Protein (P29) as a Vaccine Candidate against Cystic Echinococcosis.

Khazaei S, Dalimi A, Pirestani M, Ghafarifar F.

28-02-2023

*Arch Razi Inst.*

<https://pubmed.ncbi.nlm.nih.gov/37312723/>

### Histopathological Study to Evaluate the Effect of Aqueous Extract of *Portunuspelagicus* and Mebendazole on Hydatid Cysts in Mice.

Sabeeh E, Thamer NK, Alsaady HAM.

28-02-2023

*Arch Razi Inst.*

<https://pubmed.ncbi.nlm.nih.gov/37312708/>

## Effects of Dihydroartemisinin against Cystic Echinococcosis In Vitro and In Vivo.

Wen L, Zhang J, Zhao J, Gong Y, Zhang H, Yang J, Wang J.  
13-06-2023

*Infect Immun.*

<https://pubmed.ncbi.nlm.nih.gov/37310215/>

Cystic echinococcosis (CE) is a disease caused by the infection of *Echinococcus granulosus*. We sought to investigate the effects of dihydroartemisinin (DHA) against CE under *in vitro* and *in vivo* conditions. Protoscoleces (PSCs) from *E. granulosus* were divided into control, DMSO, ABZ, DHA-L, DHA-M, and DHA-H groups. PSC viability after DHA treatment was determined based on the eosin dye exclusion test, alkaline phosphatase content detection, and ultrastructure observation. DNA oxidative damage inducer hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), reactive oxygen species (ROS) scavenger mannitol, and the DNA damage repair inhibitor velparib were used to explore the anti-CE mechanism of DHA. The anti-CE effects and CE-induced liver injury and oxidative stress of DHA at different doses (50, 100, and 200 mg/kg) were assessed in CE mice. DHA showed antiparasitic effects on CE in both *in vivo* and *in vitro* experiments. DHA could elevate the ROS level and induce oxidative DNA damage in PSCs, thereby destroying hydatid cysts. DHA could inhibit the growth of cysts in a dose-dependent manner and reduce the content of biochemical parameters associated with liver injury in CE mice. It also significantly reversed oxidative stress in CE mice, which was characterized as the decreased tumor necrosis factor alpha and H<sub>2</sub>O<sub>2</sub> content, as well as the increase of the ratio of glutathione/oxidized glutathione and total superoxide dismutase content. DHA showed antiparasitic effects. DNA damages induced by oxidative stress played important roles in this process.

## Diagnostic accuracy of swine echinococcosis cytopathological tests and challenges for a differential diagnosis: slaughterhouse data.

Toure A, Toure L, Acapovi-Yao GL, Senin CBV, Kone N, Kachani M, Couacy-Hymann E.

Juin-2023

*Helminthologia.*

<https://pubmed.ncbi.nlm.nih.gov/37305668/>

Echinococcosis disease shows clinical signs similar to many diseases. Hence we report cases that need to be confirmed using appropriate tests. A confirmatory study has been conducted to assess the accuracy of two cytopathological tests, with the histopathology test as the reference standard. The first cytopathological test evaluates the Ziehl Neelsen staining with an epifluorescence microscope (cytopath 1). The second cytopathological test uses the same staining followed by a transmitted light microscope examination (cytopath 2). Of a total of 2524 inspected pigs, 101 suspected cases of echinococcosis were detected, of which 67 were found positive with the two cytopathological tests and the histopathological one. The specificity of cytopath 1 (100 % [95 % CI 100 - 100]) and cytopath 2 (100 % [95 % CI 100;100]) were similar, as well as their respective positive

predictive values: 100 % [95 % CI 100 - 100] vs. 100 % [95 % CI 100 - 100]. The sensitivity of cytopath 1 is 79.66 % [95 % CI 69.39 - 89.93], while cytopath 2 equals 66.10 % [95 % CI 54.02 - 78.18]. The difference in sensitivity of both tests was not significant. Negative predictive values found for cytopath 1, and cytopath 2 were 40 [95 % CI 18.53 - 61.47] and 28.57 [95 % CI 11.84 - 45.3], leading to the Generalized Estimating Equations (GEE) Model estimate for an odds ratio of 1.4 [95 % CI 0.41 - 5.2],  $p = 0.06$ . Cytopath 1 and cytopath 2 are equivalent in terms of specificity (100 % [95 % CI 100 - 100] vs. 100 % [95 % CI 100;100]) and positive predictive value (100 % [95 % CI 100 - 100]). Cytopath 1 is more sensitive than cytopath 2 but not significant (79.66 % [95 % CI 69.39 - 89.93] vs. 66.10 % [95 % CI 54.02 - 78.18]). However, the negative predictive value of cytopath 1 is better than that of cytopath 2: 40 % [95 % CI 18.53 - 61.47] vs. 28.57 % [95 % CI 11.84 - 45.3].

## A Solitary Abscessed Hydatid Cyst of the Buttock: A Rare Case.

Chablou M, Id M'barek A, Chacha R, Merhom A, Tahi M.  
10-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37303317/>

The hydatid cyst is a cosmopolitan parasitic infection caused by tapeworms of the genus *Echinococcus* and is a major public health problem in developing countries. Solitary hydatid cysts located in the buttocks are very rare, and the unusual location of the cyst can aid in the differential diagnosis of subcutaneous masses in this area, particularly in endemic areas. In this report, we present the case of a 39-year-old man who was admitted to the emergency department with a painful, abscessed cyst in the buttock region. The cyst was completely excised, and histopathological examination confirmed the diagnosis of a hydatid cyst. Further investigations did not reveal any other locations. Although the buttock region is an extremely rare site of infection for a hydatid cyst, it should be considered in cystic lesions, especially in endemic areas.

## First report of *Echinococcus orteppi* and genotype G6 of *E. canadensis* cluster from southern Punjab, Pakistan and a global overview on genetic structure and host adaptation of *E. orteppi*.

Muqaddas H, Mehmood N, Saarma U, Usman A, Ahmed F, Varcasia A, Sini MF, Ullah MI.

Août-2023  
*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37220843/>

## Differences in clinical aspects of human cystic echinococcosis caused by *Echinococcus granulosus sensu stricto* and the G6 genotype in Neuquén, Argentina.

Debiaggi MF, Alvarez Rojas CA, Lazzarini LE, Calfunao D, Titanti P, Calanni L, Iacono M, Soriano SV, Deplazes P, Pierangeli NB.

Juin-2023

*Parasitology*.

<https://pubmed.ncbi.nlm.nih.gov/37203451/>

Most human cystic echinococcosis (CE) cases worldwide are attributed to *Echinococcus granulosus sensu stricto* (s.s.), followed by the G6 and G7 genotypes. While *E. granulosus* s.s. has a cosmopolitan distribution, the G6 genotype is restricted to areas where camels and goats are present. Goats are the primary livestock in the Neuquén province in Argentina where the G6 genotype has been reported to be responsible for a significant percentage of CE human cysts genotyped. In the present study, we genotyped 124 *Echinococcus* cysts infecting 90 CE-confirmed patients. *Echinococcus granulosus* s.s. was identified in 51 patients (56.7%) with 81 cysts and the G6 genotype in 39 patients (43.3%) harbouring 43 cysts. Most CE cases ≤18 years were male suggesting pastoral work could be a risk factor for the infection. *Echinococcus granulosus* s.s. was significantly found more frequently in the liver (32/51 patients) and the G6 genotype in the lungs and extrahepatic localizations (27/39). The patients infected with *E. granulosus* s.s., presented up to 6 cysts while patients infected with G6 presented a maximum of 2. The diameter of lung cysts attributed to *E. granulosus* s.s. was significantly larger compared to lung cysts from G6. Following the WHO ultrasound classification of liver cysts, we observed inactive cysts in 55.6% of G6 cysts and only 15.3% of *E. granulosus* s.s. cysts. In conclusion, we provide evidence of differences in clinical aspects of CE caused by *E. granulosus* s.s. and the G6 genotype of *E. granulosus* s.l. complex infecting humans.

### **Cystic echinococcosis in Iceland: a brief history and genetic analysis of a 46-year-old *Echinococcus* isolate collected prior to the eradication of this zoonotic disease.**

Saarma U, Skirnisson K, Björnsdóttir TS, Laurimäe T, Kinkar L.

Juin-2023

*Parasitology*.

<https://pubmed.ncbi.nlm.nih.gov/37161714/>

Cystic echinococcosis (CE) is considered the most severe parasitic disease that ever affected the human population in Iceland. Before the start of eradication campaign in the 1860s, Iceland was a country with very high prevalence of human CE, with approximately every fifth person infected. Eradication of CE from Iceland by 1979 was a huge success story and served as a leading example for other countries on how to combat such a severe One Health problem. However, there is no genetic information on *Echinococcus* parasites before eradication. Here, we reveal the genetic identity for one of the last *Echinococcus* isolates in Iceland, obtained from a sheep 46 years ago (1977). We sequenced a large portion of the mitochondrial genome (8141 bp) and identified the isolate as *Echinococcus granulosus sensu stricto* genotype G1. As G1 is known to be highly infective genotype to humans, it may partly explain why such a large proportion of human population in Iceland was infected at a time. The study demonstrates that decades-old samples hold significant potential to uncover genetic identities of parasites in the past.

### **Exploring the genetic diversity of genotypes G8 and G10 of the *Echinococcus canadensis* cluster in Europe based on complete mitochondrial genomes (13 550-13 552 bp).**

Laurimäe T, Kinkar L, Moks E, Bagrade G, Saarma U.

Juin-2023

*Parasitology*.

<https://pubmed.ncbi.nlm.nih.gov/37005069/>

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## **Filariose lymphatique**

### **Chyluria in a Postpartum Obese Female Patient.**

Kowshik V, Moorthy S, Marappa L, Ahmed B, Bhaskar E.

12-05-2023

*Cureus*.

<https://pubmed.ncbi.nlm.nih.gov/37309336/>

Chyluria characterized by the passage of milky white urine is rarely encountered these days due to the overall reduction in the number of cases of lymphatic filariasis. Though lymphatic filariasis accounts for the majority of cases of chyluria, nonparasitic causes have also been reported. Case reports of chyluria as a complication in pregnancy have been published but chyluria presenting solely as a postpartum complication has rarely been documented. We present a case of a 29-year-old female with no known prior comorbidities, who presented with recurring complaints of the painless passage of milky white urine over the last year. Symptoms seem to have started six months post-delivery of her second child. The patient claimed significant weight gain during an otherwise normal pregnancy. She was well-built and had a BMI of 32 kg/m<sup>2</sup>. Her systemic examination and baseline laboratory workup were within normal limits. Postprandial urine was milky white, rich in chylomicrons, with urine chylomicrons of 112 mg/dl. The patient was screened for filariasis, which was negative. An ultrasound of the abdomen was done to rule out the presence of a fistula, but no evidence of one was found on imaging. Tc-99m sulfur colloid scintigraphy revealed an area of abnormal tracer accumulation in the abdomen with the passage of the tracer in the urine container, confirming the presence of chyluria. The patient was recommended to undergo conservative management with dietary modification and weight reduction. She has been closely followed up and has achieved spontaneous resolution of the chyluria. Most patients with chyluria show a good response to conservative management alone as in our case. Surgical intervention is usually indicated for cases not responding to conservative management or for refractory chyluria.

### **Evaluating the availability and quality of services for lymphatic filariasis morbidity in Ghana.**

Edmiston M, Atinbire S, Mensah EO, Mensah E, Alomatu B, Asemanyi Mensah K, Palmer S.

12-06-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/37307289/>

## Gale

### Crusted scabies.

Selvaraj R, Purushothaman S, Indra Couppoussamy K.

28-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317720/>

### Traitement à l'ivermectine par voie orale chez un nourrisson atteint de gale croûteuse.

Dixit D, Tang JW, Grolla A.

12-06-2023

*CMAJ.*

<https://pubmed.ncbi.nlm.nih.gov/37308209/>

### Scrotal and Penile Scabietic Nodules.

Narayanan A.

12-06-2023

*J Cutan Med Surg.*

<https://pubmed.ncbi.nlm.nih.gov/37306409/>

### Infection Control among Healthcare Workers and Management of a Scabies Outbreak in a Large Italian University Hospital.

Sponselli S, De Maria L, Caputi A, Stefanizzi P, Bianchi FP, Delvecchio G, Foti C, Romita P, Ambrogio F, Zagaria S, Giannelli G, Tafuri S, Vimercati L.

02-06-2023

*J Clin Med.*

<https://pubmed.ncbi.nlm.nih.gov/37298025/>

This retrospective observational study describes the results of an ad-hoc designated prevention protocol aimed at containing the spread of the scabies infestation among healthcare workers (HCWs) of a large University Hospital in Italy. The outbreak started on October 2022 and a preventive protocol was set up thanks to a multidisciplinary approach. HCWs at high scabies risk were defined as subjects working in Operative Units with a scabies prevalence higher than 2%, close contacts of a confirmed case of scabies, or HCWs with signs and symptoms of the disease. All cases at high scabies risk underwent a dermatological examination, and the infested HCWs were suspended from work until definitive healing. Mass drug administration was established for all HCWs working in Operative Units with a scabies prevalence higher than 2%. Until March 2023, out of 183 screening dermatological examinations, 21 (11.5%) were diagnostic for scabies. Between 11 October 2022 (date of the first diagnosed scabies case) and 6 March 2023 (the end of incubation period related to the last case detected), the frequency of scabies was 0.35% (21 scabies cases/6000 HCWs). The duration of the outbreak in our hospital was 14.7 weeks. Statistical analysis shows a significant association between scabies and being a nurse and having an allergy to dust mites. We obtained a low

frequency of scabies infection, limiting the duration of the outbreak and the related economic burden.

### Burden of Disease and Unmet Needs in the Diagnosis and Management of Atopic Dermatitis in Diverse Skin Types in Australia.

Courtney A, Lopez DJ, Lowe AJ, Holmes Z, Su JC.

01-06-2023

*J Clin Med.*

<https://pubmed.ncbi.nlm.nih.gov/37298007/>

Atopic dermatitis (AD) is a common, chronic, inflammatory skin disease affecting Australians of all ages, races, ethnicities, and social classes. Significant physical, psychosocial, and financial burdens to both individuals and Australian communities have been demonstrated. This narrative review highlights knowledge gaps for AD in Australian skin of colour. We searched PubMed, Wiley Online Library, and Cochrane Library databases for review articles, systematic reviews, and cross-sectional and observational studies relating to AD in Australia for skin of colour and for different ethnicities. Statistical data from the Australian Institute of Health and Welfare and the Australian Bureau of Statistics was collected. In recent years, there has been substantially increased awareness of and research into skin infections, such as scabies and impetigo, among various Australian subpopulations. Many such infections disproportionately affect First Nations Peoples. However, data for AD itself in these groups are limited. There is also little written regarding AD in recent, racially diverse immigrants with skin of colour. Areas for future research include AD epidemiology and AD phenotypes for First Nations Peoples and AD trajectories for non-Caucasian immigrants. We also note the evident disparity in both the level of understanding and the management standards of AD between urban and remote communities in Australia. This discrepancy relates to a relative lack of healthcare resources in marginalised communities. First Nations Peoples in particular experience socioeconomic disadvantage, have worse health outcomes, and experience healthcare inequality in Australia. Barriers to effective AD management must be identified and responsibly addressed for socioeconomically disadvantaged and remote-living communities to achieve healthcare equity.

### Glittering trail: feces of scabies indicated by a high-power-field dermoscopy with UVA light.

Fujimoto M, Sakai H, Watanabe R, Fujimoto M.

07-06-2023

*J Am Acad Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/37295505/>

### MOVEMENTS BY SAN JOAQUIN KIT FOXES (VULPES MACROTIS MUTICA) BETWEEN URBAN AND NONURBAN HABITATS: IMPLICATIONS FOR INTERPOPULATION DISEASE TRANSFER.



Cypher BL, Deatherage NA, Westall TL, Kelly EC, Foley JE, Clifford DL, Rudd JL.

01-04-2023

*J Wildl Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37018594/>

Sarcoptic mange epidemics erupted in two of the remaining populations of endangered San Joaquin kit foxes (*Vulpes macrotis mutica*). Both populations are in urban habitats in the cities of Bakersfield and Taft, California, USA. The risk of disease spread from the two urban populations to nearby nonurban populations, and then throughout the species range, is of considerable conservation concern. To date, mange has not been detected in any nonurban populations despite considerable surveillance effort. The reasons for the lack of detections of mange among nonurban foxes are unknown. We monitored urban kit fox movements using geographic positioning system (GPS) collars to test the hypothesis that urban foxes were not venturing into nonurban habitats. Of 24 foxes monitored December 2018 to November 2019, 19 (79%) made excursions from urban into nonurban habitats from 1-124 times. The mean number of excursions per 30 d was 5.5 (range 0.1-13.9 d). The mean proportion of locations in nonurban habitats was 29.0% (range 0.6-99.7%). The mean maximum distance that foxes traveled into nonurban areas from the urban-nonurban interface was 1.1 km (range 0.1-2.9 km). Mean number of excursions, proportion of nonurban locations, and maximum distance into nonurban habitats were similar between Bakersfield and Taft, females and males, and adults and juveniles. At least eight foxes apparently used dens in nonurban habitats; shared use of dens may be an important mode of mange mite transmission between conspecifics. Two of the collared foxes died of mange during the study and two others had mange when captured at the end of the study. Three of these four foxes had made excursions into nonurban habitats. These results confirm a significant potential for mange to spread from urban to nonurban kit fox populations. We recommend continued surveillance in nonurban populations and continued treatment efforts in the affected urban populations.

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

**An efficient method for viable cryopreservation and recovery of hookworms and other gastrointestinal nematodes in the laboratory.**

Li H, Gazzola D, Hu Y, Aroian RV.

Juil-2023

*Int J Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37201563/>

Hookworms (genera *Ancylostoma* and *Necator*) are amongst the most prevalent and important parasites of humans globally. These intestinal parasites ingest blood,

resulting in anemia, growth stunting, malnutrition, and adverse pregnancy outcomes. They are also critical parasites of dogs and other animals. In addition, hookworms and hookworm products are being explored for their use in treatment of autoimmune and inflammatory diseases. There is thus a significant and growing interest in these mammalian host-obligate parasites. Laboratory research is hampered by the lack of good means of cryopreservation and recovery of parasites. Here, we describe a robust method for long-term ( $\geq 3$  year) cryopreservation and recovery of both *Ancylostoma* and *Necator* hookworms that is also applicable to two other intestinal parasites that passage through the infective L3 stage, *Strongyloides ratti* and *Heligmosomoides polygyrus bakeri*. The key is a revised recovery method, in which cryopreserved L1s are thawed and raised to the infective L3 stage using activated charcoal mixed with uninfected feces from a permissive host. This technique will greatly facilitate research on and availability of gastrointestinal parasitic nematodes with great importance to global health, companion animal health, and autoimmune/inflammatory disease therapies.

## Continuity in intestinal parasite infection in Aalst (Belgium) from the medieval to the early modern period (12th-17th centuries).

Rabinow S, Deforce K, Mitchell PD.

Juin-2023

*Int J Paleopathol.*

<https://pubmed.ncbi.nlm.nih.gov/36947954/>

**Objective:** To characterize patterns in the taxonomic diversity of parasites infecting the population of Aalst, Belgium, between the 12th and 17th centuries. **Materials:** 14 sediment samples from seven cesspits dated 1100-1700 CE. **Methods:** Digital light microscopy and Enzyme-linked immunosorbent assay (ELISA). **Results:** We identified eggs of four species of helminths: whipworm (*Trichuris trichiura*), roundworm (*Ascaris lumbricoides*), Echinostoma fluke and Dicrocoelium fluke. ELISA results for protozoal parasites were negative. **Conclusions:** Taxonomic diversity of parasite infections remained constant from the 12th to the 17th centuries. Roundworm and whipworm, spread by poor sanitation, were dominant. Two species of zoonotic parasites were also identified, including for the first time ever in the Low Countries the Echinostoma fluke, which may have been spread by eating uncooked freshwater animal foods. **Significance:** Analysis of sediment samples spanning such a broad chronology (six centuries) from a single city offers the opportunity to track diachronic change, which is rare in paleoparasitological studies. **Limitations:** We were unable to acquire samples from cesspits dating to the 14th century. **Suggestions for further research:** Additional data from other Low Countries towns may strengthen the patterns identified in this paper. A similar approach can be used to investigate towns in different regions of the world.

## The turkey ascarid, *Ascaridia dissimilis*, as a model genetic system.

Collins JB, Andersen EC.



Juil-2023  
*Int J Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36549442/>

## Leishmaniose

### LeishIF3d is a non-canonical cap-binding protein in *Leishmania*.

**Bose P, Baron N, Pullaiahgari D, Ben-Zvi A, Shapira M.**  
30-05-2022  
*Front Mol Biosci.*  
<https://pubmed.ncbi.nlm.nih.gov/37325473/>

Translation of most cellular mRNAs in eukaryotes proceeds through a cap-dependent pathway, whereby the cap-binding complex, eIF4F, anchors the pre-initiation complex at the 5' end of mRNAs driving translation initiation. The genome of *Leishmania* encodes a large repertoire of cap-binding complexes that fulfill a variety of functions possibly involved in survival along the life cycle. However, most of these complexes function in the promastigote life form that resides in the sand fly vector and decrease their activity in amastigotes, the mammalian life form. Here we examined the possibility that LeishIF3d drives translation in *Leishmania* using alternative pathways. We describe a non-canonical cap-binding activity of LeishIF3d and examine its potential role in driving translation. LeishIF3d is required for translation, as reducing its expression by a hemizygous deletion reduces the translation activity of the LeishIF3d(+/-) mutant cells. Proteomic analysis of the mutant cells highlights the reduced expression of flagellar and cytoskeletal proteins, as reflected in the morphological changes observed in the mutant cells. Targeted mutations in two predicted alpha helices diminish the cap-binding activity of LeishIF3d. Overall, LeishIF3d could serve as a driving force for alternative translation pathways, although it does not seem to offer an alternative pathway for translation in amastigotes.

### In Silico Characterization of an Important Metacyclogenesis Marker in *Leishmania donovani*, HASPB1, as a Potential Vaccine Candidate.

**Kordi B, Basmenj ER, Majidani H, Basati G, Sargazi D, Nazari N, Shams M.**  
07-06-2023  
*Biomed Res Int.*  
<https://pubmed.ncbi.nlm.nih.gov/37323936/>

### First reported case of leishmaniasis in a cat in Trinidad and Tobago.

**Pargass I, Wint C, Suepaul R, Frontera-Acevedo K, Qurollo BA.**  
Juil-2023  
*Vet Parasitol Reg Stud Reports.*  
<https://pubmed.ncbi.nlm.nih.gov/37321792/>

Antileishmanial, cellular mechanisms, and cytotoxic effects of green synthesized zinc nanoparticles alone and in combined with

glucantime against *Leishmania major* infection.

**Ghasemian Yadegari J, Khudair Khalaf A, Ezzatkah F, Shakibaie M, Mohammadi HR, Mahmoudvand H.**  
13-06-2023  
*Biomed Pharmacother.*  
<https://pubmed.ncbi.nlm.nih.gov/37321058/>

**Background:** We decided to investigate the antileishmanial, cellular mechanisms, and cytotoxic effects of green synthesized Zinc nanoparticles (ZnNPs) alone and combined with glucantime against *Leishmania major* infection. **Methods:** The effect of green synthesized ZnNP on *L. major* amastigote was studied through macrophage cells. The mRNA expression level of iNOS and IFN- $\gamma$  followed by the exposure of J774-A1 macrophage cells to ZnNPs was assessed by Real-time PCR. The Caspase-3-like activity of promastigotes exposed to ZnNPs was studied. Effects of ZnNPs alone and combined with glucantime (MA) were studied on cutaneous leishmaniasis in BALB/c mice. **Results:** ZnNPs displayed the spherical shape with sizes ranging from 30 to 80 nm. The obtained IC<sub>50</sub> values for ZnNPs, MA, and ZnNPs + MA were 43.2, 26.3, and 12.6  $\mu\text{g/mL}$ , respectively; indicating the synergistic effects of ZnNPs in combination with MA. CL lesions had completely improved in the mice received with ZnNPs in combination with MA. The mRNA expression level of iNOS, TNF- $\alpha$ , and IFN- $\gamma$  was dose-dependently ( $p < 0.01$ ) upregulated; whereas it was downregulated in IL-10. ZnNPs markedly stimulated the caspase-3 activation with no significant toxicity on normal cells. **Conclusion:** Based on these in vitro and in vivo results, green synthesized ZnNPs, mainly along with MA, showed that has the potential to be introduced as a new drug for CL therapy. Triggering of NO production, and inhibition of infectivity rate are revealed as mechanisms of action ZnNPs on *L. major*. But, supplementary investigations are necessary to clear the efficacy and safety of these agents.

### Occurrence of Leishmaniasis in Iberian Wolves in Northwestern Spain.

**Merino Goyenechea J, Castilla Gómez de Agüero V, Palacios Alberti J, Balaña Fouce R, Martínez Valladares M.**  
30-04-2023  
*Microorganisms.*  
<https://pubmed.ncbi.nlm.nih.gov/37317153/>

Canine leishmaniasis is an important vector-borne protozoan disease in dogs that is responsible for serious deterioration in their health. In the Iberian Peninsula, as in most countries surrounding the Mediterranean Sea, canine leishmaniasis is caused by *Leishmania infantum* (zymodeme MON-1), a digenetic trypanosomatid that harbors in the parasitophorous vacuoles of host macrophages, causing severe lesions that can lead to death if the animals do not receive adequate treatment. Canine leishmaniasis is highly prevalent in Spain, especially in the Mediterranean coastal regions (Levante, Andalusia and the Balearic Islands), where the population of domestic dogs is very high. However, the presence of this disease has been spreading to other rural and sparsely populated latitudes, and cases of leishmaniasis have been

reported for years in wildlife in northwestern Spain. This work describes for the first time the presence of wolves that tested positive for leishmaniasis in the vicinity of the Sierra de la Culebra (Zamora province, northwestern Spain), a protected sanctuary of this canid species, using PCR amplification of *L. infantum* DNA from different non-invasive samples such as buccal mucosa and those from both ears and hair. In addition to live animals (21), samples from carcasses of mainly roadkill animals (18) were also included and analyzed using the same technique, obtaining a positivity rate of 18 of the 39 wolves sampled (46.1%) regardless of their origin.

### Updated estimation of cutaneous leishmaniasis incubation period in French Guiana.

**Blaizot R, Fontaine A, Demar M, Delon F, d'Oleón AB, Mayet A, de Laval F, de Santi VP, Briolant S.**

14-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37315094/>

### Population dynamics of *Nyssomyia whitmani* (Diptera: Psychodidae) in domestic and peridomestic environments in Northeast Argentina, a tegumentary leishmaniasis outbreak area.

**Manteca-Acosta M, Cueto GR, Poullain M, Santini MS, Salomón OD.**

14-06-2023

*J Med Entomol.*

<https://pubmed.ncbi.nlm.nih.gov/37313956/>

In the present study, the temporal dynamics of the main vector of *Leishmania braziliensis*, *Nyssomyia whitmani*, was measured by monthly captures of phlebotominae sandflies during 5 consecutive years (from 2011 to 2016) in the Paranaense region of South America. The captures were performed in environments where the human-vector contact risk is high: domiciliary and peridomestic environments in a rural area endemic of tegumentary leishmaniasis. *Nyssomyia whitmani* was recorded as the dominant species of the phlebotominae ensemble in all domiciliary and peridomestic environments (House, Chicken Shed, Pigsty, and Forest Edge). Using generalized additive models, intra- and interannual fluctuations were observed, modulated by meteorological variables such as the minimum temperature and the accumulated precipitation 1 wk prior to capture. The installation of a pigsty by the farmer during the study period allowed us to observe and describe the so-called "pigsty effect" where the *Ny. whitmani* population was spatially redistributed, turning the pigsty as the environment that obtained the highest phlebotominae record counts, thus maintaining the farm overall abundance, supporting the idea that the environmental management of the peridomicile could have an impact on the reduction of epidemiological risk by altering the spatial distribution of the phlebotominae ensemble in the environments.

### First molecular description of autochthonous urban cases of canine visceral leishmaniasis in the city of Belém, Pará, Brazil.

**Galvão GR, Gonçalves EC, Moura LGS, Virgolino RR, Neves AMP, Aguiar DCF.**

09-06-2023

*Braz J Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37311132/>

Leishmaniasis is an anthroponosis transmitted by vectors, with dogs being the main domestic reservoirs. Brazil is one of the countries most affected by this disease, and it has been described in humans and dogs in every region in the country. In the northern region leishmaniasis cases in humans have been described in more than 100 municipalities in the State, including the capital, Belém. This study involves two cases of canine visceral leishmaniasis in which the animals developed clinical signs compatible with the disease in urban areas in Belém, the Pará state capital. The diagnosis was confirmed via polymerase chain reaction (PCR) to detect SSUr-rDNA and kDNA of *Leishmania* sp. and *Leishmania infantum*, respectively. In one of the cases the animal died and in the other the animal underwent treatment with medicines prescribed for dogs. Through this treatment, parasitemia in the second animal has been kept under control and is being monitored through molecular tests. Previously, no canine cases had been notified from urban neighborhoods in the city of Belém, but only on the island of Cotijuba, at a distance of 29 kilometers from the city. Cases of canine and human leishmaniasis have been recorded close to the capital, Belém, which has areas of conserved vegetation and where the presence of disease vectors has been described. Thus, as has been done in several other Brazilian cities, this study uses clinical and laboratory findings to confirm the presence of autochthonous cases of canine visceral leishmaniasis in the city of Belém.

### Immunisation with Transgenic *L. tarentolae* Expressing Gamma Glutamyl Cysteine Synthetase from Pathogenic *Leishmania* Species Protected against *L. major* and *L. donovani* Infection in a Murine Model.

**Topuz Ata D, Hussain M, Jones M, Best J, Wiese M, Carter KC.**

17-05-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317296/>

### *Leishmania major* drives host phagocyte death and cell-to-cell transfer depending on intracellular pathogen proliferation rate.

**Baars I, Jaedtka M, Dewitz LA, Fu Y, Franz T, Mohr J, Gintschel P, Berlin H, Degen A, Freier S, Rygol SM, Schraven B, Kahlfuss S, van Zandbergen G, Müller AJ.**

13-06-2023

*JCI Insight.*

<https://pubmed.ncbi.nlm.nih.gov/37310793/>

### **Leishmania species and clinical characteristics of Pacific and Amazon cutaneous leishmaniasis in Ecuador and determinants of health-seeking delay: a cross-sectional study.**

**Bezemer JM, Freire-Paspuel BP, Schallig HDFH, de Vries HJC, Calvopiña M.**

12-06-2023

*BMC Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37308815/>

**Background:** Cutaneous Leishmaniasis (CL) affects up to 5.000 people in Ecuador each year. *L. guyanensis* and *L. braziliensis* are the most common of the eight CL-causing *Leishmania* species. Earlier CL research concentrated on the easily accessible Pacific region. This study aims to describe the *Leishmania* species in Pacific and Amazon ecoregions, to analyze regional differences in CL patient clinical presentation, and to identify determinants of health-seeking delay. **Methods:** All cases in this cross-sectional study were diagnosed using smear slide microscopy, PCR, or both. Cytochrome B gene sequencing was used to identify the causative *Leishmania* species in qPCR-positive samples. **Results:** This study included 245 patients, with 154 (63%) infected in the Pacific region and 91 (37%) infected in the Amazon. Causative *Leishmania* species were identified in 135 patients (73% of qPCR positives). *L. guyanensis* was identified in 76% (102/135) of the samples and *L. braziliensis* in 19% (26/135). The Pacific region had a low prevalence of 6% (5/89) of *L. braziliensis*. For the first time, we report *L. guyanensis* from the central Amazon, *L. braziliensis* from the northern Pacific, and *L. lainsoni* from both the central Amazon and northern Pacific. Amazon cases had a longer median health-seeking delay in months (2.0, IQR 3.0) than Pacific cases (1.0, IQR 1.5). Prolonged health-seeking delay was associated with older age, Amerindian ethnicity, infection at lower altitudes, non-ulcerative lesions, and lesions on the lower limbs. **Conclusions:** In the Pacific region, health-seeking delay is relatively short and *L. braziliensis* prevalence remains low. Limited access to health care and stigma might explain the prolonged health-seeking delay in the Amazon. We recommend larger studies on the distribution of *Leishmania* species in Amazon CL cases and additional regional research into diagnostic test accuracy. Furthermore, the determinants of health-seeking delay in Ecuador should be investigated further.

### **A Novel Topical Formulation of the Leishmaniasis Drug Glucantime as a Nanostructured Lipid Carrier-Based Hydrogel.**

**Dehghani F, Farhadian N, Mashayekhi Goyonlo V, Ahmadi O.**

12-06-2023

*Am J Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/37308100/>

Leishmaniasis is a parasitic disease caused by *Leishmania* parasites. Meglumine antimoniate, or Glucantime, is the primary drug used to treat this disease. Glucantime with a standard painful injection administration route has high aqueous solubility, burst release, a significant tendency to

cross into aqueous medium, rapid clearance from the body, and insufficient residence time at the injury site. Topical delivery of Glucantime can be a favorable option in the treatment of localized cutaneous leishmaniasis. In this study, a suitable transdermal formulation in the form of nanostructured lipid carrier (NLC)-based hydrogel containing Glucantime was prepared. In vitro drug release studies confirmed controllable drug release behavior for hydrogel formulation. An in vivo permeation study on healthy BALB/C female mice confirmed appropriate penetration of hydrogel into the skin and sufficient residence time in the skin. In vivo performance of the new topical formulation on the BALB/C female mice showed a significant improvement in reduction of leishmaniasis wound size, lowering parasites number in lesions, liver, and spleen compared with commercial ampule. Hematological analysis showed a significant reduction of the drug's side effects, including variance of enzymes and blood factors. NLC-based hydrogel formulation is proposed as a new topical administration to replace the commercial ampule.

### **Disseminated Skin Lesions in a Patient Living With Human Immunodeficiency Virus.**

**Villalba Ramos JR, Pereira Brunelli JG, Stankiewicz Acosta IC, Benitez Estigarribia GG, Stankiewicz Karita HC.**

30-05-2023

*Open Forum Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37305846/>

### **High prevalence of Leishmania spp. in dogs from Central West Colombia.**

**Giraldo-Martínez LA, Petano-Duque JM, Uribe-García HF, Chacón-Novoa RA, Guzmán-Barragán BL, Rondón-Barragán I.**

31-12-2023

*Vet Ital.*

<https://pubmed.ncbi.nlm.nih.gov/37303138/>

### **Co-expression analysis of lncRNA and mRNA suggests a role for ncRNA-mediated regulation of host-parasite interactions in primary skin lesions of patients with American tegumentary leishmaniasis.**

**de Almeida MC, Felix JS, Lopes MFDS, de Athayde FRF, Troiano JA, Scaramela NF, Furlan AO, Lopes FL.**

09-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37302689/>

Leishmaniasis, caused by different *Leishmania* species, manifests as cutaneous or visceral forms. In the American continent, the cutaneous form is called American tegumentary leishmaniasis (ATL) and is primarily caused by *Leishmania* (*Viannia*) *braziliensis*. Mucosal leishmaniasis (ML), the most severe form of ATL, arises in approximately 20% of patients from a primary cutaneous lesion. Evidence indicates changes in overall expression patterns of mRNAs and lncRNAs of the host in response to *Leishmania* infection, with the parasite capable of modulating host

immune response, which may contribute to disease progression. We evaluated whether the co-expression of lncRNAs and their putative target mRNAs in primary cutaneous lesions of patients with ATL could be associated with the development of ML. Previously available public RNA-Seq data from primary skin lesions of patients infected with *L. braziliensis* was employed. We identified 579 mRNAs and 46 lncRNAs differentially expressed in the primary lesion that subsequently progressed to mucosal disease. Co-expression analysis revealed 1324 significantly correlated lncRNA-mRNA pairs. Among these, we highlight the positive correlation and trans-action between lncRNA SNHG29 and mRNA S100A8, both upregulated in the ML group. S100A8 and its heterodimeric partner S100A9 form a pro-inflammatory complex expressed by immune cells and seems to participate in host innate immune response processes of infection. These findings expand the knowledge of the Leishmania-host interaction and indicate that the expression of lncRNAs in the primary cutaneous lesion could regulate mRNAs and play roles in disease progression.

### Anti-leishmanial activities of *Olea europaea* subsp. *laperrinei* extracts.

**Lahcene S, Trabelsi L, M Salem-Bekhit M, Shazly GA, Mohammed Refat M Selim H, Mohammed Alehaidib S, Sebbane H, Msela A, Benguerba Y, Houali K.**

31-05-2023

*Cell Mol Biol (Noisy-le-grand).*

<https://pubmed.ncbi.nlm.nih.gov/37300665/>

Leishmaniasis is an infectious disease that is often fatal in affected patients and represents a major public health problem. At present, no vaccine is available, and the drug treatments used are costly, long, and have numerous side effects, they also present variable effectiveness, frequent relapses, and a more and more marked resistance towards the parasites. Thus, new therapeutic strategies are urgently needed, and they are mainly based on the research of active natural products. The objective of our study is the chemical characterization and the quantification of the polyphenol contents contained in the EAF and EAT extracts of the *Laperrine* olive tree and the evaluation of their antileishmania effect against *Leishmania infantum*. The quantification of polyphenols, flavonoids and total tannins shows a higher content in the leaf extract. We find respectively  $776.76 \pm 30.64$  mg gallic acid equivalent/g DR;  $114.35 \pm 14.12$  mg quercetin equivalent/g DR and  $214.89 \pm 17$  mg tannic acid equivalent/g DR. The chemical characterization of *Olea europaea* subsp. *laperrinei* extracts show the presence of numerous antileishmanial biomolecules such as oleuropein, hydroxytyrosol, rutin, gallic acid, caffeic acid, rosmarinic acid, and quercetin. In this context, we are testing the in vitro leishmanicidal effect of *Laperrine* olive tree extracts. The results obtained are promising and highlight the effectiveness of the tested extracts against the promastigote form of *Leishmania infantum*. Indeed, the LD50 is obtained with the leaf extract at a concentration of  $7.52 \pm 2.71$  µl/ml.

### Regiospecific Reduction of 4,6-Dinitrobenzimidazoles: Synthesis,

### Characterization, and Biological Evaluation.

**Abouelhaoul EA, El Kihel A, Ahbala M, Sdassi H, Köhler LHF, Bauchat P, Roisnel T, Khan TA, Al Nasr IS, Koko WS, Schobert R, Biersack B.**

09-06-2023

*Chem Biodivers.*

<https://pubmed.ncbi.nlm.nih.gov/37294393/>

**Leishmania (Viannia) naiffi** Lainson & Shaw 1989.

**Cantanhêde LM, Cupolillo E.**

08-06-2023

*Parasit Vectors.*

<https://pubmed.ncbi.nlm.nih.gov/37291682/>

Just over 30 years ago, a new species of *Leishmania* of the subgenus *Leishmania* (*Viannia*) was described infecting the armadillo *Dasypus novemcinctus*; then, a report of human infection followed. From the Brazilian Amazon and apparently restricted to this region and its close borders, *Leishmania* (*Viannia*) *naiffi* has been characterized as a species that grows easily in axenic culture medium and causes few to no lesions after inoculation in experimental animal models. Results in the last decade indicate the occurrence of *L. naiffi* in vectors and human infections, including a report of therapeutic failure possibly associated with *Leishmania* RNA virus 1. Overall, such accounts suggest that the parasite is more dispersed and the disease less self-healing than previously expected.

### Broad anti-pathogen potential of DEAD box RNA helicase eIF4A-targeting rocaglates.

**Obermann W, Azri MFD, Konopka L, Schmidt N, Magari F, Sherman J, Silva LMR, Hermosilla C, Ludewig AH, Houhou H, Haeberlein S, Luo MY, Häcker I, Schetelig MF, Greveling CG, Schroeder FC, Lau GSK, Taubert A, Rodriguez A, Heine A, Yeo TC, Grünweller A, Taroncher-Oldenburg G.**

08-06-2032

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37291191/>

Inhibition of eukaryotic initiation factor 4A has been proposed as a strategy to fight pathogens. Rocaglates exhibit the highest specificities among eIF4A inhibitors, but their anti-pathogenic potential has not been comprehensively assessed across eukaryotes. In silico analysis of the substitution patterns of six eIF4A1 aa residues critical to rocaglate binding, uncovered 35 variants. Molecular docking of eIF4A:RNA:rocaglate complexes, and in vitro thermal shift assays with select recombinantly expressed eIF4A variants, revealed that sensitivity correlated with low inferred binding energies and high melting temperature shifts. In vitro testing with silvestrol validated predicted resistance in *Caenorhabditis elegans* and *Leishmania amazonensis* and predicted sensitivity in *Aedes* sp., *Schistosoma mansoni*, *Trypanosoma brucei*, *Plasmodium falciparum*, and *Toxoplasma gondii*. Our analysis further revealed the possibility of targeting important insect, plant, animal, and human pathogens with rocaglates. Finally, our findings



might help design novel synthetic rocaglate derivatives or alternative eIF4A inhibitors to fight pathogens.

### The leishmaniasis in Kenya: A scoping review.

Grifferty G, Shirley H, O'Brien K, Hirsch JL, Orriols AM, Amechi KL, Lo J, Chanda N, El Hamzaoui S, Kahn J, Yap SV, Watson KE, Curran C, Atef AbdelAlim A, Bose N, Cilfone AL, Wamai R.

01-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37262045/>

**Background:** The leishmaniasis are a group of four vector-borne neglected tropical diseases caused by 20 species of protozoan parasites of the genus *Leishmania* and transmitted through a bite of infected female phlebotomine sandflies. Endemic in over 100 countries, the four types of leishmaniasis-visceral leishmaniasis (VL) (known as kala-azar), cutaneous leishmaniasis (CL), mucocutaneous leishmaniasis (MCL), and post-kala-azar dermal leishmaniasis (PKDL)-put 1.6 billion people at risk. In Kenya, the extent of leishmaniasis research has not yet been systematically described. This knowledge is instrumental in identifying existing research gaps and designing appropriate interventions for diagnosis, treatment, and elimination. **Methodology/principal findings:** This study used the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) methodology to determine the state of leishmaniasis research in Kenya and identify research gaps. We searched seven online databases to identify articles published until January 2022 covering VL, CL, MCL, and/or PKDL in Kenya. A total of 7,486 articles were found, of which 479 underwent full-text screening, and 269 met our eligibility criteria. Most articles covered VL only ( $n = 141$ , 52%), were published between 1980 and 1994 ( $n = 108$ , 39%), and focused on the theme of "vectors" ( $n = 92$ , 34%). The most prevalent study types were "epidemiological research" ( $n = 88$ , 33%) tied with "clinical research" ( $n = 88$ , 33%), then "basic science research" ( $n = 49$ , 18%) and "secondary research" ( $n = 44$ , 16%). **Conclusion/significance:** While some studies still provide useful guidance today, most leishmaniasis research in Kenya needs to be updated and focused on prevention, co-infections, health systems/policy, and general topics, as these themes combined comprised less than 4% of published articles. Our findings also indicate minimal research on MCL ( $n = 1$ , <1%) and PKDL ( $n = 2$ , 1%). We urge researchers to renew and expand their focus on these neglected diseases in Kenya.

### Overexpression of *Leishmania* major protein arginine methyltransferase 6 reduces parasite infectivity in vivo.

Campagnaro GD, Lorenzon LB, Rodrigues MA, Defina TPA, Pinzan CF, Ferreira TR, Cruz AK.

Août-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37257676/>

### Matrix metalloproteinases -2 and -9 expression in dogs with visceral leishmaniasis: A systematic review.

Rocha Da Silva R, de Santana Fontes Vasconcelos F, Nunes de Santana Campos R, Dos Santos Tavares D, Lima Dos Santos P.

Août-2023

*Cytokine.*

<https://pubmed.ncbi.nlm.nih.gov/37257306/>

### Species diversity of phlebotomine sand flies and sympatric occurrence of *Leishmania* (*Mundinia*) *martiniquensis*, *Leishmania* (*Leishmania*) *donovani* complex, and *Trypanosoma* spp. in the visceral leishmaniasis focus of southern Thailand.

Preativatanyou K, Chinwirunsirisup K, Phumee A, Khositharattanakool P, Sunantaraporn S, Depaquit J, Siritayastien P.

Août-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37211153/>

Autochthonous leishmaniasis in Thailand has recently been a public health concern due to an increasing number of new clinical cases. Most indigenous cases were diagnosed with *Leishmania* (*Mundinia*) *martiniquensis*, and *Leishmania* (*Mundinia*) *orientalis*. However, some doubts regarding vector misidentification have arisen and need to be elucidated. Accordingly, we aimed to assess the species composition of sand flies and determine the molecular prevalence of trypanosomatids in the transmission area of leishmaniasis in southern Thailand. In the present study, a total of 569 sand flies were caught from the vicinity of a visceral leishmaniasis patient's house in Na Thawi District, Songkhla Province. Of these, 229 parous and gravid females consisted of *Sergentomyia* *khawi*, *Se. barraudi*, *Phlebotomus stantoni*, *Grassomyia indica*, and *Se. hivernus*, accounting for 31.4%, 30.6%, 29.7%, 7.9%, and 0.4%, respectively. However, *Se. gemmea*, which has previously been proposed as the most abundant species and putative vector of visceral leishmaniasis, was not found in the present study. Based on ITS1-PCR and sequence analysis, two specimens of *Gr. indica* and *Ph. stantoni* showed positive amplification of *L. martiniquensis* and *L. donovani* complex, respectively, the first one being presumed indigenous and the second one being not. Anuran *Trypanosoma* was also molecularly detected using SSU rRNA-PCR and ubiquitously found in 16 specimens of four dominant sand fly species except for *Se. hivernus*. The obtained sequences could be phylogenetically categorized into the two major amphibian clades (An04/Frog1 and An01+An02/Frog2). The existence of the monophyletic subgroup and distinct lineage suggests them as novel *Trypanosoma* species. The TCS network analysis of these anuran *Trypanosoma* sequences also revealed high haplotype diversity ( $H_d = 0.925 \pm 0.050$ ), but low nucleotide diversity ( $\pi = 0.019 \pm 0.009$ ). Furthermore, the living anuran trypanosomes were microscopically demonstrated in a single specimen of *Gr. indica*, supporting the vectorial capacity.

Importantly, our data confirmed the scarcity of *Se. gemmea* and also uncovered, for the first time, the co-circulation of *L. martiniquensis*, *L. donovani* complex, and suspected novel anuran *Trypanosoma* spp. in phlebotomine sand flies, implicating their potential role as vectors of trypanosomatid parasites. Therefore, the novel data from this study would greatly facilitate the comprehension of the complexity of trypanosomatid transmission and the establishment of prevention and control measures for this neglected disease more effectively.

### **Design and synthesis of N-acyl and dimeric N-Arylpiperazine derivatives as potential antileishmanial agents.**

**Ansari SB, Kamboj S, Ramalingam K, Meena R, Lal J, Kant R, Shukla SK, Goyal N, Reddy DN.**

AOût-2023

*Bioorg Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37186964/>

### **Biochemical characterization and assessment of leishmanicidal effects of a new L-amino acid oxidase from *Crotalus durissus collilineatus* snake venom (CollinLAO-I).**

**de Freitas V, Costa TR, Nogueira AR, Polloni L, Alves de Melo Fernandes T, Correia LIV, Borges BC, Teixeira SC, Silva MJB, Amorim FG, Quinton L, Saraiva AL, Espindola FS, Iwai LK, Rodrigues RS, Yoneyama KAG, de Melo Rodrigues Ávila V.**

Juil-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/37169266/>

This study reports the isolation of CollinLAO-I, a new L-amino acid oxidase from *Crotalus durissus collilineatus* snake venom, its biochemical characterization and leishmanicidal potential in *Leishmania* spp. CollinLAO-I (63.1 kDa) was successfully isolated with high purity using two chromatographic steps and represents 2.5% of total venom proteins. CollinLAO-I displayed high enzymatic activity (4262.83 U/mg/min), significantly reducing after 28 days. The enzymatic activity of CollinLAO-I revealed higher affinity for hydrophobic amino acids such as L-leucine, high enzymatic activity in a wide pH range (6.0-10.0), at temperatures from 0 to 25 °C, and showed complete inhibition in the presence of Na<sup>+</sup> and K<sup>+</sup>. Cytotoxicity assays revealed IC<sub>50</sub> of 18.49 and 11.66 µg/mL for *Leishmania* (L.) *amazonensis* and *Leishmania* (L.) *infantum*, respectively, and the cytotoxicity was completely suppressed by catalase. CollinLAO-I significantly increased the intracellular concentration of reactive oxygen species (ROS) and reduced the mitochondrial potential of both *Leishmania* species. Furthermore, CollinLAO-I decreased the parasite capacity to infect macrophages by around 70%, indicating that even subtoxic concentrations of CollinLAO-I can interfere with *Leishmania* vital processes. Thus, the results obtained for CollinLAO-I provide important support for developing therapeutic strategies against leishmaniasis.

### **Antileishmanial effects and drugability characteristics of a heterocyclic copper complex: An in silico, in vitro and molecular study.**

**Mirzaei M, Sharifi I, Mohammad-Rafi F, Anjomshoa M, Abiri A, Moqaddari AH, Nooshadokht M, Raiesi O, Amirheidari B.**

AOût-2023

*J Inorg Biochem.*

<https://pubmed.ncbi.nlm.nih.gov/37167732/>

### **G-Quadruplexes as Key Transcriptional Regulators in Neglected Trypanosomatid Parasites.**

**Monti L, Di Antonio M.**

15-06-2023

*Chembiochem.*

<https://pubmed.ncbi.nlm.nih.gov/37146230/>

G-quadruplexes (G4s) are nucleic acid secondary structures that have been linked to the functional regulation of eukaryotic organisms. G4s have been extensively characterised in humans and emerging evidence suggests that they might also be biologically relevant for human pathogens. This indicates that G4s might represent a novel class of therapeutic targets for tackling infectious diseases. Bioinformatic studies revealed a high prevalence of putative quadruplex-forming sequences (PQSs) in the genome of protozoans, which highlights their potential roles in regulating vital processes of these parasites, including DNA transcription and replication. In this work, we focus on the neglected trypanosomatid parasites, *Trypanosoma* and *Leishmania* spp., which cause debilitating and deadly diseases across the poorest populations worldwide. We review three examples where G4-formation might be key to modulate transcriptional activity in trypanosomatids, providing an overview of experimental approaches that can be used to exploit the regulatory roles and relevance of these structures to fight parasitic infections.

### **Drug repositioning to discover novel ornithine decarboxylase inhibitors against visceral leishmaniasis.**

**Sheikh SY, Ansari WA, Hassan F, Faruqui T, Khan MF, Akhter Y, Khan AR, Siddiqui MA, Al-Khedairy AA, Nasibullah M.**

Juil-2023

*J Mol Recognit.*

<https://pubmed.ncbi.nlm.nih.gov/37092713/>

### **Evaluation of heart fatty acid-binding protein as a biomarker for canine leishmaniosis.**

**Casamián-Sorrosal D, Barrera-Chacón R, Fonfara S, Cristobal-Verdejo JI, Talavera-López J, Belinchón-Lorenzo S, Miró-Corralles G, Caro-Vadillo A, Duque FJ.**

20-05-2032

*Vet Rec.*

<https://pubmed.ncbi.nlm.nih.gov/36755402/>

**Background:** Myocarditis frequently occurs in canine leishmaniasis (CanL). Heart fatty acid-binding protein (HFABP) is a biomarker of myocardial damage. **Methods:** This study aimed to compare HFABP concentration (HFABPc) in healthy dogs and dogs at different stages of CanL and evaluate the correlation of this biomarker with several clinicopathological and echocardiographic variables. Thirty-one dogs diagnosed with CanL and 10 healthy dogs were included. **Results:** HFABPc was not statistically different ( $p > 0.05$ ) between groups of dogs at different LeishVet stages of CanL or between groups with high versus low to intermediate serology titres. In 70% of CanL dogs, HFABPc was within the 95% confidence interval limits of the mean of healthy dogs. A moderate negative correlation with globulin ( $r = -0.519$ ;  $p = 0.03$ ) and haematocrit (HCT) ( $r = -0.538$ ;  $p = 0.02$ ) was observed. No other significant correlation ( $p > 0.05$ ) was observed with any other variable. **Limitations:** Many statistical tests were performed, and therefore, type I error cannot be ruled out. **Conclusion:** HFABPc is not consistently elevated in dogs with CanL and is not associated with the severity of the disease, or most echocardiographic or clinicopathological variables studied. The correlation with globulin and HCT was not strong and not considered clinically significant. HFABPc lacks sufficient predictive capacity in dogs with CanL, discouraging further research or clinical use of this biomarker in this disease.

### A case of Leishmania infection with focal splanchnic involvement without systemic symptoms: a potential anti-inflammatory role for vitamin D.

Zaghi I, Ielasi L, Stagni B, Cascavilla A, Ferri S, Ambrosini V, Riefolo M, Varani S.

Août-2023

*Acta Clin Belg.*

<https://pubmed.ncbi.nlm.nih.gov/36373331/>

**Case report:** We report the case of a 59 year-old woman with persistent nausea, hyporexia, fatigue and mild abdominal discomfort. The patient was hospitalized upon suspicion of malignancy due to multiple hepatic and splenic nodules found on an abdominal ultrasound. Hypercalcemia emerged at initial diagnostic workup, which was considered secondary to iatrogenic vitamin D intoxication. After an adequate management of hypercalcemia and normalization of serum calcium level, all symptoms presented by the patient completely regressed. In order to characterize splanchnic lesions, several biochemistry, microbiology and radiological tests were performed, including two bioptic specimens of a focal hepatic lesion. Eventually, a diagnosis of leishmanial infection was made. The patient started a specific anti-leishmanial treatment, and the focal hepatic and splenic lesions progressively disappeared. **Conclusion:** To our knowledge, this is the first reported case of asymptomatic leishmanial infection with a widespread focal splanchnic involvement. The anti-inflammatory effect of vitamin D could be related to this atypical presentation of visceral leishmaniasis without systemic symptoms.

### Coalition of Biological Agent (Melatonin) With Chemotherapeutic Agent

### (Amphotericin B) for Combating Visceral Leishmaniasis via Oral Administration of Modified Solid Lipid Nanoparticles.

Parvez S, Yadagiri G, Arora K, Javaid A, Kushwaha AK, Singh OP, Sundar S, Mudavath SL.

12-06-2023

*ACS Biomater Sci Eng.*

<https://pubmed.ncbi.nlm.nih.gov/34463477/>

## Lèpre

### Computational assessment of Withania somnifera phytomolecules as putative inhibitors of Mycobacterium tuberculosis CTP synthase PyrG.

Singh A, Kumar S, Gupta VK, Singh S, Dwivedi VD, Mina U.

Juil-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35549811/>

Genome evolution of *Mycobacterium tuberculosis* (Mtb) produces new strains resistant to various pre-existing anti-tubercular drugs. Hence, there is an urgent need to explore potent compounds with the most negligible side effects and effective Mtb inhibition. Mtb PyrG (CTP synthase) is a crucial enzyme for the conversion of the uridine triphosphate (UTP) into cytidine triphosphate (CTP) and is essential for the growth of Mtb. Thus, in this study, phytochemicals of *Withania somnifera* (*W. somnifera*) were screened to find the potential inhibitors against Mtb PyrG. Molecular docking resulted in the identification of quercetin 3-rutinoside-7-glucoside, rutin, chlorogenic acid and isochlorogenic acid C with a substantial docking score (from -12.6 to -10.8 kcal/mol) contributed by significant intermolecular interactions. Furthermore, 100 ns molecular dynamics simulation, ADME analysis and free binding energy calculations support the stability of docked complexes and drug-likeness for selected compounds, respectively. Collectively, these findings suggest that phytochemicals present in *W. somnifera* can be considered for further evaluation against Mtb in a series of *in vitro* and *in vivo* models. Communicated by Ramaswamy H. Sarma.

### Role of Nerve Conduction Studies in Hansen's Disease.

Chaudhary SK, Kalita J, Misra UK.

Mai-Juin 2023

*Neurol India.*

<https://pubmed.ncbi.nlm.nih.gov/37322740/>

### Relapsing Polychondritis With Palmoplantar Pustulosis.

Comarmond C, Chimon A, Salfrant M, Sène D.

15-06-2023

*J Rheumatol.*

<https://pubmed.ncbi.nlm.nih.gov/37321639/>

### **T-BACCO SCORE: A predictive scoring tool for tuberculosis (TB) loss to follow-up among TB smokers.**

Sharani ZZ, Ismail N, Yasin SM, Isa MR, Razali A, Sherzkawee MA, Ismail AI.

15-06-2023

*PLoS One.*

<https://pubmed.ncbi.nlm.nih.gov/37319310/>

**Introduction:** Loss to follow-up (LTFU) and smoking during TB treatment are major challenges for TB control programs. Smoking increases the severity and prolongs TB treatment duration, which lead to a higher rate of LTFU. We aim to develop a prognostic scoring tool to predict LTFU among TB patients who smoke to improve successful TB treatment outcomes. **Materials and methods:** The development of the prognostic model utilized prospectively collected longitudinal data of adult TB patients who smoked in the state of Selangor between 2013 until 2017, which were obtained from the Malaysian Tuberculosis Information System (MyTB) database. Data were randomly split into development and internal validation cohorts. A simple prognostic score (T-BACCO SCORE) was constructed based on the regression coefficients of predictors in the final logistic model of the development cohort. Estimated missing data was 2.8% from the development cohort and was completely at random. Model discrimination was determined using c-statistics (AUCs), and calibration was based on the Hosmer and Lemeshow goodness of fit test and calibration plot. **Results:** The model highlights several variables with different T-BACCO SCORE values as predictors for LTFU among TB patients who smoke (e.g., age group, ethnicity, locality, nationality, educational level, monthly income level, employment status, TB case category, TB detection methods, X-ray categories, HIV status, and sputum status). The prognostic scores were categorized into three groups that predict the risk for LTFU: low-risk (<15 points), medium-risk (15 to 25 points) and high-risk (> 25 points). The model exhibited fair discrimination with a c-statistic of 0.681 (95% CI 0.627-0.710) and good calibration with a nonsignificant chi-square Hosmer–Lemeshow's goodness of fit test  $\chi^2 = 4.893$  and accompanying p value of 0.769. **Conclusion:** Predicting LTFU among TB patients who smoke in the early phase of TB treatment is achievable using this simple T-BACCO SCORE. The applicability of the tool in clinical settings helps health care professionals manage TB smokers based on their risk scores. Further external validation should be carried out prior to use.

### **Rupioid psoriasis with inverse psoriasis.**

Sharma V, Mohanty S, Chaudhary G.

01-04-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317774/>

### **Cervicofacial actinomycosis with an atypical presentation.**

Dash S, Behera B, Sethy M, Garg S, Mishra J, Sarkar N.

01-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317764/>

### **Clown nose: A marker for lung carcinoma.**

Gupta S, Gupta P, Singh P, Prasad Asati D.

01-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317749/>

### **"Degeneration" in Dermatopathology.**

Parekh AR, Shah HA.

03-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317736/>

### **Crusted scabies.**

Selvaraj R, Purushothaman S, Indra Couppoussamy K.

28-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317720/>

### **Inadvertent intra-arterial injection: Cutaneous complications and management.**

Pathania S, Rai A, Kumar S, Tyagi V, Agrawal T, Suvirya S.

28-05-2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/37317718/>

### **Massive and Lengthy Clonal Nosocomial Expansion of Mycobacterium abscessus subsp. massiliense among Patients Who Are Ventilator Dependent without Cystic Fibrosis.**

Komiya K, Yoshida M, Uchida S, Takikawa S, Yamasue M, Matsumoto T, Morishige Y, Aono A, Hiramatsu K, Yamaoka Y, Nishizono A, Ato M, Kadota JI, Mitarai S.

14-06-2032

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37314340/>

Nontuberculous mycobacterial infections are generally believed to be independently acquired from the environment. Although person-to-person transmission of nontuberculous mycobacteria, especially *Mycobacterium abscessus* subsp. *massiliense*, is a serious concern among individuals with cystic fibrosis (CF), evidence of its spread among patients without CF has never been established. We unexpectedly found a number of *M. abscessus* subsp. *massiliense* cases among patients without CF in a hospital. This study aimed to define the mechanism of *M. abscessus* subsp. *massiliense* infection among patients who were ventilator dependent and without CF who had progressive neurodegenerative diseases in our long-term care wards from 2014 to 2018 during suspected nosocomial outbreaks. We conducted whole-genome sequencing of *M. abscessus* subsp. *massiliense* isolates from 52 patients and environmental samples. Potential opportunities for in-hospital transmission were analyzed using epidemiological data. *M. abscessus* subsp. *massiliense* was isolated from one air sample obtained near a patient without CF who was colonized with *M. abscessus* subsp. *massiliense* but



not from other potential sources. Phylogenetic analysis of the strains from these patients and the environmental isolate revealed clonal expansion of near-identical *M. abscessus* subsp. *massiliense* isolates, with the isolates generally differing by fewer than 22 single nucleotide polymorphisms (SNPs). Approximately half of the isolates differed by fewer than nine SNPs, indicating interpatient transmission. Whole-genome sequencing revealed a potential nosocomial outbreak among patients who were ventilator dependent and without CF. **IMPORTANCE** The isolation of *M. abscessus* subsp. *massiliense* from the air, but not from environmental fluid samples, may suggest airborne transmission. This was the first report to demonstrate person-to-person transmission of *M. abscessus* subsp. *massiliense*, even among patients without CF. *M. abscessus* subsp. *massiliense* may spread among patients who are ventilator dependent without CF through direct or indirect in-hospital transmission. The current infection control measures should address potential transmission among patients without CF, particularly in facilities that treat patients who are ventilator dependent and patients with preexisting chronic pulmonary diseases, such as CF.

### **Risk predictions of hospital-acquired pressure injury in the intensive care unit based on a machine learning algorithm.**

**Tehrany PM, Zabihi MR, Ghorbani Vajargah P, Tamimi P, Ghaderi A, Norouzkhani N, Zaboli Mahdiabadi M, Karkhah S, Akhoondian M, Farzan R.**

13-06-2023

*Int Wound J.*

<https://pubmed.ncbi.nlm.nih.gov/37312659/>

### **A Rare Case of Acral Lentiginous Melanoma.**

**Meghe S, Kashikar Y, Chopra S, Madke B, Jawade S.**

12-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37309332/>

Acral lentiginous melanoma (ALM) is named so for its site and histological orientation. It is an infrequent form of melanoma that usually presents with lesions on the palms, soles, or nails. Although rare, it's the most commonly discovered subtype of melanoma in the non-Caucasian population, including Africans, Chinese, Koreans, and Latin Americans. It's most likely to be diagnosed in the sixth or seventh decade of life. Acral lentiginous melanoma can clinically mimic ulceration, verrucous lesions, onychomycosis, subungual hematomas, vascular lesions, and infections. Here, we are presenting the case of a 65-year-old male who was admitted to the surgery ward in Acharya Vinobha Bhave Rural Hospital with a chief complaint of a lesion over the plantar surface of his left foot for the last one or two years and was referred to the Department of Dermatology for the same. The lesion was sighted by the patient a long time before his visit to Acharya Vinobha Bhave Rural Hospital. A physical examination showed a blackish, poorly delineated soft tissue lesion on the left heel. An excisional biopsy and proper management were carried out for the patient.

Patient education and greater awareness about this tumor and its early detection can serve as important weapons to increase the patient survival rate and prognosis of acral lentiginous melanoma.

### **Evaluating the availability and quality of services for lymphatic filariasis morbidity in Ghana.**

**Edmiston M, Atinbire S, Mensah EO, Mensah E, Alomatu B, Asemanyi Mensah K, Palmer S.**

12-05-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37307289/>

### **Immune Targeting of Mycobacteria through Cell Surface Glycan Engineering.**

**Dzigba P, Rylski AK, Angera IJ, Banahene N, Kavunja HW, Greenlee-Wacker MC, Swarts BM.**

12-06-2023

*ACS Chem Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37306676/>

Mycobacteria and other organisms in the order Mycobacteriales cause a range of significant human diseases, including tuberculosis, leprosy, diphtheria, Buruli ulcer, and non-tuberculous mycobacterial (NTM) disease. However, the intrinsic drug tolerance engendered by the mycobacterial cell envelope undermines conventional antibiotic treatment and contributes to acquired drug resistance. Motivated by the need to augment antibiotics with novel therapeutic approaches, we developed a strategy to specifically decorate mycobacterial cell surface glycans with antibody-recruiting molecules (ARMs), which flag bacteria for binding to human-endogenous antibodies that enhance macrophage effector functions. Mycobacterium-specific ARMs consisting of a trehalose targeting moiety and a dinitrophenyl hapten (Tre-DNPs) were synthesized and shown to specifically incorporate into outer-membrane glycolipids of *Mycobacterium smegmatis* via trehalose metabolism, enabling recruitment of anti-DNP antibodies to the mycobacterial cell surface. Phagocytosis of Tre-DNP-modified *M. smegmatis* by macrophages was significantly enhanced in the presence of anti-DNP antibodies, demonstrating proof-of-concept that our strategy can augment the host immune response. Because the metabolic pathways responsible for cell surface incorporation of Tre-DNPs are conserved in all Mycobacteriales organisms but absent from other bacteria and humans, the reported tools may be enlisted to interrogate host-pathogen interactions and develop immune-targeting strategies for diverse mycobacterial pathogens.

### **An Updated Review on Current Treatment of Alopecia Areata and Newer Therapeutic Options.**

**Malhotra K, Madke B.**

Jan-Fév 2023

*Int J Trichology.*

<https://pubmed.ncbi.nlm.nih.gov/37305188/>

Alopecia areata (AA) is a dermatological disease that causes nonscarring hair loss. It can occur at any age and has an unpredictable and variable evolution in individuals. The aim of this review is to provide an update on the novel therapies currently being used, as well as upcoming therapeutic options in the treatment of AA.

### **Efficacy of Low-Level Laser Therapy in Androgenetic Alopecia - A Randomized Controlled Trial.**

**Sondagar DM, Mehta HH, Agharia RS, Jhavar MK.**

Jan-Fév 2023

*Int J Trichology.*

<https://pubmed.ncbi.nlm.nih.gov/37305186/>

### **A Comparative Study of Intralesional Acyclovir vs Immunotherapy for Treatment of Viral Warts.**

**Meghana Reddy E, Rajashekar TS, Suresh Kumar K.**

09-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37303436/>

**Background:** Viral warts are caused by human papillomavirus (HPV), are difficult to treat with conventional modalities, and are cosmetically disfiguring; hence, immunomodulators are being used. The viral origin of warts suggests the antiviral drug acyclovir as a potential therapeutic option. The current study compares the effect of intralesional acyclovir (nucleoside analogue) and intralesional purified protein derivative (PPD) (immunotherapy) in treating various viral warts.

**Methodology:** Prospective observational comparative study was conducted to determine the efficacy of acyclovir, and PPD administered via the intralesional route in patients with viral warts. The study population was categorized into two groups. One group received intralesional acyclovir, and the other received intralesional PPD. Patients were followed-up with for three months. Outcomes considered in our study were recovery (complete, partial, and no recovery) and side effects like pain, burning sensation, and desquamation. Statistical analysis was carried out by coguide software. **Results:** In our study total of 40 participants, 20 in each group were included. 25 and 15 were of age <30, and ≥ 30, respectively, while 20 were males, and 20 females. Our study reported 60%, and 30% of complete recovery with intralesional acyclovir treatment and intralesional PPD treatment, respectively, in the twelfth week. However, p-value > 0.05 represented no significance between groups. 90% in the acyclovir-treated group presented with pain, and 100% presented with burning sensation, while in the case of PPD-treated group, 60% presented no side effects and the rest 40% showed pain. **Conclusions:** Intralesional acyclovir is more effective in treating viral warts than PPD. The focus is to be laid on anticipated side effects.

### **Prominent corneal nerves in pure mucosal neuroma syndrome, a clinical phenotype distinct from multiple endocrine neoplasia type 2B.**

**Yin L, Wang Y, Zhu J, Tan CY, Sun C, Yao Y.**

12-06-2023

*BMC Ophthalmol.*

<https://pubmed.ncbi.nlm.nih.gov/37303040/>

### **Inhaled Adjunct Therapy with Second-Line Drug Candidates for Dose Reduction in Chemotherapeutic Regimens for Multi-drug-Resistant Tuberculosis.**

**Verma S, Dal NK, Srivastava A, Bharti R, Siva Reddy DV, Sofi HS, Roy T, Verma K, Raman SK, Azmi L, Ray L, Mugale MN, Singh AK, Singh J, Griffiths G, Misra A.**

08-06-2023

*AAPS PharmSciTech.*

<https://pubmed.ncbi.nlm.nih.gov/37291443/>

Chemotherapy of multi-drug-resistant tuberculosis (TB) requires prolonged administration of multiple drugs. We investigated whether pulmonary delivery of minute doses of drugs, along with reduced oral doses of the same agents, would affect preclinical efficacy. We prepared dry powder inhalation (DPI) formulations comprising sutezolid (SUT), the second-generation pretomanid analog TBA-354 (TBA), or a fluorinated derivative of TBA-354 (32,625) in a matrix of the biodegradable polymer poly(L-lactide). We established formulation characteristics, doses inhaled by healthy mice, and preclinical efficacy in a mouse model of TB. Oral doses of 100 mg/kg/day or DPI doses of 0.25-0.5 mg/kg/day of drugs SUT, TBA-354, or 32,625 administered over 28 days were sub-optimally effective in reducing lung and spleen burden of *Mycobacterium tuberculosis* (Mtb) in infected mice. The addition of 0.25-0.5 mg/kg/day of SUT, TBA-354, or 32,625 as DPI to oral doses of 50 mg/kg/day was non-inferior in clearing Mtb from the lungs of infected mice. We concluded that adjunct therapy with inhaled second-line agents has the potential to reduce the efficacious oral dose.

### **Phytochemical profiling of *Symplocos tanakana* Nakai and *S. sawafutagi* Nagam. leaf and identification of their antioxidant and anti-diabetic potential.**

**Seong SH, Kim BR, Park JS, Jeong DY, Kim TS, Im S, Jeong JW, Cho ML.**

05-09-2023

*J Pharm Biomed Anal.*

<https://pubmed.ncbi.nlm.nih.gov/37148699/>

### **Analysis of intronic SNP (rs4147358) and expression of SMAD3 gene in Atopic Dermatitis: A case-control study.**

**Shafi T, Rasool R, Ayub S, Bhat IA, Gull A, Hussain S, Hassan Shah I, Shah ZA.**

Mai-2023

*Immunobiology.*

<https://pubmed.ncbi.nlm.nih.gov/37100019/>

### **Little Doctors: Agents of change in Indian rural communities.**

**Premkumar K, Ramasamy R, Ramasamy M, Aiyer H.**

Jul-2023

*Med Teach.*

<https://pubmed.ncbi.nlm.nih.gov/37053445/>

The child-to-child approach to health advocacy is one that draws on the strengths and agency of children to make a positive impact within their communities. The approach has been popularly used for health education in low- and middle-income countries. This article describes the 'Little Doctors' program that implemented the child-to-child approach in the towns of KC Patty and Oddanchatram, located in remote hilly regions of Tamil Nadu, India starting in 1986 to train middle- and high school children to respond to diseases prevalent in their communities along with practices for preventative measures. The program involved sessions that used a combination of creative instructional methods to engage students and provided take-home messages for them to act on with their families and community. The program was successful in creating a creative learning environment for children, offering a shift from the traditional methods of classroom instruction. Students who successfully completed the program were awarded certificates as 'Little Doctors' in their communities. Although the program did not conduct formal evaluations of the program effectiveness, students reported successfully recalling complex topics such as early signs of diseases like tuberculosis and leprosy that were prevalent in the community during the time. The program experienced several challenges and had to be discontinued despite its continued benefits to the communities.

### **Painful purpura on bilateral earlobes.**

**Yumnam D, Paonam R, Moirangthem A.**

Jul-2023

*Int J Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/36939091/>

### **Be aware: 'Leprosy'! Not for nothing an NTD.**

**Naafs B.**

Jul-2023

*J Eur Acad Dermatol Venereol.*

<https://pubmed.ncbi.nlm.nih.gov/36883806/>

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## **Morsures de serpent**

### **Chronic Kidney Disease of Unknown Origin: Think Beyond Common Etiologies.**

**Trivedi A, Kumar S.**

12-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37309333/>

Chronic kidney disease has an increased health impact on a global scale, with the most common etiologies being hypertension and diabetes. It is most frequently linked to noncommunicable conditions, including diabetes and hypertension, among high-income nations. However, it has a couple of new potential etiologies in low- and middle-income countries, many of which are yet unknown,

including viral infections and environmental toxins. The phrase "CKD of unknown etiology" (CKDu) has been used to refer to CKD that is not caused by a typical risk factor such as diabetes, high blood pressure, or HIV. Environmental variables have been investigated as potential contributors to CKDu, including heavy metal exposure, elevated seasonal temperatures, pesticide use, mycotoxins, contamination of water supplies, and snake bites. Furthermore, the underlying causes have not been definitively established in the majority of areas and identifying serious health consequences across different international contexts and populations may be crucial for comprehending and avoiding CKDu.

### **Fangs in the Ghats: Preclinical Insights into the Medical Importance of Pit Vipers from the Western Ghats.**

**Khochare S, Senji Laxme RR, Jaikumar P, Kaur N, Attarde S, Martin G, Sunagar K.**

30-05-2023

*Int J Mol Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37298463/>

### **Nationwide and long-term epidemiological research of snakebite envenomation in Taiwan during 2002-2014 based on the use of snake antivenoms: A study utilizing National Health Insurance Database.**

**Hsu JY, Chiang SO, Yang CC, Hsieh TW, Chung CJ, Mao YC.**

08-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37289739/>

### **A retrospective analysis of epidemiology, clinical features of envenomation, and in-patient management of snakebites in a model secondary hospital of Assam, North-east India.**

**Kakati H, Giri S, Patra A, Taye SJ, Agarwalla D, Boruah H, Choudhary G, Kalita B, K Mukherjee A.**

Jul-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/37257518/>

Assam, a Northeastern State of India, is inhabited by several venomous snake species causing substantial morbidity and mortality. The data on the epidemiology of snakebites and their management is underreported in this region. Hence, a secondary health-based retrospective study was carried out at Demow Model Hospital, Sivasagar, Assam, to evaluate the clinical and epidemiological profile of snakebite cases reported in this rural hospital and their management. Snakebites occurring between April 2018 to August 2022 were reviewed based on socio-demographic details of the patient, clinical symptoms, and treatment using a standard questionnaire. Out of the 1011 registered snakebite cases, 139 patients (13.7%) counted for venomous bites, among which 92 patients (66.19%) accounted for viper bites (green pit viper and Salazar's pit viper), and 30 patients

(21.5%) were bitten by elapid snakes (Indian monocled Cobra, banded krait, and greater/lesser black krait). A maximum number of snakebite cases (80.5%) were reported from the interior rural villages and documented from July to September (51.3%). Elapid snake envenomed patients, except one, were successfully treated with commercial antivenom, neostigmine, and glycopyrrolate. Because commercial polyvalent antivenom against "Big Four" venomous snakes of India showed poor neutralization of pit-vipers envenomation; therefore, pit-viper bite patients were treated with repurposed drugs magnesium sulfate and glycerin compression dressing. Adverse serum reactions were reported only in 3 (11.1%) cases. The preventive measures and facilities adopted at the Demow Model Hospital significantly reduce snakebite death and morbidity; therefore, they can be practised across various states in India as a prototype.

### Medically important snakes and snakebite envenoming in Iran.

**Dehghani R, Monzavi SM, Mehrpour O, Shirazi FM, Hassanian-Moghaddam H, Keyler DE, Wüster W, Westerström A, Warrell DA.**

Jul-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/37187227/>

Snakebite is a relatively common health condition in Iran with a diverse snake fauna, especially in tropical southern and mountainous western areas of the country with a plethora of snake species. The list of medically important snakes, circumstances and effects of their bite, and necessary medical care require critical appraisal and should be updated regularly. This study aims to review and map the distributions of medically important snake species of Iran, re-evaluate their taxonomy, review their venomics, describe the clinical effects of envenoming, and discuss medical management and treatment, including the use of antivenom. Nearly 350 published articles and 26 textbooks with information on venomous and mildly venomous snake species and snakebites of Iran, were reviewed, many in Persian (Farsi) language, making them relatively inaccessible to an international readership. This has resulted in a revised updated list of Iran's medically important snake species, with taxonomic revisions of some, compilation of their morphological features, remapping of their geographical distributions, and description of species-specific clinical effects of envenoming. Moreover, the antivenom manufactured in Iran is discussed, together with treatment protocols that have been developed for the hospital management of envenomed patients.

### Envenomation by *Vipera aspis* in Piedmont (Italy): A report of three cases, including one case with neurological symptoms.

**Sassoè M.**

Jul-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/37169267/>

## Mycétome

### Epidemiology and etiology of brain cancer in Africa: A systematic review.

**Uwishema O, Frederiksen KS, Badri R, Pradhan AU, Shariff S, Adanur I, Dost B, Esene I, Rosseau G.**

14-06-2023

*Brain Behav.*

<https://pubmed.ncbi.nlm.nih.gov/37312649/>

**Background:** Cancer is a significant threat to public health and a leading cause of morbidity across the globe. Of all cancers, brain cancer can be particularly catastrophic as treatment often fails to achieve the desired degree of effectiveness and diagnosis remains associated with a high mortality rate. Africa, as a continent with resource-limited countries, needs to allocate the necessary proper healthcare infrastructure to significantly reduce cancer rates and improve patient survival. In addition, the relative paucity of data within this field in Africa makes effective management a challenge. **Objective:** This review is aimed at elucidating the currently available evidence base with regard to the epidemiology and etiology of brain cancer within resource-limited African countries. This review hopes to bring to the attention of the wider clinical community the growing burden of brain cancer within Africa and to encourage future research into this field of research. **Methods:** The available literature for this Systematic Review was searched on two bibliographic databases, PubMed and Scopus, using an individually verified, prespecified approach. In addition, the Global Cancer Observatory and Global Burden of Disease databases were also utilized. Studies reporting on the epidemiology, etiology, and impact of brain cancer in Africa were suitable for inclusion. The level of evidence of the included studies was considered as per the Centre for Evidence-Based Medicine recommendations.

**Results:** Out of the four databases searched, 3848 articles were initially screened rigorously, filtered into 54 articles, and finally assessed qualitatively and quantitatively. We have demonstrated a poor survival rate and lack of proper funds/resources necessary to report, identify, and treat cases, as well as the dearth of comprehensive research on the subject of brain cancer that has become a challenging healthcare concern in many African developing nations. Also, because of the gradual improvement in healthcare facilities and the increasing population within many countries in Africa, the number of patients with central nervous system and intracranial tumors is rising specifically in the elder population. In addition, the population in West Africa is at a higher risk of HIV-related malignancies due to the high prevalence of HIV in West Africa. The burden of brain cancer in Africa is increasing in comparison with the developed parts of the world in which it is decreasing. Moreover, the mismanagement of cancers in Africa leads to higher morbidity and mortality and decreased quality of life. **Conclusion:** This study addresses the burden of brain cancer as a major public health crisis in Africa. Improved treatment modalities and access to screening are required to better address the burden of this disease. Therefore, there is a clear need for more substantial and comprehensive research on etiology,



epidemiology, and treatment of brain cancer within Africa to understand its epidemiological distribution and provide a means for managing and reducing the associated morbidity and mortality.

### Unusual Fungal Endocarditis Causing Disseminated Infection After Renal Transplant.

Ali W, Casey B, Al Salman I, Mazek H, Alemu R, Younus U.

11-05-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/37303459/>

Fungal endocarditis is a relatively uncommon disease; it mostly affects those with intracardiac devices and those with compromised immune systems. *Scedosporium apiospermum* (*S. apiospermum*), the asexual state of *Pseudoallescheria boydii*, has become increasingly reported as an opportunistic pathogen. These filamentous fungi present in soil, sewage, and polluted waters, and was previously recognized to cause human infection after their inhalation or traumatic subcutaneous implantation. In immunocompetent individuals, it usually causes localized diseases depending on the site of entry such as skin mycetoma. However, in immunocompromised hosts, the fungus species appear to disseminate and cause invasive infections, frequently reported to be life-threatening with poor response to antifungal medications. *S. apiospermum* invasive endocarditis remains a rare complication, mostly cited in immunocompetent hosts with prosthetic cardiac valves or other intracardiac devices and severely immunocompromised patients with hematologic neoplasia. Herein, we describe the case of a renal transplant patient on immunosuppressive medications who presented with *S. apiospermum* fungal septic infection that invaded the left ventricular outflow tract (LVOT) causing endocarditis with disseminated infection and resulted in poor clinical outcome.

### Madura foot: The role of imaging in early diagnosis.

López Banet E, Litrán López G.

23-06-2023

*Med Clin (Barc).*

<https://pubmed.ncbi.nlm.nih.gov/37002020/>

## Onchocercose

### Onchocerciasis-associated epilepsy in Maridi, South Sudan: Modelling and exploring the impact of control measures against river blindness.

Bhattacharyya S, Vinkeles Melchers NVS, Siewe Fodjo JN, Vutha A, Coffeng LE, Logora MY, Colebunders R, Stolk WA.

26-05-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37235598/>

**Background:** Onchocerciasis, also known as "river blindness", is caused by the bite of infected female blackflies (genus *Simuliidae*) that transmit the parasite *Onchocerca volvulus*. A high onchocerciasis microfilarial load increases the risk to develop epilepsy in children between the ages of 3 and 18 years. In resource-limited settings in Africa where onchocerciasis has been poorly controlled, high numbers of onchocerciasis-associated epilepsy (OAE) are reported. We use mathematical modeling to predict the impact of onchocerciasis control strategies on the incidence and prevalence of OAE.

**Methodology:** We developed an OAE model within the well-established mathematical modelling framework ONCHOSIM. Using Latin-Hypercube Sampling (LHS), and grid search technique, we quantified transmission and disease parameters using OAE data from Maridi County, an onchocerciasis endemic area, in southern Republic of South Sudan. Using ONCHOSIM, we predicted the impact of ivermectin mass drug administration (MDA) and vector control on the epidemiology of OAE in Maridi. **Principal findings:** The model estimated an OAE prevalence of 4.1% in Maridi County, close to the 3.7% OAE prevalence reported in field studies. The OAE incidence is expected to rapidly decrease by >50% within the first five years of implementing annual MDA with good coverage (≥70%). With vector control at a high efficacy level (around 80% reduction of blackfly biting rates) as the sole strategy, the reduction is slower, requiring about 10 years to halve the OAE incidence. Increasing the efficacy levels of vector control, and implementing vector control simultaneously with MDA, yielded better results in preventing new cases of OAE. **Conclusions/significances:** Our modeling study demonstrates that intensifying onchocerciasis eradication efforts could substantially reduce OAE incidence and prevalence in endemic foci. Our model may be useful for optimizing OAE control strategies.

## Rage

### Immune-adjuvant effect of vitamin A and probiotics supplementation on humoral response to cell culture rabies vaccine in rabbits.

Najam A, Ahmad S, Abid R, Ali H, Husnain M, Aziz T, Adeel SS, Muhammad N, Ghazanfar S.

Jul-2023

*3 Biotech.*

<https://pubmed.ncbi.nlm.nih.gov/37323857/>

This study was carried out to evaluate the effects of vitamin A (Vit A) and probiotic co-supplementation with rabies vaccine on humoral immune response in New Zealand white (NZW) rabbits. For this experiment, 54 rabbits were randomized into six experimental and three control groups. Mixed cultures of commercial probiotics supplements and a dose of Vit A were administered to each animal. Results were compared with the control group fed with only basal diet. Animals in different treatment groups showed significantly higher sero-conversions against rabies vaccine. There was a significant increase ( $p < 0.001$ ) in the titers of rabies antibodies in all treatment groups on 14th and 35th days than control C3

group. Both commercial probiotics irrespective of brand increase the humoral immune response of rabbits against rabies vaccine. The mean titer values of all groups G1-G6 and sub-controls (C1, C2) were generally above 3.6 EU/ml on day 14th and between 3.7 and 3.9 EU/ml, showing highest sero-conversion on 35th day than mean titer of C3 control = 3.091 and 3.505 EU/ml respectively on both days. The maximum titer values were obtained with the addition of organic carrots to the daily diet. These results suggest that simple dietary interventions using probiotics and Vit A in natural form may enhance the efficacy of rabies vaccine in the host. These cost-effective strategies can be applied for getting higher yields of polyclonal antibody production in animal models, thus providing promising means of improving the final product yield and can be adopted easily by the manufacturers.

### **Determination of Vaccine Immunogenicity Using Bovine Monocyte-Derived Dendritic Cells.**

**Liaqat F, Kangethe RT, Pichler R, Liu B, Huber J, Wijewardana V, Cattoli G, Porfiri L.**

19-05-2023

*J Vis Exp.*

<https://pubmed.ncbi.nlm.nih.gov/37318241/>

### **Inclusion of Rabishield in the WHO guidelines for rabies postexposure prophylaxis.**

**Kaza VK, Nathan B.**

Mars-avr 2023

*Indian J Pharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37313941/>

### **Louis Pasteur-The life of a controversial scientist with a prepared mind, driven by curiosity, motivation, and competition.**

**Brogren CH.**

13-06-2023

*APMIS.*

<https://pubmed.ncbi.nlm.nih.gov/37310124/>

Louis Pasteur, born December 27, 1822 in Dole, France, showed in his childhood and youth great abilities as an artistic painter; however by an age of 19, his interest changed toward science, and he moved to Paris to study chemistry and physics at École Normale Supérieure. During graduation, he initiated research on chiral crystallography and stereochemistry and got his doctorates in 1847 in both chemistry and physics. In 1848, he started as high school teacher in Dijon, but shortly after he became a deputy professor at the University of Strasbourg in chemistry and got married to the rector's daughter Marie Laurent. They had five children, of which only two survived. The family moved to Lille in 1854, where he worked as professor in chemistry and became the dean at the new Faculty of Science at the University of Lille. He initiated his famous research on fermentation in 1855. Louis Pasteur moved back to École Normale Supérieure in 1857, where a major part of his innovative research on fermentation took place ending up with the development of pasteurization in 1864. Through genius

experiments, he disputed the spontaneous genesis theory and founded the basis for the germ theory, later confirmed by his enemy Robert Koch and several other research teams, which he for lifetime competed with on the cure and prevention against infectious disease causes by both bacteria such as cholera, anthrax, and virus-induced infections as yellow fever and rabies. However, most of his experiments were done on animals since Pasteur and his colleagues at École Normale Supérieure were not physicians but scientists. The first successful attenuated vaccine used in humans against rabies was, when the 9-year-old Joseph Meister was cured or prevented from rabies in 1885 after 13 vaccine injections done by the young pediatrician Joseph Grancher. This worldwide known intervention is both world famous and ethically criticized and disputed. The Pasteur Institute was inaugurated in 1888-now an international prestigious research institute-which has been expanded since in a network of affiliated Pasteur institutes over the whole world. There were multiple links to Danish scientists of the 19th century and to the Danish brewery industry. Most well known is the strong friendship between Louis Pasteur and the Carlsberg brewery and especially to its founder Jacob Christian Jacobsen, who was a great believer on a scientific approach to a cleaner fermentation process and better beer quality. Louis Pasteur stands as a milestone example of the fruitful outcome of scientific competition and collaboration and should therefore be remembered as an inspiration for present and future scientists.

### **Hindlimb muscle representations in mouse motor cortex defined by viral tracing.**

**Maurer L, Brown M, Saggi T, Cardiges A, Kolarcik CL.**

25-05-2023

*Front Neuroanat.*

<https://pubmed.ncbi.nlm.nih.gov/37303816/>

**Introduction:** Descending pathways from the cortex to the spinal cord are involved in the control of natural movement. Although mice are widely used to study the neurobiology of movement and as models of neurodegenerative disease, an understanding of motor cortical organization is lacking, particularly for hindlimb muscles. **Methods:** In this study, we used the retrograde transneuronal transport of rabies virus to compare the organization of descending cortical projections to fast- and slow-twitch hindlimb muscles surrounding the ankle joint in mice. **Results:** Although the initial stage of virus transport from the soleus muscle (predominantly slow-twitch) appeared to be more rapid than that associated with the tibialis anterior muscle (predominantly fast-twitch), the rate of further transport of virus to cortical projection neurons in layer V was equivalent for the two injected muscles. After appropriate survival times, dense concentrations of layer V projection neurons were identified in three cortical areas: the primary motor cortex (M1), secondary motor cortex (M2), and primary somatosensory cortex (S1). **Discussion:** The origin of the cortical projections to each of the two injected muscles overlapped almost entirely within these cortical areas. This organization suggests that cortical projection neurons maintain a high degree of specificity; that is, even when

cortical projection neurons are closely located, each neuron could have a distinct functional role (controlling fast- versus slow-twitch and/or extensor versus flexor muscles). Our results represent an important addition to the understanding of the mouse motor system and lay the foundation for future studies investigating the mechanisms underlying motor system dysfunction and degeneration in diseases such as amyotrophic lateral sclerosis and spinal muscular atrophy.

### Assessing the effect of a canine surgical-neutering educational programme on the knowledge and confidence of Indian veterinary participants.

Rayner EL, Airikkala-Otter I, Mellanby RJ, Gibson AD, Susheelan A, Gamble L, Mazeri S.

25-05-2023

*Front Vet Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37303735/>

### Microfluidic Biosensor Based on Molybdenum Disulfide (MoS<sub>2</sub>) Modified Thin-Core Microfiber for Immune Detection of *Toxoplasma gondii*.

Chen H, Luo B, Wu S, Shi S, Dai Q, Peng Z, Zhao M.

31-05-2023

*Sensors (Basel).*

<https://pubmed.ncbi.nlm.nih.gov/37299945/>

*Toxoplasma gondii* (*T. gondii*) is a zoonotic parasite that is widely distributed and seriously endangers public health and human health. Therefore, accurate and effective detection of *T. gondii* is crucial. This study proposes a microfluidic biosensor using a thin-core microfiber (TCMF) coated with molybdenum disulfide (MoS<sub>2</sub>) for immune detection of *T. gondii*. The single-mode fiber was fused with the thin-core fiber, and the TCMF was obtained by arc discharging and flame heating. In order to avoid interference and protect the sensing structure, the TCMF was encapsulated in the microfluidic chip. MoS<sub>2</sub> and *T. gondii* antigen were modified on the surface of TCMF for the immune detection of *T. gondii*. Experimental results showed that the detection range of the proposed biosensor for *T. gondii* monoclonal antibody solutions was 1 pg/mL to 10 ng/mL with sensitivity of 3.358 nm/log(mg/mL); the detection of limit was calculated to be 87 fg/mL through the Langmuir model; the dissociation constant and the affinity constant were calculated to be about  $5.79 \times 10^{-13}$  M and  $1.727 \times 10^{14}$  M<sup>-1</sup>, respectively. The specificity and clinical characteristics of the biosensor was explored. The rabies virus, pseudorabies virus, and *T. gondii* serum were used to confirm the excellent specificity and clinical characteristics of the biosensor, indicating that the proposed biosensor has great application potential in the biomedical field.

### The Price of Hospital Reshaping: Nasal Myiasis Caused by Flesh Fly (Diptera: Sarcophagidae) in Reallocated COVID-19 Intensive Care Unit.

Dolinaj V, Grujić J, Križanović D, Potkonjak A, Pape T, Banović P.

24-05-2023

*Healthcare (Basel).*

<https://pubmed.ncbi.nlm.nih.gov/37297672/>

### Risk of Rabies and Implications for Postexposure Prophylaxis Administration in the US.

Charniga K, Nakazawa Y, Brown J, Jeon S, Wallace RM.

01-06-2023

*JAMA Netw Open.*

<https://pubmed.ncbi.nlm.nih.gov/37294570/>

### Distribution of *Baylisascaris procyonis* in Raccoons (*Procyon lotor*) in Florida, USA.

Cunningham MW, Wolf DP, Sayler KA, Milleson M, Bankovich B, Schueller P, Haley BS, Stura S, Yabsley MJ.

01-04-2023

*J Wildl Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37074793/>

## Schistosomiasis

### Associations of water contact frequency, duration, and activities with schistosome infection risk: A systematic review and meta-analysis.

Reitzug F, Ledien J, Chami GF.

14-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37315020/>

**Background:** Schistosomiasis is a water-borne parasitic disease which affects over 230 million people globally. The relationship between contact with open freshwater bodies and the likelihood of schistosome infection remains poorly quantified despite its importance for understanding transmission and parametrising transmission models.

**Methods:** We conducted a systematic review to estimate the average effect of water contact duration, frequency, and activities on schistosome infection likelihood. We searched Embase, MEDLINE (including PubMed), Global Health, Global Index Medicus, Web of Science, and the Cochrane Central Register of Controlled Trials from inception until May 13, 2022. Observational and interventional studies reporting odds ratios (OR), hazard ratios (HR), or sufficient information to reconstruct effect sizes on individual-level associations between water contact and infection with any *Schistosoma* species were eligible for inclusion. Random-effects meta-analysis with inverse variance weighting was used to calculate pooled ORs and 95% confidence intervals (CIs). **Results:** We screened 1,411 studies and included 101 studies which represented 192,691 participants across Africa, Asia, and South America. Included studies mostly reported on water contact activities (69%; 70/101) and having any water contact (33%; 33/101). Ninety-six percent of studies (97/101) used surveys to measure exposure. A meta-analysis of 33 studies showed that individuals with water contact were 3.14 times more likely to be infected (OR 3.14; 95% CI: 2.08-4.75) when compared to individuals

with no water contact. Subgroup analyses showed that the positive association of water contact with infection was significantly weaker in children compared to studies which included adults and children (OR 1.67; 95% CI: 1.04-2.69 vs. OR 4.24; 95% CI: 2.59-6.97). An association of water contact with infection was only found in communities with  $\geq 10\%$  schistosome prevalence. Overall heterogeneity was substantial ( $I^2 = 93\%$ ) and remained high across all subgroups, except in direct observation studies ( $I^2$  range = 44%-98%). We did not find that occupational water contact such as fishing and agriculture (OR 2.57; 95% CI: 1.89-3.51) conferred a significantly higher risk of schistosome infection compared to recreational water contact (OR 2.13; 95% CI: 1.75-2.60) or domestic water contact (OR 1.91; 95% CI: 1.47-2.48). Higher duration or frequency of water contact did not significantly modify infection likelihood. Study quality across analyses was largely moderate or poor. **Conclusions:** Any current water contact was robustly associated with schistosome infection status, and this relationship held across adults and children, and schistosomiasis-endemic areas with prevalence greater than 10%. Substantial gaps remain in published studies for understanding interactions of water contact with age and gender, and the influence of these interactions for infection likelihood. As such, more empirical studies are needed to accurately parametrise exposure in transmission models. Our results imply the need for population-wide treatment and prevention strategies in endemic settings as exposure within these communities was not confined to currently prioritised high-risk groups such as fishing populations.

### Prevalence and distribution of urinary schistosomiasis among senior primary school pupils of Siphofaneni area in the low veld of Eswatini: A cross-sectional study.

Maseko TSB, Masuku SKS, Dlamini SV, Fan CK.

04-06-2023

*Helminthologia*.

<https://pubmed.ncbi.nlm.nih.gov/37305666/>

A cross-sectional survey of *Schistosoma haematobium* prevalence was conducted among senior primary school pupils of Siphofaneni area, Eswatini. This area is devoid of potable water, with a newly constructed Lubovane dam and an LUSIP irrigation scheme. The objective of the study was to investigate the distribution of urinary schistosomiasis among Siphofaneni senior primary school pupils. Using simple random sampling, 200 participants were enrolled from four of six schools in the area. Ten millimetres (10 ml) of urine samples were obtained from each participant and examined for *S. haematobium* eggs. The intensity of the infection was estimated by calculating the total number of *S. haematobium* eggs present in 10 ml urine. Out of 200 participants, 45% ( $n = 91$ ) were males, and 55% ( $n = 109$ ) were females. The mean age for participants was 13 years, and almost half (47%,  $n = 94$ ) were in Grade 5. Overall, the prevalence of *S. haematobium* infection was 16% (32/200). More than half (59%, 19/32) of the Schistosomiasis cases were from females. Positive and significant associations were observed between the number of eggs ( $\chi^2=170.9$ ) and the

presence of red blood cells ( $\chi^2=49.2$ ) at  $p = 0.001$ . In conclusion, the prevalence of Schistosomiasis is high among pupils enrolled in Siphofaneni area primary schools that needs comprehensive treatment and education to prevent from *S. haematobium* infection.

### Molecular characterization of Smtde-1 and Smdde-1 discloses roles as male-competence factors for the sexual maturation of Schistosoma mansoni females.

Li X, Weth O, Haeberlein S, Grevelding CG.

26-05-2023

*Front Cell Infect Microbiol*.

<https://pubmed.ncbi.nlm.nih.gov/37305409/>

### The interaction of Schistosoma mansoni infection with diabetes mellitus and obesity in mice.

Amer AS, Othman AA, Dawood LM, El-Nouby KA, Gobert GN, Abou Rayia DM.

09-06-2023

*Sci Rep*.

<https://pubmed.ncbi.nlm.nih.gov/37296126/>

Human schistosomiasis is one of the most prevalent parasitic diseases worldwide. Various host factors can affect the host-parasite interactions. Therefore, the aim of the present work was to determine the parasitological, histopathological, biochemical, and immunological status of *Schistosoma mansoni*-infected hosts with metabolic disorders to identify the underlying possible mechanisms of these comorbidities. The study animals were divided into four groups. Group I represented the control groups, namely, the normal control group, the *S. mansoni*-infected control group, and the noninfected type 1 diabetes (T1DM), type 2 diabetes (T2DM), and obesity groups. The mice of the other three groups underwent induction of T1DM (Group II), T2DM (Group III) and obesity (Group IV) before being infected with *S. mansoni*. All mice were subjected to body weight measurement, blood glucose and insulin assessment, parasitological evaluation of adult worm count, tissue egg count and intestinal oogram. Histopathological and immunohistochemical study using anti-glial fibrillary acidic protein (GFAP) in hepatic stellate cells (HSCs) and image analysis of Masson's trichrome-stained liver sections using ImageJ (Fiji) software were carried out. Additionally, immunological analysis of tumour necrosis factor (TNF) beta, interleukin-5 (IL-5), IL-10, Forkhead box P3 (FOXP3) and pentraxin 3 (PTX3) levels besides biochemical study of total lipid profile were evaluated. The present study revealed a significant increase in the adult worm count and tissue egg output in the obesity group compared to the infected control group. The oogram of counted eggs showed prevalence of immature eggs in T1DM group, while T2DM and obese groups showed prevalence of mature eggs. The fibrosis area percentage showed significant increase in T2DM and obese groups while it was decreased in T1DM group in comparison to infected control group. Our data also showed significant increase in the levels of TNF- $\beta$ , IL-5, PTX3 in T1DM, T2DM and obesity groups in comparison to



infected control group, whilst the levels of FOXP3 and IL-10 were increased in the infected groups in comparison to their noninfected controls. Moreover, infected T1DM, T2DM and obesity groups showed higher blood glucose and lipid profile in comparison to the infected control group. However, these parameters were improved in comparison to their noninfected controls. In sum, induction of T2DM and obesity increased tissue egg counts, mature egg percentage, and fibrosis density, while schistosome infection induced changes in the lipid profile and blood glucose levels in infected diabetic and obese groups and impacted favorably insulin levels in obese mice. By better understanding the complexities of host-parasite interactions, efforts to reduce the burden of these debilitating diseases can be improved.

### **In vitro activity, ultrastructural analysis and in silico pharmacokinetic properties (ADMET) of thiazole compounds against adult worms of *Schistosoma mansoni*.**

da Silva DVSP, Henrique do Bomfim Nascimento P, da Rocha JVR, Marques DSC, Brayner FA, Alves LC, de Araújo HDA, da Cruz Filho IJ, de Azevedo Albuquerque MCP, do Carmo Alves de Lima M, de Lima Aires A.

07-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37295486/>

### **Broad anti-pathogen potential of DEAD box RNA helicase eIF4A-targeting rocaglates.**

Obermann W, Azri MFD, Konopka L, Schmidt N, Magari F, Sherman J, Silva LMR, Hermosilla C, Ludewig AH, Houhou H, Haeblerlein S, Luo MY, Häcker I, Schetelig MF, Grevelding CG, Schroeder FC, Lau GSK, Taubert A, Rodriguez A, Heine A, Yeo TC, Grünweller A, Taroncher-Oldenburg G.

08-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37291191/>

### **Schistosome egg antigen stimulates the secretion of miR-33-carrying extracellular vesicles from macrophages to promote hepatic stellate cell activation and liver fibrosis in schistosomiasis.**

Qi X, Pu Y, Chen F, Dong L, Ma Y, Wang J, Yin G, Lu D, Chen X, Zhu J, Li Y, Zhou S, Su C.

30-05-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37253066/>

### **Evaluation of 43 species of Congolese medicinal plants used traditionally for the treatment of schistosomiasis leading to the isolation of an anti-schistosomal phaeophytin from *Pseudolachnostylis maprouneifolia* Pax.**

Muya K, Kalonji M, Ilunga NW, Maseho M, Kitambala M, Kalonda M, Ndoumba K, Byanga K, Wright CW, Häberli C, Keiser J, Simbi L.

28-10-2023

*J Ethnopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37245710/>

Schistosomiasis is a serious and neglected disease with a high prevalence in tropical and subtropical countries. The primary pathology of hepatic schistosomiasis caused by *Schistosoma japonicum* (*S. japonicum*) or *Schistosoma mansoni* (*S. mansoni*) infection is egg-induced granuloma and subsequent fibrosis in the liver. Activation of hepatic stellate cells (HSCs) is the central driver of liver fibrosis. Macrophages (M $\phi$ ), making up 30% of cells in hepatic granulomas, directly or indirectly regulate HSC activation by paracrine mechanisms, via secreting cytokines or chemokines. Currently, M $\phi$ -derived extracellular vesicles (EVs) are broadly involved in cell communication with adjacent cell populations. However, whether M $\phi$ -derived EVs could target neighboring HSCs to regulate their activation during schistosome infection remains largely unknown. Schistosome egg antigen (SEA) is considered to be the main pathogenic complex mixture involved in liver pathology. Here, we demonstrated that SEA induced M $\phi$  to produce abundant extracellular vesicles, which directly activated HSCs by activating their autocrine TGF- $\beta$ 1 signaling. Mechanistically, EVs derived from SEA-stimulated M $\phi$  contained increased miR-33, which were transferred into HSCs and subsequently upregulated autocrine TGF- $\beta$ 1 in HSCs through targeting and downregulating SOCS3 expression, thereby promoting HSC activation. Finally, we validated that EVs derived from SEA-stimulated M $\phi$  utilized enclosed miR-33 to promote HSC activation and liver fibrosis in *S. japonicum*-infected mice. Overall, our study indicates that M $\phi$ -derived EVs play important roles in the paracrine regulation of HSCs during the progression of hepatic schistosomiasis, representing a potential target for the prevention of liver fibrosis in hepatic schistosomiasis.

### **Antischistosomal effects of green and chemically synthesized silver nanoparticles: In vitro and in vivo murine model.**

Hamdan ZK, Soliman MI, Taha HA, Khalil MMH, Nigm AH.

01-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37236335/>

Schistosomiasis is one of the most important neglected tropical diseases in Africa, caused by blood fluke, *Schistosoma* sp. The use of nanotechnology in the treatment of this type of disease is urgently important to avoid the unwanted side effects of chemotherapy. The present study aimed to evaluate the efficacy of green silver nanoparticles (G-AgNPs), fabricated by (*Calotropis procera*), comparing with both chemically prepared silver ones (C-AgNPs) and Praziquantel (PZQ) treatments. The study included in vitro and in vivo evaluations. In in vitro study, 4 groups of schistosome worms were exposed to treatments as follows: the first one with a dose of PZQ (0.2  $\mu$ g/ml), the 2nd and 3rd groups with different concentrations of G-AgNPs and C-AgNPs, respectively and

the last one act as a negative control group. In in vivo study, six groups of mice were infected and then treated as follows: the first one with a dose of PZQ, the second with G-AgNPs, the third with C-AgNPs, the fourth with G-AgNPs plus a half dose of PZQ, the fifth with C-AgNPs accompanied by a half dose of PZQ, and the last group acted as a positive control group. The parasitological (worm burden, egg count & oogram) and histopathological parameters (hepatic granuloma profile) were used to evaluate antischistosomal activities in experimental groups. Additionally, the subsequent ultrastructural alterations were observed in adult worms using scanning electron microscopy (SEM). Transmission electron microscopy analysis showed that G-AgNPs and C-AgNPs have 8-25 and 8-11 nm in diameter, respectively, besides, fourier transform infrared analysis (FTIR) revealed the presence of organic compounds (aromatic ring groups) which act as capping agents around the surfaces of biogenic silver nanoparticles. In in vitro experiment, adult worms incubated either with G-AgNPs or C-AgNPs at concentrations higher than 100 µg/ml or 80 µg/ml, respectively, showed full mortality of parasites after 24 h. In the infected treated groups (with G-AgNPs plus PZQ & C-AgNPs plus PZQ) showed the most significant reduction in the total worm burdens (92.17% & 90.52%, respectively). Combined treatment with C-AgNPs and PZQ showed the highest value of dead eggs (93,6%), followed by G-AgNPs plus PZQ-treated one (91%). This study showed that mice treated with G-AgNPs plus PZQ significantly has the highest percentage of reduction in granuloma size and count (64.59%, 70.14%, respectively). Both G-AgNPs plus PZQ-treated & C-AgNPs plus PZQ treated groups showed the highest similar values of reduction percentage of total ova count in tissues (98.90% & 98.62%, respectively). Concerning SEM, G-AgNPs-treated worms showed more variability in ultrastructural alterations than G-AgNPs plus PZQ-treated one, besides, worms treated with C-AgNPs plus PZQ exhibited the maximum level of contractions or (shrinkage) as a major impact.

### **Electrophysiological characterization of a schistosome transient receptor potential channel activated by praziquantel.**

**Chulkov EG, Palygin O, Yahya NA, Park SK, Marchant JS.**  
Juil-2023  
*Int J Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36610556/>

### **Use the force, fluke: Ligand-independent gating of *Schistosoma mansoni* ion channel TRPM2PZQ.**

**Chulkov EG, Isaeva E, Stucky CL, Marchant JS.**  
Juil-2023  
*Int J Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36610555/>

## **Trachome**

### **Chlamydia trachomatis-An Emerging Old Entity?**

**Grygiel-Górniak B, Folga BA.**  
14-05-2023

*Microorganisms.*

<https://pubmed.ncbi.nlm.nih.gov/37317257/>

*Chlamydia trachomatis* is an evasive pathogen that can prompt severe clinical manifestations in humans such as vaginitis, epididymitis, lymphogranuloma venereum, trachoma, conjunctivitis and pneumonia. If left untreated, chronic infections with *C. trachomatis* can give rise to long-lasting and even permanent sequelae. To shed some light on its widespread nature, data from original research, systematic reviews and meta-analyses from three databases was collected and analyzed in the context of chlamydial infection, related symptoms and appropriate treatment modalities. This review describes the bacterium's pervasiveness on a global scale, especially in developing countries, and suggests ways to halt its transmission and spread. Infections with *C. trachomatis* often go unnoticed, as many individuals are asymptomatic and unaware of their diagnosis, contributing to a delay in diagnosis and treatment. The high prevalence of chlamydial infection highlights the need for a universal screening and detection method enabling immediate treatment at its onset. Prognosis is favorable with antibiotic therapy and education for high-risk groups and their sexual partners. In the future, a quick, easily accessible, and inexpensive test should be developed to diagnose and treat infected individuals early on. Along with a vaccine against *C. trachomatis*, it would halt the transmission and spread of the pathogen worldwide.

### **Pharmacokinetics, feasibility and safety of co-administering azithromycin, albendazole, and ivermectin during mass drug administration: A review.**

**McPherson S, Solomon AW, Seife F, Solomon H, Gebre T, Mabey DCW, Marks M.**  
14-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37315102/>

**Introduction:** Traditionally, health ministries implement mass drug administration programmes for each neglected tropical disease (NTD) as separate and distinct campaigns. Many NTDs have overlapping endemicity suggesting co-administration might improve programme reach and efficiency, helping accelerate progress towards 2030 targets. Safety data are required to support a recommendation to undertake co-administration. **Methodology:** We aimed to compile and summarize existing data on co-administration of ivermectin, albendazole and azithromycin, including both data on pharmacokinetic interactions and data from previous experimental and observational studies conducted in NTD-endemic populations. We searched PubMed, Google Scholar, research and conference abstracts, gray literature, and national policy documents. We limited the

publication language to English and used a search period from January 1st, 1995 through October 1st, 2022. Search terms were: azithromycin and ivermectin and albendazole, mass drug administration co-administration trials, integrated mass drug administration, mass drug administration safety, pharmacokinetic dynamics, and azithromycin and ivermectin and albendazole. We excluded papers if they did not include data on co-administration of azithromycin and both albendazole and ivermectin, or azithromycin with either albendazole or ivermectin alone. **Results:** We identified a total of 58 potentially relevant studies. Of these we identified 7 studies relevant to the research question and which met our inclusion criteria. Three papers analyzed pharmacokinetic and pharmacodynamic interactions. No study found evidence of clinically significant drug-drug interactions likely to impact safety or efficacy. Two papers and a conference presentation reported data on the safety of combinations of at least two of the drugs. A field study in Mali suggested the rates of adverse events were similar with combined or separate administration, but was underpowered. A further field study in Papua New Guinea used all three drugs as part of a four-drug regimen also including diethylcarbamazine; in this setting, co-administration appeared safe but there were issues with the consistency in how adverse events were recorded. **Conclusion:** There are relatively limited data on the safety profile of co-administering ivermectin, albendazole and azithromycin as an integrated regimen for NTDs. Despite the limited amount of data, available evidence suggests that such a strategy is safe with an absence of clinically important drug-drug interactions, no serious adverse events reported and little evidence for an increase in mild adverse events. Integrated MDA may be a viable strategy for national NTD programmes.

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

**Prevalence of gastrointestinal parasites and molecular identification of beta-tubulin mutations associated with benzimidazole resistance in *Haemonchus contortus* in goats from selected districts of Uganda.**

Kalule F, Vudriko P, Nanteza A, Ekiri AB, Alafiatayo R, Betts J, Betson M, Mijten E, Varga G, Cook A.

Juil-2023

*Vet Parasitol Reg Stud Reports.*

<https://pubmed.ncbi.nlm.nih.gov/37321794/>

**Morphological and molecular characterization of *Fasciola* isolates**

**from livestock in Golestan province, northern Iran.**

Sharbatkhori M, Nasibi S, Mohammadi MA, Aryaeipour M, Raeghi S, Fasihi Harandi M.

15-06-2023

*Vet Med Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37317979/>

**Background:** Fascioliasis, caused by the liver flukes *Fasciola hepatica* and *Fasciola gigantica*, is a global zoonotic helminthic disease. The livestock and human are the final hosts of the parasites. Northern Iran is an important endemic region for fascioliasis. Few studies have been conducted on the characterization of *Fasciola* isolates from eastern regions of the Caspian littoral of the country.

**Objective:** The aim of the present study was to identify *F. hepatica*, *F. gigantica* and intermediate/hybrid forms of *Fasciola* isolates from livestock in Golestan province, northern Iran, using morphometric and molecular tools.

**Methods:** Livestock livers naturally infected with *Fasciola* spp. were collected from Golestan slaughterhouse during 2019-2020. The worms were morphometrically studied using a calibrated stereomicroscope. Genomic DNA was extracted from all samples, and polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) was performed on internal transcribed spacer (ITS1) region using *Rsa*I restriction enzyme. All the isolates were then analysed by multiplex PCR on *Pepck* region. **Results:** A total of 110 *Fasciola* isolates were collected from the infected livers, including 94 sheep, 12 cattle and 4 goats. Morphometric analysis of 61 adult *Fasciola* isolates indicated that, 44 and 17 isolates belonged to *F. hepatica* and *F. gigantica*, respectively. Eighty-one and 29 isolates belonged to *F. hepatica* and *F. gigantica* using ITS1-RFLP, respectively. However, *Pepck* Multiplex PCR indicated 72 *F. hepatica*, 26 *F. gigantica* and 12 intermediate/hybrid forms. All 12 hybrid isolates were found in sheep host. Two isolates were identified as *F. gigantica* using morphometry and *F. hepatica* using both molecular methods. **Conclusion:** The present study confirmed the existence of both *F. hepatica* and *F. gigantica* species and reported the first molecular evidence of hybrid *Fasciola* isolates in ruminants of Golestan province.

**Plasma lipopolysaccharide elevations in cattle associated with early-stage infection by *Fasciola hepatica*.**

Marendy D, Gabor L, George SD, Parker A, Doyle E.

14-06-2023

*Aust Vet J.*

<https://pubmed.ncbi.nlm.nih.gov/37317661/>

**High endemicity of *Opisthorchis viverrini* infection among people in northern Cambodia confirmed by adult worm expulsion.**

Jung BK, Hong S, Chang T, Cho J, Ryoo S, Lee KH, Lee J, Sohn WM, Hong SJ, Khieu V, Huy R, Chai JY.

14-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37316679/>

### Secretory Excretory and Somatic Immunogenic Antigens Profiles of Adult *Fasciola* spp.

Dezhabad A, Dalimi A, Hoghooghi Rad N, Madani R.

28-02-2023

Arch Razi Inst.

<https://pubmed.ncbi.nlm.nih.gov/37312739/>

Fascioliasis is a common human-animal disease that is reported in most parts of the world. Fascioliasis is also prevalent in different provinces of Iran. Since it has done no study on the excretory/secretory and somatic immunogenic antigens profiles of adult *Fasciola* in Iran, the present study was performed on the *Fasciola* spp. collected from Mazandaran province. For this purpose, the *Fasciola* worm was isolated from the liver of infected sheep, then its excretory/secretory and somatic antigens were prepared from adult worms. The protein of the samples was measured by the Lowry method. Then, somatic and secretory excretions were examined by SDS-PAGE and the protein profile of the two substances was determined. To evaluate the immunogenicity, the somatic and secretory excretions antigens of *Fasciola* spp. were injected into white rabbits and after boosting, the blood serum of the rabbits was collected and then Western blotting was performed on them and the results were evaluated. According to the results of Western blotting, 11 somatic antigen bands with a molecular weight of 149, 122, 99, 85, 75, 65, 50, 46, 40, 37, 30 kDa and 12 protein bands of excretory/secretory antigens with molecular weights of 100, 82, 75, 70, 58, 55, 47, 40, 38, 37, 30, 25 kDa were observed in adult *Fasciola* spp. that immunogenic, which appear to have a protective effect or can be used to prepare a diagnostic kit.

### Ethanol extract of *Etlingera elatior* flower exhibits anthelmintic properties to *Fasciola gigantica* in vitro.

Wulandari AR, Nurlaelasari A, Nugroho HA, Cahyadi M, Kurniawan W, Hamid PH.

Mai-2023

Open Vet J.

<https://pubmed.ncbi.nlm.nih.gov/37304615/>

### High prevalence of liver fluke infestation, *Fasciola gigantica*, among slaughtered cattle in Boyolali District, Central Java.

Prasetyo DA, Nurlaelasari A, Wulandari AR, Cahyadi M, Wardhana AH, Kurnianto H, Kurniawan W, Kristianingrum YP, Muñoz-Caro T, Hamid PH.

Mai-2023

Open Vet J.

<https://pubmed.ncbi.nlm.nih.gov/37304607/>

### A socio-ecological framework for examining foodborne parasitic infection risk.

Wang YC, Namsanor J, Law A, Sithithaworn P.

Aug-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37269890/>

Human liver fluke infection through the consumption of raw freshwater fish is one of the foodborne parasitic infections of global concern. Despite decades of health campaign efforts, high prevalence of infection remains in different areas of the Lower Mekong Basin. This necessitates the consideration of the infection differences between places and the human-environment complexities of disease transmission. This paper used the socio-ecological model as a framework to unravel the social science dimensions of liver fluke infection. We conducted questionnaire surveys in Northeast Thailand to gather participants' knowledge on liver fluke infection and reasons for raw fish consumption. We synthesized our findings with prior work to identify factors influencing liver fluke infection at four socio-ecological levels. At the individual level, gender and age differences in food consumption habits and personal hygiene of open defecation presented the behavioral risks. At the interpersonal level, family tradition and social gathering affected the disease risk. At the community level, physical-social-economic environments of land use and modernization, community health infrastructure and health volunteer support accounted for the varying degree of infection. At the policy level, impacts of regional and national regulations on disease control, health system organization structure, and government development projects were of concern. The findings provide insights into how infection risks are shaped by people's behavior, social connectedness, interactions with places, and the interplay of these multi-level socio-ecological influences. The framework therefore allows a more comprehensive understanding of liver fluke infection risks to inform a culturally sensitive and sustainable disease control program.

### Proteomic characterization of *Opisthorchis felinus* exosome-like vesicles and their uptake by human cholangiocytes.

Pakharukova MY, Savina E, Ponomarev DV, Gubanov NV, Zaporina O, Zakirova EG, Cheng G, Tikhonova OV, Mordvinov VA.

15-07-2023

J Proteomics.

<https://pubmed.ncbi.nlm.nih.gov/37225040/>

The epidemiologically important food-borne trematode *Opisthorchis felinus* infests the liver biliary tract of fish-eating mammals and causes disorders, including bile duct neoplasia. Many parasitic species release extracellular vesicles (EVs) that mediate host-parasite interaction. Currently, there is no information on *O. felinus* EVs. Using gel electrophoresis followed by liquid chromatography coupled with tandem mass spectrometry, we aimed to characterize the proteome of EVs released by the adult *O. felinus* liver fluke. Differential abundance of proteins between whole adult worms and EVs was assessed by semiquantitative iBAQ (intensity-based absolute quantification). Imaging, flow cytometry, inhibitor assays, and colocalization assays were performed to monitor the uptake of the EVs by H69 human cholangiocytes. The proteomic analysis reliably identified 168 proteins (at least



two peptides matched a protein). Among major proteins of EVs were ferritin, tetraspanin CD63, helminth defense molecule 1, globin 3, saposin B type domain-containing protein, 60S ribosomal protein, glutathione S-transferase GST28, tubulin, and thioredoxin peroxidase. Moreover, as compared to the whole adult worm, EVs proved to be enriched with tetraspanin CD63, saposin B, helminth defense molecule 1, and Golgi-associated plant pathogenesis-related protein 1 (GAPR1). We showed that EVs are internalized by human H69 cholangiocytes via clathrin-dependent endocytosis, whereas phagocytosis and caveolin-dependent endocytosis do not play a substantial role in this process. Our study describes for the first time proteomes and differential abundance of proteins in whole adult *O. felinus* worms and EVs released by this food-borne trematode. Studies elucidating the regulatory role of individual components of EVs of liver flukes should be continued to determine which components of EV cargo play the most important part in the pathogenesis of fluke infection and in a closely linked pathology: bile duct neoplasia. **SIGNIFICANCE:** The food-borne trematode *Opisthorchis felinus* is a pathogen that causes hepatobiliary disorders in humans and animals. Our study describes for the first time the release of EVs by the liver fluke *O. felinus*, their microscopic and proteomic characterization, and internalization pathways by human cholangiocytes. Differential abundance of proteins between whole adult worms and EVs was assessed. EVs are enriched with canonical EV markers as well as parasite specific proteins, i.e. tetraspanin CD63, saposin B, helminth defense molecule 1, and others. Our findings will form the basis of the search for potential immunomodulatory candidates with therapeutic potential in the context of inflammatory diseases, as well as novel vaccine candidates.

### **Worm-migration track of *Paragonimus westermani* infection.**

**Itoh R, Tomoda Y, Takeuchi C, Awaya Y.**

08-06-2023

*QJM.*

<https://pubmed.ncbi.nlm.nih.gov/36633295/>

## **Trypanosomes (trypanosomiasis et maladie de Chagas)**

### **The high identity of the *Trypanosoma cruzi* Group-I of trans-sialidases points them as promising vaccine immunogens.**

**Pacini MF, Perdomini A, Bulfoni Balbi C, Dinatale B, Herrera FE, Perez AR, Marcipar I.**

16-06-2023

*Proteins.*

<https://pubmed.ncbi.nlm.nih.gov/37323089/>

Trans-sialidase (TS) superfamily of proteins comprises eight subgroups, being the proteins of Group-I (TS-GI) promising immunogens in vaccine approaches against *Trypanosoma cruzi*. Strikingly, TS-GI antigenic variability

among parasite lineages and their influence on vaccine development has not been previously analyzed. Here, a search in GenBank detects 49 TS-GI indexed sequences, whereas the main infecting human different parasite discrete typing units (DTU) are represented. In silico comparison among these sequences indicate that they share an identity above 92%. Moreover, the antigenic regions (T-cell and B-cell epitopes) are conserved in most sequences or present amino acid substitutions that scarcely may alter the antigenicity. Additionally, since the generic term TS is usually used to refer to different immunogens of this broad family, a further in silico analysis of the TS-GI-derived fragments tested in preclinical vaccines was done to determine the coverage and identity among them, showing that overall amino acid identity of vaccine immunogens is high, but the segment coverage varies widely. Accordingly, strong H-2K, H-2I, and B-cell epitopes are dissimilarly represented among vaccine TS-derived fragments depending on the extension of the TG-GI sequence used. Moreover, bioinformatic analysis detected a set of 150 T-cell strong epitopes among the DTU-indexed sequences that strongly bind human HLA-I supertypes. In all currently reported experimental vaccines based on TS-GI fragments, mapping these 150 epitopes showed that they are moderately represented. However, despite vaccine epitopes do not present all the substitutions observed in the DTUs, these regions of the proteins are equally recognized by the same HLAs. Interestingly, the predictions regarding global and South American population coverage estimated in these 150 epitopes are similar to the estimations in experimental vaccines when the complete sequence of TS-GI is used as an antigen. In silico prediction also shows that a number of these MHC-I restricted T-cell strong epitopes could be also cross-recognized by HLA-I supertypes and H-2K<sup>b</sup> or H-2K<sup>d</sup> backgrounds, indicating that these mice may be used to improve and facilitate the development of new TS-based vaccines and suggesting an immunogenic and protective potential in humans. Further molecular docking analyses were performed to strengthen these results. Taken together, different strategies that would cover more or eventually fully of these T-cell and also B-cell epitopes to reach a high level of coverage are considered.

### **Parasitological and molecular detection of *Trypanosoma evansi* in a dog from Tocache, San Martin, Peru.**

**Villena FE, Puicón VH, López AM, Rivera K, Pannebaker D, Valdivia HO, Arévalo H.**

Jul-2023

*Vet Parasitol Reg Stud Reports.*

<https://pubmed.ncbi.nlm.nih.gov/37321797/>

This study presents the first case report of canine trypanosomiasis caused by *Trypanosoma evansi* in Peru. The case was admitted to a veterinary clinic in the Peruvian Amazon region of San Martin with severe clinical symptomatology which resulted in the dog's death. Microscopy screening showed the presence of trypomastigotes in blood and bone marrow and postmortem histopathology found damage at the cardiac, lung, kidney and spleen levels. Collected specimens were tested by nested-PCR which were positive for

Trypanosoma spp., but negative for T. cruzi. High-throughput sequencing determined that the infecting species was closely related to T. equiperdom/evansi and subsequent phylogenetic analysis confirmed that the sample was related to T. evansi. The presence of T. evansi in the area highlights the need for increased surveillance to assess the impact of surra in the region and to develop measures to prevent socioeconomic damage resulting from infections in domestic and farm animals as well as prevent zoonotic transmission.

### **Temporal assessment of entomological surveillance of Trypanosoma cruzi vectors in an endemic area of northeastern Brazil.**

**Sampaio GHF, da Silva ANB, de Negreiros CCA, Honorato NRM, Martins RR, Aguiar LMA, Sales LML, Brito CRDN, Guedes PMDM, da Câmara ACJ, Galvão LMDC.**

15-06-2023

*PLoS One.*

<https://pubmed.ncbi.nlm.nih.gov/37319301/>

Entomological surveillance is essential for the control of triatomines and the prevention of Trypanosoma cruzi infection in humans and domestic animals. Thus, the objective of this study was to evaluate entomological indicators and triatomine control during the period from 2005 to 2015 in an endemic area in the state of Rio Grande do Norte, Brazil. This observational and retrospective study was developed based on data analysis related to active entomological surveillance activities and chemical control of infested housing units (HU) in the Agreste mesoregion of the state of Rio Grande do Norte, Brazil, in the period between 2005 to 2015. The quantitative analysis of housing units surveyed for entomological indicators was performed by linear regression of random effects ( $p < 0.05$ ). The effect of the number of HU surveyed on the entomological indicators was analyzed by fitting a linear random effects regression model and an increasing intradomiciliary colonization rate was significant. In the period evaluated 92,156 housing units were investigated and the presence of triatomines was reported in 4,639 (5.0%). A total of 4,653 specimens of triatomines were captured and the species recorded were Triatoma pseudomaculata ( $n = 1,775$ ), Triatoma brasiliensis ( $n = 1,569$ ), Rhodnius nasutus ( $n = 741$ ) and Panstrongylus lutzi ( $n = 568$ ), with an index of natural infection by T. cruzi of 2.2%. Only 53.1% of the infested HU were subjected to chemical control. Moreover, there was a decrease in the total number of HU surveyed over time associated with an increase in the index of intradomiciliary colonization ( $p = 0.004$ ). These data demonstrated that entomological surveillance and control of vectors in the Agreste mesoregion of the state has been discontinued, emphasizing the need for more effective public policies to effectively control the vectors, in order to avoid the exposure of humans and domestic animals to the risk of T. cruzi infection.

### **Chagas disease prevalence among migrants from El Salvador in Milan: a cross-sectional study of an often-overlooked population.**

**Beltrami M, Grande R, Giacomelli A, Sabaini F, Biondo L, Longo M, Grosso S, Oreni L, Fadelli S, Galimberti L, Ridolfo AL, Antinori S.**

15-06-2023

*Infect Dis (Lond).*

<https://pubmed.ncbi.nlm.nih.gov/37317783/>

### **Biomarkers and Echocardiographic Predictors of Cardiovascular Outcome in Patients With Chronic Chagas Disease.**

**Mendes VG, Rimolo L, de Lima ACB, Ferreira RR, Oliveira LS, Nisimura LM, Horita SIM, Costa AR, da Silva GMS, Sangenis LHC, Mendes FSNS, Sousa AS, Veloso HH, Holanda MT, Mediano MFF, Waghbi MC, Garzoni LR, Moreira OC, Britto C, Cunha AB, Hasslocher-Moreno AM, Saraiva RM.**

14-06-2023

*J Am Heart Assoc.*

<https://pubmed.ncbi.nlm.nih.gov/37313975/>

### **"Bunch of acai berries sign": a new radiological sign in patients with CNS involvement in Chagas disease.**

**Fonseca APA, de Melo RFQ, Menezes T, Soares CMA, Rodrigues V, Alves RPM, Pincerato RCM, Roca F, da Rocha AJ.**

14-06-2023

*Neuroradiology.*

<https://pubmed.ncbi.nlm.nih.gov/37311984/>

Chagas disease is an infection caused by Trypanosoma cruzi, a parasite endemic in Latin America. Acute involvement of the CNS by Chagas has been considered rare, but presumed reactivation of chronic disease in immunosuppressed patients has been the subject of recent reports. Our objective is to describe the clinical and imaging characteristics of four patients with Chagas disease and CNS involvement, and the patients had to have available MRI and a diagnosis confirmed by biopsy. The imaging findings were similar, highlighting the presence of focal cerebral lesions with hypointensity on T2-WI, and these lesions assume a "bunch of acai berries appearance", a fruit involved in the transmission of T. cruzi. The post Gd T1-WI shows punctate enhancement. Knowledge of this pattern may be crucial to recognize this disease in immunocompromised patients from endemic areas.

### **In vitro activity and mechanism of cell death induction of cyanomethyl vinyl ethers derivatives against Trypanosoma cruzi.**

**Bethencourt-Estrella CJ, Delgado-Hernández S, López-Arencibia A, San Nicolás-Hernández D, Tejedor D, García-Tellado F, Lorenzo-Morales J, Piñero JE.**

31-05-2023

*Int J Parasitol Drugs Drug Resist.*

<https://pubmed.ncbi.nlm.nih.gov/37311268/>

### **Formulation of benznidazole-lipid nanocapsules: Drug release,**

### permeability, biocompatibility, and stability studies.

Arrua EC, Hartwig O, Loretz B, Murgia X, Ho DK, Bastiat G, Lehr CM, Salomón CJ.

10-06-2023

*Int J Pharm.* 2023

<https://pubmed.ncbi.nlm.nih.gov/37307960/>

Benznidazole, a poorly soluble in water drug, is the first-line medication for the treatment of Chagas disease, but long treatment periods at high dosages cause several adverse effects with insufficient activity in the chronic phase. According to these facts, there is a serious need for novel benznidazole formulations for improving the chemotherapy of Chagas disease. Thus, this work aimed to incorporate benznidazole into lipid nanocapsules for improving its solubility, dissolution rate in different media, and permeability. Lipid nanocapsules were prepared by the phase inversion technique and were fully characterized. Three formulations were obtained with a diameter of 30, 50, and 100 nm and monomodal size distribution with a low polydispersity index and almost neutral zeta potential. Drug encapsulation efficiency was between 83 and 92% and the drug loading was between 0.66 and 1.04%. Loaded formulations were stable under storage for one year at 4 °C. Lipid nanocapsules were found to protect benznidazole in simulated gastric fluid and provide a sustained release platform for the drug in a simulated intestinal fluid containing pancreatic enzymes. The small size and the almost neutral surface charge of these lipid nanocarriers improved their penetration through mucus and such formulations showed a reduced chemical interaction with gastric mucin glycoproteins. LNCs. The incorporation of benznidazole in lipid nanocapsules improved the drug permeability across intestinal epithelium by 10-fold compared with the non-encapsulated drug while the exposure of the cell monolayers to these nanoformulations did not affect the integrity of the epithelium.

### Valorizing Constituents of Cashew Nut Shell Liquid toward the Sustainable Development of New Drugs against Chagas Disease.

Nunes Lemes LF, Magoulas GE, Souza de Oliveira A, Barrias E, de Camargo Nascente L, Granado R, Teixeira de Macedo Silva S, Assimomytis N, de Souza W, Bolognesi ML, Romeiro LAS, Calogeropoulou T.

12-06-2023

*ACS Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37307287/>

Six new ether phospholipid analogues encompassing constituents from cashew nut shell liquid as the lipid portion were synthesized in an effort to valorize byproducts of the cashew industry toward the generation of potent compounds against Chagas disease. Anacardic acids, cardanols, and cardols were used as the lipid portions and choline as the polar headgroup. The compounds were evaluated for their *in vitro* antiparasitic activity against different developmental stages of *Trypanosoma cruzi*. Compounds **16** and **17** were found to be the most potent against *T. cruzi* epimastigotes,

trypomastigotes, and intracellular amastigotes exhibiting selectivity indices against the latter 32-fold and 7-fold higher than current drug benznidazole, respectively. Hence, four out of six analogues can be considered as hit-compounds toward the sustainable development of new treatments for Chagas disease, based on inexpensive agro-waste material.

### The macrophage infectivity potentiator of *Trypanosoma cruzi* induces innate IFN- $\gamma$ and TNF- $\alpha$ production by human neonatal and adult blood cells through TLR2/1 and TLR4.

Ait Djebbara S, Mcheik S, Percier P, Segueni N, Poncelet A, Truyens C.

26-05-2023

*Front Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/37304288/>

### Correction: N-glycosylation modulates enzymatic activity of *Trypanosoma congolense* trans-sialidase.

Rosenau J, Grothaus IL, Yang Y, Kumar ND, Ciacchi LC, Kelm S, Waespy M.

09-06-2023

*J Biol Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37302382/>

### First identification of *Tyrophagus curvipenis* (Acari: Acaridae) and pathogen detection in *Apis mellifera* colonies in the Republic of Korea.

Nguyen TT, Yoo MS, Truong AT, Lee JH, Youn SY, Lee SJ, Kim DH, Yoon SS, Cho YS.

10-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37301922/>

Mites of the genus *Tyrophagus* (Acari: Acaridae) are among the most widely distributed mites. The species in this genus cause damage to stored products and crops, and pose a threat to human health. However, the influence of *Tyrophagus* spp. in apiculture remains unknown. In 2022, a study focusing on the identification of *Tyrophagus* species within five apiaries was conducted in Chungcheongnam Province, Republic of Korea. Its specific objective was to investigate the presence of *Tyrophagus* mites in response to the reported high mortality of honey bee colonies in this area. Morphological identification and phylogenetic analysis using the mitochondrial gene cytochrome-c oxidase subunit 1 (CO1) confirmed for the first time the presence of the mite species *Tyrophagus curvipenis* in a honey bee colony in the Republic of Korea. Two honey bee pathogens were detected in the mite, a viral pathogen (deformed wing virus, DWV) and a protozoal pathogen (*Trypanosoma* spp.). The presence of the two honey bee pathogens in the mite suggests that this mite could contribute to the spread of related honey bee diseases. However, the direct influence of the mite *T. curvipenis* on honey bee health remains unknown and should be further investigated.

### **Oxidative stress evaluation in patients with chronic Chagas disease.**

de Carvalho FCT, de Oliveira LRC, Gatto M, Tasca KI, da Silva LDM, Dos Santos KC, Pierine DT, da Costa EAPN, Francisqueti-Ferron FV, Dos Santos RM, Camacho CRC.

08-06-2023

*Parasitol Int.*

<https://pubmed.ncbi.nlm.nih.gov/37301364/>

### **Barbellatanic acid, a new antitrypanosomal pseudo-disquiterpenoid isolated from *Nectandra barbellata*, displayed interaction with protozoan cell membrane.**

Londero VS, Rosa ME, Baitello JB, Costa-Silva TA, Cruz LMS, Tempone AG, Caseli L, Lago JHG.

08-06-2023

*Biochim Biophys Acta Biomembr.*

<https://pubmed.ncbi.nlm.nih.gov/37301246/>

As part of our ongoing studies involving the discovery of new natural prototypes with antiprotozoal activity against *Trypanosoma cruzi* from Brazilian plant species, the chromatographic fractionation of hexane extract from leaves of *Nectandra barbellata* afforded one new pseudo-disquiterpenoid, barbellatanic acid. The structure of this compound was elucidated by NMR and HR-ESIMS data analysis. Barbellatanic acid displayed a trypanocidal effect with  $IC_{50}$  of 13.2  $\mu$ M to trypomastigotes and no toxicity against NCTC cells ( $CC_{50} > 200 \mu$ M), resulting in an SI value higher than 15.1. The investigation of the lethal mechanism of barbellatanic acid in trypomastigotes, using both fluorescence microscopy and spectrofluorimetric analysis, revealed a time-dependent permeation of the plasma membrane. Based on these results, this compound was incorporated in cellular membrane models built with lipid Langmuir monolayers. The interaction of barbellatanic acid with the models was inferred by tensiometric, rheological, spectroscopical, and morphological techniques, which showed that this compound altered the thermodynamic, viscoelastic, structural, and morphological properties of the film. Taking together, these results could be employed when this prodrug interacts with lipidic interfaces, such as protozoa membranes or liposomes for drug delivery systems.

### **Piplartine-Inspired 3,4,5-Trimethoxycinnamates: Trypanocidal, Mechanism of Action, and In Silico Evaluation.**

Filho CSMB, de Menezes RRPPB, Magalhães EP, Castillo YP, Martins AMC, de Sousa DP.

02-06-2023

*Molecules.*

<https://pubmed.ncbi.nlm.nih.gov/37298988/>

Chagas disease (CD) is one of the main neglected tropical diseases that promote relevant socioeconomic impacts in several countries. The therapeutic options for the treatment of CD are limited, and parasite resistance has

been reported. Piplartine is a phenylpropanoid imide that has diverse biological activities, including trypanocidal action. Thus, the objective of the present work was to prepare a collection of thirteen esters analogous to pipilartine (1-13) and evaluate their trypanocidal activity against *Trypanosoma cruzi*. Of the tested analogues, compound **11** ((*E*)-furan-2-ylmethyl 3-(3,4,5-trimethoxyphenyl)acrylate) showed good activity with  $IC_{50}$  values =  $28.21 \pm 5.34 \mu$ M and  $47.02 \pm 8.70 \mu$ M, against the epimastigote and trypomastigote forms, respectively. In addition, it showed a high rate of selectivity to the parasite. The trypanocidal mechanism of action occurs through the induction of oxidative stress and mitochondrial damage. In addition, scanning electron microscopy showed the formation of pores and leakage of cytoplasmic content. Molecular docking indicated that **11** probably produces a trypanocidal effect through a multi-target mechanism, including affinity with proteins CRK1, MPK13, GSK3B, AKR, UCE-1, and UCE-2, which are important for the survival of the parasite. Therefore, the results suggest chemical characteristics that can serve for the development of new trypanocidal prototypes for researching drugs against Chagas disease.

### **Pharmacological potential of new metronidazole/eugenol/dihydroeugenol hybrids against *Trypanosoma cruzi* in vitro and in vivo.**

Gonçalves-Santos E, Caldas IS, Fernandes VÂ, Franco LL, Pelozo MF, Feltrim F, Maciel JS, Machado JVC, Gonçalves RV, Novaes RD.

07-06-2023

*Int Immunopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37295025/>

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## **Ulcère de Buruli**

### **Memory B-cells are enriched in the blood of patients with acute Buruli ulcer disease: a prospective observational study.**

Adjei JK, Aniagyei W, Adankwah E, Seyfarth J, Mayatepek E, Berko DA, Ackam N, Annani-Akollor ME, Sakyi SA, Amoako YA, Owusu D, Jacobsen M, Phillips RO.

12-06-2023

*BMC Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37308884/>

**Background:** Buruli ulcer disease (BUD) caused by *Mycobacterium* (M.) ulcerans is characterized by necrotic skin lesions. As for other mycobacterial infections, e.g., tuberculosis, the immune response is important for host protection. B-cells may play a role in antimycobacterial immunity but studies characterizing the B-cell repertoire and memory generation in BUD and during the course of treatment are scarce. **Methods:** We investigated the adaptive immune cell repertoire in children with BUD and healthy matched controls by flow cytometry. Analyses prior to treatment, also in a study group of patients with tuberculosis, as well as three time points during BUD treatment (i.e., week 8, 16, and 32) were performed. In addition, BUD disease severity as well as treatment



response were analysed for association with B-cell repertoire differences. **Results:** Children with BUD had comparable total B- and T-cell proportions but differed largely in B-cell subsets. Memory B-cell ( $B_{\text{mem}}$ ) proportions were higher in children with BUD whereas regulatory B-cell ( $B_{\text{reg}}$ ) proportions were lower as compared to healthy controls and tuberculosis patients. Lower naïve ( $B_{\text{naïve}}$ ) and higher transitional B-cell ( $B_{\text{trans}}$ ) proportions characterized children with BUD in comparison with tuberculosis patients. Under treatment,  $B_{\text{mem}}$  proportions decreased significantly whereas proportions of  $B_{\text{reg}}$  and  $B_{\text{naïve}}$  increased concomitantly in children with BUD. Also, we found significant correlation between lesion size and  $B_{\text{mem}}$  as well as  $B_{\text{reg}}$ . However, we did not detect associations between treatment efficacy and B-cell proportions. **Conclusions:** These results suggest a role of B-cell subsets in the immune response against *M. ulcerans*. Furthermore, changes in B-cell subset proportions may be used as markers for treatment monitoring in BUD.

### Immune Targeting of Mycobacteria through Cell Surface Glycan Engineering.

Dzigba P, Rylski AK, Angera IJ, Banahene N, Kavunja HW, Greenlee-Wacker MC, Swarts BM.

12-06-2023

*ACS Chem Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37306676/>