



## **Veille scientifique**

### **Maladies tropicales négligées**

**Semaine 5**  
*19 au 25 juin 2023*

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## Cysticercose

### Triplex ELISA for Assessing Durability of *Taenia solium* Seropositivity after Neurocysticercosis Cure.

Tang NL, Nash TE, Corda M, Nutman TB, O'Connell EM.  
Juil-2023

*Emerg Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37347506/>

Neurocysticercosis prevalence estimates often are based on serosurveys. However, assessments of *Taenia solium* seropositivity durability in patients with various neurocysticercosis types are lacking. We optimized a triplex serologic ELISA by using synthetic GP50, T24H, and Ts18var3 antigens for *T. solium*. We used that assay to test sequential serologic responses over several years after neurocysticercosis cure in 46 patients, 9 each with parenchymal or ventricular neurocysticercosis and 28 with subarachnoid disease. Triplex results were concordant with 98% of positive and 100% of negative enzyme-linked immunoelectrotransfer blots. Eight years after neurocysticercosis cure, 11.1% of patients with parenchymal, 47.3% with subarachnoid, and 41.7% with ventricular disease were still seropositive. Median time to seroreversion after cure in this cohort in a *T. solium* nonendemic area was 2 years for parenchymal disease, 4 years for ventricular disease, and 8 years for subarachnoid disease. Our findings can inform epidemiologic models that rely on serosurveys to estimate disease burden.

### In Vitro and In Vivo Cysticidal Effects of *Carica Papaya* Cell Suspensions.

Guzmán C, Villalobos N, Ortiz Caltempa A, Hernández M, Núñez G, Salazar J, Bobes RJ, Fragoso G, Sciutto E, Villarreal ML.

21-06-2023

*Infect Immun.*

<https://pubmed.ncbi.nlm.nih.gov/37341599/>

### Subcutaneous *Taenia crassiceps* Cysticercosis in a Ring-Tailed Lemur (*Lemur catta*) in a Serbian Zoo.

Simin S, Vračar V, Kozoderović G, Stevanov S, Alić A, Lalošević D, Lalošević V.

Juin-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37099074/>

### Cysticercosis & Heart: A Systematic Review.

García-Martínez CE, Scatularo CE, Farina JM, Saldarriaga C, Pérez GE, Wyss F, Spina S, Mendoza I, Lopez Santi R, Martínez-Sellés M, Baranchuk A.

Août-2023

*Curr Probl Cardiol.*

<https://pubmed.ncbi.nlm.nih.gov/35395330/>

Cysticercosis is a parasitic tissue infection caused by larval cysts of the tapeworm *Taenia solium*. These larval cysts infect brain, muscle, or other tissue, and are a major cause

of adult-onset seizures in most low-income countries with tropical climate. Prevalence it's around 50 million people. Although cardiovascular system is not the most affected, this disease can also be associated with multiple and randomly distributed cysts in the subpericardium, subendocardium and myocardium in up to 25% of infected patients. Most cardiac cysticercosis' cases are asymptomatic, but it can manifest with ventricular arrhythmias and conduction disorders. Area Covered: The "Neglected Tropical Diseases and other Infectious Diseases affecting the Heart" (NET-Heart project) is an initiative by the Emerging Leaders group of the Interamerican Society of Cardiology to systematically review all these endemic conditions affecting the heart. A systematic review was conducted following preferred reporting items for systematic review and meta-analysis guidelines and including articles published in MEDLINE, ScienceDirect, PubMed and LILACS databases. A total of 41 papers were included in this review. Expert Opinion: In the areas of greatest prevalence, unhealthiness and poverty favor the development of this disease, which highlights the need to establish global health policies that reduce morbidity and mortality, economic losses of the affected population, and health costs related to hospitalizations for cardiovascular involvement. Authors provide an algorithm to evaluate the possibility of Cysticercosis' cardiovascular complications.

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## Dengue, chikungunya et maladie à virus Zika

### Broad-Spectrum Small-Molecule Inhibitors Targeting the SAM-Binding Site of Flavivirus NS5 Methyltransferase.

Samrat SK, Bashir Q, Huang Y, Trieschmann CW, Tharappel AM, Zhang R, Chen K, Zheng YG, Li Z, Li H.

22-06-2023

*ACS Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37348028/>

Flavivirus infections, such as those caused by dengue virus (DENV), West Nile virus (WNV), yellow fever virus (YFV), and Zika virus (ZIKV), pose a rising threat to global health. There are no FDA-approved drugs for flaviviruses, although a small number of flaviviruses have vaccines. For flaviviruses or unknown viruses that may appear in the future, it is particularly desirable to identify broad-spectrum inhibitors. The NS5 protein is regarded as one of the most promising flavivirus drug targets because it is conserved across flaviviruses. In this study, we used FL-NAH, a fluorescent analog of the methyl donor *S*-adenosyl methionine (SAM), to develop a fluorescence polarization (FP)-based high throughput screening (HTS) assay to specifically target methyltransferase (MTase), a vital enzyme for flaviviruses that methylates the N7 and 2'-O positions of the viral 5'-RNA cap. Pilot screening identified two candidate MTase inhibitors, NSC 111552 and 288387. The two compounds inhibited the FL-NAH binding to the DENV3 MTase with low micromolar IC<sub>50</sub>. Functional assays verified the inhibitory potency of these molecules for the flavivirus MTase activity. Binding studies indicated that

these molecules are bound directly to the DENV3 MTase with similar low micromolar affinity. Furthermore, we showed that these compounds greatly reduced ZIKV replication in cell-based experiments at dosages that did not cause cytotoxicity. Finally, docking studies revealed that these molecules bind to the SAM-binding region on the DENV3 MTase, and further mutagenesis studies verified residues important for the binding of these compounds. Overall, these compounds are innovative and attractive candidates for the development of broad-spectrum inhibitors for the treatment of flavivirus infections.

### Reemergence of Dengue Virus Serotype 3, Brazil, 2023.

Naveca FG, Santiago GA, Maito RM, Ribeiro Meneses CA, do Nascimento VA, de Souza VC, do Nascimento FO, Silva D, Mejía M, Gonçalves L, de Figueiredo RMP, Ribeiro Cruz AC, Diniz Nunes BT, Presibella MM, Quallio Marques NF, Riediger IN, de Mendonça MCL, de Bruycker-Nogueira F, Sequeira PC, de Filippis AMB, Resende P, Campos T, Wallau GL, Gräf T, Delatorre E, Kopp E, Morrison A, Muñoz-Jordán JL, Bello G.

Jul-2023

*Emerg Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37347884/>

### Singapore's 5 decades of dengue prevention and control-Implications for global dengue control.

Ho SH, Lim JT, Ong J, Hapuarachchi HC, Sim S, Ng LC.

22-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37347767/>

This paper summarises the lessons learnt in dengue epidemiology, risk factors, and prevention in Singapore over the last half a century, during which Singapore evolved from a city of 1.9 million people to a highly urban globalised city-state with a population of 5.6 million. Set in a tropical climate, urbanisation among green foliage has created ideal conditions for the proliferation of *Aedes aegypti* and *Aedes albopictus*, the mosquito vectors that transmit dengue. A vector control programme, largely for malaria, was initiated as early as 1921, but it was only in 1966 that the Vector Control Unit (VCU) was established to additionally tackle dengue haemorrhagic fever (DHF) that was first documented in the 1960s. Centred on source reduction and public education, and based on research into the bionomics and ecology of the vectors, the programme successfully reduced the Aedes House Index (HI) from 48% in 1966 to <5% in the 1970s. Further enhancement of the programme, including through legislation, suppressed the Aedes HI to around 1% from the 1990s. The current programme is characterised by 4 key features: (i) proactive inter-epidemic surveillance and control that is stepped up during outbreaks; (ii) risk-based prevention and intervention strategies based on advanced data analytics; (iii) coordinated inter-sectoral cooperation between the public, private, and people sectors; and (iv) evidence-based adoption of new tools and strategies. Dengue seroprevalence and force of infection (FOI) among

residents have substantially and continuously declined over the 5 decades. This is consistent with the observation that dengue incidence has been delayed to adulthood, with severity highest among the elderly. Paradoxically, the number of reported dengue cases and outbreaks has increased since the 1990s with record-breaking epidemics. We propose that Singapore's increased vulnerability to outbreaks is due to low levels of immunity in the population, constant introduction of new viral variants, expanding urban centres, and increasing human density. The growing magnitude of reported outbreaks could also be attributed to improved diagnostics and surveillance, which at least partially explains the discord between rising trend in cases and the continuous reduction in dengue seroprevalence. Changing global and local landscapes, including climate change, increasing urbanisation and global physical connectivity are expected to make dengue control even more challenging. The adoption of new vector surveillance and control tools, such as the Gravitrap and Wolbachia technology, is important to impede the growing threat of dengue and other Aedes-borne diseases.

### Serum ferritin level as a prognostic biomarker for predicting dengue disease severity: A systematic review and meta-analysis.

Shukla S, Jadhav SM, Gurav YK, Parashar D, Alagarasu K.

22-06-2023

*Rev Med Virol.*

<https://pubmed.ncbi.nlm.nih.gov/37347209/>

Serum ferritin levels serves as biomarkers in many inflammatory and infectious diseases. This current systematic review and meta-analysis evaluated whether serum ferritin levels are associated with severe dengue and its utility as a biomarker of disease severity. Literature searches were conducted in PubMed, Scopus, ScienceDirect, the Cochrane library, and Google Scholar. A total of 18 studies examining the serum ferritin levels in dengue cases in the context of disease severity (nine studies having dengue classification as non-severe vs. severe dengue cases, and nine studies having dengue classification as dengue without warning signs (DwoWS), dengue with warning signs (DwWS), and severe dengue cases) were included and the quality of the studies was assessed using the Quality in Prognostic Factor Studies tool. The meta-analysis was performed using STATA software to calculate the effect size as a standardized mean difference (SMD) or Hedges 'g' for the continuous outcome. Higher serum ferritin levels were found in severe dengue cases compared to non-severe cases [SMD (Hedges 'g') 4.05 (95% C.I. 2.09-6.00), ( $I^2 = 98.8\%$ )]. In the second group, DwWS cases showed high serum ferritin levels compared to DwoWS [SMD 2.01 (95% C.I. 0.92-3.10), ( $I^2 = 97.89\%$ )], and severe dengue cases showed higher levels of serum ferritin compared to DwWS [SMD 2.66 (95% C.I. 1.72-4.48), ( $I^2 = 98.78\%$ )] and DwoWS cases [SMD 6.65 (95% C.I. 1.72-11.59), ( $I^2 = 99.78\%$ )]. Subgroup analysis for the country of study (India vs. others), ferritin testing methods, and ferritin measurement day revealed testing method as a significant contributor to heterogeneity. To conclude, the present study suggests

serum ferritin as a prognostic marker for dengue disease severity. Multi-centric studies involving a large number of dengue patients with a uniform case definition accounting for all the confounding variables might help in determining a universal cut-off value to discriminate between non-severe and severe dengue.

### **Peru's health minister resigns as country reels from worst dengue outbreak in history.**

**Taylor L.**

21-06-2023

*BMJ.*

<https://pubmed.ncbi.nlm.nih.gov/37343965/>

### **Metformin restrains ZIKV replication and alleviates virus-induced inflammatory responses in microglia.**

**Wang X, Wang H, Yi P, Baker C, Casey G, Xie X, Luo H, Cai J, Fan X, Soong L, Hu H, Shi PY, Liang Y, Sun J.**

19-06-2023

*Int Immunopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37343373/>

The re-emergence of Zika virus (ZIKV) remains a major public health threat that has raised worldwide attention. Accumulating evidence suggests that ZIKV can cause serious pathological changes to the human nervous system, including microcephaly in newborns. Recent studies suggest that metformin, an established treatment for diabetes may play a role in viral infection; however, little is known about the interactions between ZIKV infection and metformin administration. Using fluorescent ZIKV by flow cytometry and immunofluorescence imaging, we found that ZIKV can infect microglia in a dose-dependent manner. Metformin diminished ZIKV replication without the alteration of viral entry and phagocytosis. Our study demonstrated that metformin downregulated ZIKV-induced inflammatory response in microglia in a time- and dose-dependent manner. Our RNA-Seq and qRT-PCR analysis found that type I and III interferons (IFN), such as IFN $\alpha$ 2, IFN $\beta$ 1 and IFN $\lambda$ 3 were upregulated in ZIKV-infected cells by metformin treatment, accompanied with the downregulation of GBP4, OAS1, MX1 and ISG15. Together, our results suggest that metformin-mediated modulation in multiple pathways may attribute to restraining ZIKV infection in microglia, which may provide a potential tool to consider for use in unique clinical circumstances.

### **Amid Paraguay Chikungunya Outbreak, Vaccine Candidate Safe, Immunogenic.**

**Harris E.**

21-06-2023

*JAMA.*

<https://pubmed.ncbi.nlm.nih.gov/37342059/>

### **Travel vaccines-priorities determined by incidence and impact.**

**Steffen R, Chen LH, Leggat PA.**

21-06-2023

*J Travel Med.*

<https://pubmed.ncbi.nlm.nih.gov/37341307/>

### **Viral evasion of the interferon response at a glance.**

**Zhu J, Chiang C, Gack MU.**

15-06-2023

*J Cell Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37341132/>

Re-emerging and new viral pathogens have caused significant morbidity and mortality around the world, as evidenced by the recent monkeypox, Ebola and Zika virus outbreaks and the ongoing COVID-19 pandemic. Successful viral infection relies on tactical viral strategies to derail or antagonize host innate immune defenses, in particular the production of type I interferons (IFNs) by infected cells. Viruses can thwart intracellular sensing systems that elicit IFN gene expression (that is, RIG-I-like receptors and the cGAS-STING axis) or obstruct signaling elicited by IFNs. In this Cell Science at a Glance article and the accompanying poster, we review the current knowledge about the major mechanisms employed by viruses to inhibit the activity of intracellular pattern-recognition receptors and their downstream signaling cascades leading to IFN-based antiviral host defenses. Advancing our understanding of viral immune evasion might spur unprecedented opportunities to develop new antiviral compounds or vaccines to prevent viral infectious diseases.

### **Inhibitory effect of $\beta$ -escin on Zika virus infection through the interruption of viral binding, replication, and stability.**

**Lai ZZ, Shen HH, Lee YM.**

30-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37340032/>

### **Dietary Patterns and Anti-Flavivirus IgG Seroconversion in Colombian Children.**

**Arjomand T, Herrán OF, Mantilla LC, Estupiñán MI, Lozano-Parra A, Gelvez RM, Herrera VM, Villar LA, Villamor E.**

20-06-2023

*Am J Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/37339760/>

The burden of flaviviral infections, especially dengue and Zika, is high in the Americas. Malnutrition affects the risk and response to infections, but the role of diet on flaviviral infection risk is uncertain. The objective of this study was to investigate the relations between dietary patterns adherence and anti-flavivirus IgG seroconversion in children during a Zika epidemic in a dengue-endemic area of Colombia. In 2015-2016, we followed 424 anti-flavivirus IgG seronegative children aged 2 to 12 years for 1 year. Baseline data included children's sociodemographic, anthropometric, and dietary information collected through a 38-item food frequency questionnaire (FFQ). IgG testing was repeated at the end of follow-up. The primary exposure was adherence to each of four dietary

patterns (animal foods, traditional, ultraprocessed foods, and prudent) that were identified from the FFQ through principal component analysis. Secondary exposures were intake frequencies of foods contributing to relevant patterns. We estimated risk of seroconversion by quartiles of adherence scores and compared them using relative risks (RR) and 95% CI from Poisson regression adjusted for sex, age, and socioeconomic status indicators. Seroconversion risk was 32.1%. Adherence to the traditional pattern was positively related to seroconversion. RR comparing fourth versus first quartiles of adherence was 1.52 (95% CI: 1.04-2.21; P trend = 0.02). Of the most representative foods in this pattern, potato and sugarcane water intake frequencies were related to increased seroconversion risk. In conclusion, adherence to a traditional foods pattern, including potatoes and sugarcane water, was positively associated with anti-flavivirus IgG seroconversion.

### **Modeling the sequence dependence of differential antibody binding in the immune response to infectious disease.**

**Chowdhury R, Taguchi AT, Kelbauskas L, Stafford P, Diehnelt C, Zhao ZG, Williamson PC, Green V, Woodbury NW.**

20-06-2023

*PLoS Comput Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37339137/>

### **Is the presence of mosquitoes an indicator of poor environmental sanitation?**

**Olagunju EA.**

Mars-2023

*J Water Health.*

<https://pubmed.ncbi.nlm.nih.gov/37338318/>

The World Health Organization has designated mosquitoes as the most lethal animal since they are known to spread pathogen-transmitting organisms. Understanding the many environmental elements that contribute to the spread of these vectors is one of the many strategies used to stop them. If there are mosquitoes around people, it may indicate that there is not an appropriate environmental sanitation program in place in the community or region. Environmental sanitation involves improving any elements of the physical environment that could have a negative impact on a person's survival, health, or physical environment. Keywords containing 'Aedes,' 'Culex,' 'Anopheles,' 'dengue,' 'malaria,' 'yellow fever,' 'Zika,' 'West Nile,' 'chikungunya,' 'resident,' 'environment,' 'sanitation,' 'mosquito control,' and 'breeding sites' of published articles on PubMed, Google Scholar, and ResearchGate were reviewed. It was discovered that the general population should be involved in mosquito and mosquito-borne disease control. Collaboration between health professionals and the general population is essential. The purpose of this paper is to increase public awareness of environmental health issues related to diseases carried by mosquitoes.

### **Comparative phylogenetic analysis and transcriptomic profiling of Dengue (DENV-3 genotype I) outbreak in 2021 in Bangladesh.**

**Sarkar MMH, Rahman MS, Islam MR, Rahman A, Islam MS, Banu TA, Akter S, Goswami B, Jahan I, Habib MA, Uddin MM, Mia MZ, Miah MI, Shaikh AA, Khan MS.**

19-06-2023

*Viro J.*

<https://pubmed.ncbi.nlm.nih.gov/37337232/>

### **Study of kaempferol in the treatment of COVID-19 combined with Chikungunya co-infection by network pharmacology and molecular docking technology.**

**Hossain MA, Sohel M, Sultana T, Hasan MI, Khan MS, Kibria KMK, Mahmud SMH, Rahman MH.**

2023

*Inform Med Unlocked.*

<https://pubmed.ncbi.nlm.nih.gov/37346467/>

Chikungunya (CHIK) patients may be vulnerable to coronavirus disease (COVID-19). However, presently there are no anti-COVID-19/CHIK therapeutic alternatives available. The purpose of this research was to determine the pharmacological mechanism through which kaempferol functions in the treatment of COVID-19-associated CHIK co-infection. We have used a series of network pharmacology and computational analysis-based techniques to decipher and define the binding capacity, biological functions, pharmacological targets, and treatment processes in COVID-19-mediated CHIK co-infection. We identified key therapeutic targets for COVID-19/CHIK, including TP53, MAPK1, MAPK3, MAPK8, TNF, IL6 and NFKB1. Gene ontology, molecular and upstream pathway analysis of kaempferol against COVID-19 and CHIK showed that DEGs were confined mainly to the cytokine-mediated signalling pathway, MAP kinase activity, negative regulation of the apoptotic process, lipid and atherosclerosis, TNF signalling pathway, hepatitis B, toll-like receptor signaling, IL-17 and IL-18 signaling pathways. The study of the gene regulatory network revealed several significant TFs including KLF16, GATA2, YY1 and FOXC1 and miRNAs such as let-7b-5p, mir-16-5p, mir-34a-5p, and mir-155-5p that target differential-expressed genes (DEG). According to the molecular coupling results, kaempferol exhibited a high affinity for 5 receptor proteins (TP53, MAPK1, MAPK3, MAPK8, and TNF) compared to control inhibitors. In combination, our results identified significant targets and pharmacological mechanisms of kaempferol in the treatment of COVID-19/CHIK and recommended that core targets be used as potential biomarkers against COVID-19/CHIK viruses. Before conducting clinical studies for the intervention of COVID-19 and CHIK, kaempferol might be evaluated in wet lab tests at the molecular level.

### **'I was terrified for my child': understanding the link between the Dengvaxia® controversy and the measles vaccine hesitancy in Pasay City, Philippines.**

Miras AP, Regencia ZJG, Baja ES.

20-06-2023

*J Public Health (Oxf).*

<https://pubmed.ncbi.nlm.nih.gov/37340460/>

### Public health impact of the spread of *Anopheles stephensi* in the WHO Eastern Mediterranean Region countries in Horn of Africa and Yemen: need for integrated vector surveillance and control.

Al-Eryani SM, Irish SR, Carter TE, Lenhart A, Aljasari A, Montoya LF, Awash AA, Mohammed E, Ali S, Esmail MA, Hussain A, Amran JG, Kayad S, Nouredayem M, Adam MA, Azkoul L, Assada M, Baheshm YA, Eltahir W, Hutin YJ.

19-06-2023

*Malar J.*

<https://pubmed.ncbi.nlm.nih.gov/37337209/>

### Modified vaccinia Ankara-Bavarian Nordic vaccine against mpox in children.

Turtle L, Subramaniam K.

16-06-2023

*Lancet Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37336223/>

### Dengue hepatitis: Incidence, spectrum and outcome.

Prajapati R, Mehta R, Kabrawala M, Nandwani S, Patel N, Sethia M, Magnani K, Tandel R, Kumar A.

19-06-2023

*Indian J Gastroenterol.*

<https://pubmed.ncbi.nlm.nih.gov/37335522/>

**Background and aims:** While dengue infection is common in India, there is scarce information on dengue hepatitis. The aim of this study was to analyze the incidence, spectrum and outcome of dengue hepatitis. **Methods:** We retrospectively analyzed consecutive patients, who had hepatitis among those with dengue infection admitted to two tertiary care hospitals in western India from January 2016 to March 2021. Diagnosis of dengue infection was made by serology. Dengue hepatitis was diagnosed and the severity of dengue was categorized by standard criteria. **Results:** Of 1664 patients admitted with dengue fever during the study period, 199 patients had hepatitis (i.e. incidence of dengue hepatitis was 11.9%). Of the 199 dengue hepatitis patients (age: 29 [13 - 80] years, median [range], 67% males), 100 patients (50%) had severe dengue, 73 (36%) had severe dengue hepatitis, 32 (16%) had dengue shock syndrome and eight (4%) had acute liver failure. Forty-five patients (23%) had acute lung injury and 32 (16%) had acute kidney injury. The dengue hepatitis patients were treated with standard medical care, including vital organ support, as needed-166 (83%) patients survived, while 33 patients (17%) died (cause of death: multi-organ failure: 24 patients, septic shock: nine patients). The presence of shock independently predicted mortality (odds ratio 6.4, 95% confidence interval: 1.2 - 34). Among patients with dengue hepatitis, mortality rate was higher in those with severe dengue (23%), dengue shock syndrome (47%), severe dengue hepatitis (24%) and

acute liver failure (38%). **Conclusion:** In this large series of hospitalized patients with dengue infection, the incidence of dengue hepatitis was 11.9%. Among 199 dengue hepatitis, 17% died; multi-organ failure was the commonest cause for death and death rate was higher in patients with more severe disease. The presence of shock at presentation independently predicted mortality.

### Insulin reduces the transmission potential of chikungunya virus and activates the toll pathway in *Aedes aegypti* mosquitoes.

Rai P, Webb EM, Kang L, Weger-Lucarelli J.

19-06-2023

*Insect Mol Biol.*

<https://pubmed.ncbi.nlm.nih.gov/37334906/>

Chikungunya virus (CHIKV) is an alphavirus that has re-emerged globally over the last two decades and has the potential to become endemic in the United States due to the presence of competent mosquito vectors, *Aedes aegypti* and *Aedes albopictus*. CHIK disease is characterised by fever, rash, and joint pain, and causes chronic debilitating joint pain and swelling in >50% of infected individuals. Given the disease severity caused by CHIKV and the global presence of vectors to facilitate its spread, strategies to reduce viral transmission are desperately needed; however, the human biological factors driving CHIKV transmission are poorly understood. Towards that end, we have previously shown that mosquitoes fed on alphavirus-infected obese mice have reduced infection and transmission rates compared to those fed on infected lean mice despite similar viremia in lean and obese mice. One of the many host factors that increase in obese hosts is insulin, which was previously shown to impact the infection of mosquitoes by several flaviviruses. However, insulin's impact on alphavirus infection of live mosquitoes is unknown and whether insulin influences mosquito-borne virus transmission has not been tested. To test this, we exposed *A. aegypti* mosquitoes to bloodmeals with CHIKV in the presence or absence of physiologically relevant levels of insulin and found that insulin significantly lowered both infection and transmission rates. RNA sequencing analysis on mosquito midguts isolated at 1-day-post-infectious-bloodmeal (dpbm) showed enrichment in genes in the Toll immune pathway in the presence of insulin, which was validated by reverse transcription-quantitative polymerase chain reaction (RT-qPCR). We then sought to determine if the Toll pathway plays a role in CHIKV infection of *Ae. aegypti* mosquitoes; therefore, we knocked down Myd88, a critical immune adaptor molecule for the Toll pathway, in live mosquitoes, and found increased CHIKV infection compared to the mock knockdown control group. Overall, these data demonstrate that insulin reduces CHIKV transmission by *Ae. aegypti* and activates the Toll pathway in mosquitoes, suggesting that conditions resulting in higher serum insulin concentrations may reduce alphavirus transmission. Finally, these studies suggest that strategies to activate insulin or Toll signalling in mosquitoes may be an effective control strategy against medically relevant alphaviruses.

### **Zika virus: Critical crosstalk between pathogenesis, cytopathic effects, and macroautophagy.**

**Bernardo-Menezes LC, Agrelli A, Oliveira ASLE, Azevedo EAN, Morais CNL.**

19-06-2023

*J Cell Biochem.*

<https://pubmed.ncbi.nlm.nih.gov/37334850/>

### **Dengue virus neutralizing antibody: a review of targets, cross-reactivity, and antibody-dependent enhancement.**

**Sarker A, Dhama N, Gupta RD.**

02-06-2023

*Front Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/37334355/>

Dengue is the most common viral infection spread by mosquitoes, prevalent in tropical countries. The acute dengue virus (DENV) infection is a benign and primarily febrile illness. However, secondary infection with alternative serotypes can worsen the condition, leading to severe and potentially fatal dengue. The antibody raised by the vaccine or the primary infections are frequently cross-reactive; however, weakly neutralizing, and during subsequent infection, they may increase the odds of antibody-dependent enhancement (ADE). Despite that, many neutralizing antibodies have been identified against the DENV, which are thought to be useful in reducing dengue severity. Indeed, an antibody must be free from ADE for therapeutic application, as it is pretty common in dengue infection and escalates disease severity. Therefore, this review has described the critical characteristics of DENV and the potential immune targets in general. The primary emphasis is given to the envelope protein of DENV, where potential epitopes targeted for generating serotype-specific and cross-reactive antibodies have critically been described. In addition, a novel class of highly neutralizing antibodies targeted to the quaternary structure, similar to viral particles, has also been described. Lastly, we have discussed different aspects of the pathogenesis and ADE, which would provide significant insights into developing safe and effective antibody therapeutics and equivalent protein subunit vaccines.

### **Exploring the inhibitory potential of *Nigella sativa* against dengue virus NS2B/NS3 protease and NS5 polymerase using computational approaches.**

**Mukhtar M, Khan HA, Zaidi NUSS.**

16-06-2023

*RSC Adv.*

<https://pubmed.ncbi.nlm.nih.gov/37333789/>

### **Dengue in Cambodia 2002-2020: Cases, Characteristics and Capture by National Surveillance.**

**Yek C, Li Y, Pacheco AR, Lon C, Duong V, Dussart P, Chea S, Lay S, Man S, Kimsan S, Huch C, Leang R, Huy R, Brook CE, Manning JE.**

28-04-2023

*medRxiv.*

<https://pubmed.ncbi.nlm.nih.gov/37333247/>

### **Integrative systems biology characterizes immune-mediated neurodevelopmental changes in murine Zika virus microcephaly.**

**Fujimura K, Guise AJ, Nakayama T, Schlaffner CN, Meziani A, Kumar M, Cheng L, Vaughan DJ, Kodani A, Van Haren S, Parker K, Levy O, Durbin AF, Bosch I, Gehrke L, Steen H, Mochida GH, Steen JA.**

19-05-2023

*iScience.*

<https://pubmed.ncbi.nlm.nih.gov/37332674/>

Characterizing perturbation of molecular pathways in congenital Zika virus (ZIKV) infection is critical for improved therapeutic approaches. Leveraging integrative systems biology, proteomics, and RNA-seq, we analyzed embryonic brain tissues from an immunocompetent, wild-type congenital ZIKV infection mouse model. ZIKV induced a robust immune response accompanied by the downregulation of critical neurodevelopmental gene programs. We identified a negative correlation between ZIKV polyprotein abundance and host cell cycle-inducing proteins. We further captured the downregulation of genes/proteins, many of which are known to be causative for human microcephaly, including Eomesodermin/T-box Brain Protein 2 (EOMES/TBR2) and Neuronal Differentiation 2 (NEUROD2). Disturbances of distinct molecular pathways in neural progenitors and post-mitotic neurons may contribute to complex brain phenotype of congenital ZIKV infection. Overall, this report on protein- and transcript-level dynamics enhances understanding of the ZIKV immunopathological landscape through characterization of fetal immune response in the developing brain.

### **Employing Oxford Nanopore Technologies (ONT) for understanding the ecology and transmission dynamics of flaviviruses in mosquitoes (Diptera: Culicidae) from eastern Colombia.**

**Martínez D, Gómez M, De Las Salas JL, Hernández C, Flórez AZ, Muñoz M, Ramírez JD.**

16-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37331645/>

Studies focused on identifying the viral species of Flavivirus in vectors are scarce in Latin America and particularly in Colombia. Therefore, the frequency of infection of the Flavivirus genus and its feeding preferences were identified in the mosquito species circulating in the municipality of Puerto Carreño-Vichada, located in the Eastern Plains of Colombia. This was done by sequencing the viral NS5 and vertebrate 12S rRNA genes, respectively, using Oxford Nanopore Technologies (ONT). A total of 1,159 mosquitoes were captured, with the most abundant species being *Aedes serratus* at 73.6% (n=853). All the mosquitoes were processed in 230 pools (2-6 individuals) and 51 individuals, where 37.01% (n=104)

were found to be infected with Flavivirus. In these samples, infection by arboviruses of epidemiological importance, such as dengue virus (DENV), Zika virus (ZIKV), and chikungunya virus (CHIKV), was ruled out by PCR. However, through sequencing, infection by different insect-specific viruses (ISFVs) and a medically important virus, West Nile virus (WNV), were identified in a mosquito of the *Culex browni* species. Additionally, the feeding patterns showed that most species present a generalist behavior. Given the above, conducting entomovirological surveillance studies is crucial, especially in areas of low anthropogenic intervention, due to the high probability that potentially pathogenic viruses could generate spillover events under deforestation scenarios.

### **Clinical Characteristics and Outcomes Among Travelers With Severe Dengue : A GeoSentinel Analysis.**

Huits R, Angelo KM, Amatya B, Barkati S, Barnett ED, Bottieau E, Emetulu H, Epelboin L, Eperon G, Medebb L, Gobbi F, Grobusch MP, Itani O, Jordan S, Kelly P, Leder K, Díaz-Menéndez M, Okumura N, Rizwan A, Rothe C, Saio M, Waggoner J, Yoshimura Y, Libman M, Hamer DH, Schwartz E.

20-06-2023

*Ann Intern Med.*

<https://pubmed.ncbi.nlm.nih.gov/37335991/>

### **A new cluster of chikungunya virus West Africa genotype isolated from *Aedes albopictus* in China.**

Li N, Peng C, Yuan Y, Hao Y, Ma W, Xiao P.

16-06-2023

*J Infect.*

<https://pubmed.ncbi.nlm.nih.gov/37331428/>

### **An in vitro workflow to create and modify infectious clones using replication cycle reaction.**

Marano JM, Cereghino C, Finkelstein CV, Weger-Lucarelli J.

13-06-2023

*Virology.*

<https://pubmed.ncbi.nlm.nih.gov/37331111/>

### **Crude saliva of *Amblyomma cajennense* sensu stricto (Acari: Ixodidae) reduces locomotor activity and increases the hemocyte number in the females of *Aedes aegypti* (Diptera: Culicidae).**

Cerri F, Araujo MDS, Aguirre AAR, Evaristo GPC, Evaristo JAM, Nogueira FCS, de Medeiros JF, Dias QM.

15-6-2023

*Exp Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37330106/>

### **Amniotic fluid metabolomics identifies impairment of glycerophospholipid and amino acid metabolism during congenital Zika syndrome development.**

Sosa-Acosta P, Evaristo GPC, Evaristo JAM, Carneiro GRA, Quiñones-Vega M, Monnerat G, Melo A, Garcez PP, Nogueira FCS, Domont GB.

17-06-2023

*Proteomics Clin Appl.*

<https://pubmed.ncbi.nlm.nih.gov/37329193/>

### **Investigating the etiology of acute febrile illness: a prospective clinic-based study in Uganda.**

Kigozi BK, Kharod GA, Bukenya H, Shadomy SV, Haberling DL, Stoddard RA, Galloway RL, Tushabe P, Nankya A, Nsibambi T, Mbidde EK, Lutwama JJ, Perniciaro JL, Nicholson WL, Bower WA, Bwogi J, Blaney DD.

16-06-2023

*BMC Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37328808/>

**Background:** Historically, malaria has been the predominant cause of acute febrile illness (AFI) in sub-Saharan Africa. However, during the last two decades, malaria incidence has declined due to concerted public health control efforts, including the widespread use of rapid diagnostic tests leading to increased recognition of non-malarial AFI etiologies. Our understanding of non-malarial AFI is limited due to lack of laboratory diagnostic capacity. We aimed to determine the etiology of AFI in three distinct regions of Uganda. **Methods:** A prospective clinic-based study that enrolled participants from April 2011 to January 2013 using standard diagnostic tests. Participant recruitment was from St. Paul's Health Centre (HC) IV, Ndejje HC IV, and Adumi HC IV in the western, central and northern regions, which differ by climate, environment, and population density. A Pearson's chi-square test was used to evaluate categorical variables, while a two-sample t-test and Kruskal-Wallis test were used for continuous variables. **Results:** Of the 1281 participants, 450 (35.1%), 382 (29.8%), and 449 (35.1%) were recruited from the western, central, and northern regions, respectively. The median age (range) was 18 (2-93) years; 717 (56%) of the participants were female. At least one AFI pathogen was identified in 1054 (82.3%) participants; one or more non-malarial AFI pathogens were identified in 894 (69.8%) participants. The non-malarial AFI pathogens identified were chikungunya virus, 716 (55.9%); Spotted Fever Group rickettsia (SFGR), 336 (26.2%) and Typhus Group rickettsia (TGR), 97 (7.6%); typhoid fever (TF), 74 (5.8%); West Nile virus, 7 (0.5%); dengue virus, 10 (0.8%) and leptospirosis, 2 (0.2%) cases. No cases of brucellosis were identified. Malaria was diagnosed either concurrently or alone in 404 (31.5%) and 160 (12.5%) participants, respectively. In 227 (17.7%) participants, no cause of infection was identified. There were statistically significant differences in the occurrence and distribution of TF, TGR and SFGR, with TF and TGR observed more frequently in the western region ( $p = 0.001$ ;  $p < 0.001$ ) while SFGR in the northern region ( $p < 0.001$ ). **Conclusion:** Malaria, arboviral infections, and rickettsioses are major causes of AFI in Uganda. Development of a Multiplexed Point-of-Care test would help identify the etiology of non-malarial AFI in regions with high AFI rates.

### Neurotoxic properties of the Zika virus envelope protein.

Steiner JP, Bachani M, Malik N, Li W, Tyagi R, Sampson K, Abrams RPM, Kousa Y, Solis J, Johnson TP, Nath A.  
14-06-2023

*Exp Neurol.*

<https://pubmed.ncbi.nlm.nih.gov/37327963/>

Prenatal Zika virus (ZIKV) infection is a serious global concern as it can lead to brain injury and many serious birth defects, collectively known as congenital Zika syndrome. Brain injury likely results from viral mediated toxicity in neural progenitor cells. Additionally, postnatal ZIKV infections have been linked to neurological complications, yet the mechanisms driving these manifestations are not well understood. Existing data suggest that the ZIKV envelope protein can persist in the central nervous system for extended periods of time, but it is unknown if this protein can independently contribute to neuronal toxicity. Here we find that the ZIKV envelope protein is neurotoxic, leading to overexpression of poly adenosine diphosphate -ribose polymerase 1, which can induce parthanatos. Together, these data suggest that neuronal toxicity resulting from the envelope protein may contribute to the pathogenesis of post-natal ZIKV-related neurologic complications.

### Pre-pandemic cross-reactive humoral immunity to SARS-CoV-2 in Africa: systematic review and meta-analysis.

Ioannidis JPA, Contopoulos-Ioannidis DG.

14-06-2023

*Int J Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37327857/>

### Zika virus infection induces expression of NRF2 and antioxidant systems in trophoblast cells.

Cervantes MAV, Martinez JAV, García LDG, Ortega OL, Romero HA, Estrada AM, Castillo MM, Pliego AF, Reyes GL, Repetto ACH, Cordero JG, Juárez ML.

16-06-2023

*Virus Genes.*

<https://pubmed.ncbi.nlm.nih.gov/37326824/>

The nuclear factor erythroid 2-related factor 2 (NRF2) is a transcription factor that plays a critical role in the xenobiotic and stress responses. During viral infection, NRF2 can modulate the host metabolism and innate immunity; however, the most common activity of NRF2 in viral diseases is controlling reactive oxygen species (ROS). The Zika virus (ZIKV) is involved in a vertical infection in pregnancy, with reported fetal health consequences. However, the possibility that ZIKV regulates NRF2 expression in placental trophoblasts has not been investigated. In this report, we evaluated the upregulation of NRF2 and antioxidant enzymes in a trophoblast-like cell. These findings could help us understand the antioxidant mechanism underlying the ZIKV infection in the placenta during pregnancy

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

Akter S, Jin Z.

27-05-2023

*Math Biosci Eng.*

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

### 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/>

### N<sup>6</sup>-methyladenosine is required for efficient RNA synthesis of Ebola virus and other haemorrhagic fever viruses.

Wendt L, Pickin MJ, Bodmer BS, Reiche S, Fénéant L, Höpfer JE, Fuchs W, Groseth A, Hoenen T.

Déc-2023

*Emerg Microbes Infect.*

<https://pubmed.ncbi.nlm.nih.gov/37306620/>

N<sup>6</sup>-methyladenosine (m<sup>6</sup>A) is one of the most abundant modifications of cellular RNA, where it serves various functions. m<sup>6</sup>A methylation of many viral RNA species has also been described; however, little is known about the m<sup>6</sup>A epitranscriptome of haemorrhagic fever-causing viruses like Ebola virus (EBOV). Here, we analysed the importance of the methyltransferase METTL3 for the life cycle of this virus. We found that METTL3 interacts with the EBOV nucleoprotein and the transcriptional activator VP30 to support viral RNA synthesis, and that METTL3 is recruited into EBOV inclusions bodies, where viral RNA synthesis occurs. Analysis of the m<sup>6</sup>A methylation pattern of EBOV mRNAs showed that they are methylated by METTL3. Further studies revealed that METTL3 interaction with the viral nucleoprotein, as well as its importance for RNA synthesis and protein expression, is also observed for other haemorrhagic fever viruses such as Junín virus (JUNV) and Crimean-Congo haemorrhagic fever virus (CCHFV). The negative effects on viral RNA synthesis due to loss of m<sup>6</sup>A methylation are independent of innate immune sensing, as METTL3 knockout did not affect type I interferon induction in response to viral RNA synthesis or infection. Our results suggest a novel function for m<sup>6</sup>A that is conserved among diverse haemorrhagic fever-causing viruses (i.e. EBOV, JUNV and CCHFV), making METTL3 a promising target for broadly-acting antivirals.

### Dengue transmission dynamics prediction by combining metapopulation networks and Kalman filter algorithm.

Zeng Q, Yu X, Ni H, Xiao L, Xu T, Wu H, Chen Y, Deng H, Zhang Y, Pei S, Xiao J, Guo P.

07-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37285385/>

Predicting the specific magnitude and the temporal peak of the epidemic of individual local outbreaks is critical for infectious disease control. Previous studies have indicated that significant differences in spatial transmission and epidemic magnitude of dengue were influenced by multiple factors, such as mosquito population density, climatic conditions, and population movement patterns. However, there is a lack of studies that combine the above factors to explain their complex nonlinear relationships in dengue transmission and generate accurate predictions. Therefore, to study the complex spatial diffusion of dengue, this research combined the above factors and developed a network model for spatiotemporal transmission prediction of dengue fever using metapopulation networks based on human mobility. For improving the prediction accuracy of the epidemic model, the ensemble adjusted Kalman filter (EAKF), a data assimilation algorithm, was used to iteratively assimilate the observed case data and adjust the model and parameters. Our study demonstrated that the metapopulation network-EAKF system provided accurate predictions for city-level dengue transmission trajectories in retrospective forecasts of 12 cities in Guangdong province, China. Specifically, the system accurately predicts local dengue outbreak magnitude and the temporal peak of the epidemic up to 10 wk in advance. In addition, the system predicted the peak time, peak intensity, and total number of dengue cases more accurately than isolated city-specific forecasts. The general metapopulation assimilation framework presented in our study provides a methodological foundation for establishing an accurate system with finer temporal and spatial resolution for retrospectively forecasting the magnitude and temporal peak of dengue fever outbreaks. These forecasts based on the proposed method can be interoperated to better support intervention decisions and inform the public of potential risks of disease transmission.

### **Zika virus RNA persistence and recovery in water and wastewater: An approach for Zika virus surveillance in resource-constrained settings.**

Zhu K, Hill C, Muirhead A, Basu M, Brown J, Brinton MA, Hayat MJ, Venegas-Vargas C, Reis MG, Casanovas-Massana A, Meschke JS, Ko AI, Costa F, Stauber CE.  
01-08-2023  
*Water Res.*  
<https://pubmed.ncbi.nlm.nih.gov/37270953/>

### **Aetiology of Acute Undifferentiated Fever Among Children Under the Age of Five in Vietnam: A Prospective Study.**

Tran XD, Hoang VT, Dang TTD, Vu TP, To MM, Tran TK, Do MD, Nguyen DC, Nguyen QT, Colson P, Parola P, Marty P, Gautret P.  
Juin-2023  
*J Epidemiol Glob Health.*  
<https://pubmed.ncbi.nlm.nih.gov/37258852/>

**Background:** To investigate the aetiology of acute undifferentiated fever (AUF) among children under the

age of five in Vietnam. **Methods:** This prospective study was conducted in the Thai Binh paediatric hospital, between July 2020 and July 2021 among children with AUF at admission. Real-time PCR testing 18 microbial pathogens were done on blood samples. **Results:** 286 children were included, with median age of 16 months. 64.7% were male. 53.9% were positive for at least one pathogen by PCR. Enterovirus, human herpesvirus 6, adenovirus, and varicella zoster virus PCR were positive for 31.1, 12.6, 1.4, and 1.0% patients, respectively. Other pathogens tested negative by PCR. During the hospital stay, based on clinical criteria 47.2% children secondarily presented with signs of respiratory tract infections, 18.9% had hand, foot and mouth disease, 4.6% had chickenpox. 4.2% presented signs of central nervous system infections, 1.0% had dengue (antigenic test) and 1.0% had signs of gastrointestinal infection. Finally, 23.1% patients presented a fever with or without a rash and no other symptoms and ultimately received a diagnosis of AUF. **Conclusion:** Real-time PCR of blood is useful for detecting pathogens and diagnosing infectious causes of AUF. Further prospective studies with blood and urine culture testing and PCR investigation of not only blood but also cerebrospinal fluid, throat, and skin samples according to symptoms would be of interest to confirm the predominance of viral infections in children with AUF and to guide therapeutic options.

### **A booster regime of liposome-delivered live-attenuated CHIKV vaccine RNA genome protects against chikungunya virus disease in mice.**

Rao S, Abeyratne E, Freitas JR, Yang C, Tharmarajah K, Mostafavi H, Liu X, Zaman M, Mahalingam S, Zaid A, Taylor A.  
19-06-202  
*Vaccine.*  
<https://pubmed.ncbi.nlm.nih.gov/37230889/>

### **Comparative Infections of Zika, Dengue, and Yellow Fever Viruses in Human Cytotrophoblast-Derived Cells Suggest a Gating Role for the Cytotrophoblast in Zika Virus Placental Invasion.**

Viettri M, Caraballo G, Sanchez ME, Espejel-Nuñez A, Betanzos A, Ortiz-Navarrete V, Estrada-Gutierrez G, Nava P, Ludert JE.  
15-06-2023  
*Microbiol Spectr.*  
<https://pubmed.ncbi.nlm.nih.gov/37227282/>

The Zika virus (ZIKV) is teratogenic and considered a TORCH pathogen (toxoplasmosis [Toxoplasma gondii], rubella, cytomegalovirus, herpes simplex virus [HSV], and other microorganisms capable of crossing the blood-placenta barrier). In contrast, the related flavivirus dengue virus (DENV) and the attenuated yellow fever virus vaccine strain (YFV-17D) are not. Understanding the mechanisms used by ZIKV to cross the placenta is necessary. In this work, parallel infections with ZIKV of African and Asian lineages, DENV, and YFV-17D were compared for kinetics and growth efficiency, activation of mTOR pathways, and

cytokine secretion profile using cytotrophoblast-derived HTR8 cells and monocytic U937 cells differentiated to M2 macrophages. In HTR8 cells, ZIKV replication, especially the African strain, was significantly more efficient and faster than DENV or YFV-17D. In macrophages, ZIKV replication was also more efficient, although differences between strains were reduced. Greater activation of the mTORC1 and mTORC2 pathways in HTR8 cells infected with ZIKV than with DENV or YFV-17D was observed. HTR8 cells treated with mTOR inhibitors showed a 20-fold reduction in ZIKV yield, versus 5- and 3.5-fold reductions for DENV and YFV-17D, respectively. Finally, infection with ZIKV, but not DENV or YFV-17D, efficiently inhibited the interferon (IFN) and chemoattractant responses in both cell lines. These results suggest a gating role for the cytotrophoblast cells in favoring entry of ZIKV, but not DENV and YFV-17D, into the placental stroma. **IMPORTANCE** Zika virus acquisition during pregnancy is associated with severe fetal damage. The Zika virus is related to dengue virus and yellow fever virus, yet fetal damage has not been related to dengue or inadvertent vaccination for yellow fever during pregnancy. Mechanisms used by the Zika virus to cross the placenta need to be deciphered. By comparing parallel infections of Zika virus strains belonging to the African and Asian lineages, dengue virus, and the yellow fever vaccine virus strain YFV-17D in placenta-derived cytotrophoblast cells and differentiated macrophages, evidence was found that Zika virus infections, especially by the African strains, were more efficient in cytotrophoblast cells than dengue virus or yellow fever vaccine virus strain infections. Meanwhile, no significant differences were observed in macrophages. Robust activation of the mTOR signaling pathways and inhibition of the IFN and chemoattractant response appear to be related to the better growth capacity of the Zika viruses in the cytotrophoblast-derived cells.

### Dengue fever: the impact of increasing temperatures and heatwaves.

Frentiu FD.

Juin-2023

EBioMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37182266/>

### The Conundrum of Differentiating MIS-C from Dengue and Other Tropical Infections.

Singhal T.

Juil-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37165252/>

### Prevalence and Risk Factors of Acute Kidney Injury in Hospitalized Children with Dengue Infection Using Kidney Disease Improving Global Outcomes Criteria: Authors' Reply.

Mekangkul E, Siripen N, Rianthavorn P.

Juil-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37133750/>

### Prevalence and Risk Factors of Acute Kidney Injury in Hospitalized Children with Dengue Infection Using Kidney Disease Improving Global Outcomes Criteria: Correspondence.

Sookaromdee P, Wiwanitkit V.

Juil-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37097535/>

### Hydration and clinical warning signs of dengue fever in primary care: An observational prospective study.

Besnard O, Maillard O, Franco JM, Lebreton N, Reix G, Legrand F, Bertolotti A, Leruste S.

Juin-2023

Infect Dis Now.

<https://pubmed.ncbi.nlm.nih.gov/37054972/>

**Objectives:** Dengue fever is an arbovirus expanding worldwide, for which hydration has been reported to reduce the risk of hospitalization. Our objective was to estimate the volume of hydration in Reunionese patients with dengue. **Methods:** A prospective observational study included patients presenting with a 'dengue-like' syndrome in ambulatory care. General practitioners recruited patients during consultation, and beverage consumption over the previous 24 hours was reported at two different times. Warning signs were defined according to the 2009 WHO guidelines. **Results:** GPs included 174 patients from April to July 2019. Average oral hydration volume was 1863 mL and 1944 mL, at the 1st and 2nd medical consultations, respectively. Water was the most wide consumed liquid. Drinking at least 5 glasses of liquid was significantly associated with fewer clinical warning signs at the 1st medical consultation ( $p = 0.044$ ). **Conclusions:** Sufficient hydration volume could prevent dengue warning signs. Further studies with standardized measurement of hydration would be needed.

### The First Genomic Characterization of the Chikungunya Virus in Saudi Arabia.

Alguridi HI, Alzahrani F, Altayb HN, Almalki S, Zaki E, Algarni S, Assiri A, Memish ZA.

Juin-2023

J Epidemiol Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37029884/>

### ASFV transcription reporter screening system identifies ailanthone as a broad antiviral compound.

Zhang Y, Zhang Z, Zhang F, Zhang J, Jiao J, Hou M, Qian N, Zhao D, Zheng X, Tan X.

Juin-2023

Viol Sin.

<https://pubmed.ncbi.nlm.nih.gov/36948461/>

African swine fever (ASF) is an acute, highly contagious and deadly viral disease in swine that jeopardizes the worldwide pig industry. Unfortunately, there are no authoritative vaccine and antiviral drug available for ASF control. African swine fever virus (ASFV) is the etiological

agent of ASF. Among the ASFV proteins, p72 is the most abundant component in the virions and thus a potential target for anti-ASFV drug design. Here, we constructed a luciferase reporter system driven by the promoter of p72, which is transcribed by the co-transfected ASFV RNA polymerase complex. Using this system, we screened over 3200 natural product compounds and obtained three potent candidates against ASFV. We further evaluated the anti-ASFV effects and proved that among the three candidates, ailanthone (AIL) inhibits the replication of ASFV at the nanomolar concentration ( $IC_{50} = 15 \text{ nmol/L}$ ). Our in vitro experiments indicated that the antiviral effect of AIL is associated with its inhibition of the HSP90-p23 cochaperone. Finally, we showed the antiviral activity of AIL on Zika virus and hepatitis B virus (HBV), which supports that AIL is a potential broad-spectrum antiviral agent.

### Toward a global virus genomic surveillance network.

Hill V, Githinji G, Vogels CBF, Bento AI, Chaguza C, Carrington CVF, Grubaugh ND.

14-06-2023

*Cell Host Microbe*.

<https://pubmed.ncbi.nlm.nih.gov/36921604/>

### Nonparametric estimation of the causal effect of a stochastic threshold-based intervention.

van der Laan L, Zhang W, Gilbert PB.

Juin-2023

*Biometrics*.

<https://pubmed.ncbi.nlm.nih.gov/35526218/>

### Dengue in Myanmar: Spatiotemporal epidemiology, association with climate and short-term prediction.

Zaw W, Lin Z, Ko Ko J, Rotejanaprasert C, Pantanilla N, Ebener S, Maude RJ.

05-06-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/37276226/>

### Comparison of Multisystem Inflammatory Syndrome (MIS-C) and Dengue in Hospitalized Children.

Randhawa MS, Angurana SK, Nallasamy K, Kumar M, Ravikumar N, Awasthi P, Ghosh A, Ratho RK, Minz RW, Kumar RM, Bansal A, Jayashree M.

Juil-2023

*Indian J Pediatr*.

<https://pubmed.ncbi.nlm.nih.gov/35511400/>

**Objective:** Multisystem inflammatory syndrome (MIS-C) in children is a febrile illness that has overlapping presentation with other locally prevalent illnesses. Clinicolaboratory profile of children admitted with MIS-C and dengue were compared to understand their presentation at the outset. **Methods:** This was a retrospective study of children  $\leq 12$  y admitted with MIS-C (WHO definition) or laboratory-confirmed dengue

between August 2020 and January 2021 at a tertiary center in North India. **Results:** A total of 84 children (MIS-C - 40; dengue - 44) were included. The mean (SD) age [83.5 (39) vs. 91.6 (35) mo] was comparable. Rash (72.5% vs. 22.7%), conjunctival injection (60% vs. 2.3%), oral mucocutaneous changes (27.5% vs. 0) and gallop rhythm (15% vs. 0) were seen more frequently with MIS-C, while petechiae [29.5% vs. 7.5%], myalgia (38.6% vs. 10%), headache (22.7% vs. 2.5%), and hepatomegaly (68.2% vs. 27.5%) were more common with dengue. Children with MIS-C had significantly higher C-reactive protein (124 vs. 3.2 mg/L) and interleukin 6 (95.3 vs. 20.7 ng/mL), while those with dengue had higher hemoglobin (12 vs. 10.2 g/dL) lower mean platelet count ( $26$  vs.  $140 \times 10^9/L$ ), and greater elevation in aspartate (607 vs. 44 IU/L) and alanine (235.5 vs. 56 IU/L) aminotransferases. The hospital stay was longer with MIS-C; however, PICU stay and mortality were comparable. **Conclusion:** In hospitalized children with acute febrile illness, the presence of mucocutaneous features and highly elevated CRP could distinguish MIS-C from dengue. The presence of petechiae, hepatomegaly, and hemoconcentration may favor a diagnosis of dengue.

### Self-replicating vehicles based on negative strand RNA viruses.

Lundstrom K.

Juin-2023

*Cancer Gene Ther*.

<https://pubmed.ncbi.nlm.nih.gov/35169298/>

## Dracunculose

### Patterns and drivers of heat production in the plant genus *Amorphophallus*.

Claudel C, Loiseau O, Silvestro D, Lev-Yadun S, Antonelli A.

20-06-2023

*Plant J*.

<https://pubmed.ncbi.nlm.nih.gov/37340521/>

### Removal of benzotriazole micropollutants using *Spirodela polyrhiza* (L.) Schleid. And *Azolla caroliniana* Willd.

Polińska W, Kotowska U, Karpińska J, Piotrowska-Niczyporuk A.

01-09-2023

*Environ Pollut*.

<https://pubmed.ncbi.nlm.nih.gov/37301460/>

### Constructed wetlands and duckweed ponds as a treatment step in liquid manure handling - A life cycle assessment.

Beyers M, Ravi R, Devlamynck R, Meers E, Jensen LS, Bruun S.

01-09-2023

*Sci Total Environ*.

<https://pubmed.ncbi.nlm.nih.gov/37149194/>

Life cycle assessment (LCA) was applied to evaluate duckweed ponds and constructed wetlands as polishing steps in pig manure liquid fraction treatment. Using nitrification-denitrification (NDN) of the liquid fraction as the starting point, the LCA compared direct land application of the NDN effluent with different combinations of duckweed ponds, constructed wetlands and discharge into natural waterbodies. Duckweed ponds and constructed wetlands are viewed as a viable tertiary treatment option and potential remedy for nutrient imbalances in areas of intense livestock farming, such as in Belgium. As the effluent stays in the duckweed pond, settling and microbial degradation reduce the remaining phosphorous and nitrogen concentrations. Combined with duckweed and/or wetland plants that take up nutrients in their plant body, this approach can reduce over-fertilisation and prevent excessive nitrogen losses to aquatic environments. In addition, duckweed could serve as an alternative livestock feed and replace imports of protein destined for animal consumption. The environmental performance of the overall treatment systems studied was found to depend greatly on assumptions about the possible avoidance of potassium fertiliser production through the field application of effluents. If it is assumed that the potassium contained in the effluent replaces mineral fertiliser, direct field application of the NDN effluent performed best. If the application of NDN effluent does not lead to mineral fertiliser savings or if the replaced K fertiliser is of low grade, duckweed ponds seem to be a viable additional step in the manure treatment chain. Consequently, whenever background concentrations of N and/or P in fields allow for effluent application and potassium fertiliser substitution, direct application should be favoured over further treatment. If direct land application of the NDN effluent is not an option, the focus should be on long residence times in duckweed ponds to allow for maximum nutrient uptake and feed production.

### **Revealing the mechanisms of *Arisaema cum Bile* on allergic asthma with systematic pharmacology approach-experimental validation.**

**Wu X, Wang J, Zou T, He SR, Zhong L, Zhang Q, Song YJ, Wang CL, Zhao CB.**

Jul-2023

*Fitoterapia.*

<https://pubmed.ncbi.nlm.nih.gov/37121408/>

*Arisaema cum Bile* (Dan Nanxing in Chinese, DNX) have been employed to treat allergic asthma. However, the active components and its mechanisms remain unknown. Therefore, the systematic pharmacology approach-experimental validation was performed in this study. Each 5, 6, and 10 compounds of DNX were obtained by HPLC analysis, TCMSP, and literature report, respectively. A total of 379 targets on all these compounds were acquired from Swiss Target Prediction, and 1973 targets on allergic asthma were predicated. The KEGG enrichment analysis was performed. Furthermore, a rat model of allergic asthma was established and DNX (450 mg/kg, p.o.) was given for 2 weeks. DNX treatment prevented OVA-induced pathological changes in lung cell of irregular arrange and

necrotic bronchial epithelial. It also decreased inflammatory cytokines IL-4, IL-5, and IL-13 of serum and BALF, and increased IL-12 and IFN- $\gamma$ . The main MAPK signaling pathway predicted by KEGG enrichment was verified, as indicated by the decreased protein expression of JNK ( $p < 0.05$  &  $p < 0.01$ ), ERK ( $p < 0.05$ ), and p38 MAPK ( $p < 0.01$ ) in lung tissue. These findings indicated that DNX attenuated OVA-induced allergic asthma mainly by decreasing the MAPK signaling pathway.

## **Echinococcosis**

### **Endobronchial hydatid cyst causing variable intrathoracic airflow limitation selectively during expiration acting as a ball valve.**

**Dammalapati PK, Kar SK, Dasgupta CS.**

Jul-2023

*Indian J Thorac Cardiovasc Surg.*

<https://pubmed.ncbi.nlm.nih.gov/37346445/>

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

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

12-06-2023

*Pathol Res Pract.*

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

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

was treated with albendazole and at the six-month follow-up he was in good clinical conditions. Our case highlights the importance of considering rare infections, particularly in individuals from endemic areas. Frozen tissue analyses can be a diagnostic challenge and often require ancillary tools such as imprint cytology and serial sections for more sensitive and accurate diagnosis.

### **A Very Rare Cause of Dyspnea in a Child: A Hydatid Cyst From Echinococcus.**

**Carrel T, Sharipov I, Vogt PR.**

20-06-2023

*World J Pediatr Congenit Heart Surg.*

<https://pubmed.ncbi.nlm.nih.gov/37340730/>

Hydatid cyst is a human parasitic disease caused by *Echinococcus granulosus* that affects mainly the liver or the lungs but may be found in any organ, including the heart in up to 2% of the cases. Humans are infected as accidental hosts by contaminated vegetables or water and by contact with saliva from infected animals. Although cardiac echinococcosis can be fatal, it is rare and often asymptomatic in the early stage. We present the case of a young boy living on a farm who suffered from mild exertional dyspnea. He suffered from pulmonary and cardiac echinococcosis and was treated surgically through median sternotomy to prevent potential cystic rupture.

### **Detection of Echinococcus multilocularis in repurposed environmental DNA samples from river water.**

**Mori K, Imamura A, Hirayama I, Minamoto T.**

14-06-2023

*PeerJ.*

<https://pubmed.ncbi.nlm.nih.gov/37334136/>

### **Posterior Mediastinal Hydatid Cyst with Spine and Chest Wall Involvement.**

**Tadasa S, Dencha B, Gebrekidan M, Bedasso S, Tsehay Abebe A.**

14-06-2023

*Int Med Case Rep J.*

<https://pubmed.ncbi.nlm.nih.gov/37333036/>

Hydatid cyst, which is caused by *Echinococcus* larvae, is a worldwide zoonotic disease which can affect virtually any organ in the body. Although the liver and lungs are the most commonly affected, it can occur in other parts of the body. Mediastinal hydatid cysts are incredibly rare, but imaging is crucial to diagnose and determine the extent of involvement and complications. In this article, we present a case of posterior Mediastinal hydatid cyst with adjacent chest wall and spinal involvement, diagnosed through chest CT and histopathology.

### **Experimental cystic echinococcosis as a proof of concept for the development of peptide-based vaccines following a novel rational workflow.**

**Miles S, Dematteis S, Mourglia-Ettlin G.**

Mai-2023

*Biologicals.*

<https://pubmed.ncbi.nlm.nih.gov/37201271/>

### **Mucins Shed from the Laminated Layer in Cystic Echinococcosis Are Captured by Kupffer Cells via the Lectin Receptor Clec4F.**

**Barrios AA, Mouhape C, Schreiber L, Zhang L, Nell J, Suárez-Martins M, Schlapp G, Meikle MN, Mulet AP, Hsu TL, Hsieh SL, Mourglia-Ettlin G, González C, Crispo M, Barth TFE, Casaravilla C, Jenkins SJ, Díaz Á.**

15-06-2023

*Infect Immun.*

<https://pubmed.ncbi.nlm.nih.gov/37162364/>

Cystic echinococcosis is caused by the larval stages (hydatids) of cestode parasites belonging to the species cluster *Echinococcus granulosus sensu lato*, with *E. granulosus sensu stricto* being the main infecting species. Hydatids are bladderlike structures that attain large sizes within various internal organs of livestock ungulates and humans. Hydatids are protected by the massive acellular laminated layer (LL), composed mainly of mucins. Parasite growth requires LL turnover, and abundant LL-derived particles are found at infection sites in infected humans, raising the question of how LL materials are dealt with by the hosts. In this article, we show that *E. granulosus sensu stricto* LL mucins injected into mice are taken up by Kupffer cells, the liver macrophages exposed to the vascular space. This uptake is largely dependent on the intact mucin glycans and on Clec4F, a C-type lectin receptor which, in rodents, is selectively expressed in Kupffer cells. This uptake mechanism operates on mucins injected both in soluble form intravenously (i.v.) and in particulate form intraperitoneally (i.p.). In mice harboring intraperitoneal infections by the same species, LL mucins were found essentially only at the infection site and in the liver, where they were taken up by Kupffer cells via Clec4F. Therefore, shed LL materials circulate in the host, and Kupffer cells can act as a sink for these materials, even when the parasite grows in sites other than the liver.

### **Molecular characterization and immunological properties of Echinococcus granulosus sensu stricto (G1) ADK1 and ADK8.**

**Song HY, Zhan JF, Hua RQ, He X, Du XD, Xu J, He R, Xie Y, Gu XB, Peng XR, Yang GY.**

Jul-2023

*Parasitol Res.*

<https://pubmed.ncbi.nlm.nih.gov/37148368/>

### **A Diverse Virome Is Identified in Parasitic Flatworms of Domestic Animals in Xinjiang, China.**

**Zhang P, Zhang Y, Cao L, Li J, Wu C, Tian M, Zhang Z, Zhang C, Zhang W, Li Y.**

15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37042768/>

Parasitic flatworms infect diverse vertebrates and are major threats to animal and even human health; however, little is known about the virome of these lower life forms. Using viral metagenomic sequencing, we characterized the virome of the parasitic flatworms collected from major domestic animals, including *Dicrocoelium lanceatum* and *Taenia hydatigena*, *Echinococcus granulosus sensu stricto* and *Echinococcus multilocularis*. Seven and three different viruses were discovered from *D. lanceatum* and *T. hydatigena*, respectively, and no viral sequences were found in adult tapeworms and protoscoleces of *E. granulosus sensu stricto* and *E. multilocularis*. Two out of the five parasitic flatworm species carry viruses, showing a host specificity of these viruses. These viruses belong to the *Parvoviridae*, *Circoviridae*, unclassified circular, Rep-encoding single-stranded (CRESS) DNA virus, *Rhabdoviridae*, *Endornaviridae*, and unclassified RNA viruses. The presence of multiple highly divergent RNA viruses, especially those that cluster with viruses found in marine animals, implies a deep evolutionary history of parasite-associated viruses. In addition, we found viruses with high identity to common pathogens in dogs, including canine circovirus and canine parvovirus 2. The presence of these viruses in the parasites implies that they may infect parasitic flatworms but does not completely exclude the possibility of contamination from host intestinal contents. Furthermore, we demonstrated that certain viruses, such as CRESS DNA virus may integrate into the genome of their host. Our results expand the knowledge of viral diversity in parasites of important domestic animals, highlighting the need for further investigations of their prevalence among other parasites of key animals. **IMPORTANCE** Characterizing the virome of parasites is important for unveiling the viral diversity, evolution, and ecology and will help to understand the "Russian doll" pattern among viruses, parasites, and host animals. Our data indicate that diverse viruses are present in specific parasitic flatworms, including viruses that may have an ancient evolutionary history and viruses currently circulating in parasite-infected host animals. These data also raise the question of whether parasitic flatworms acquire and/or carry some viruses that may have transmission potential to animals. In addition, through the study of virus-parasite-host interactions, including the influence of viral infection on the life cycle of the parasite, as well as its fitness and pathogenicity to the host, we could find new strategies to prevent and control parasitic diseases.

### **Popliteal Echinococcosis: A Long Journey from the Liver.**

**Erginöz E, Ergün S, Tunç E, Pekmezci S.**

Juin-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36995509/>

### **Anti-Tumor Effect of Protoscolex Hydatid Cyst Somatic Antigen on Inhibition Cell Growth of K562.**

**Asouli A, Sadr S, Mohebalian H, Borji H.**

Juin-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36991291/>

### **Diagnosis, treatment, and outcome of four dogs with alveolar echinococcosis in the northwestern United States.**

**Williams LBA, Walzthoni N.**

17-02-2023

*J Am Vet Med Assoc.*

<https://pubmed.ncbi.nlm.nih.gov/36800299/>

### **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/>

The larval stage of the cestode *Echinococcus multilocularis* is the causative agent of alveolar echinococcosis. To investigate the biology of these stages and to test novel compounds, metacestode cultures represent a suitable *in vitro* model system. These metacestodes are vesicles surrounded by an envelope formed by the vesicle tissue (VT), which is formed by the laminated and germinal layer, and filled with vesicle fluid (VF). We analyzed the proteome of VF and VT by liquid chromatography tandem mass spectrometry (LC-MS/MS) and identified a total of 2,954 parasite proteins. The most abundant protein in VT was the expressed conserved protein encoded by EmuJ\_000412500, followed by the antigen B subunit AgB8/3a encoded by EmuJ\_000381500 and Endophilin B1 (protein p29). In VF, the pattern was different and dominated by AgB subunits. The most abundant protein was the AgB8/3a subunit followed by three other AgB subunits. In total, the AgB subunits detected in VF represented 62.1% of the parasite proteins. In culture media (CM), 63 *E. multilocularis* proteins were detected, of which AgB subunits made up 93.7% of the detected parasite proteins. All AgB subunits detected in VF (encoded by EmuJ\_000381100-700, corresponding to AgB8/2, AgB8/1, AgB8/4, AgB8/3a, AgB8/3b, and AgB8/3c) were also found in CM, except the subunit encoded by EmuJ\_000381800 (AgB8/5) that was very rare in VF and not detected in CM. The relative abundance of the AgB subunits in VF and CM followed the same pattern. In VT, only the subunits EmuJ\_000381500 (AgB8/3a) and EmuJ\_000381200 (AgB8/1) were detected among the 20 most abundant proteins. To see whether this pattern was specific to VF from *in vitro* cultured metacestodes, we analyzed the proteome of VF from metacestodes grown in a mouse model. Here, the AgB subunits encoded by EmuJ\_000381100-700 constituted the most abundant proteins, namely, 81.9% of total protein, with the same order of abundance as *in vitro*. Immunofluorescence on metacestodes showed that AgB is co-localized to calcareous corpuscles of *E. multilocularis*. Using targeted proteomics with HA-tagged EmuJ\_000381200 (AgB8/1) and EmuJ\_000381100 (AgB8/2), we could show that

uptake of AgB subunits from CM into VF occurs within hours.

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## Filariose lymphatique

### Assessment of wing geometric morphometrics of urban *Culex quinquefasciatus* (Diptera: Culicidae) populations.

Oliveira-Christe R, de Carvalho GC, Wilke ABB, Marrelli MT.

16-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37331646/>

*Culex quinquefasciatus* is a cosmopolitan species distributed throughout tropical and subtropical areas of the world. The species is of great epidemiological importance as it is responsible for vectoring the causative agent of lymphatic filariasis and several arboviruses, including West Nile virus. Wing geometric morphometrics has been widely used to assess phenotypic variations in mosquito species. Here, we hypothesize that *Cx. quinquefasciatus* populations in urban parks in the city of São Paulo, Brazil, have been subjected to anthropogenic selective pressures that are responsible for driving their ecology and behavior. Mosquitoes were collected by CDC traps in five municipal parks in the city of São Paulo. Eighteen anatomical landmark coordinates on each female right wing were digitized. Canonical variate analysis, wireframe graphs, cross-validated reclassification tests and the neighbor-joining method were used to assess phenotypical dissimilarity in wing shape between populations. Centroid size was calculated to assess differences in wing size between populations, which can result from different environmental conditions during immature mosquito development. Moderately heterogeneous wing shape and wing size patterns were found in the populations analyzed, indicating that selective pressures in the urban environment are affecting the wing patterns of *Cx. quinquefasciatus* populations in the city of São Paulo, Brazil.

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## Gale

### *Bacillus velezensis* K-9 as a potential biocontrol agent for managing potato scab.

Ma S, Wang T, Wang Y.

19-06-2023

*Plant Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37337440/>

### New Ionone Glycosides from the Aerial Parts of *Allium sativum* and Their Anti-Platelet Aggregation Activity.

Hu B, Hu H, Pu C, Peng D, Wei Z, Kuang H, Wang Q.

Juin-2023

*Planta Med.*

<https://pubmed.ncbi.nlm.nih.gov/36513370/>

The bulbs of *Allium sativum* known as garlic are widely used as food or seasoning. In China they have been used as a traditional Chinese medicine (TCM) since ancient times for the treatment of scabies, tuberculosis, pertussis, diarrhea and dysentery. *A. sativum* has reportedly shown platelet aggregation inhibition and has been used in the treatment of cardiovascular diseases. However, there are only few studies focussing on the aerial parts, which are normally discarded during harvest. In this study, two new ionone glycosides, dasuanxinosides D and E (1, 2: ), are isolated from the aerial parts together with 13 known compounds including alkanes derivatives and alkyl glycosides (3 - 15: ), which are reported for the first time from this plant. Their structures are identified by extensive NMR and HRMS analyses. The isolated compounds are evaluated for their inhibitory effect on adenosine diphosphate (ADP)-induced platelet aggregation *in vitro*.

### Lessons to learn from the analysis of routine health data from Moria Refugee Camp on Lesbos, Greece.

Hart PL, Zahos H, Salt N, Schofield R, Mahroof-Shaffi S, Simonek T, Harkensee C.

14-06-2023

*J Public Health (Oxf).*

<https://pubmed.ncbi.nlm.nih.gov/36415082/>

**Background:** Refugees in humanitarian settings commonly experience many health needs and barriers to access healthcare; health data from these settings are infrequently reported, preventing effective healthcare provision. This report describes health needs of refugees in Moria Camp on Lesbos, Greece-Europe's largest refugee camp. **Methods:** A set of routinely collected service data of 18 131 consultations of 11 938 patients, attending a primary care clinic in the camp over 6 months in 2019-20, was analysed retrospectively, focusing on chronic health conditions. **Results:** The most frequent chronic conditions were musculoskeletal pain (25.1%), mental health (15.9%), cardiac (12.7%) and endocrine conditions (8.9%). In all, 70.4% of consultations were for acute health problems, with high rates of injuries and wounds (20.8%), respiratory infections (12.5%), gastroenteritis (10.7%) and skin problems (9.7%), particularly scabies. **Conclusions:** The prevalence of acute and chronic health problems is high in this setting, with some likely attributable to the deplorable living conditions in the camp. Despite its magnitude, the interpretability of routine health data is limited. A research agenda is identified, and a framework for chronic disease management in refugee camps is proposed.

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## Leishmaniose

### Bayesian multivariate longitudinal model for immune responses to *Leishmania*: A tick-borne co-infection study.

Pabon-Rodriguez FM, Brown GD, Scorza BM, Petersen CA.

23-06-2023

Stat Med.

<https://pubmed.ncbi.nlm.nih.gov/37350148/>

### **Deciphering anti-infectious compounds from Peruvian medicinal Cordoncillos extract library through multiplexed assays and chemical profiling.**

Vásquez-Ocmín PG, Cojean S, Roumy V, Marti G, Pomel S, Gadea A, Leblanc K, Dennemont I, Ruiz-Vásquez L, Ricopa Cotrina H, Ruiz Mesia W, Bertani S, Ruiz Mesia L, Maciuk A.

05-06-2023

Front Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37342590/>

High prevalence of parasitic or bacterial infectious diseases in some world areas is due to multiple reasons, including a lack of an appropriate health policy, challenging logistics and poverty. The support to research and development of new medicines to fight infectious diseases is one of the sustainable development goals promoted by World Health Organization (WHO). In this sense, the traditional medicinal knowledge substantiated by ethnopharmacology is a valuable starting point for drug discovery. This work aims at the scientific validation of the traditional use of *Piper* species ("*Cordoncillos*") as firsthand anti-infectious medicines. For this purpose, we adapted a computational statistical model to correlate the LCMS chemical profiles of 54 extracts from 19 *Piper* species to their corresponding anti-infectious assay results based on 37 microbial or parasites strains. We mainly identified two groups of bioactive compounds (called features as they are considered at the analytical level and are not formally isolated). Group 1 is composed of 11 features being highly correlated to an inhibiting activity on 21 bacteria (principally Gram-positive strains), one fungus (*C. albicans*), and one parasite (*Trypanosoma brucei gambiense*). The group 2 is composed of 9 features having a clear selectivity on *Leishmania* (all strains, both axenic and intramacrophagic). Bioactive features in group 1 were identified principally in the extracts of *Piper strigosum* and *P. xanthostachyum*. In group 2, bioactive features were distributed in the extracts of 14 *Piper* species. This multiplexed approach provided a broad picture of the metabolome as well as a map of compounds putatively associated to bioactivity. To our knowledge, the implementation of this type of metabolomics tools aimed at identifying bioactive compounds has not been used so far.

### **Leishmania donovani Induces Multiple Dynamic Responses in the Metabolome Associated with Amastigote Differentiation and Maturation Inside the Human Macrophage.**

Fernández-García M, Mesquita I, Ferreira C, Araújo M, Saha B, Rey-Stolle MF, García A, Silvestre R, Barbas C.

20-06-2023

J Proteome Res.

<https://pubmed.ncbi.nlm.nih.gov/37339249/>

*Leishmania donovani* infection of macrophages drives profound changes in the metabolism of both the host macrophage and the parasite, which undergoes different phases of development culminating in replication and propagation. However, the dynamics of this parasite-macrophage cometabolome are poorly understood. In this study, a multiplatform metabolomics pipeline combining untargeted, high-resolution CE-TOF/MS and LC-QTOF/MS with targeted LC-QqQ/MS was followed to characterize the metabolome alterations induced in *L. donovani*-infected human monocyte-derived macrophages from different donors at 12, 36, and 72 h post-infection. The set of alterations known to occur during *Leishmania* infection of macrophages, substantially expanded in this investigation, characterized the dynamics of the glycerophospholipid, sphingolipid, purine, pentose phosphate, glycolytic, TCA, and amino acid metabolism. Our results showed that only citrulline, arginine, and glutamine exhibited constant trends across all studied infection time points, while most metabolite alterations underwent a partial recovery during amastigote maturation. We determined a major metabolite response pointing to an early induction of sphingomyelinase and phospholipase activities and correlated with amino acid depletion. These data represent a comprehensive overview of the metabolome alterations occurring during promastigote-to-amastigote differentiation and maturation of *L. donovani* inside macrophages that contributes to our understanding of the relationship between *L. donovani* pathogenesis and metabolic dysregulation.

### **Morphology does not allow differentiating the species of the Phlebotomus perniciosus complex: Molecular characterization and investigation of their natural infection by Leishmania infantum in Morocco.**

Gijón-Robles P, Gómez-Mateos M, Corpas-López E, Abattouy N, Merino-Espinosa G, Morillas-Márquez F, Corpas-López V, Díaz-Sáez V, Riyad M, Martín-Sánchez J.

19-06-2023

Zoonoses Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37337345/>

Morphological and DNA-based complemented approaches were applied for characterization of sympatric populations of *Phlebotomus longicuspis* and *Phlebotomus perniciosus* in Morocco. Both sand fly species are generally recorded in sympatry in North Africa but on few occasions have been molecularly characterized. The diagnostic confusion of these species has led to errors in their geographical distribution and probably, in the assignment of their role in the transmission of *L. infantum*. Sand flies were caught inside households in El Borouj, central Morocco, in 2014-2015. For female sand flies, detection of *L. infantum* natural infection and blood meal identification were carried out. According to morphological identification, *Phlebotomus longicuspis* s.l. (34.7%) was the second most abundant *Phlebotomus* species after *P. sergenti*, followed by atypical *Phlebotomus perniciosus* (7.1%); 11.6% of the male specimens of *P. longicuspis* s.l. were identified as *P. longicuspis* LCx according to the

number of coxite setae. The density of *Larroussius* species was very high (31 *Larroussius*/light trap/night) in the peripheral neighbourhood of Oulad Bouchair ( $p = 0.001$ ) where the first case of cutaneous leishmaniasis due to *Leishmania infantum* was detected in 2017. Phylogenetic trees based on three independent genes highlighted three well-supported clusters within *P. perniciosus* complex that could be interpreted as corresponding to *P. perniciosus*, *P. longicuspis* s.s. and an undescribed species, all coexisting in sympatry. Some females with typical morphology of *P. longicuspis* were genetically homologous to *P. perniciosus*. The taxa cannot be differentiated by morphological methods but characterized by a distinctive genetic lineage for which the synapomorphic characters are described. *Leishmania infantum* was detected in females of all clusters with a low parasite load. Population genetics will help to assess the threat of the geographical spread of *L. infantum* in Morocco by determining the density, abundance and vector role of the species of the *P. perniciosus* complex identified correctly.

### Versatile anti-infective properties of pyrido- and dihydropyrido[2,3-d]pyrimidine-based compounds.

Al Nasr IS, Corona A, Koko WS, Khan TA, Ben Said R, Daoud I, Rahali S, Tramontano E, Schobert R, Amdouni N, Biersack B.

15-06-2023

*Bioorg Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37336083/>

### One piece of the puzzle: Modeling vector presence and environment reveals seasonality, distribution, and prevalence of sandflies and *Leishmania* in an expansion area.

Thomaz-Soccol V, Gonçalves AL, Baggio RA, Bisetto A Jr, Celestino A, Hospinal-Santiani M, de Souza A, Mychalizen M, Borges ME, Piechnik CA.

09-06-2023

*One Health.*

<https://pubmed.ncbi.nlm.nih.gov/37332885/>

### Identification of molecular mechanisms causing skin lesions of cutaneous leishmaniasis using weighted gene coexpression network analysis (WGCNA).

Momeni K, Ghorbian S, Ahmadpour E, Sharifi R.

17-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37330553/>

### An integrative in silico and in vitro study identifies *Leishmania donovani* MAP kinase12 as a probable virulence factor.

Mazire PH, Roy A.

15-06-2023

*Int Immunopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37329806/>

### Molecular Detection of *Leishmania* in Wild Caught Sand Flies of *Larroussius* Subgenus in Iran: Combined Use of Internal and External Morphological Characters as a Mean to Differentiate Morphologically Similar Females.

Vaziri VM, Behniafar H, Spotin A, Absavarand A, Badakhshan M.

17-06-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37328624/>

**Objective:** Phlebotomine sand flies are the primary vectors of leishmaniasis; visceral form of disease is transmitted mainly by species belonging to *Larroussius* and *Adlerius* subgenus. Species identification of some females in *Larroussius* subgenus is not easy due to the high similarity. Accurate species identification enables control operations to target only main vectors and increase understanding of ecological needs, bionomic characteristics, and behavioral traits. The purpose of current study was to use two approaches based on internal and external morphological characters to identify the wild caught of female specimens belonged to *Larroussius* subgenus and investigate *Leishmania* infection. **Methods:** Totally, 128 specimens belonging to *Larroussius* subgenus were collected from a VL focus in northwestern Iran, species differentiation was done by two approaches proposed in literature: (1) characters of pharyngeal armature, number of Spermathecal segment, length of spermathecal neck, palpal and ascoid formulae; (2) blindly on the basis of the shape of the base of spermathecal duct. Their potential infection to *Leishmania* was investigated by kDNA-Nested-PCR. **Results:** The results of species identification were consistent based on two methods. Among three identified species, *Phlebotomus perfiliewi* was found to be the dominant species, followed by *Ph. neglectus* and *Ph. tobbi*. Two specimens of *Ph. perfiliewi* were found to be infected by *Leishmania infantum*, which emphasizes the role of this species in VL transmission in study area. **Conclusion:** It is suggested that combination of the characters used here be considered for species identification of female of *Larroussius* subgenus to take advantage of maximum characters, especially where species present sympatrically.

### Generation of dysbiotic microbiota in cutaneous leishmaniasis and enhancement of skin inflammation.

Naz S, Ali Z, Minhas A, Fatima A, Waseem S.

14-06-2023

*Microb Pathog.*

<https://pubmed.ncbi.nlm.nih.gov/37327948/>

### Synthesis and biological evaluation of carbohydrate-Coumarin/vanillic acid hybrid as a promising antiparasitic agent.

Sharma A, Saikia P, Saha S, Kumar D, Panchadhayee R.

11-06-2023

*Carbohydr Res.*

<https://pubmed.ncbi.nlm.nih.gov/37327765/>

### Hypercalcemia during initiation of antiretroviral therapy in human immunodeficiency virus and Leishmania coinfection: A case report.

Yu T, Tang J.

16-06-2023

*Medicine (Baltimore).*

<https://pubmed.ncbi.nlm.nih.gov/37327295/>

**Rationale:** Hypercalcemia is a common complication of many granulomatous diseases but is not typically associated with leishmaniasis. Here we report an unusual case of hypercalcemia during the initiation of antiviral therapy in a patient with acquired immunodeficiency syndrome coinfecting with visceral leishmaniasis. **Patient concerns:** Our patient presented with malaise and altered mental status following antiretroviral therapy initiation. He was found to have de novo hypercalcemia complicated by acute kidney injury. **Diagnosis, interventions, and outcomes:** An extensive workup for other etiologies of hypercalcemia was negative. The patient was ultimately thought to have hypercalcemia secondary to visceral leishmaniasis in the setting of immune reconstitution inflammatory syndrome. He was treated with intravenous volume expansion, bisphosphonates, and oral corticosteroid therapy with complete resolution. **Lessons:** This case highlights an unusual presentation of immune reconstitution inflammatory syndrome, in which proinflammatory cytokine signaling during the restoration of cellular immunity may have led to increased ectopic calcitriol production by granuloma macrophages, thereby altering bone-mineral metabolism and driving hypercalcemia.

### 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, Quorllo BA.

Juil-2023

*Vet Parasitol Reg Stud Reports.*

<https://pubmed.ncbi.nlm.nih.gov/37321792/>

A 3-year-old, female, domestic shorthair cat, was presented to the Veterinary Teaching Hospital at the School of Veterinary Medicine (SVM), Trinidad and Tobago for a swollen nose, and multiple, variably sized small masses on both ears. The initial diagnostic tests included a CBC, serum biochemistry profile, cytological evaluation of masses on the ear and nose, and FeLV/FIV testing. The CBC and biochemistry results were unremarkable except for a hyperproteinemia and hyperglobulinemia. Cytology of the nose and ear lesions revealed mixed inflammation and

high numbers of intracellular and extracellular organisms consistent with Leishmania amastigotes. The cat was FeLV/FIV negative. Histopathology and Leishmania IFA and PCR analysis were subsequently performed, confirming the Leishmania diagnosis. The PCR, DNA sequencing and phylogenetic tree analyses identified L. amazonensis. This is the first reported case of L. amazonensis infection in a domestic animal in Trinidad with molecular characterization indicating it exists in the region and is likely being transmitted by sandflies.

### 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.

Aug-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  $\mu$ 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.

### Discovery, SAR and mechanistic studies of quinazolinone-based acetamide derivatives in experimental visceral leishmaniasis.

Ansari A, Seth A, Dutta M, Qamar T, Katiyar S, Jaiswal AK, Rani A, Majhi S, Kumar M, Bhatta RS, Guha R, Mitra K, Sashidhara KV, Kar S.

05-09-2023

*Eur J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37290183/>

### **Variants of CARD8 in *Leishmania guyanensis*-cutaneous leishmaniasis and influence of the variants genotypes on circulating plasma cytokines IL-1 $\beta$ , TNF $\alpha$ and IL-8.**

Sequera HDG, Souza JL, Junior JDES, Silva LSD, Pinheiro SK, Kerr HKA, Souza MLG, Guerra MVF, Mesquita TGR, Ramasawmy R.

05-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37276232/>

### **Association between the potential distribution of *Lutzomyia longipalpis* and *Nyssomyia whitmani* and leishmaniasis incidence in Piauí State, Brazil.**

de Sousa RLT, Araujo-Pereira T, Leal ARDS, Freire SM, Silva CLM, Mallet JRDS, Vilela ML, Vasconcelos SA, Gomes R, Teixeira C, Britto C, Pita Pereira D, Carvalho BM.

05-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37276231/>

**Background:** Leishmaniasis are vector borne diseases caused by *Leishmania* spp. parasites transmitted by female sandflies (Diptera: Psychodidae) whose geographic distribution is influenced by environmental factors. Among the main tools for studying the distribution of vector species, modeling techniques are used to analyze the influence of climatic and environmental factors on the distribution of these insects and their association with human cases of the disease. **Methodology/principal findings:** Here, we used a multiscale ecological niche modeling approach to assess the environmental suitability of sandfly vectors of the etiological agents of Visceral (VL) and American Cutaneous Leishmaniasis (ACL) in Piauí state, northeastern Brazil, and then evaluated their relationship with human disease incidence. For this, we obtained the geographic coordinates of the vector species *Lutzomyia longipalpis* and *Nyssomyia whitmani* through literature review, online databases and unpublished records. These data were used for the development of predictive models of the distribution of both sandflies species based on climatic and environmental variables. Finally, the environmental suitability for the presence of these vectors was compared with the incidence of both the diseases at the municipality level. The final models for each sandfly species showed good predictive powers with performance metric values of 0.889 for *Lu. longipalpis* and 0.776 for *Ny. whitmani*. The areas with greater environmental suitability for the presence of these species were concentrated in the central-north region of Piauí and coincide with the location of those municipalities presenting higher incidences of VL and ACL, situated in the central-north and extreme north of the state, respectively. The south and southeast regions of Piauí state have low incidence of these diseases and presented low environmental suitability for the presence of both vectors.

**Conclusions/significance:** We discuss how predictive modeling can guide entomological and epidemiological surveillances and recommend an increased supervision and control activities in Teresina (capital of the state of Piauí), Altos and Pedro II, in addition to other municipalities with similar social and environmental characteristics.

### **Tetrahydrobenzo[h]quinoline derivatives as a novel chemotype for dual antileishmanial-antimalarial activity graced with antitubercular activity: Design, synthesis and biological evaluation.**

Ibrahim TM, Abada G, Dammann M, Maklad RM, Eldehna WM, Salem R, Abdelaziz MM, El-Domany RA, Bekhit AA, Beockler FM.

05-09-2023

*Eur J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37269671/>

### **Molecular-level strategic goals and repressors in Leishmaniasis - Integrated data to accelerate target-based heterocyclic scaffolds.**

Abirami M, Karan Kumar B, Faheem, Dey S, Johri S, Reguera RM, Balaña-Fouce R, Gowri Chandra Sekhar KV, Sankaranarayanan M.

05-09-2023

*Eur J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37257213/>

Leishmaniasis is a complex of neglected tropical diseases caused by various species of leishmanial parasites that primarily affect the world's poorest people. A limited number of standard medications are available for this disease that has been used for several decades, these drugs have many drawbacks such as resistance, higher cost, and patient compliance, making it difficult to reach the poor. The search for novel chemical entities to treat leishmaniasis has led to target-based scaffold research. Among several identified potential molecular targets, enzymes involved in the purine salvage pathway include polyamine biosynthetic process, such as arginase, ornithine decarboxylase, S-adenosylmethionine decarboxylase, spermidine synthase, trypanothione reductase as well as enzymes in the DNA cell cycle, such as DNA topoisomerases I and II plays vital role in the life cycle survival of leishmanial parasite. This review mainly focuses on various heterocyclic scaffolds, and their specific inhibitory targets against leishmaniasis, particularly those from the polyamine biosynthesis pathway and DNA topoisomerases with estimated activity studies of various heterocyclic analogs in terms of their IC<sub>50</sub> or EC<sub>50</sub> value, reported molecular docking analysis from available published literatures.

### **Nonbacterial Microflora in Wastewater Treatment Plants: an Underappreciated Potential Source of Pathogens.**

Ariyadasa S, Taylor W, Weaver L, McGill E, Billington C, Pattis I.

15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37222623/>

Wastewater treatment plants (WWTPs) receive and treat large volumes of domestic, industrial, and urban wastewater containing pathogenic and nonpathogenic microorganisms, chemical compounds, heavy metals, and other potentially hazardous substances. WWTPs play an essential role in preserving human, animal, and environmental health by removing many of these toxic and infectious agents, particularly biological hazards. Wastewater contains complex consortiums of bacterial, viral, archaeal, and eukaryotic species, and while bacteria in WWTP have been extensively studied, the temporal and spatial distribution of nonbacterial microflora (viruses, archaea, and eukaryotes) is less understood. In this study, we analyzed the viral, archaeal, and eukaryotic microflora in wastewater throughout a treatment plant (raw influent, effluent, oxidation pond water, and oxidation pond sediment) in Aotearoa (New Zealand) using Illumina shotgun metagenomic sequencing. Our results suggest a similar trend across many taxa, with an increase in relative abundance in oxidation pond samples compared to influent and effluent samples, except for archaea, which had the opposite trend. Additionally, some microbial families, such as *Podoviridae* bacteriophages and Apicomplexa alveolates, appeared largely unaffected by the treatment process, with their relative abundance remaining stable throughout. Several groups encompassing pathogenic species, such as *Leishmania*, *Plasmodium*, *Toxoplasma*, *Apicomplexa*, *Cryptococcus*, *Botrytis*, and *Ustilago*, were identified. If present, these potentially pathogenic species could be a threat to human and animal health and agricultural productivity; therefore, further investigation is warranted. These nonbacterial pathogens should be considered when assessing the potential for vector transmission, distribution of biosolids to land, and discharge of treated wastewater to waterways or land. **IMPORTANCE** Nonbacterial microflora in wastewater remain understudied compared to their bacterial counterparts despite their importance in the wastewater treatment process. In this study, we report the temporal and spatial distributions of DNA viruses, archaea, protozoa, and fungi in raw wastewater influent, effluent, oxidation pond water, and oxidation pond sediments by using shotgun metagenomic sequencing. Our study indicated the presence of groups of nonbacterial taxa which encompass pathogenic species that may have potential to cause disease in humans, animals, and agricultural crops. We also observed higher alpha diversity in viruses, archaea, and fungi in effluent samples than in influent samples. This suggests that the resident microflora in the wastewater treatment plant may be making a greater contribution to the diversity of taxa observed in wastewater effluent than previously thought. This study provides important insights to better understand the potential human, animal, and environmental health impacts of discharged treated wastewater.

**Multi-target withaferin-A analogues as promising anti-kinetoplastid agents through the programmed cell death.**

San Nicolás-Hernández D, Hernández-Álvarez E, Bethencourt-Estrella CJ, López-Arencibia A, Sifaoui I, Bazzocchi IL, Lorenzo-Morales J, Jiménez IA, Piñero JE. Août-2023

*Biomed Pharmacother.*

<https://pubmed.ncbi.nlm.nih.gov/37210899/>

**C3/CD11b-Mediated *Leishmania major* Internalization by Neutrophils Induces Intraphagosomal NOX2-Mediated Respiratory Burst but Fails to Eliminate Parasites and Induces a State of Stalled Apoptosis.**

Ranson AJ, Carneiro MB, Perks B, Penner R, Melo L, Canton J, Egen J, Peters NC.

Juil-2023

*J Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/37195185/>

**Identification of infection by *Leishmania* spp. in wild and domestic animals in Brazil: a systematic review with meta-analysis (2001-2021).**

Ratzlaff FR, Osmari V, da Silva D, de Paula Vasconcellos JS, Pötter L, Fernandes FD, de Mello Filho JA, de Avila Botton S, Vogel FSF, Sangioni LA.

Juil-2023

*Parasitol Res.*

<https://pubmed.ncbi.nlm.nih.gov/37154922/>

Leishmaniasis is a zoonosis caused by protozoan species of the genus *Leishmania*. It generates different clinical manifestations in humans and animals, and it infects multiple hosts. *Leishmania* parasites are transmitted by sandfly vectors. The main objective of this systematic review was to identify the host, or reservoir animal species, of *Leishmania* spp., with the exception of domestic dogs, that were recorded in Brazil. This review included identification of diagnostic methods, and the species of protozoan circulating in the country. For this purpose, a literature search was conducted across index journals. This study covered the period from 2001 to 2021, and 124 studies were selected. Eleven orders possible hosts were identified, including 229 mammalian species. *Perissodactyla* had the highest number of infected individuals (30.69%, 925/3014), with the highest occurrence in horses. In Brazil, the most commonly infected species were found to be: horses, domestic cats, rodents, and marsupials. Bats, that were infected by one or more protozoan species, were identified as potential reservoirs of *Leishmania* spp. Molecular tests were the most commonly used diagnostic methods (94 studies). Many studies have detected *Leishmania* spp. (n = 1422): *Leishmania* (*Leishmania*) *infantum* (n = 705), *Leishmania* (*Viannia*) *braziliensis* (n = 319), and *Leishmania* (*Leishmania*) *amazonensis* (n = 141). Recognizing the species of animals involved in the epidemiology and biological cycle of the protozoan is important, as this allows for the identification of environmental biomarkers, knowledge of *Leishmania* species can improve the control zoonotic leishmaniasis.

### **Prevalence of *Trypanosoma lainsoni* and its effects of parasitism on the health of non-volant small mammals from the Brazilian Cerrado.**

de Oliveira MM, Ferrando CPR, Gómez-Hernández C, de Oliveira KR, Araújo IAC, Ribeiro PVA, Mineo TWP, Leiner NO, Mineo JR, da Silva SM.

Jul-2023

*Parasitol Res.*

<https://pubmed.ncbi.nlm.nih.gov/37129625/>

### ***Leishmania donovani* Attenuates Dendritic Cell Trafficking to Lymph Nodes by Inhibiting C-Type Lectin Receptor 2 Expression via Transforming Growth Factor- $\beta$ .**

Yadav M, Akhtar MN, Mishra M, Kumar S, Kumar R, Shubham, Nandal A, Sen P.

15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37125906/>

### **New antiprotozoal sesquiterpene derivatives from *Dorema glabrum* Fisch & C.A.Mey.**

Delnavazi MR, Ebrahimi SN, Hadjiakhoondi A, Yassa N.

Jul-2023

*Fitoterapia.*

<https://pubmed.ncbi.nlm.nih.gov/37121409/>

Seven undescribed sesquiterpene derivatives, Azerins A-G (3-6, 8, 14 and 15), three known sesquiterpene phenols, kopetdaghin A (1), kopetdaghin B (2) and latisectin (7), together with five known sesquiterpene coumarins (9-13), were isolated from the roots of *Dorema glabrum*. The structures were elucidated by comprehensive 1D- and 2D-NMR spectral analysis as well as HR-ESI-MS. Compounds were assessed for their in vitro antiprotozoal activity against *Trypanosoma brucei* rhodesiense, *T. cruzi*, *Leishmania donovani*, and *Plasmodium falciparum*. Cytotoxic potentials of the compounds were also tested on L6 rat skeletal myoblasts. Azerin G (15) showed a potent preferential growth inhibitory activity against *T. b. rhodesiense* with IC<sub>50</sub> value of 0.01  $\mu$ M and selectivity index of 329. Compounds 1, 4, 7 and 8 were also found as the most active compounds with selective growth inhibitory effects toward *P. falciparum* with selectivity indices ranging from 11.6 to 16.7 (IC<sub>50</sub>: 1.8-24.6  $\mu$ M).

### **Development of a Novel Enzyme-Linked Immunosorbent Assay and Lateral Flow Test System for Improved Serodiagnosis of Visceral Leishmaniasis in Different Areas of Endemicity.**

Mahdavi R, Shams-Eldin H, Witt S, Latz A, Heinz D, Fresco-Taboada A, Aira C, Hübner MP, Sukyte D, Visekruna A, Teixeira HC, Abass E, Steinhoff U.

15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37074181/>

Visceral leishmaniasis (VL) is caused by protozoan parasites of the *Leishmania donovani* complex and is one of the most prominent vector-borne infectious diseases with epidemic and mortality potential if not correctly diagnosed and treated. East African countries suffer from a very high incidence of VL, and although several diagnostic tests are available for VL, diagnosis continues to represent a big challenge in these countries due to the lack of sensitivity and specificity of current serological tools. Based on bioinformatic analysis, a new recombinant kinesin antigen from *Leishmania infantum* (rKLi8.3) was developed. The diagnostic performance of rKLi8.3 was evaluated by enzyme-linked immunosorbent assay (ELISA) and lateral flow test (LFT) on a panel of sera from Sudanese, Indian, and South American patients diagnosed with VL or other diseases, including tuberculosis, malaria, and trypanosomiasis. The diagnostic accuracy of rKLi8.3 was compared with rK39 and rKLO8 antigens. The VL-specific sensitivity of rK39, rKLO8, and rKLi8.3 ranged from 91.2% over 92.4% to 97.1% and specificity ranged from 93.6% over 97.6% to 99.2%, respectively. In India, all tests showed a comparable specificity of 90.9%, while the sensitivity ranged from 94.7% to 100% (rKLi8.3). In contrast to commercial serodiagnostic tests, rKLi8.3-based ELISA and LFT showed improved sensitivity and no cross-reactivity with other parasitic diseases. Thus, rKLi8.3-based ELISA and LFT offer improved VL serodiagnostic efficiency in East Africa and other areas of endemicity. **IMPORTANCE** Reliable and field suitable serodiagnosis of visceral leishmaniasis (VL) in East Africa has until now been a big challenge due to low sensitivity and cross-reactivity with other pathogens. To improve VL serodiagnosis, a new recombinant kinesin antigen from *Leishmania infantum* (rKLi8.3) was developed and tested with a panel of sera from Sudanese, Indian, and South American patients diagnosed with VL or other infectious diseases. Both prototype rKLi8.3-based enzyme-linked immunosorbent assay (ELISA) and lateral flow test (LFT) showed improved sensitivity and no cross-reactivity with other parasitic diseases. Thus, rKLi8.3-based ELISA and LFT offer substantially increased diagnostic efficiency for VL in East Africa and other areas of endemicity, compared to currently commercially available serodiagnostic tests.

### **Evaluation of the Antiparasitic and Antifungal Activities of Synthetic Piperlongumine-Type Cinnamide Derivatives: Booster Effect by Halogen Substituents.**

Khan TA, Al Nasr IS, Koko WS, Ma J, Eckert S, Brehm L, Ben Said R, Daoud I, Hanachi R, Rahali S, van de Sande WWJ, Ersfeld K, Schobert R, Biersack B.

15-06-2023

*ChemMedChem.*

<https://pubmed.ncbi.nlm.nih.gov/37021847/>

A series of synthetic N-acylpyrrolidone and -piperidone derivatives of the natural alkaloid piperlongumine were prepared and tested for their activities against *Leishmania* major and *Toxoplasma gondii* parasites. Replacement of one of the aryl meta-methoxy groups by halogens such as chlorine, bromine and iodine led to distinctly increased antiparasitic activities. For instance, the new bromo- and

iodo-substituted compounds 3 b/c and 4 b/c showed strong activity against *L. major* promastigotes ( $IC_{50}$  =4.5-5.8  $\mu$ M). Their activities against *L. major* amastigotes were moderate. In addition, the new compounds 3 b, 3 c, and 4 a-c exhibited high activity against *T. gondii* parasites ( $IC_{50}$  =2.0-3.5  $\mu$ M) with considerable selectivities when taking their effects on non-malignant Vero cells into account. Notable antitrypanosomal activity against *Trypanosoma brucei* was also found for 4 b. Antifungal activity against *Madurella mycetomatis* was observed for compound 4 c at higher doses. Quantitative structure-activity relationship (QSAR) studies were carried out, and docking calculations of test compounds bound to tubulin revealed binding differences between the 2-pyrrolidone and 2-piperidone derivatives. Microtubules-destabilizing effects were observed for 4 b in *T. b. brucei* cells.

### **Molecular Diagnosis of Leishmaniasis in Spain: Development and Validation of Ready-To-Use Gel-Form Nested and Real-Time PCRs To Detect Leishmania spp.**

Chicharro C, Nieto J, Miguelañez S, García E, Ortega S, Peña A, Rubio JM, Flores-Chavez M.  
15-06-2023  
*Microbiol Spectr.*  
<https://pubmed.ncbi.nlm.nih.gov/37014253/>

### **Diagnosis of Human Cutaneous Leishmaniasis: A Comparative Study Using CL Detect™ Dipstick, Direct Smear and Polymerase Chain Reaction Methods.**

Zamanpour M, Mohebbi M, Khamesipour A, Mohammadi AMA, Akhoundi B.  
Juin-2023  
*Acta Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36913075/>

### **Zinc and Manganese Imbalances in BALB/c Mice Experimentally Infected with Leishmania (Leishmania) amazonensis.**

Sobotyk C, Baldissera FG, Rodrigues Junior LC, Romão PRT, de Oliveira JS, Dornelles GL, de Andrade CM, Maciel RM, Danesi CC, de Padua Ferreira RV, Bellini MH, de Avila Botton S, Vogel FSF, Sangioni LA.  
Juin-2023  
*Acta Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36884141/>

**Purpose:** The clinical progression of *Leishmania* (*Leishmania*) *amazonensis* infection depends on multiple factors, including immunological status of the host and their genotypic interaction. Several immunological processes depend directly on minerals for an efficient performance. Therefore, this study used an experimental model to investigate the alterations of trace metals in *L. amazonensis* infection associate with clinical outcome, parasite load, and histopathological lesions, and the effect of CD4 + T cells depletion on these parameters. **Methods:**

A total of 28 BALB/c mice were divided into 4 groups: 1- non-infected; 2-treated with anti-CD4 antibody; 3- infected with *L. amazonensis*; and 4-treated with anti-CD4 antibody and infected with *L. amazonensis*. After 24 weeks post-infection, levels of calcium (Ca), iron (Fe), magnesium (Mg), manganese (Mn), Cu, and Zn were determined by inductively coupled plasma optical emission spectroscopy using tissue samples of the spleen, liver, and kidneys. Additionally, parasite burdens were determined in the infected footpad (inoculation site) and samples of inguinal lymph node, spleen, liver, and kidneys were submitted to histopathological analysis. **Results:** Despite no significant difference was observed between groups 3 and 4, *L. amazonensis*-infected mice had a significant reduction of Zn (65.68-68.32%) and Mn (65.98 to 82.17%) levels. Presence of *L. amazonensis* amastigotes was also detected in the inguinal lymph node, spleen, and liver samples in all infected animals. **Conclusion:** The results showed that significant alterations in micro-elements levels occur in BALB/c mice experimentally infected with *L. amazonensis* and may increase the susceptibility of individuals to the infection.

### **Metallopeptidases as Key Virulence Attributes of Clinically Relevant Protozoa: New Discoveries, Perspectives, and Frontiers of Knowledge.**

Vargas Rigo G, Gomes Cardoso F, Bongiorno Galego G, da Rosa DF, Dos Santos ALS, Tasca T.  
2023  
*Curr Protein Pept Sci.*  
<https://pubmed.ncbi.nlm.nih.gov/36876838/>

### **Parasite Metallo-aminopeptidases as Targets in Human Infectious Diseases.**

Aguado ME, Izquierdo M, González-Matos M, Varela AC, Méndez Y, Del

Rivero MA, Rivera DG, González-Bacerio J.  
2023  
*Curr Drug Targets.*  
<https://pubmed.ncbi.nlm.nih.gov/36825701/>

### **Antileishmanial Activity of the Essential Oils from Three Trees Obtained in Different Phenological Stages.**

Rguez S, Essid R, Bettaieb I, Bourguou S, Hammami M, Hamrouni Sellami I.  
Juin-2023  
*Acta Parasitol.*  
<https://pubmed.ncbi.nlm.nih.gov/36810938/>

**Purpose:** Leishmaniasis is a parasitic disease found in tropical areas, and it affects up to 12 million individuals globally. Chemotherapies now available include drawbacks such as toxicity, high cost, and parasite resistance. This work aimed to evaluate the antileishmanial properties of essential oils (EOs) extracted from aerial parts of *Cupressus sempervirens* (*C. sempervirens*), *Tetraclinis articulata* (*T. articulata*), and

*Pistacia lentiscus* (*P. lentiscus*) trees. **Methods:** The EOs were obtained by hydro-distillation, and chemical composition was determined by gas chromatography coupled to mass spectrometry at three phenological stages. The EOs were evaluated in vitro for antileishmanial activities against *Leishmania major* (*L. major*) and *Leishmania infantum* (*L. infantum*). The cytotoxicity effect was also tested against murine macrophagic cells (Raw264.7 lines). **Results:** Results showed that *P. lentiscus* and *T. articulata* EOs presented low and moderate antileishmanial activity against *L. infantum* and *L. major*. However, *C. sempervirens* EO from the fructification stage gave an important selectivity index (23.89 and 18.96 against *L. infantum* and *L. major*, respectively). This activity was more interesting than those of amphotericin chemical drugs. Antileishmanial activity for this EO was highly correlated with germacrene D content ( $r = 1.00$ ). This compound presented a SI equal to 13.34 and 10.38 for the two strains. According to the Principal Component Analysis (PCA), the distribution of the three phenological stages proved that the chemical composition of the EOs affected the antileishmanial activity. PCA revealed that SI was positively correlated with  $\alpha$ -pinene, germacrene D and the sesquiterpene hydrocarbon class. *Cupressus sempervirens* EO can provide a source of germacrene D that can be used as a new alternative to chemical drugs for the treatment of antileishmanial diseases. **Conclusion:** *C. sempervirens* EO seemed to be a highly active antileishmanial agent and a natural alternative for chemical drugs to treat several leishmanial strains.

## Lèpre

### Systematic Review of Hansen Disease Attributed to *Mycobacterium lepromatosis*.

Collin SM, Lima A, Heringer S, Sanders V, Pessotti HA, Deps P.

Juil-2023

*Emerg Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37347507/>

In 2008, bacilli from 2 Hansen disease (leprosy) cases were identified as a new species, *Mycobacterium lepromatosis*. We conducted a systematic review of studies investigating *M. lepromatosis* as a cause of HD. Twenty-one case reports described 27 patients with PCR-confirmed *M. lepromatosis* infection (6 dual *M. leprae*/*M. lepromatosis*): 10 case-patients in the United States (7 originally from Mexico), 6 in Mexico, 3 in the Dominican Republic, 2 each in Singapore and Myanmar, and 1 each in Indonesia, Paraguay, Cuba, and Canada. Twelve specimen surveys reported 1,098 PCR-positive findings from 1,428 specimens, including *M. lepromatosis* in 44.9% (133/296) from Mexico, 3.8% (5/133) in Colombia, 12.5% (10/80) in Brazil, and 0.9% (2/224) from the Asia-Pacific region. Biases toward investigating *M. lepromatosis* as an agent in cases of diffuse lepromatous leprosy or from Mesoamerica precluded conclusions about clinicopathologic manifestations and geographic

distribution. Current multidrug treatments seem effective for this infection.

### Exploratory study of ultraviolet B (UVB) radiation and age of onset of bipolar disorder.

Bauer M, Glenn T, Achtyes ED, Alda M, Agaoglu E, Altınbaş K, Andreassen OA, Angelopoulos E, Arda R, Aydın M, Ayhan Y, Baethge C, Bauer R, Baune BT, Balaban C, Becerra-Palars C, Behere AP, Behere PB, Belete H, Belete T, Belizario GO, Bellivier F, Belmaker RH, Benedetti F, Berk M, Bersudsky Y, Bicaçci S, Birabwa-Oketcho H, Bjella TD, Brady C, Cabrera J, Cappucciati M, Castro AMP, Chen WL, Cheung EYW, Chiesa S, Crowe M, Cuomo A, Dallaspezia S, Del Zompo M, Desai P, Dodd S, Etain B, Fagiolini A, Fellendorf FT, Ferensztajn-Rochowiak E, Fiedorowicz JG, Fountoulakis KN, Frye MA, Geoffroy PA, Gitlin MJ, Gonzalez-Pinto A, Gottlieb JF, Grof P, Haarman BCM, Harima H, Hasse-Sousa M, Henry C, Hoffding L, Houenou J, Imbesi M, Isometsä ET, Ivkovic M, Janno S, Johnsen S, Kapczinski F, Karakatsoulis GN, Kardell M, Kessing LV, Kim SJ, König B, Kot TL, Koval M, Kunz M, Lafer B, Landén M, Larsen ER, Lenger M, Licht RW, Lopez-Jaramillo C, MacKenzie A, Madsen HØ, Madsen SAKA, Mahadevan J, Mahardika A, Manchia M, Marsh W, Martinez-Cengotitabengoa M, Martini J, Martiny K, Mashima Y, McLoughlin DM, Meesters Y, Melle I, Meza-Urzuá F, Mikolas P, Mok YM, Monteith S, Moorthy M, Morken G, Mosca E, Mozzhegorov AA, Munoz R, Mythri SV, Nacef F, Nadella RK, Nakanotani T, Nielsen RE, O'Donovan C, Omrani A, Osher Y, Ouali U, Pantovic-Stefanovic M, Pariwatcharakul P, Petite J, Petzold J, Pfennig A, Ruiz YP, Pinna M, Pompili M, Porter RJ, Quiroz D, Rabelo-da-Ponte FD, Ramesar R, Rasgon N, Ratta-Apha W, Ratzenhofer M, Redahan M, Reddy MS, Reif A, Reininghaus EZ, Richards JG, Ritter P, Rybakowski JK, Sathyaputri L, Scippa AM, Simhandl C, Smith D, Smith J, Stackhouse PW Jr, Stein DJ, Stilwell K, Strejilevich S, Su KP, Subramaniam M, Sulaiman AH, Suominen K, Tanra AJ, Tatebayashi Y, Teh WL, Tondo L, Torrent C, Tuinstra D, Uchida T, Vaaler AE, Vieta E, Viswanath B, Yoldi-Negrete M, Yalcinkaya OK, Young AH, Zgueb Y, Whybrow PC.

22-06-2023

*Int J Bipolar Disord.*

<https://pubmed.ncbi.nlm.nih.gov/37347392/>

### Reaching those at risk: Active case detection of leprosy and contact tracing at Kokosa, a hot spot district in Ethiopia.

Lema T, Bobosha K, Kasang C, Tarekegne A, Lambert S, Mengiste A, Britton S, Aseffa A, Woldeamanuel Y.

21-06-2023

*PLoS One.*

<https://pubmed.ncbi.nlm.nih.gov/37343000/>

**Introduction:** Leprosy is a chronic mycobacterial disease of public health importance. It is one of the leading causes of permanent physical disability. The prevalence of leprosy in Ethiopia has remained stagnant over the last decades. The aim of the study was to identify new leprosy cases and trace household contacts at risk of developing leprosy by

active case detection. The study area was Kokosa district, West Arsi zone, Oromia region, Ethiopia. **Method:** A prospective longitudinal study was conducted from June 2016-September 2018 at Kokosa district. Ethical approvals were obtained from all relevant institutions. Health extension workers screened households by house-to-house visits. Blood samples were collected and the level of anti-PGL-I IgM measured at two-time points. **Results:** More than 183,000 people living in Kokosa district were screened. Dermatologists and clinical nurses with special training on leprosy confirmed the new cases, and their household contacts were included in the study. Of the 91 new cases diagnosed and started treatment, 71 were recruited into our study. Sixty-two percent were males and 80.3% were multibacillary cases. A family history of leprosy was found in 29.6% of the patients with cohabitation ranging from 10 to 30 years. Eight new leprosy cases were diagnosed among the 308 household contacts and put on multi-drug therapy. The New Case Detection Rate increased from 28.3/100,000 to 48.3/100,000 between 2015/2016 and 2016/2017. Seventy one percent of leprosy patients and 81% of the household contacts' level of anti-PGL-I IgM decreased after treatment. In conclusion, the results of the study showed the importance of active case detection and household contact tracing. It enhances early case finding, and promotes early treatment, thereby interrupting transmission and preventing potential disability from leprosy.

### Exploring the potential of a polyvinyl alcohol/chitosan-based nanofibrous matrix for erythromycin delivery: fabrication, in vitro and in vivo evaluation.

**Cheng Y, Farasati Far B, Jahanbakhshi M, Bahrami S, Tamimi P, Sedaghat M, Ghazizadeha E.**

19-06-2023

RSC Adv.

<https://pubmed.ncbi.nlm.nih.gov/37342809/>

This study aimed to investigate the potential of polyvinyl alcohol/chitosan nanofibers as a drug delivery system for erythromycin. Polyvinyl alcohol/chitosan nanofibers were fabricated using the electrospinning method and characterized using SEM, XRD, AFM, DSC, FTIR, swelling assessment and viscosity analysis. The *in vitro* drug release kinetics, biocompatibility, and cellular attachments of the nanofibers have been evaluated using *in vitro* release studies and cell culture assays. The results showed that the polyvinyl alcohol/chitosan nanofibers displayed improved *in vitro* drug release and biocompatibility compared to the free drug. The study provides important insights into the potential of polyvinyl alcohol/chitosan nanofibers as a drug delivery system for erythromycin and highlights the need for further investigation into the development of nanofibrous drug delivery systems based on polyvinyl alcohol/chitosan for improved therapeutic efficacy and reduced toxicity. The nanofibers prepared in this approach use less antibiotics, which may be beneficial to the environment. The resulting nanofibrous matrix can be used for external drug delivery applications, such as wound healing or topical antibiotic therapy.

### Evaluating the impact of cash transfers on tuberculosis (ExaCT TB): a stepped wedge cluster randomised controlled trial.

**Shete PB, Kadota JL, Nanyunja G, Namale C, Nalugwa T, Oyuku D, Turyahabwe S, Kiwanuka N, Cattamanchi A, Katamba A.**

19-06-2023

ERJ Open Res.

<https://pubmed.ncbi.nlm.nih.gov/37342088/>

### Quantitative Real-Time Polymerase Chain Reaction for Detection of Mycobacterium leprae DNA in Tissue Specimens from Patients with Leprosy.

**Sarath IM, Joseph NM, Jamir I.**

20-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37339763/>

### Mycobacterium kiyosense sp. nov., a scotochromogenic slow-growing species isolated from respiratory specimens.

**Fukano H, Kazumi Y, Sakagami N, Fujiwara N, Ato M, Mitarai S, Hoshino Y.**

Juin-2023

Int J Syst Evol Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37339072/>

Scotochromogenic slow-growing mycobacteria were isolated from the sputum or bronchoalveolar lavage fluid of 12 patients in Japan. From a comparison of the whole-genome sequences, the representative strain IWGMT90018-18076<sup>T</sup> and the unknown strains obtained from the patients were found to represent a novel species related to the *Mycobacterium gordonae* complex. The average nucleotide identity values of IWGMT90018-18076<sup>T</sup> with *Mycobacterium vicinigordonae*, *Mycobacterium paragordonae* and *M. gordonae* were 86.7, 82.5 and 82.2 %, respectively. The genome size of the representative strain IWGMT90018-18076<sup>T</sup> was approximately 6.3 Mbp, and the genomic DNA G+C content was 67.1 %. The major fatty acid methyl esters were C<sub>16</sub>:<sub>0</sub> (37.71 %), C<sub>18</sub>:<sub>1</sub>ω<sub>9c</sub> (29.5 %) and C<sub>16</sub>:<sub>1</sub>ω<sub>7c</sub> (10.32 %). In this study, we performed phylogenetic analyses, physiological and biochemical characteristic tests, drug susceptibility tests and fatty acid profiling of the clinical isolates. On the basis of the results obtained, we propose that the unknown clinical isolates represent a novel species, '*Mycobacterium kiyosense* sp. nov.', with the type strain being IWGMT90018-18076<sup>T</sup> (=JCM 34837<sup>T</sup> =KCTC 49725<sup>T</sup>).

### Rare concurrence of lepromatous leprosy and cutaneous tuberculosis.

**Muna B, Neerukonda P.**

Avr-Juin 2023

Int J Mycobacteriol.

<https://pubmed.ncbi.nlm.nih.gov/37338487/>

The coinfection of leprosy and tuberculosis has been rarely reported in literature. A middle-aged man who was a

known case of hepatitis B infection had presented with ichthyosis with claw hand deformity and submandibular swelling, which were diagnosed with lepromatous leprosy and scrofuloderma, respectively.

### Psoriasis and Leprosy: An Arcane Relationship.

Ge G, Shang J, Gan T, Chen Z, Pan C, Mei Y, Long S, Wu A, Wang H.

14-06-2023

*J Inflamm Res.*

<https://pubmed.ncbi.nlm.nih.gov/37337513/>

### Gene Expression of Human Beta-Defensin-3 and Cathelicidin in the Skin of Leprosy Patients, Household Contacts, and Healthy Individuals from Indonesia.

Argentina F, Suwarsa O, Gunawan H, Berbudi A.

12-06-2023

*Clin Cosmet Investig Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/37333516/>

**Background:** Leprosy, a chronic infectious peripheral neuropathy, is caused by *Mycobacterium leprae*. This bacterium produces triacylated lipopeptides that can induce the immune system via the Toll-like receptor 2/1 (TLR 2/1) complex. Activation of TLR 2/1 produces proinflammatory cytokines and antimicrobial peptides (AMPs), including human beta-defensin-3 (HBD-3) and cathelicidin. **Purpose:** To analyze differences in gene expression of HBD-3 and cathelicidin in the skin of leprosy patients, household contacts, and healthy individuals. **Patients and methods:** An analytic observational study was conducted at the Outpatient Clinic of Dermatology and Venereology of Dr Mohammad Hoesin General Hospital, Palembang, Indonesia, from January 2021 to June 2022. In each group of 18 subjects, 72 samples were collected, including skin lesion in leprosy patients, normal skin in leprosy patients, household contacts, and healthy individuals. A comparison of HBD-3 and cathelicidin gene expression between the four groups was analyzed using Pearson Chi Square, Kruskal-Wallis, and Mann-Whitney Test. **Results:** The median value of HBD-3 gene expression on skin lesion in leprosy patients was 260.61 (0.19-3734.10); normal skin in leprosy patients was 1.91 (0.01-151.17); household contacts skin was 7.93 (0.27-121.10); and healthy individuals' skin was 1.00 (1.00-1.00) is highly significant difference ( $p < 0.0001$ ). The median value of cathelicidin gene expression on skin lesion in leprosy patients was 38.72 (0.28-1852.17); normal skin in leprosy patients was 0.48 (0.01-15.83); household contacts skin was 9.8 (0.04-128.0); and healthy individual skin was 1.00 (1.00-1.00), also highly significant difference ( $p < 0.0001$ ).

### Hi-plex deep amplicon sequencing for identification, high-resolution genotyping and multidrug resistance prediction of *Mycobacterium leprae* directly from patient biopsies by using Deeplex Myc-Lep.

Jouet A, Braet SM, Gaudin C, Bisch G, Vasconcellos S, Epaminondas Nicacio de Oliveira do Livramento RE, Prado Palacios YY, Fontes AB, Lucena N, Rosa P, Moraes M, La K, Badalato N, Lenoir E, Ferré A, Clément M, Hasker E, Grillone SH, Abdou W, Said A, Assoumani Y, Attoumani N, Laurent Y, Cambau E, de Jong BC, Suffys PN, Supply P.

14-06-2023

*EBioMedicine.*

<https://pubmed.ncbi.nlm.nih.gov/37327675/>

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

Chaudhary SK, Kalita J, Misra UK.

Mai-Juin 2023

*Neural India.*

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

**Background and objective:** To report the role of nerve conduction study (NCS) in diagnosis, monitoring, and prognosis of Hansen's disease (HD). **Materials and methods:** In a hospital-based prospective observational study, the patients with HD as per World Health Organization (WHO) criteria were included; muscle wasting power, reflexes, and sensations were recorded. Motor NCS of median, ulnar, and peroneal nerves and sensory NCS of ulnar, median, and sural nerves were recorded. Disability was graded using WHO grading scale. The outcome was assessed after 6 months using modified Rankin scale. **Results:** In the present study, 38 patients with a median age of 40 (15-80) years and five females were included. The diagnosis was tuberculoid in seven, borderline tuberculoid in 23, borderline lepromatous in two, and borderline in six patients. The disability was grade 1 and 2 in 19 patients each. Out of 480 nerves studied, NCS was normal in 139 sensory (57.4%) and 160 (67.2%) motor nerves. NCSs were axonal in seven sensory and eight motor nerves, demyelinating in three nerves, and mixed in one in seven patients who had lepra reaction. NCS findings did not correlate with disability ( $p = 1.0$ ) or outcome (0.304) and provided additional information in 11 nerves (seven patients). Peripheral nerves were enlarged in 79. NCSs were normal in 32 (29.90%) in thickened nerves. **Conclusion:** In HD, NCS abnormalities correlated with respective sensory or motor abnormality but related with neither disability nor the outcome.

### 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/>

### Evidencing leprosy neuronal inflammation by 18-Fluoro-deoxy-glucose.

Penna PS, De Souza SAL, De Lacerda PGLN, Rodrigues Pitta IJ, Spitz CN, Sales AM, Lara FA, De Souza ACS, Sarno EN, Pinheiro RO, Jardim MR.

05-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37276237/>

**Background:** Leprosy is caused by multiple interactions between *Mycobacterium leprae* (*M. leprae*) and the host's peripheral nerve cells. *M. leprae* primarily invades Schwann cells, causing nerve damage and consequent development of disabilities. Despite its long history, the pathophysiological mechanisms of nerve damage in the lepromatous pole of leprosy remain poorly understood. This study used the findings of 18F-FDG PET/CT on the peripheral nerves of eight lepromatous patients to evaluate the degree of glucose uptake by peripheral nerves and compared them with clinical, electrophysiological, and histopathological evaluations. **Methods:** Eight patients with lepromatous leprosy were included in this study. Six patients were evaluated up to three months after leprosy diagnosis using neurological examination, nerve conduction study, 18F-FDG PET/CT, and nerve biopsy. Two others were evaluated during an episode of acute neuritis, with clinical, neurophysiological, and PET-CT examinations to compare the images with the first six. **Results:** Initially, six patients already had signs of peripheral nerve injury, regardless of symptoms; however, they did not present with signs of neuritis, and there was little or no uptake of 18F-FDG in the clinically and electrophysiologically affected nerves. Two patients with signs of acute neuritis had 18F-FDG uptake in the affected nerves. **Conclusions:** 18F-FDG uptake correlates with clinical neuritis in lepromatous leprosy patients but not in silent neuritis patients. 18F-FDG PET-CT could be a useful tool to confirm neuritis, especially in cases that are difficult to diagnose, such as for the differential diagnosis between a new episode of neuritis and chronic neuropathy.

### Bohn's Nodules.

Yumnam D, Moirangthem A.

Mai-Juin 2023

*J Cutan Med Surg.*

<https://pubmed.ncbi.nlm.nih.gov/37113022/>

### Diagnosis of Human Cutaneous Leishmaniasis: A Comparative Study Using CL Detect™ Dipstick, Direct Smear and Polymerase Chain Reaction Methods.

Zamanpour M, Mohebbali M, Khamesipour A, Mohammadi AMA, Akhoundi B.

Juin-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36913075/>

**Introduction:** In most of the endemic areas, the detection of CL is based on searching for amastigotes using the direct smear method. Since expert microscopists are not usually available in every laboratory, false diagnoses are a disaster that happens. Therefore, the aim of current research is to evaluate the validity of the CL Detect™ Rapid Test (CDRT) for diagnosis CL in comparison to direct smear and polymerase chain reaction (PCR) methods. **Methods:** A total of 70 patients with skin lesions suspected to be CL were recruited. Skin samples from the lesions were

collected and used for direct microscopic examination and the PCR method. Furthermore, the skin sample was collected in accordance with the manufacturer's instructions for the CDRT-based rapid diagnostic test. **Results:** Of 70 samples, 51 and 35 samples were positive by direct smear examination and the CDRT, respectively. The PCR showed positive results in 59 samples; 50 and 9 samples were identified as *Leishmania major* and *Leishmania tropica*, respectively. The sensitivity and specificity were calculated to be 68.6% (95% CI 54.11-80.89%) and 100% (95% CI 82.35-100%). When the results of CDRT were compared to the microscopic examinations, an agreement of 77.14% was seen between the CDRT and microscopic examination. In addition, the sensitivity and specificity were 59.32% (95% CI 45.75-71.93%) and 100% (95% CI 71.5-100%) when the CDRT was compared to PCR assay (as gold standard) and an agreement (65.71%) was found between CDRT and PCR assay. **Conclusion:** As the CDRT is simple, rapid, and does not require great proficiency, it is recommended for use in the detection of CL caused by *L. major* or *L. tropica* as a diagnostic method, especially in areas with limited access to expert microscopists.

### Emerging hepatitis C virus and neuron-allied neuroviral intertwine and its therapeutic approaches.

Mukerjee N, Chaudhari SY, Jha S, Sinha S, Jadhav SB, Dhar R, Rathod VD, Nanaware RB, Chakole RD, Sharma D, Sharma PP, Pawar SD, Ghosh A.

01-06-2023

*Int J Surg.*

<https://pubmed.ncbi.nlm.nih.gov/36906766/>

### MiR-1290: a potential therapeutic target for regenerative medicine or diagnosis and treatment of non-malignant diseases.

Kalhari MR, Soleimani M, Yari K, Moradi M, Kalhari AA.

Juil-2023

*Clin Exp Med.*

<https://pubmed.ncbi.nlm.nih.gov/35802264/>

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## Morsures de serpent

### Antivenom access impacts severity of Brazilian snakebite envenoming: A geographic information system analysis.

Isaacson JE, Ye JJ, Silva LL, Hernandez Rocha TA, de Andrade L, Scheidt JFHC, Wen FH, Sachett J, Monteiro WM, Staton CA, Vissoci JRN, Gerardo CJ.

21-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37343007/>

**Background:** Snakebite envenoming (SBE) is a neglected tropical disease capable of causing both significant disability and death. The burden of SBE is especially high in low- and middle-income countries. The aim of this study was to perform a geospatial analysis evaluating the association of sociodemographics and access to care

indicators on moderate and severe cases of SBE in Brazil.

**Methods:** We conducted an ecological, cross-sectional study of SBE in Brazil from 2014 to 2019 using the open access National System Identification of Notifiable Diseases (SINAN) database. We then collected a set of indicators from the Brazil Census of 2010 and performed a Principal Component Analysis to create variables related to health, economics, occupation, education, infrastructure, and access to care. Next, a descriptive and exploratory spatial analysis was conducted to evaluate the geospatial association of moderate and severe events. These variables related to events were evaluated using Geographically Weighted Poisson Regression. T-values were plotted in choropleth maps and considered statistically significant when values were  $<-1.96$  or  $>+1.96$ .

**Results:** We found that the North region had the highest number of SBE cases by population (47.83/100,000), death rates (0.18/100,000), moderate and severe rates (22.96/100,000), and proportion of cases that took more than three hours to reach healthcare assistance (44.11%). The Northeast and Midwest had the next poorest indicators. Life expectancy, young population structure, inequality, electricity, occupation, and more than three hours to reach healthcare were positively associated with greater cases of moderate and severe events, while income, illiteracy, sanitation, and access to care were negatively associated. The remaining indicators showed a positive association in some areas of the country and a negative association in other areas. **Conclusion:** Regional disparities in SBE incidence and rates of poor outcomes exist in Brazil, with the North region disproportionately affected. Multiple indicators were associated with rates of moderate and severe events, such as sociodemographic and health care indicators. Any approach to improving snakebite care must work to ensure the timeliness of antivenom administration.

### Comparing modified Lee and White method against 20-minute whole blood clotting test as bedside coagulation screening test in snake envenomation victims.

Suseel A, Abraham SV, Paul S, Tomy MML, Rafi AM.  
19-06-2023

*J Venom Anim Toxins Incl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37342654/>

### Snakebite-associated thrombotic microangiopathy: a spotlight on pharmaceutical interventions.

Noutsos T, Isbister GK.

Jan-Juin 2023

*Expert Rev Clin Pharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37259708/>

### Detection of cytotoxins by sandwich-ELISA for discrimination of cobra envenomation and indication of necrotic severity.

Liu CC, Chou YS, Wu CJ, Hsieh CH, Hsiao YC, Chu LJ, Ouyang CH, Lin CC, Liaw GW, Chen CK.

01-06-2032

*Int J Biol Macromol.*

<https://pubmed.ncbi.nlm.nih.gov/37210050/>

Snake envenoming is both a healthcare and socioeconomic problem for developing countries and underserved communities. In Taiwan, clinical management of *Naja atra* envenomation is a major challenge, since cobra venom-induced symptoms are usually confused with hemorrhagic snakebites and current antivenom treatments do not effectively prevent venom-induced necrosis for which early surgical debridement should be administered. Identification and validation of biomarkers of cobra envenomation is critical for progress in setting a realistic goal for snakebite management in Taiwan. Previously, cytotoxin (CTX) was determined as one of potential biomarker candidates; however, its ability to discriminate cobra envenoming remains to be verified, especially in clinical practice. In this study, we selected a monoclonal single-chain variable fragment (scFv) and a polyclonal antibody to develop a sandwich enzyme-linked immunosorbent assay (ELISA) for CTX detection, which successfully recognized CTX from *N. atra* venom over that from other snake species. Using this specific assay, the CTX concentration in envenoming mice was shown to remain consistent in about 150 ng/mL during the 2-hour post-injection period. The measured concentration was highly correlated with the size of local necrosis in mouse dorsal skin, which the correlation coefficient is about 0.988. Furthermore, our ELISA method displayed 100 % of specificity and sensitivity in discriminating cobra envenoming among snakebite victims through CTX detection and the level of CTX in victim plasma was ranged from 5.8 to 253.9 ng/mL. Additionally, patients developed tissue necrosis at plasma CTX concentrations higher than 150 ng/mL. Thus, CTX not only serves as a verified biomarker for discrimination of cobra envenoming but also a potential indicator of severity of local necrosis. In this context, detection of CTX may facilitate reliable identification of envenoming species and improve snakebite management in Taiwan.

### Snakebite envenomation-induced posterior reversible encephalopathy syndrome presenting with Bálint syndrome.

Ghosh R, León-Ruiz M, Das S, Dubey S, Benito-León J.

Juil-Août 2023

*Neurologia (Engl Ed).*

<https://pubmed.ncbi.nlm.nih.gov/35878800/>

### The concept of Big Four: Road map from snakebite epidemiology to antivenom efficacy.

Gopal G, Muralidar S, Prakash D, Kamalakkannan A, Indhuprakash ST, Thirumalai D, Ambi SV.

01-06-2023

*Int J Biol Macromol.*

<https://pubmed.ncbi.nlm.nih.gov/37169043/>

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## Mycétome

### Primary mycetoma of the calcaneum: Case report on an unusual hazard of barefoot walking.

Nasir MU, Mukhtar MU, Nasir Z, Mehmood Q, Raza MS, Ali MN.

17-06-2023

*Int J Surg Case Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37343500/>

### The Rise of AI: How Artificial Intelligence is Revolutionizing Infectious Disease Control.

Siddig EE, Eltigani HF, Ahmed A.

19-06-2023

*Ann Biomed Eng.*

<https://pubmed.ncbi.nlm.nih.gov/37335374/>

Artificial Intelligence (AI) has proven to be an effective tool in predicting, detecting, and mitigating the spread of infectious diseases, especially during the COVID-19 pandemic. The technology is increasingly playing a role in preventing future health crises by predicting outbreaks, identifying high-risk areas, and aiding in vaccine development. AI can track and trace infected individuals and identify potential hotspots, help reduce the spread of infectious diseases, and monitor patient symptoms, enabling healthcare professionals to provide effective treatment.

### The critical state of children's health during the Sudan crisis.

Aborode AT, Fasawe AS, Agwuna FO, Badri R, Adewunmi RO.

15-06-2023

*Lancet Child Adolesc Health.*

<https://pubmed.ncbi.nlm.nih.gov/37331357/>

### Evaluation of the Antiparasitic and Antifungal Activities of Synthetic Piperlongumine-Type Cinnamide Derivatives: Booster Effect by Halogen Substituents.

Khan TA, Al Nasr IS, Koko WS, Ma J, Eckert S, Brehm L, Ben Said R, Daoud I, Hanachi R, Rahali S, van de Sande WWJ, Ersfeld K, Schobert R, Biersack B.

15-06-2023

*ChemMedChem.*

<https://pubmed.ncbi.nlm.nih.gov/37021847/>

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## Onchocercose

### Sociodemographics, Clinical Factors, and Biological Factors Associated with Loiasis in Endemic Onchocerciasis Areas in Southern Gabon.

Moutongo Mouandza R, Mourou JR, Moutombi Ditombi B, Roger Sibi Matotou H, Ekomi B, Bouyou-Akotet MK, Mawili-Mboumba DP.

20-06-2023

*Am J Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/37339766/>

To implement the appropriate strategies for scale-up interventions to eliminate onchocerciasis without severe adverse events, clinical and biological factors associated with loiasis were analyzed in onchocerciasis-endemic areas. Blood was collected from volunteers after examination by a physician. Detection of microfilariae and measurement of Ov16 IgG4 were performed using direct microscopic examination of blood and onchocerciasis rapid test detection, respectively. Areas with sporadic, hypoendemic, and hyperendemic onchocerciasis endemicity were found. Participants with microfilaremia were considered microfilaremic, and those without microfilaremia were seen as amicrofilaremic. Of the 471 study participants, 40.5% (n = 191) had microfilariae. Among them, *Mansonella* spp. was the most common (78.2%, n = 147), followed by *Loa loa* (41.4%, n = 79). The association between the two species represented 18.3% (n = 35). The specific immunoglobulins of *Onchocerca volvulus* were detected in 24.2% of participants (n = 87/359). Overall prevalence of *L. loa* was 16.8%. Hypermicrofilaremia was found in 3% (N = 14), and one participant had more than 30,000 microfilariae per milliliter. The frequency of *L. loa* did not vary according to the level of onchocerciasis transmission. Pruritus was the most common clinical sign (60.5%, n = 285) reported, mainly in microfilaremic participants (72.2%, n = 138/191). The prevalence of *L. loa* microfilaria in the study population was below the threshold at risk for the occurrence of serious side effects due to ivermectin. Clinical manifestations frequently observed could be exacerbated by microfilaremia in areas where onchocerciasis transmission is high.

### Nodding syndrome, a case-control study in Mahenge, Tanzania: *Onchocerca volvulus* and not *Mansonella perstans* as a risk factor.

Amaral LJ, Bhwana D, Mhina AD, Mmbando BP, Colebunders R.

20-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37339148/>

**Background:** Nodding syndrome (NS) has been consistently associated with onchocerciasis. Nevertheless, a positive association between NS and a *Mansonella perstans* infection was found in South Sudan. We aimed to determine whether the latter parasite could be a risk factor for NS in Mahenge. **Methods:** Cases of epilepsy were identified in villages affected by NS in Mahenge, Tanzania, and matched with controls without epilepsy of the same sex, age and village. We examined blood films of cases and controls to identify *M. perstans* infections. The participants were also asked for sociodemographic and epilepsy information, examined for palpable onchocercal nodules and onchocerciasis-related skin lesions and tested for anti-*Onchocerca volvulus* antibodies (Ov16 IgG4) by

ELISA. Clinical characteristics of cases and controls, *O. volvulus* exposure status and relevant sociodemographic variables were assessed by a conditional logistic regression model for NS and epilepsy status matched for age, sex and village. **Results:** A total of 113 epilepsy cases and 132 controls were enrolled, of which, respectively, 56 (49.6%) and 64 (48.5%) were men. The median age in cases and controls was 28.0 (IQR: 22.0-35.0) and 27.0 (IQR: 21.0-33.3) years. Of the persons with epilepsy, 43 (38.1%) met the probable NS criteria and 106 (93.8%) had onchocerciasis-associated epilepsy (OAE). *M. perstans* infection was absent in all participants, while *Ov16* seroprevalence was positively associated with probable NS (odds ratio (OR): 5.05, 95%CI: 1.79-14.27) and overall epilepsy (OR: 2.03, 95%CI: 1.07-3.86). Moreover, onchocerciasis-related skin manifestations were only found in the cases ( $n = 7$ ,  $p = 0.0040$ ), including persons with probable NS ( $n = 4$ ,  $p = 0.0033$ ). Residing longer in the village and having a family history of seizures were positively correlated with *Ov16* status and made persons at higher odds for epilepsy, including probable NS. **Conclusion:** In contrast to *O. volvulus*, *M. perstans* is most likely not endemic to Mahenge and, therefore, cannot be a co-factor for NS in the area. Hence, this filaria is unlikely to be the primary and sole causal factor in the development of NS. The main risk factor for NS remains onchocerciasis.

### In Vitro Filaricidal Properties of Hydro-Methanolic Extracts of Powdery Fractions of *Khaya senegalensis* (Meliaceae) on *Onchocerca ochengi*.

Galani Tietcheu BR, Betrosse T, Ayiseh RB, Yuunoeone EI, Mfotie Njoya E, Nveikoueng F, Njintang NY, Ndjinka D.

19-06-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37336863/>

### Survival of worm masses of *Onchocerca ochengi* in gerbils and hamsters: implications for the development of an in vivo macrofilaricide screening model.

Ayiseh RB, Mbah GE, Manfo FPT, Kulu TK, Njotu FN, Monya E, Ndi EM, Tumanjong IM, Mainsah EN, Sakanari J, Lustigman S, Cho-Ngwa F.

Juil-2023

*Parasitol Res.*

<https://pubmed.ncbi.nlm.nih.gov/37154921/>

Onchocerciasis, the second leading infectious cause of blindness, afflicts approximately 21 million people globally. Its control is limited to the use of the microfilaricidal drugs, ivermectin and moxidectin. Both drugs are unable to kill the adult worms which can survive for up to 15 years in patients, justifying the urgent need for potent and novel macrofilaricides that kill adult worms. The development of such drugs has been hindered by the lack of an appropriate small laboratory animal model to evaluate potential drug candidates in vivo. This study assessed the survival of *O. ochengi* female worms and their embryos over time in two laboratory rodents: gerbils

and hamsters and tested using "proof-of-concept" studies, whether known macrofilaricidal drugs can kill these worms. Animals were surgically implanted with mechanical or collagenase-liberated *O. ochengi* worm masses, and necropsied at various time points to test for survival. Recovered worm masses were assessed for viability by biochemical analysis (MTT/formazan assay) or fecundity (embryogram). Flubendazole (FBZ) administered at 20 mg/kg body weight was used to validate both rodent models. By day 26 post-implantation of 15 worm masses, a median of 7.00 (4.00-10.00) was recovered from hamsters, and 2.50 (2.00-4.00) from gerbils. Worm masses recovered from gerbils were mostly disintegrated or fragmented, with significantly higher fragmentation observed with collagenase-liberated worm masses. FBZ had no significant effect on the number of worm masses recovered, but enhanced embryo degradation in gerbils and reduced worm mass viability in hamsters. This exploratory study has revealed the gerbil and hamster as permissible rodents to adult female worms of *O. ochengi*. The hamsters appeared to maintain the worms longer, compared to gerbils.

## Rage

### Unmodified rabies mRNA vaccine elicits high cross-neutralizing antibody titers and diverse B cell memory responses.

Hellgren F, Cagigi A, Arcoverde Cerveira R, Ols S, Kern T, Lin A, Eriksson B, Dodds MG, Jasny E, Schwendt K, Freuling C, Müller T, Corcoran M, Karlsson Hedestam GB, Petsch B, Loré K.

22-06-2023

*Nat Commun.*

<https://pubmed.ncbi.nlm.nih.gov/37349310>

### Whole-brain monosynaptic inputs and outputs of leptin receptor b neurons of the nucleus tractus solitarius in mice.

Sun L, Zhu M, Wang M, Hao Y, Hao Y, Jing X, Yu H, Shi Y, Zhang X, Wang S, Yuan F, Yuan XS.

20-06-2023

*Brain Res Bull.*

<https://pubmed.ncbi.nlm.nih.gov/37348822/>

The nucleus tractus solitarius (NTS) is the primary central station that integrates visceral afferent information and regulates respiratory, gastrointestinal, cardiovascular, and other physiological functions. Leptin receptor b (LepRb)-expressing neurons of the NTS (NTS<sup>LepRb</sup> neurons) are implicated in central respiration regulation, respiratory facilitation, and respiratory drive enhancement. Furthermore, LepRb dysfunction is involved in obesity, insulin resistance, and sleep-disordered breathing. However, the monosynaptic inputs and outputs of NTS<sup>LepRb</sup> neurons in whole-brain mapping remain to be elucidated. Therefore, the exploration of its whole-brain connection system may provide strong support for comprehensively understanding the physiological and pathological functions of NTS<sup>LepRb</sup> neurons. In the present study, we used a cell type-specific, modified rabies virus and adeno-associated virus with the Cre-loxp system to map

monosynaptic inputs and outputs of NTS<sup>LepRb</sup> neurons in LepRb-Cre mice. The results showed that NTS<sup>LepRb</sup> neurons received inputs from 48 nuclei in the whole brain from five brain regions, including especially the medulla. We found that NTS<sup>LepRb</sup> neurons received inputs from nuclei associated with respiration, such as the pre-Bötzinger complex, ambiguus nucleus, and parabrachial nucleus. Interestingly, some brain areas related to cardiovascular regulation-i.e., the ventrolateral periaqueductal gray and locus coeruleus-also sent a small number of inputs to NTS<sup>LepRb</sup> neurons. In addition, anterograde tracing results demonstrated that NTS<sup>LepRb</sup> neurons sent efferent projections to 15 nuclei, including the dorsomedial hypothalamic nucleus and arcuate hypothalamic nucleus, which are involved in regulation of energy metabolism and feeding behaviors. Quantitative statistical analysis revealed that the inputs of the whole brain to NTS<sup>LepRb</sup> neurons were significantly greater than the outputs. Our study comprehensively revealed neuronal connections of NTS<sup>LepRb</sup> neurons in the whole brain and provided a neuroanatomical basis for further research on physiological and pathological functions of NTS<sup>LepRb</sup> neurons.

### **Short-Chain Fatty Acids Alleviate Vancomycin-Caused Humoral Immunity Attenuation in Rabies-Vaccinated Mice by Promoting the Generation of Plasma Cells via Akt-mTOR Pathway.**

**Wu Q, Zhang Y, Wang C, Hou Y, He W, Wang L, Xiong J, Ren Z, Wang H, Sui B, Zhou D, Zhou M, Fu ZF, Zhao L.**  
20-06-2023  
*J Virol.*

<https://pubmed.ncbi.nlm.nih.gov/37338411/>

Mounting evidence suggests that gut microbial composition and its metabolites, including short-chain fatty acids (SCFAs), have beneficial effects in regulating host immunogenicity to vaccines. However, it remains unknown whether and how SCFAs improve the immunogenicity of the rabies vaccine. In this study, we investigated the effect of SCFAs on the immune response to rabies vaccine in vancomycin (Vanco)-treated mice and found that oral gavage with butyrate-producing bacteria (*C. butyricum*) and butyrate supplementation elevated RABV-specific IgM, IgG, and virus-neutralizing antibodies (VNAs) in Vanco-treated mice. Supplementation with butyrate expanded antigen-specific CD4<sup>+</sup> T cells and IFN- $\gamma$ -secreting cells, augmented germinal center (GC) B cell recruitment, promoted plasma cells (PCs) and RABV-specific antibody-secreting cells (ASCs) generation in Vanco-treated mice. Mechanistically, butyrate enhanced mitochondrial function and activated the Akt-mTOR pathway in primary B cells isolated from Vanco-treated mice, ultimately promoting B lymphocyte-induced maturation protein-1 (Blimp-1) expression and CD138<sup>+</sup> PCs generation. These results highlight the important role of butyrate in alleviating Vanco-caused humoral immunity attenuation in rabies-vaccinated mice and maintaining host immune homeostasis. **IMPORTANCE** The gut microbiome plays many crucial roles in the maintenance of immune homeostasis. Alteration of the gut microbiome and metabolites has been shown to impact vaccine

efficacy. SCFAs can act as an energy source for B-cells, thereby promoting both mucosal and systemic immunity in the host by inhibiting HDACs and activation of GPR receptors. This study investigates the impact of orally administered butyrate, an SCFA, on the immunogenicity of rabies vaccines in Vanco-treated mice. The results showed that butyrate ameliorated humoral immunity by facilitating the generation of plasma cells via the Akt-mTOR in Vanco-treated mice. These findings unveil the impact of SCFAs on the immune response of the rabies vaccine and confirm the crucial role of butyrate in regulating immunogenicity to rabies vaccines in antibiotic-treated mice. This study provides a fresh insight into the relationship of microbial metabolites and rabies vaccination.

### **Side-by-side comparative study of the immunogenicity of the intramuscular and intradermal rabies post-exposure prophylaxis regimens in a cohort of suspected RABV exposed individuals.**

**Auerswald H, Maestri A, Touch S, In S, Ya N, Heng B, Bosch-Castells V, Augard C, Petit C, Dussart P, Peng Y, Cantaert T, Ly S.**

20-06-2023

*Clin Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37337899/>

### **Emergence, Tropism, Disease, and Treatment of Australian Bat Lyssavirus Infections in Humans.**

**Young AR, Stobart CC.**

19-06-2023

*Vector Borne Zoonotic Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37335942/>

### **Comparison of Anti-rabies Virus Nucleoprotein IgY Prepared by DNA Immunization and Protein Immunization.**

**Kubo N, Park CH, Inoue S, Hatta H.**

17-06-2023

*J Poult Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37334105/>

Immunization of egg-laying hens with viral antigens efficiently produces large amounts of virus-specific IgY antibodies from egg yolks. A supply of practical and economical antibodies against the rabies virus is being desired worldwide. We immunized hens with the antigen gene DNA of the rabies virus, purified specific IgY antibodies from the egg yolk, and characterized the immuno-protein chemistry for use as a diagnosis. To prepare specific IgY antibodies against rabies virus nucleoprotein (RV-N) by DNA immunization, laying hens were pre-injected with  $\lambda$ -carrageenan or Freund's complete adjuvant to increase local immune activity (pre-immune stimulation), and then immunized with RV-N recombinant plasmid DNA. RV-N-specific IgY antibodies were prepared from egg yolks of immunized hens. For comparison, conventional protein antigen immunization was also used to induce the production of RV-N-specific

IgY antibodies. Laying hens were immunized with an RV-N protein antigen and RV-N-specific IgY was purified from egg yolks. The binding activity against RV-N antigens was examined using IgY samples prepared by DNA (with pre-immune stimulation) and protein immunization. Immunohistochemical staining showed that IgY antibodies prepared by protein immunization strongly detected viral antigens in the brain sections of dogs infected with the virus, whereas IgY antibodies prepared by DNA immunization did not. Enzyme-linked immunosorbent assay was performed using a commercially available rabies vaccine (inactivated virus) treated with 10% formalin and heating (60°C, 30 min and 90°C, 5 min). IgY prepared by DNA immunization had weaker reactivity with denatured antigens and lower antigen concentrations than IgY prepared by protein immunization. These results suggest that it is necessary to develop a DNA immunization method for inducing IgY antibodies against the rabies virus that strongly bind to native and denatured antigens to prepare specific IgYs that can be used for antigen detection in clinical tests.

### **Rabies in an imported dog, Ontario, 2021.**

**Rebellato S, Choi M, Gitelman J, Ratiu F, Magnusson K, Armstrong B, Fehlner-Gardiner C, McClinchey H, Tataryn J, Anderson ME, Di Salvo P, Gardner C.**

09-06-2022

*Can Commun Dis Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37333573/>

In July 2021, a dog was imported into Canada from Iran and subsequently developed clinical signs of rabies within 11 days of arrival. Following laboratory confirmation of the diagnosis of rabies, local, provincial and federal inter-agency collaboration was required to complete contact tracing to identify all persons and domestic animals that may have been exposed to the rabid dog during the potential virus shedding period. This case highlights the risks of importing animals from known canine rabies-endemic areas, identifies gaps in current dog importation policies that pose potential risk to human and animal health and prompts ongoing vigilance for this deadly disease among human and animal health partners, as well as members of the public who adopt imported dogs.

### **Integrating a community-based continuous mass dog vaccination delivery strategy into the veterinary system of Tanzania: A process evaluation using normalization process theory.**

**Duamor CT, Hampson K, Lankester F, Lugelo A, Chagalucha J, Lushasi KS, Czapryna A, Mpolya E, Kreppel K, Cleaveland S, Wyke S.**

03-06-2023

*One Health.*

<https://pubmed.ncbi.nlm.nih.gov/37332884/>

### **One Health at gunpoint: Impact of wild boars as exotic species in Brazil - A review.**

**Kmetiuk LB, Biondo LM, Pedrosa F, Favero GM, Biondo AW.**

08-06-2023

*One Health.*

<https://pubmed.ncbi.nlm.nih.gov/37332883/>

Wild boars have been listed among the 100 most invasive species worldwide, spreading impacts to all continents, with the exception of Antarctica. In Brazil, a major source of introduction was a commercial livestock importation for exotic meat market, followed by successive escapes and releases to natural ecosystems. Currently found in all six Brazilian biomes, with reports in 11 Brazilian states, wild boars have invaded natural and agricultural areas. Wild boars have been reportedly indicated as hosts and reservoirs of several zoonotic diseases in Brazil, including toxoplasmosis, salmonellosis, leptospirosis, brucellosis, tuberculosis, trichinellosis, and hepatitis E. Wild boars have been also associated with Brazilian spotted fever and rabies, infected while providing plentiful exotic blood supply for native ticks and hematophagous bats. Due to their phylogenetic proximity, wild boars may present ecological niche overlapping and direct disease risk to native white-lipped and collared peccaries. Moreover, wild boars may pose an economical threat to Brazilian livestock industry due to restrictive diseases such as Aujeszky, enzootic pneumonia, neosporosis, hemoplasmosis, and classic swine fever. Finally, wild boars have directly impacted in environmentally protected areas, silting up water springs, rooting and wallowing native plants, decreasing native vegetal coverage, disbalancing of soil components, altering soil structure and composition. Wild boar hunting has failed as a control measure to date, according to the Brazilian Ministry of Environment, due to private hunting groups mostly targeting males, intentionally leaving females and piglets alive, disseminating wild boar populations nationwide. Meanwhile, non-government animal welfare organizations have pointed to animal cruelty of hunting dogs and wild boars (and native species) during hunting. Despite unanimous necessity of wild boar control, eradication and prevention, methods have been controversial and should focus on effective governmental measures instead occasional game hunting, which has negatively impacted native wildlife species while wild boars have continuously spread throughout Brazil.

### **Diagnosis of rabies using reverse-transcription polymerase chain reaction on post-mortem skin tissue specimens of the nasolabial plate in a rabies suspected cow: a case study.**

**Sharma AK, Prashar P, Bharti OK, Thachamvally R, Thakur R, Kumar N, Shanmugasundaram K, Singha H, Bhattacharya TK, Gulati BR, Isloor S, Panda AK, Sharma J, Hara M, Knobel D.**

19-06-2023

*J Vet Med Sci.*

<https://pubmed.ncbi.nlm.nih.gov/37331817/>

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## Schistosomiase

### Schistosoma japonicum-derived peptide SJMHE1 ameliorates allergic symptoms and responses in mice with allergic rhinitis.

Gao X, Mao C, Zheng T, Xu X, Luo X, Zhang S, Liu J, Wang X, Chen X, Dong L.

06-06-2023

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/37346033/>

### Defining an optimal control for RNAi experiments with adult *Schistosoma mansoni*.

Moescheid MF, Puckelwaldt O, Beutler M, Haeblerlein S, Greveling CG.

16-06-2023

*Sci Rep.*

<https://pubmed.ncbi.nlm.nih.gov/37328492/>

### How do disease control measures impact spatial predictions of schistosomiasis and hookworm? The example of predicting school-based prevalence before and after preventive chemotherapy in Ghana.

Kulinkina AV, Farnham A, Biritwum NK, Utzinger J, Walz Y.

16-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37327211/>

**Background:** Schistosomiasis and soil-transmitted helminth infections are among the neglected tropical diseases (NTDs) affecting primarily marginalized communities in low- and middle-income countries. Surveillance data for NTDs are typically sparse, and hence, geospatial predictive modeling based on remotely sensed (RS) environmental data is widely used to characterize disease transmission and treatment needs. However, as large-scale preventive chemotherapy has become a widespread practice, resulting in reduced prevalence and intensity of infection, the validity and relevance of these models should be re-assessed. **Methodology:** We employed two nationally representative school-based prevalence surveys of *Schistosoma haematobium* and hookworm infections from Ghana conducted before (2008) and after (2015) the introduction of large-scale preventive chemotherapy. We derived environmental variables from fine-resolution RS data (Landsat 8) and examined a variable distance radius (1-5 km) for aggregating these variables around point-prevalence locations in a non-parametric random forest modeling approach. We used partial dependence and individual conditional expectation plots to improve interpretability. **Principal findings:** The average school-level *S. haematobium* prevalence decreased from 23.8% to 3.6% and that of hookworm from 8.6% to 3.1% between 2008 and 2015. However, hotspots of high-prevalence locations persisted for both diseases. The models with

environmental data extracted from a buffer radius of 2-3 km around the school location where prevalence was measured had the best performance. Model performance (according to the R<sup>2</sup> value) was already low and declined further from approximately 0.4 in 2008 to 0.1 in 2015 for *S. haematobium* and from approximately 0.3 to 0.2 for hookworm. According to the 2008 models, land surface temperature (LST), modified normalized difference water index (MNDWI), elevation, slope, and streams variables were associated with *S. haematobium* prevalence. LST, slope, and improved water coverage were associated with hookworm prevalence. Associations with the environment in 2015 could not be evaluated due to low model performance. **Conclusions/significance:** Our study showed that in the era of preventive chemotherapy, associations between *S. haematobium* and hookworm infections and the environment weakened, and thus predictive power of environmental models declined. In light of these observations, it is timely to develop new cost-effective passive surveillance methods for NTDs as an alternative to costly surveys, and to focus on persisting hotspots of infection with additional interventions to reduce reinfection. We further question the broad application of RS-based modeling for environmental diseases for which large-scale pharmaceutical interventions are in place.

### *Schistosoma japonicum* Tyrosine Hydroxylase is promising targets for immunodiagnosis and immunoprotection of Schistosomiasis japonica.

Piao X, Duan J, Jiang N, Liu S, Hou N, Chen Q.

05-06-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37276235/>

Identification of promising schistosome antigen targets is crucial for the development of anti-schistosomal strategies. Schistosomes rely on their neuromuscular systems to coordinate important locomotory behaviors. Tyrosine hydroxylase (TH) is critical in the initial rate-limiting step in biosynthesis of catecholamine, the important neuroactive agents, which promote the lengthening of the worm through muscular relaxation and are therefore of great importance to the movement of the organism both within and between its hosts. THs from both *Schistosoma mansoni* and *Schistosoma japonicum* and their enzyme activities have been discovered; however, the role of these proteins during infection have not been explored. Herein, a recombinant protein of the nonconserved fragment of *S. japonicum* TH (SjTH) was produced and the corresponding polyclonal antibody was generated. The expression and antigenicity of SjTH were detected by qRT-PCR, western blotting, immunofluorescence assays, and ELISA. Mice immunized with the recombinant SjTH were challenged with cercariae to evaluate the immunoprotective value of this protein. Our results showed SjTH not only distributed in the head associated with the central nervous system, but also expressed along the tegument and the intestinal intima, which are involved in the movement, coupling and digestion of the parasites and associated with the peripheral nervous system. This protein can effectively

stimulate humoral immune responses in mammalian hosts and has high potential as a biomarker for schistosomiasis immunodiagnosis. Furthermore, immunization with recombinant SjTH showed to reduce the worm and egg burden of challenged mice, and to contribute to the systemic balance of the Th1/Th2 responses. Taken together, these results suggest that SjTH is an important pathogenic molecule in *S. japonicum* and may be a possible target for anti-schistosomal approaches.

### A Co-Expressed Natural Antisense RNA FCER1A-AS Controls IgE-Dependent Immunity by Promoting Expression of FcεRIα.

Tang RY, Yin L, Yao L, Zhang QF, Chen XP.  
15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37154775/>

As the α-subunit of the high-affinity receptor for the Fc portion of immunoglobulin E (FcεRIα), FcεRIα plays a central role in IgE-mediated allergic disorders and in the immunity and immunopathology of some parasitic infections. FcεRIα is specifically expressed on basophils and mast cells, but the mechanism that controls FcεRIα expression in these cells is poorly understood. In this study, we found that the natural antisense transcript (NAT) of FcεRIα (*FCER1A-AS*) is co-expressed with the sense transcript (*FCER1A-S*) in both interleukin (IL)-3-induced FcεRIα-expressing cells and in the high FcεRIα-expressing cell line MC/9. When *FCER1A-AS* is selectively knocked down by the CRISPR/RfxCas13d (CasRx) approach in MC/9 cells, the expression of both *FCER1A-S* mRNA and proteins is markedly decreased. Furthermore, *FCER1A-AS* deficiency was also found to be associated with a lack of *FCER1A-S* expression *in vivo*. Correspondingly, homozygous mice deficient in *FCER1A-AS* demonstrated a similar phenotype to *FCER1A* knockout mice in *Schistosoma japonicum* infection and in IgE-FcεRIα-mediated cutaneous anaphylaxis. Thus, we uncovered a novel pathway for the control of FcεRIα expression by its co-expressed natural antisense transcript. **IMPORTANCE** FcεRIα is responsible for high-affinity binding with the Fc portion of IgE, which is critical for IgE-dependent disease responses such as allergy responses and anti-parasite immunity. FcεRIα is expressed on a few cell types, including mast cells and basophils. Although the expression of FcεRIα is known to be promoted by the IL-3-GATA-2 pathway during its differentiation, the mechanism by which FcεRIα expression is maintained remains unknown. In this study, we discovered that a natural antisense transcript, *FCER1A-AS*, is co-expressed with the sense transcript. The presence of *FCER1A-AS* is essential for sense transcript expression in mast cells and basophils, but not for the differentiation of these cells through *cis*-regulation. Like FcεRIα knockout mice, mice lacking *FCER1A-AS* also exhibit reduced survival after *Schistosoma japonicum* infection and a lack of IgE-mediated cutaneous anaphylaxis. Thus, a novel pathway for regulating IgE-mediated allergic diseases through noncoding RNAs has been revealed.

### Schistosoma transmission: scaling-up competence from hosts to ecosystems.

Douchet P, Gourbal B, Loker ES, Rey O.

Juil-2023

*Trends Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37120369/>

### Parasite Metallo-aminopeptidases as Targets in Human Infectious Diseases.

Aguado ME, Izquierdo M, González-Matos M, Varela AC, Méndez Y, Del Rivero MA, Rivera DG, González-Bacero J.

2023

*Curr Drug Targets.*

<https://pubmed.ncbi.nlm.nih.gov/36825701/>

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## Trachome

### WHO Vision 2020: Have We Done It?

Abdulhussein D, Abdul Hussein M.

Août-2023

*Ophthalmic Epidemiol.*

<https://pubmed.ncbi.nlm.nih.gov/36178293/>

**Background:** Eye health has widespread implications across many aspects of life, ranging from the individual to the societal level. Vision 2020: The Right to Sight is an initiative that was conceptualised in 1997 and launched in 1999. It was led by the World Health Organization (WHO) and the International Agency for the Prevention of Blindness (IAPB) in response to the increasing prevalence of blindness. Approximately 80% of the causes of blindness were avoidable. Hence, the initiative set out to eliminate the major causes of avoidable blindness. These included cataract, uncorrected refractive error, trachoma, onchocerciasis, and childhood blindness. **Methods:** An electronic literature search was performed using PubMed, MEDLINE and Embase databases to assess the impacts of the Vision 2020 initiative. **Results and conclusion:** The Vision 2020 initiative was ambitious and was essential in catapulting the issue of avoidable blindness in the spotlight and putting it on the global health agenda. The causes of avoidable blindness remain and have not been eliminated. However, there have been noticeable changes in the distribution of the causes of avoidable blindness since the conception of Vision 2020, and this is mainly due to demographic shifts globally. We highlight some of the remaining challenges to achieving avoidable blindness including, population size, gender disparities in access to eyecare services, and the professional workforce.

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

### A survey for antibodies against *Fasciola hepatica* in cattle and sheep in Finland indicates a low level of exposure.

Gröning H, Oksanen A, Skrzypczak T, Autio T.  
22-06-2023

*Acta Vet Scand.*

<https://pubmed.ncbi.nlm.nih.gov/37349804/>

### The systematic position of *Cryptopotamonanacoluthon* (Kemp, 1918), with the description of a new species of *Sinolapotamon* Tai & Sung, 1975 (Crustacea, Decapoda, Brachyura, Potamidae) from southern China.

Lu YB, Zhang YX, Zou JX.

08-06-2023

*Zookeys.*

<https://pubmed.ncbi.nlm.nih.gov/37333901/>

The systematics of the potamid freshwater crab *Cryptopotamonanacoluthon* (Kemp, 1918) is clarified, and its generic position in *Sinolapotamon* Tai & Sung, 1975, is confirmed based on morphological comparisons, geographical information and phylogenetic analyses. A new species of *Sinolapotamon*, *Sinolapotamoncirratum* sp. nov. is described from the Guangxi Zhuang Autonomous Region of China. *Sinolapotamoncirratum* sp. nov. is distinguished from its congeners by the combination of characters of its carapace, third maxilliped, anterolateral margin, and unique male first gonopod. Phylogenetic analyses based on partial COX1, 16S rRNA and 28S rRNA genes also support the species as new.

### Protein Modelling and Molecular Docking Analysis of *Fasciola hepatica* $\beta$ -Tubulin's Interaction Sites, with Triclabendazole, Triclabendazole Sulphoxide and Triclabendazole Sulphone.

Olivares-Ferretti P, Beltrán JF, Salazar LA, Fonseca-Salamanca F.

18-06-2023

*Acta Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37330945/>

**Purpose:** *Fasciola hepatica* is a globally distributed trematode that causes significant economic losses. Triclabendazole is the primary pharmacological treatment for this parasite. However, the increasing resistance to triclabendazole limits its efficacy. Previous pharmacodynamics studies suggested that

triclabendazole acts by interacting mainly with the  $\beta$  monomer of tubulin. **Methods:** We used a high-quality method to model the six isotypes of *F. hepatica*  $\beta$ -tubulin in the absence of three-dimensional structures. Molecular dockings were conducted to evaluate the destabilization regions in the molecule against the ligands triclabendazole, triclabendazole sulphoxide and triclabendazole sulphone. **Results:** The nucleotide binding site demonstrates higher affinity than the binding sites of colchicine, albendazole, the T7 loop and p $\beta$ VII ( $p < 0.05$ ). We suggest that the binding of the ligands to the polymerization site of  $\beta$ -tubulin can lead a microtubule disruption. Furthermore, we found that triclabendazole sulphone exhibited significantly higher binding affinity than other ligands ( $p < 0.05$ ) across all isotypes of  $\beta$ -tubulin. **Conclusions:** Our investigation has yielded new insight on the mechanism of action of triclabendazole and its sulphometabolites on *F. hepatica*  $\beta$ -tubulin through computational tools. These findings have significant implications for ongoing scientific research ongoing towards the discovery of novel therapeutics to treat *F. hepatica* infections.

### A promising new target to control fasciolosis: *Fasciola hepatica* leucine aminopeptidase 2.

Checa J, Salazar C, Goyeche A, Rivera M, Silveira F, Maggioli G.

05-06-2023

*Vet Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/37329826/>

### 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.

Jul-2023

*Vet Parasitol Reg Stud Reports.*

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

### Identification and prevalence of fluke infection in yak and Tibetan sheep around Qinghai Lake, China.

Fu Y, Zhang X, Li Z, Meng R, Duo H, Shen X, Ma Y, Guo Z.

Jul-2023

*Parasitol Res.*

<https://pubmed.ncbi.nlm.nih.gov/37202562/>

### Mitogenomic and nuclear ribosomal transcription unit datasets support the synonymy of *Paragonimus iloktsuenensis* and *P. ohirai* (Paragonimidae: Platyhelminthes).

Le TH, Nguyen KT, Pham LTK, Doan HTT, Roan DT, Le XTK, Agatsuma T, Blair D.

Jul-2023

The complete mitogenome (mtDNA) of nominal *Paragonimus iloktsuenensis* (Paragonimidae: Trematoda) and the nuclear ribosomal transcription unit (rTU) coding region (rTU\*: from 5'-terminus of 18S to 3'-terminus of 28S rRNA gene, excluding the external spacer region) of this species and of *P. ohirai* were obtained and used to further support the previously suggested synonymy of these taxa in the *P. ohirai* complex. The complete mitogenome of *P. iloktsuenensis* was 14,827 bp long (GenBank: ON961029) and nearly identical to that of *P. ohirai* (14,818 bp; KX765277), with a 99.12% nucleotide identity. The rTU\* was 7543 bp and 6932 bp in these two taxa, respectively. All genes and spacers in the rTU were identical in length, with exception of the first internal transcribed spacer, which contained multiple tandem repeat units (6.7 for *P. iloktsuenensis* and 5.7 for *P. ohirai*). There was near 100% identity for the rTU genes. The phylogenetic topology inferred from the mtDNA and from individual gene regions (partial *cox1* of 387 bp and the ITS-2 of 282 bp - 285 bp) indicated a very close relationship consistent with synonymy of *P. iloktsuenensis* and *P. ohirai*. The datasets provided here will be useful for taxonomic reappraisal as well as studies of evolutionary and population genetics of the genus *Paragonimus* and family Paragonimidae.

### **Praziquantel - 50 Years of Research.**

Waechtler A, Cezanne B, Maillard D, Sun R, Wang S, Wang J, Harder A.

15-06-2023

*ChemMedChem.*

<https://pubmed.ncbi.nlm.nih.gov/37009677/>

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

### **Clinical and epidemiological aspects of the infection by Babesia, Theileria and Trypanosoma species in horses from northeastern Colombia.**

Jaimes-Dueñez J, Jiménez-Leaño Á, Enrique-Niño S, Arias-Landazábal N, Bedoya-Ríos M, Rangel-Pachón D.

20-06-2023

*Ticks Tick Borne Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37348426/>

Piroplasmosis and trypanosomiasis are debilitating diseases of great economic impact on the equine industry of Latin America. Considering the lack of studies in the northeastern part of Colombia, this study aimed to determine the epidemiological, clinical and genetic features associated with infection of the *Babesia*, *Theileria*, and *Trypanosoma* species in horses from this geographical area. Two hundred and eighty horses from the Arauca, Meta, and Santander departments were molecularly analyzed for infection with *Babesia caballi*, *Theileria equi*, *Trypanosoma evansi*, and *Trypanosoma*

*vivax*. Furthermore, clinical, epidemiological and entomological analyses were performed on the data sets. Molecular analysis showed 25.7% and 3.9% prevalence for *T. equi* and *T. evansi*, respectively, without positive animals for *B. caballi* and *T. vivax*. There were no differences in the prevalence of *T. equi* between departments, whereas *T. evansi* was detected exclusively in Santander. A total of 633 ticks were collected from 72 horses across the three departments, with 84.7% corresponding to *Dermacentor nitens*, 10.9% to *Amblyomma cajennense* (sensu lato) (s.l.) and 4.4% to *Rhipicephalus microplus*. For *T. equi*, genetic analyses showed that Colombian isolates belong to genotype C of species, along with sequences of Brazil and Mexico. Epidemiological analysis revealed a significant association between tick infestation and lack of vector control with molecular infection of *T. equi*, whereas clinical analysis revealed a significant reduction in packed cell volume, red blood cells, and mean corpuscular volume in positive animals to this pathogen. Furthermore, molecular infection by *T. evansi* was associated with epidemiological characteristics in the Santander department. In conclusion, our analysis revealed a moderate infection rate by *T. equi* of genotype C in horses from northeastern Colombia, which affects their clinical conditions. Control of ticks and treatment of symptomatic animals should be considered to reduce the economic impact associated with these infections in the equine industry.

### **Trypanosoma cruzi Tc24 Antigen Expressed and Orally Delivered by Schizochytrium sp. Microalga is Immunogenic in Mice.**

Ramos-Vega A, Monreal-Escalante E, Rosales-Mendoza S, Bañuelos-Hernández B, Dumonteil E, Angulo C.

21-06-2023

*Mol Biotechnol.*

<https://pubmed.ncbi.nlm.nih.gov/37344711/>

### **Development of a 2,4-Diaminothiazole Series for the Treatment of Human African Trypanosomiasis Highlights the Importance of Static-Cidal Screening of Analogues.**

Cleghorn LAT, Wall RJ, Albrecht S, MacGowan SA, Norval S, De Rycker M, Woodland A, Spinks D, Thompson S, Patterson S, Corpas Lopez V, Dey G, Collie IT, Hallyburton I, Kime R, Simeons FRC, Stojanovski L, Frearson JA, Wyatt PG, Read KD, Gilbert IH, Wyllie S.

21-06-2023

*J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37343180/>

### **Deciphering anti-infectious compounds from Peruvian medicinal Cordoncillos extract library through multiplexed assays and chemical profiling.**

Vásquez-Ocmín PG, Cojean S, Roumy V, Marti G, Pomel S, Gadea A, Leblanc K, Dennemont I, Ruiz-Vásquez L, Ricopa Cotrina H, Ruiz Mesia W, Bertani S, Ruiz Mesia L, Maciuk A.

05-06-2023

*Front Pharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/37342590/>

High prevalence of parasitic or bacterial infectious diseases in some world areas is due to multiple reasons, including a lack of an appropriate health policy, challenging logistics and poverty. The support to research and development of new medicines to fight infectious diseases is one of the sustainable development goals promoted by World Health Organization (WHO). In this sense, the traditional medicinal knowledge substantiated by ethnopharmacology is a valuable starting point for drug discovery. This work aims at the scientific validation of the traditional use of *Piper* species ("Cordoncillos") as firsthand anti-infectious medicines. For this purpose, we adapted a computational statistical model to correlate the LCMS chemical profiles of 54 extracts from 19 *Piper* species to their corresponding anti-infectious assay results based on 37 microbial or parasites strains. We mainly identified two groups of bioactive compounds (called features as they are considered at the analytical level and are not formally isolated). Group 1 is composed of 11 features being highly correlated to an inhibiting activity on 21 bacteria (principally Gram-positive strains), one fungus (*C. albicans*), and one parasite (*Trypanosoma brucei gambiense*). The group 2 is composed of 9 features having a clear selectivity on *Leishmania* (all strains, both axenic and intramacrophagic). Bioactive features in group 1 were identified principally in the extracts of *Piper strigosum* and *P. xanthostachyum*. In group 2, bioactive features were distributed in the extracts of 14 *Piper* species. This multiplexed approach provided a broad picture of the metabolome as well as a map of compounds putatively associated to bioactivity. To our knowledge, the implementation of this type of metabolomics tools aimed at identifying bioactive compounds has not been used so far.

### Targeting Cysteine Proteases and their Inhibitors to Combat Trypanosomiasis.

**Saha A, Pushpa, Moitra S, Basak D, Brahma S, Mondal D, Molla SH, Samadder A, Nandi S.**

19-06-2023

*Curr Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37340748/>

**Background:** Trypanosomiasis, caused by protozoan parasites of the *Trypanosoma* genus, remains a significant health burden in several regions of the world. Cysteine proteases play a crucial role in the pathogenesis of *Trypanosoma* parasites and have emerged as potential therapeutic targets for the development of novel antiparasitic drugs. **Introduction:** This review article aims to provide a comprehensive overview of the role of cysteine proteases in trypanosomiasis and their potential as therapeutic targets. We discuss the biological significance of cysteine proteases in *Trypanosoma* parasites and their involvement in essential processes, such as host immune evasion, cell invasion, and nutrient acquisition. **Methods:** A comprehensive literature search was conducted to identify relevant studies and research articles on the role of cysteine proteases and their inhibitors in trypanosomiasis. The selected studies were

critically analyzed to extract key findings and provide a comprehensive overview of the topic. **Results:** Cysteine proteases, such as cruzipain, TbCatB and TbCatL, have been identified as promising therapeutic targets due to their essential roles in *Trypanosoma* pathogenesis. Several small molecule inhibitors and peptidomimetics have been developed to target these proteases and have shown promising activity in preclinical studies. **Conclusion:** Targeting cysteine proteases and their inhibitors holds great potential for the development of novel antiparasitic drugs against trypanosomiasis. The identification of potent and selective cysteine protease inhibitors could significantly contribute to the combat against trypanosomiasis and improve the prospects for the treatment of this neglected tropical disease

### Congenital Transmission of *Trypanosoma cruzi* in Naturally Infected Dogs.

**Avalos-Borges EE, Jiménez-Coello M, Chan-Pérez JI, Cigarroa-Toledo N, Garg NJ, Guillermo-Cordero L, Segura-Correa JC, Ortega-Pacheco A.**

20-06-2023

*Vector Borne Zoonotic Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37339451/>

**Background:** Congenital transmission (CT) of *Trypanosoma cruzi* in dogs has not been clearly demonstrated, even though dogs are important reservoirs of this agent. **Materials and Methods:** Seventeen late pregnant dogs seropositive for *T. cruzi* were selected, and a total of 84 fetuses were obtained. Blood and heart tissues from the fetuses and dams, and placental tissue from dam were collected. All tissues were analyzed by quantitative polymerase chain reaction (qPCR) for *T. cruzi* DNA (*TcDNA*) and inflammatory infiltrate and pathology by histological examination. CT was determined when physical, histological, or molecular evidence of *T. cruzi* was detected in blood or tissues of the fetuses. **Results:** A general transmission frequency of 59% was found, and  $0.20 \pm 0.24$  of fetuses per litter were infected. Dams that were qPCR positive for *TcDNA* in cardiac tissue or blood displayed a transmission frequency of 100% and 67%, respectively. The highest parasite burden was noted in dams that were positive for *TcDNA* in both blood ( $82E-01 \pm 1.54E-01$ ) and cardiac ( $5.28E+03 \pm 8.85E+03$ ) tissues. In fetuses, higher parasitic burden in blood and cardiac tissue was found in those carried by dams that were seropositive and qPCR positive for *TcDNA* in cardiac tissue and blood. No amastigote nests were recorded in the cardiac tissue of fetuses in the histopathological studies, but typical lesions of *T. cruzi* infection were identified in all fetuses where CT occurred. **Conclusions:** CT of *T. cruzi* occurred at a high frequency in naturally infected pregnant dogs from the endemic areas.

### [The ancestral shape of the access proton path of mitochondrial ATP synthases revealed by a split subunit-a.](#)

**Wong JE, Zíková A, Gahura O.**

20-06-2023

*Mol Biol Evol.*

<https://pubmed.ncbi.nlm.nih.gov/37338543/>

### **State-of-the-Art in the Drug Discovery Pathway for Chagas Disease: A Framework for Drug Development and Target Validation.**

**Gabaldón-Figueira JC, Martínez-Peinado N, Escabia E, Ros-Lucas A, Chatelain E, Scandale I, Gascon J, Pinazo MJ, Alonso-Padilla J.**

14-06-2023

*Res Rep Trop Med.*

<https://pubmed.ncbi.nlm.nih.gov/37337597/>

Chagas disease is the most important protozoan infection in the Americas, and constitutes a significant public health concern throughout the world. Development of new medications against its etiologic agent, *Trypanosoma cruzi*, has been traditionally slow and difficult, lagging in comparison with diseases caused by other kinetoplastid parasites. Among the factors that explain this are the incompletely understood mechanisms of pathogenesis of *T. cruzi* infection and its complex set of interactions with the host in the chronic stage of the disease. These demand the performance of a variety of in vitro and in vivo assays as part of any drug development effort. In this review, we discuss recent breakthroughs in the understanding of the parasite's life cycle and their implications in the search for new chemotherapeutics. For this, we present a framework to guide drug discovery efforts against Chagas disease, considering state-of-the-art preclinical models and recently developed tools for the identification and validation of molecular targets.

### **Exploring N-myristoyltransferase as a promising drug target against parasitic neglected tropical diseases.**

**Nascimento IJDS, Cavalcanti MAT, de Moura RO.**

08-06-2023

*Eur J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37336067/>

Neglected tropical diseases (NTDs) constitute a group of approximately 20 infectious diseases that mainly affect the impoverished population without basic sanitation in tropical countries. These diseases are responsible for many deaths worldwide, costing billions of dollars in public health investment to treat and control these infections. Among them are the diseases caused by protozoa of the Trypanosomatid family, which constitute *Trypanosoma cruzi* (Chagas disease), *Trypanosoma brucei* (sleeping sickness), and Leishmaniasis. In addition, there is a classification of other diseases, called the big three, AIDS, tuberculosis, and malaria, which are endemic in countries with tropical conditions. Despite the high mortality rates, there is still a gap in the treatment. The drugs have a high incidence of side effects and protozoan resistance, justifying the investment in developing new alternatives. In fact, the Target-Based Drug Design (TBDD) approach is responsible for identifying several promising compounds, and among the targets explored through this approach, N-myristoyltransferase (NMT) stands out. It is an enzyme related to the co-translational myristoylation of N-terminal glycine in various peptides. The myristoylation

process is a co-translation that occurs after removing the initiator methionine. This process regulates the assembly of protein complexes and stability, which justifies its potential as a drug target. In order to propose NMT as a potential target for parasitic diseases, this review will address the entire structure and function of this enzyme and the primary studies demonstrating its promising potential against Leishmaniasis, *T. cruzi*, *T. brucei*, and malaria. We hope our information can help researchers worldwide search for potential drugs against these diseases that have been threatening the health of the world's population.

### **Bioactivity-guided isolation of trypanocidal coumarins and dihydropyranochromones from selected Apiaceae plant species.**

**Krishnan SR, Skiba A, Luca SV, Marcourt L, Wolfender JL, Skalicka-Woźniak K, Gertsch J.**

16-06-2023

*Phytochemistry.*

<https://pubmed.ncbi.nlm.nih.gov/37331573/>

### **Phylogenetic description of Trypanosoma cruzi isolates from Dipetalogaster maxima: Occurrence of TcI, TcIV, and TcIV-USA.**

**Flores-López CA, Esquivias-Flores EA, Guevara-Carrizales A.**

16-06-2023

*Infect Genet Evol.*

<https://pubmed.ncbi.nlm.nih.gov/37331498/>

### **Can infection with Trypanosoma cruzi modify the toxicological response of Triatoma infestans susceptible and resistant to deltamethrin?**

**Lobbía PA, Rodríguez C, Mougabure-Cueto G.**

13-06-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/37328120/>

Chemical control plays a central role in interrupting the vector transmission of Chagas disease. In recent years, high levels of resistance to pyrethroids have been detected in the main vector *Triatoma infestans*, which were associated with less effectiveness in chemical control campaigns in different regions of Argentina and Bolivia. The presence of the parasite within its vector can modify a wide range of insect physiological processes, including toxicological susceptibility and the expression of resistance to insecticides. This study examined for the first time the possible effects of *Trypanosoma cruzi* infection on susceptibility and resistance to deltamethrin in *T. infestans*. Using WHO protocol resistance monitoring assays, we exposed resistant and susceptible strains of *T. infestans*, uninfected and infected with *T. cruzi* to different concentrations of deltamethrin in fourth-instar nymphs at days 10-20 post-emergence and monitored survival at 24, 48, and 72 h. Our findings suggest that the infection affected the toxicological susceptibility of the susceptible strain, showing higher mortality than uninfected

susceptible insects when exposed to both deltamethrin and acetone. On the other hand, the infection did not affect the toxicological susceptibility of the resistant strain, infected and uninfected showed similar toxic responses and the resistance ratios was not modified. This is the first report of the effect of *T. cruzi* on the toxicological susceptibility of *T. infestans* and triatomines in general and, to our knowledge, one of the few on the effect of a parasite on the insecticide susceptibility of its insect vector.

### Putative 14th Century Outbreak of Foodborne Chagas Disease, Mexico.

Reperant LA.

15-06-2023

*Vector Borne Zoonotic Dis.*

<https://pubmed.ncbi.nlm.nih.gov/37327016/>

### Structure-based discovery of novel cruzain inhibitors with distinct trypanocidal activity profiles.

Santos VC, Leite PG, Santos LH, Pascutti PG, Kolb P, Machado FS, Ferreira RS.

05-09-2023

*Eur J Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/37290182/>

Over 110 years after the first formal description of Chagas disease, the trypanocidal drugs thus far available have limited efficacy and several side effects. This encourages the search for novel treatments that inhibit *T. cruzi* targets. One of the most studied anti-*T. cruzi* targets is the cysteine protease cruzain; it is associated with metacyclogenesis, replication, and invasion of the host cells. We used computational techniques to identify novel molecular scaffolds that act as cruzain inhibitors. First, with a docking-based virtual screening, we identified compound 8, a competitive cruzain inhibitor with a  $K_i$  of 4.6  $\mu$ M. Then, aided by molecular dynamics simulations, cheminformatics, and docking, we identified the analog compound 22 with a  $K_i$  of 27  $\mu$ M. Surprisingly, despite sharing the same isoquinoline scaffold, compound 8 presented higher trypanocidal activity against the epimastigote forms, while compound 22, against the trypomastigotes and amastigotes. Taken together, compounds 8 and 22 represent a promising scaffold for further development of trypanocidal compounds as drug candidates for treating Chagas disease.

## Ulcère de Buruli

### PPE Barcoding Identifies Biclinal *Mycobacterium ulcerans* Buruli Ulcer, Côte d'Ivoire.

Tchan BGO, Ngazoa-Kakou S, Aka N, Apia NKB, Hammoudi N, Drancourt M, Saad J.

15-06-2023

*Microbiol Spectr.*

<https://pubmed.ncbi.nlm.nih.gov/37222600/>

*Mycobacterium ulcerans*, an environmental opportunistic pathogen, causes necrotic cutaneous and subcutaneous

lesions, named Buruli ulcers, in tropical countries. PCR-derived tests used to detect *M. ulcerans* in environmental and clinical samples do not allow one-shot detection, identification, and typing of *M. ulcerans* among closely related *Mycobacterium marinum* complex mycobacteria. We established a 385-member *M. marinum*/*M. ulcerans* complex whole-genome sequence database by assembling and annotating 341 *M. marinum*/*M. ulcerans* complex genomes and added 44 *M. marinum*/*M. ulcerans* complex whole-genome sequences already deposited in the NCBI database. Pangenome, core genome, and single-nucleotide polymorphism (SNP) distance-based comparisons sorted the 385 strains into 10 *M. ulcerans* taxa and 13 *M. marinum* taxa, correlating with the geographic origin of strains. Aligning conserved genes identified one *PPE* (proline-proline-glutamate) gene sequence to be species and intraspecies specific, thereby genotyping the 23 *M. marinum*/*M. ulcerans* complex taxa. PCR sequencing of the *PPE* gene correctly genotyped nine *M. marinum*/*M. ulcerans* complex isolates among one *M. marinum* taxon and three *M. ulcerans* taxa in the African taxon (T2.4). Further, successful *PPE* gene PCR sequencing in 15/21 (71.4%) swabs collected from suspected Buruli ulcer lesions in Côte d'Ivoire exhibited positive *M. ulcerans* IS2404 real-time PCR and identified the *M. ulcerans* T2.4.1 genotype in eight swabs and *M. ulcerans* T2.4.1/T2.4.2 mixed genotypes in seven swabs. *PPE* gene sequencing could be used as a proxy for whole-genome sequencing for the one-shot detection, identification, and typing of clinical *M. ulcerans* strains, offering an unprecedented tool for identifying *M. ulcerans* mixed infections. **IMPORTANCE** We describe a new targeted sequencing approach that characterizes the *PPE* gene to disclose the simultaneous presence of different variants of a single pathogenic microorganism. This approach has direct implications on the understanding of pathogen diversity and natural history and potential therapeutic implications when dealing with obligate and opportunistic pathogens, such as *Mycobacterium ulcerans* presented here as a prototype.

### An Overview of 10 Years of Activity of a Molecular Laboratory for Buruli Ulcer Diagnosis at a Field Hospital in Benin.

Fajloun F, Ganlonon L, Gnimavo RS, Sodjinou E, Habib A, Claco E, Agoundoté I, Adeye A, Catraye P, Al-Bayssari C, Moussa EH, Robbe-Saule M, Houezo JG, Kpoton GG, Ayélo AG, Gomez B, Johnson RC, Marsollier L, Marion E, Kempf M.

20-06-2023

*J Clin Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/37212702/>