

**Veille scientifique**

**Maladies tropicales négligées**

**Semaine 05**

*30 janvier au 05 février 2023*

[Dengue, chikungunya et maladie à virus Zika 2](#_Toc126654894)

[Rage 13](#_Toc126654895)

[Trachome 14](#_Toc126654896)

[Ulcère de Buruli 15](#_Toc126654897)

[Lèpre 15](#_Toc126654898)

[Trypanosomes (trypanosomiase et maladie de Chagas) 18](#_Toc126654899)

[Leishmaniose 21](#_Toc126654900)

[Cysticercose 27](#_Toc126654901)

[Dracunculose 27](#_Toc126654902)

[Echinococcose 28](#_Toc126654903)

[Trématodoses d’origine alimentaire (clonorchiase, opisthorchiase, fasciolase et paragonimose 30](#_Toc126654904)

[Filariose lymphatique 31](#_Toc126654905)

[Mycétome 32](#_Toc126654906)

[Onchocercose 33](#_Toc126654907)

[Schistosomiase 33](#_Toc126654908)

[Helminthiases transmises par le sol (ascaridiose, trichuriase, ankylostomiase) 34](#_Toc126654909)

[Gale 35](#_Toc126654910)

[Morsures de serpent 36](#_Toc126654911)

# Dengue, chikungunya et maladie à virus Zika

Mapping patient pathways and understanding clinical decision-making in dengue management to inform the development of digital health tools.

Nguyen QH, Ming DK, Luu AP, Chanh HQ, Tam DTH, Truong NT, Huy VX, Hernandez B, Van Nuil JI, Paton C, Georgiou P, Nguyen NM, Holmes A, Tho PV, Yacoub S; Vietnam ICU Translational Applications Laboratory (VITAL) investigators.

02-02-2023

*BMC Med Inform Decis Mak*.

<https://pubmed.ncbi.nlm.nih.gov/36732718/>

**Background:** Dengue is a common viral illness and severe disease results in life-threatening complications. Healthcare services in low- and middle-income countries treat the majority of dengue cases worldwide. However, the clinical decision-making processes which result in effective treatment are poorly characterised within this setting. In order to improve clinical care through interventions relating to digital clinical decision-support systems (CDSS), we set out to establish a framework for clinical decision-making in dengue management to inform implementation. **Methods:** We utilised process mapping and task analysis methods to characterise existing dengue management at the Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam. This is a tertiary referral hospital which manages approximately 30,000 patients with dengue each year, accepting referrals from Ho Chi Minh city and the surrounding catchment area. Initial findings were expanded through semi-structured interviews with clinicians in order to understand clinical reasoning and cognitive factors in detail. A grounded theory was used for coding and emergent themes were developed through iterative discussions with clinician-researchers. **Results:** Key clinical decision-making points were identified: (i) at the initial patient evaluation for dengue diagnosis to decide on hospital admission and the provision of fluid/blood product therapy, (ii) in those patients who develop severe disease or other complications, (iii) at the point of recurrent shock in balancing the need for fluid therapy with complications of volume overload. From interviews the following themes were identified: prioritising clinical diagnosis and evaluation over existing diagnostics, the role of dengue guidelines published by the Ministry of Health, the impact of seasonality and caseload on decision-making strategies, and the potential role of digital decision-support and disease scoring tools. **Conclusions:** The study highlights the contemporary priorities in delivering clinical care to patients with dengue in an endemic setting. Key decision-making processes and the sources of information that were of the greatest utility were identified. These findings serve as a foundation for future clinical interventions and improvements in healthcare. Understanding the decision-making process in greater detail also allows for development and implementation of CDSS which are suited to the local context.

The Genetic Variant TNFA (rs361525) Is Associated with Increased Susceptibility to Developing Dengue Symptoms.

Villanueva-Aguilar ME, Rizo-de-la-Torre LDC, Granados-Muñiz MDP, Montoya-Fuentes A, Montoya-Fuentes H.

01-02-2023

*Viral Immunol*.

<https://pubmed.ncbi.nlm.nih.gov/36730734/>

Dengue virus (DENV) is the causal agent of dengue fever. The symptoms and signs of dengue vary from febrile illness to hemorrhagic syndrome. *IFITM3* and *TNFA* are genes of the innate immune system. Variants *IFITM3* (rs12252 T>C) and *TNFA* (rs1800629 G > A and rs361525 G>A) might alter gene expression and change the course of the disease. Our first objective was to determine whether these variants were associated with the susceptibility and severity of dengue. The second was to assess the association of these variants with each symptom. We studied 272 cases with suspected dengue infection, of which 102 were confirmed dengue cases (DENV+) and 170 were dengue-like cases without DENV infection (DENV-). Samples of 201 individuals from the general population of Mexico were included as a reference. Genotyping was performed by the polymerase chain reaction-restriction fragment length polymorphism technique. Odds ratios and confidence intervals were calculated using Pearson's chi-square test and later adjusted for age and sex with a binary logistic regression model. Haldane correction is applied when necessary. We found a significantly higher frequency of the A allele of *TNFA* rs361525 in both the DENV+ and DENV- groups compared with the general population. Focusing on DENV+ and DENV-, the frequency of the A allele of *TNFA* rs361525 was higher in the DENV+ group. A broad spectrum of symptoms was related to the A allele of both *TNFA* variants. We conclude that *TNFA* rs361525 increases the susceptibility to symptomatic dengue but can also be associated with susceptibility to other dengue-like symptoms from unknown causes.

Features of the urban environment associated with Aedes aegypti abundance in high-rise public apartments in Singapore: An environmental case-control study.

Fernandez SA, Sun H, Dickens BL, Ng LC, Cook AR, Lim JT.

02-02-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36730440/>

Quantifying heterogeneities in arbovirus transmission: Description of the rationale and methodology for a prospective longitudinal study of dengue and Zika virus transmission in Iquitos, Peru (2014-2019).

Morrison AC, Paz-Soldan VA, Vazquez-Prokopec GM, Lambrechts L, Elson WH, Barrera P, Astete H, Briesemeister V, Leguia M, Jenkins SA, Long KC, Kawiecki AB, Reiner RC Jr, Perkins TA, Lloyd AL, Waller LA, Hontz RD, Stoddard ST, Barker CM, Kitron U, Elder JP, Rothman AL, Scott TW; Proyecto Dengue Group.

02-02-2023

*PLoS One*.

<https://pubmed.ncbi.nlm.nih.gov/36730229/>

Inhibition of chikungunya virus replication by N-ω-Chloroacetyl-L-Ornithine in C6/36, Vero cells and human fibroblast BJ.

Rojas-Luna L, Posadas-Modragón A, Avila-Trejo AM, Alcántara-Farfán V, Rodríguez-Páez LI, Santiago-Cruz JA, Pastor-Alonso MO, Aguilar-Faisal JL.

Feb-2023

*Antivir Ther*.

<https://pubmed.ncbi.nlm.nih.gov/36724136/>

**Background:** Polyamines are involved in several cellular processes and inhibiting their synthesis affects chikungunya virus (CHIKV) replication and translation, and, therefore, reduces the quantity of infectious viral particles produced. In this study, we evaluated the inhibition of CHIKV replication by N-ω-chloroacetyl-L-ornithine (NCAO), a competitive inhibitor of ornithine decarboxylase, an enzyme which is key in the biosynthesis of polyamines (PAs). **Methods:** The cytotoxicity of NCAO was evaluated by MTT in cell culture. The inhibitory effect of CHIKV replication by NCAO was evaluated in Vero and C6/36 cells. The intracellular polyamines were quantified by HPLC in CHIKV-infected cells. We evaluated the yield of CHIKV in titres via the addition of PAs in Vero, C6/36 cells and human fibroblast BJ treated with NCAO. **Results:** We found that NCAO inhibits the replication of CHIKV in Vero and C6/36 cells in a dose-dependent manner, causing a decrease in the PFU/mL of at least 4 logarithms (*p* < 0.01) in both cell lines. Viral yields were restored by the addition of exogenous polyamines, mainly putrescine. The HPLC analyses showed that NCAO decreases the content of intracellular PAs, even though it is predominantly spermidines and spermines which are present in infected cells. Inhibition of CHIKV replication was observed in human fibroblast BJ treated with 100 μM NCAO 24 h before and 48 h after the infection at a MOI 1. **Conclusions:** NCAO inhibits CHIKV replication by depleting the intracellular polyamines in Vero, C6/36 cells and human fibroblast BJ, suggesting that this compound is a possible antiviral agent for CHIKV.

The 1H, 15N and 13C resonance assignments of dengue virus capsid protein with the deletion of the intrinsically disordered N-terminal region.

Barbosa GM, Morando MA, Da Poian AT, Almeida FCL.

01-02-2032

*Biomol NMR Assign*.

<https://pubmed.ncbi.nlm.nih.gov/36723824/>

Recombinant Protein Mimicking the Antigenic Structure of the Viral Surface Envelope Protein Reinforces Induction of an Antigen-Specific and Virus-Neutralizing Immune Response Against Dengue Virus.

Kim J, Lim TY, Park J, Jang YS.

01-02-2023

*J Microbiol*.

<https://pubmed.ncbi.nlm.nih.gov/36723792/>

Dengue virus (DENV), belonging to the family Flaviviridae, is the causative agent of dengue and comprises four serotypes. A second heterologous DENV infection is a critical risk factor for severe dengue, and no effective vaccine is available to prevent infection by all four DENV serotypes. Recombinant DENV vaccines are primarily based on the envelope proteins, prM and E. The E protein and its envelope domain III (EDIII) have been investigated as candidate antigens (Ags) for recombinant subunit vaccines. However, most EDIII-based Ags are monomers that do not display the cognate antigenic structure of E protein, which is essential for induction of virus-neutralizing immunity. Here, we developed recombinant DENV-2 envelope domain (r2ED) protein as an Ag that mimics the quaternary structure of E protein on the DENV surface. We confirmed that r2ED retained the conformational epitope displayed at the E-dimer interface, which reportedly exhibits broad virus-neutralizing capacity, without displaying the fusion loop epitope that causes antibody (Ab)-dependent enhancement. Furthermore, compared with EDIII alone, r2ED elicited stronger Ag-specific and cross-reactive neutralizing Ab and T cell-mediated immune responses in mice. This Ag-specific immunity was maintained at an elevated level 6 months after the last immunization, suggesting sustained Ag-specific immune memory. Taken together, these observations suggest that r2ED could be used to develop an improved subunit vaccine capable of inducing a broadly cross-reactive and long-lasting immune response against DENV infection.

Predictive Factors for the Complications of Dengue Fever in Children: A Retrospective Analysis.

Uthraraj NS, Sriraam LM, Hiriyur Prakash M, Kumar M, Palanisamy U, Chettiakkapalayam Venkatachalam KU.

27-12-2022

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/36721616/>

Developing Wolbachia-based disease interventions for an extreme environment.

Ross PA, Elfekih S, Collier S, Klein MJ, Lee SS, Dunn M, Jackson S, Zhang Y, Axford JK, Gu X, Home JL, Nassar MS, Paradkar PN, Tawfik EA, Jiggins FM, Almalik AM, Al-Fageeh MB, Hoffmann AA.

31-01-2023

*PLoS Pathog*.

<https://pubmed.ncbi.nlm.nih.gov/36719928/>

Aedes aegypti mosquitoes carrying self-spreading, virus-blocking Wolbachia bacteria are being deployed to suppress dengue transmission. However, there are challenges in applying this technology in extreme environments. We introduced two Wolbachia strains into Ae. aegypti from Saudi Arabia for a release program in the hot coastal city of Jeddah. Wolbachia reduced infection and dissemination of dengue virus (DENV2) in Saudi Arabian mosquitoes and showed complete maternal transmission and cytoplasmic incompatibility. Wolbachia reduced egg hatch under a range of environmental conditions, with the Wolbachia strains showing differential thermal stability. Wolbachia effects were similar across mosquito genetic backgrounds but we found evidence of local adaptation, with Saudi Arabian mosquitoes having lower egg viability but higher adult desiccation tolerance than Australian mosquitoes. Genetic background effects will influence Wolbachia invasion dynamics, reinforcing the need to use local genotypes for mosquito release programs, particularly in extreme environments like Jeddah. Our comprehensive characterization of Wolbachia strains provides a foundation for Wolbachia-based disease interventions in harsh climates.

Electrochemical biosensor detection on respiratory and flaviviruses.

Ang PC, Perumal V, Ibrahim MNM, Adnan R, Mohd Azman DK, Gopinath SCB, Raja PB.

31-12-2023

*Appl Microbiol Biotechnol*.

<https://pubmed.ncbi.nlm.nih.gov/36719432/>

Distinct cytokine profiles in malaria coinfections: A systematic review.

Kotepui M, Mala W, Kwankaew P, Kotepui KU, Masangkay FR, Wilairatana P.

30-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36716305/>

**Background:** Few data exist on the distinct cytokine profiles of individuals with malaria coinfections and other diseases. This study focuses on data collation of distinct cytokine profiles between individuals with malaria coinfections and monoinfections to provide evidence for further diagnostic or prognostic studies. **Methods:** We searched five medical databases, including Embase, MEDLINE, PubMed, Ovid, and Scopus, for articles on cytokines in malaria coinfections published from January 1, 1983 to May 3, 2022, after which the distinct cytokine patterns between malaria coinfection and monoinfection were illustrated in heat maps. **Results:** Preliminary searches identified 2127 articles, of which 34 were included in the systematic review. Distinct cytokine profiles in malaria coinfections with bacteremia; HIV; HBV; dengue; filariasis; intestinal parasites; and schistosomiasis were tumor necrosis factor (TNF), interferon (IFN)-γ, IFN-α, interleukin (IL)-1, IL-1 receptor antagonist (Ra), IL-4, IL-7, IL-12, IL-15, IL-17; TNF, IL-1Ra, IL-4, IL-10, IL-12, IL-18, CCL3, CCL5, CXCL8, CXCL9, CXCL11, granulocyte colony-stimulating factor (G-CSF); TNF, IFN-γ, IL-4, IL-6, IL-10, IL-12, CCL2; IFN-γ, IL-1, IL-4, IL-6, IL-10, IL-12, IL-13, IL-17, CCL2, CCL3, CCL4, G-CSF; IL-1Ra, IL-10, CXCL5, CXCL8, CXCL10; TNF, IL-2, IL-4, IL-6, IL-10; and TNF, IFN-γ, IL-4, IL-5, IL-10, transforming growth factor-β, CXCL8, respectively. **Conclusion:** This systematic review provides information on distinct cytokine profiles of malaria coinfections and malaria monoinfections. Further studies should investigate whether specific cytokines for each coinfection type could serve as essential diagnostic or prognostic biomarkers for malaria coinfections.

Identification of Novel Anti-ZIKV Drugs from Viral-Infection Temporal Gene Expression Profiles.

Zhang N, Tan Z, Wei J, Zhang S, Liu Y, Miao Y, Ding Q, Yi W, Gan M, Li C, Liu B, Wang H, Zheng Z.

30-01-2023

*Emerg Microbes Infect.*

<https://pubmed.ncbi.nlm.nih.gov/36715162/>

Zika virus (ZIKV) infections are typically asymptomatic but cause severe neurological complications (e.g. Guillain-Barré syndrome in adults, and microcephaly in newborns). There are currently no specific therapy or vaccine options available to prevent ZIKV infections. Temporal gene expression profiles of ZIKV-infected human brain microvascular endothelial cells (HBMECs) were used in this study to identify genes essential for viral replication. These genes were then used to identify novel anti-ZIKV agents and validated in publicly available data and functional wet-lab experiments. Here, we found that ZIKV effectively evaded activation of immune response-related genes and completely reprogrammed cellular transcriptional architectures. Knockdown of genes, which gradually upregulated during viral infection but showed distinct expression patterns between ZIKV- and mock infection, discovered novel proviral and antiviral factors. One-third of the 74 drugs found through signature-based drug repositioning and cross-reference with the Drug Gene Interaction Database (DGIdb) were known anti-ZIKV agents. In cellular assays, two promising antiviral candidates (Luminespib/NVP-AUY922, L-161982) were found to reduce viral replication without causing cell toxicity. Overall, our time-series transcriptome-based methods offer a novel and feasible strategy for antiviral drug discovery. Our strategies, which combine conventional and data-driven analysis, can be extended for other pathogens causing pandemics in the future.

Changing epidemiology of dengue fever in children in South America.

Fonseca SNS.

31-01-2023

*Curr Opin Pediatr*.

<https://pubmed.ncbi.nlm.nih.gov/36715049/>

Wolbachia wAlbB remains stable in Aedes aegypti over 15 years but exhibits genetic background-dependent variation in virus blocking.

Liang X, Tan CH, Sun Q, Zhang M, Wong PSJ, Li MI, Mak KW, Martín-Park A, Contreras-Perera Y, Puerta-Guardo H, Manrique-Saide P, Ng LC, Xi Z.

22-09-2022

*PNAS Nexus.*

<https://pubmed.ncbi.nlm.nih.gov/36714832/>

Risk of adverse outcomes in offspring with RT-PCR confirmed prenatal Zika virus exposure: An individual participant data meta-analysis of 13 cohorts in the Zika Brazilian Cohorts Consortium.

**de Alencar Ximenes RA, Miranda-Filho DB, Brickley EB, Barreto de Araújo TV, Montarroyos UR, Abtibol-Bernardino MR, Mussi-Pinhata MM, Duarte G, Coutinho CM, Biason de Moura Negrini SF, Costa Alecrim MDG, Albuquerque de Almeida Peixoto LF, Lopes Moreira ME, Zin A, Pereira Júnior JP,** **Nielsen-Saines K, Turchi Martelli CM, Rodrigues LC, de Souza WV, Ventura LO, de Oliveira CS, de Matos H, Furtado Serra EM, Souza Gomes LT, Nogueira ML, Estofolete C, Vaz-Oliani DC, Passos SD, Moron A, Duarte Rodrigues MM, Pereira Sarmento SG, Turchi MD, Pela Rosado LE, de Sene Amâncio Zara AL, Franco Gomes MB, Schuler-Faccini L, Herrero-Silva J, Amorim MM, Melo AO, Ledo Alves da Cunha AJ, Prata-Barbosa A, Amim J Jr, Rezende-Filho J, Calcagno JI, Júnior Alcântara LC, de Almeida BL, Hofer CB, Machado ES, de Siqueira IC, Martinez-Espinoza FE, Brasil P.**

Jan-2023

*Lancet Reg Health Am*.

<https://pubmed.ncbi.nlm.nih.gov/36714276/>

**Background:** Knowledge regarding the risks associated with Zika virus (ZIKV) infections in pregnancy has relied on individual studies with relatively small sample sizes and variable risk estimates of adverse outcomes, or on surveillance or routinely collected data. Using data from the Zika Brazilian Cohorts Consortium, this study aims, to estimate the risk of adverse outcomes among offspring of women with RT-PCR-confirmed ZIKV infection during pregnancy and to explore heterogeneity between studies. **Methods:** We performed an individual participant data meta-analysis of the offspring of 1548 pregnant women from 13 studies, using one and two-stage meta-analyses to estimate the absolute risks. **Findings:** Of the 1548 ZIKV-exposed pregnancies, the risk of miscarriage was 0.9%, while the risk of stillbirth was 0.3%. Among the pregnancies with liveborn children, the risk of prematurity was 10,5%, the risk of low birth weight was 7.7, and the risk of small for gestational age (SGA) was 16.2%. For other abnormalities, the absolute risks were: 2.6% for microcephaly at birth or first evaluation, 4.0% for microcephaly at any time during follow-up, 7.9% for neuroimaging abnormalities, 18.7% for functional neurological abnormalities, 4.0% for ophthalmic abnormalities, 6.4% for auditory abnormalities, 0.6% for arthrogryposis, and 1.5% for dysphagia. This risk was similar in all sites studied and in different socioeconomic conditions, indicating that there are not likely to be other factors modifying this association. **Interpretation:** This study based on prospectively collected data generates the most robust evidence to date on the risks of congenital ZIKV infections over the early life course. Overall, approximately one-third of liveborn children with prenatal ZIKV exposure presented with at least one abnormality compatible with congenital infection, while the risk to present with at least two abnormalities in combination was less than 1.0%.

RIG-I and MDA5 are modulated by bone morphogenetic protein (BMP6) and are essential for restricting Zika virus infection in human Sertoli cells.

**Jiyarom B, Giannakopoulos S, Strange DP,** **Panova N, Gale M Jr, Verma S.**

12-01-2023

*Front Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36713156/>

Broad-spectrum antiviral inhibitors targeting pandemic potential RNA viruses.

Garcia G, Irudayam JI, Jeyachandran AV, Dubey S, Chang C, Cario SC, Price N, Arumugam S, Marquez AL, Shah A, Fanaei A, Chakravarty N, Joshi S, Sinha S, French SW, Parcells M, Ramaiah A, Arumugaswami V.

20-01-2023

*bioRxiv*.

<https://pubmed.ncbi.nlm.nih.gov/36711787/>

Variable effects of Wolbachia on alphavirus infection in Aedes aegypti.

Dodson BL, Pujhari S, Brustolin M, Metz HC, Rasgon JL.

21-01-2023

*bioRxiv*.

<https://pubmed.ncbi.nlm.nih.gov/36711723/>

*Wolbachia pipientis* (= *Wolbachia* ) has promise as a tool to suppress virus transmission by *Aedes aegypti* mosquitoes. However, *Wolbachia* can have variable effects on mosquito-borne viruses. This variation remains poorly characterized, yet the multimodal effects of *Wolbachia* on diverse pathogens could have important implications for public health. Here, we examine the effects of somatic infection with two strains of *Wolbachia* ( *w* AlbB and *w* Mel) on the alphaviruses Sindbis virus (SINV), O'nyong-nyong virus (ONNV), and Mayaro virus (MAYV) in *Ae. aegypti* . We found variable effects of *Wolbachia* including enhancement and suppression of viral infections, with some effects depending on *Wolbachia* strain. Both *w* AlbB- and *w* Mel-infected mosquitoes showed enhancement of SINV infection rates one week post-infection, with *w* AlbB-infected mosquitoes also having higher viral titers than controls. Infection rates with ONNV were low across all treatments and no significant effects of *Wolbachia* were observed. The effects of *Wolbachia* on MAYV infections were strikingly strain-specific; *w* Mel strongly blocked MAYV infections and suppressed viral titers, while *w* AlbB did not influence MAYV infection. The variable effects of *Wolbachia* on vector competence underscore the importance of further research into how this bacterium impacts the virome of wild mosquitoes including the emergent human pathogens they transmit. **Impact statement:** In recent years, wild populations of *Aedes aegypti* mosquitoes have been deliberately infected with *Wolbachia* -a bacterium that helps to curb the spread of some pathogens including dengue virus. But how does *Wolbachia* affect the ability of mosquitoes to become infected with and spread the many different viruses they encounter in nature? Here, we characterize the effects of *Wolbachia* on three alphaviruses that cause illness in humans- Sindbis virus, O'nyong-nyong virus, and Mayaro virus. We find *Wolbachia* has variable effects on these pathogens, including significant enhancement of Sindbis virus infections. Our research has important implications for the design of vector control strategies, and suggests further research is needed to understand how *Wolbachia* shapes the replication and transmission of diverse viruses.

Adipokine levels and their association with clinical disease severity in patients with dengue.

Kuruppu H, Wickramanayake WPRH, Jeewandara C, Peranantharajah D, Colambage HS, Perera L, Gomes L, Wijewickrama A, Ogg GS, Malavige GN.

09-01-2023

*medRxiv*.

<https://pubmed.ncbi.nlm.nih.gov/36711706/>

Insight parameter drug design for human β-tryptase inhibition integrated molecular docking, QSAR, molecular dynamics simulation, and pharmacophore modelling studies of α-keto-[1,2,4]-oxadiazoles.

Yu CX, Tan JW, Rullah K, Imran S, Tham CL.

29-01-2023

*J Biomol Struct Dyn*.

<https://pubmed.ncbi.nlm.nih.gov/36709457/>

Scaffold identification and drug repurposing for finding potential Dengue envelope inhibitors through ligand-based pharmacophore model.

Priya S, Alli VJ, Jadav SS.

29-01-2023

*J Biomol Struct Dyn*.

<https://pubmed.ncbi.nlm.nih.gov/36709443/>

Most of the existing DENV entry inhibitors were discovered through structure-based, high-throughput screening techniques and optimization approaches by aiming β-OG pocket. However, the class of precise chemical scaffolds with superior antiviral activity targeting the early stages of virus infection that is considered to be beneficial in therapeutics and is still in process. In this study, ligand-based pharmacophore modeling using existing DENV entry inhibitors provided two best models, AADRR-2 and AAADR-2 (A- accepter, D- donor, R-ring) to screen public and DrugBank datasets. Further, approximately 36000 molecules were filtered using Zinc13 by employing the ideal validated models. Additionally, using β-OG binding pocket as target site, molecular docking experiments including induced-fit studies were conducted that provided further structurally divergent ligands. Moreover, the refined list of preferential hits were filtered out based on the best fitness score, binding energy and interaction paradigm, among them fused pyrimidine, hydrazone and biphenyl core comprising scaffolds were identified possessing profound interaction profile with key amino acid residues, ALA-50, GLN-200, PHE-193 and PHE-279 in 100 ns MD simulations. Additionally, the search for similar chemical fingerprints from DrugBank library was also carried out and Eltrombopag (Promacta/Revolade® prescribed in thrombocytopenia) was identified as a preferential β-OG pocket binder. The identified pyrazole-based hydrazone class of drug, Eltrombopag is in phase II clinical trials employed to treat dengue-mediated thrombocytopenia.Communicated by Ramaswamy H. Sarma.

Infections in travellers returning to the UK: a retrospective analysis (2015-2020).

Warner JC, Hatziioanou D, Osborne JC, Bailey DJ, Brooks TJG, Semper AE.

27-01-2023

*J Travel Med*.

<https://pubmed.ncbi.nlm.nih.gov/36708032/>

Correlations between COVID-19 and dengue obtained via the study of South America, Africa and Southeast Asia during the 2020s.

Bergero P, Schaposnik LP, Wang G.

27-01-2023

*Sci Rep*.

<https://pubmed.ncbi.nlm.nih.gov/36707624/>

A dramatic increase in the number of outbreaks of dengue has recently been reported, and climate change is likely to extend the geographical spread of the disease. In this context, this paper shows how a neural network approach can incorporate dengue and COVID-19 data as well as external factors (such as social behaviour or climate variables), to develop predictive models that could improve our knowledge and provide useful tools for health policy makers. Through the use of neural networks with different social and natural parameters, in this paper we define a Correlation Model through which we show that the number of cases of COVID-19 and dengue have very similar trends. We then illustrate the relevance of our model by extending it to a Long short-term memory model (LSTM) that incorporates both diseases, and using this to estimate dengue infections via COVID-19 data in countries that lack sufficient dengue data.

Typhoid Fever among Patients Diagnosed with Dengue in a Tertiary Care Centre: A Descriptive Cross-sectional Study.

Mahato AK, Shrestha N, Gharti SB, Shah M.

01-08-2022

*JNMA J Nepal Med Assoc*.

<https://pubmed.ncbi.nlm.nih.gov/36705211/>

**Introduction:** Dengue and typhoid fever are different entities with overlapping signs and symptoms which are indistinguishable and there have been few reports of co-infections from endemic areas. The resemblance of symptoms makes accurate clinical diagnosis and treatment difficult. Both are major health problems mainly during monsoon and co-infection, if not timely diagnosed and treated can be fatal. The aim of this study was to find out the prevalence of typhoid fever among patients diagnosed with dengue at a tertiary care centre. **Methods:** A descriptive cross-sectional study was done among patients of age >15 years with dengue fever attending the medicine outpatient department in a tertiary care centre from 1 July 2021 to 30 June 2022. Ethical approval was taken from the Institutional Review Committee (Reference number: 466/2020). Convenience sampling was used. Patients with other risk factors for febrile illness were excluded from the study. Point estimate and 90% Confidence Interval were calculated. **Results:** Among 95 dengue cases, typhoid fever was observed in 18 (18.95%) (12.36-25.54, 90% Confidence Interval). The mean age of presentation was 35±9 years with a male to female ratio of 0.8:1. Fever was the most common presentation with a mean temperature of 100.8±2.1°F. **Conclusions:** The prevalence of typhoid fever among dengue-positive cases was higher as compared to other studies done in similar settings.

Admitted Dengue Cases among the Adult Dengue Positive Cases in a Tertiary Care Centre: A Descriptive Cross-sectional Study.

Dhungana D, Banstola B, Banjara M.

01-09-2022

*JNMA J Nepal Med Assoc*.

<https://pubmed.ncbi.nlm.nih.gov/36705129/>

**Introduction:** Dengue is an infectious disease. This disease is prevalent mainly in the terai belts of Nepal. But in the last few years, the cases are in increasing trend in the hilly areas of Nepal. The aim of this study was to find out the prevalence of admitted dengue cases among adult dengue-positive cases in a tertiary care centre. **Methods:** This was a descriptive cross-sectional study done at a tertiary teaching hospital after obtaining ethical approval from the Institutional Review Committee (Reference number: 063/2077/2078). Convenience sampling was used. The data of serologically confirmed dengue cases, during the period of 1 August 2019 to 1 December 2019, of ages above 15 years, were collected from the hospital records. Point estimate and 95% Confidence Interval were calculated. **Results:** Out of 922 adult dengue-positive patients, 347 (37.63%) (36.04-39.22, 95% Confidence Interval) were admitted. Among them, 154 (44.38%) cases were seen during the month of September. A total of 264 (76.08%) were the inhabitants of the Kaski district. A total of one hundred seventy eight (51.29%) cases were males. The most common symptoms seen were fever among 335 (96.54%) patients and headache among 141 (40.63%) patients. Leukopenia was seen in 192 (55.33%) patients and thrombocytopenia was seen in 165 (47.55%) of the admitted cases. **Conclusions:** The prevalence of admitted dengue cases was higher as compared to other studies done in similar settings.

Experiencing Dengue as a Medical Student.

Shrestha S.

01-12-2022

*JNMA J Nepal Med Assoc*.

<https://pubmed.ncbi.nlm.nih.gov/36705100/>

Dengue is a disease which spreads by the bite of an infected Aedes mosquito. Reading about a disease in a textbook and experiencing it as a patient is a completely different thing. This article highlights the feeling of a medical student as a patient. It provides the reader with an idea of how Basic Science knowledge can be used for rational decision-making. Self- prescription of medication without consulting a doctor can be more harmful in many circumstances. We also need to be aware of the warning signs of Dengue virus infection.

Clinical Profile, Histopathology, and Outcomes in Infection-Related Glomerulonephritis - Single-Center Experience.

Sanathkumar HT, Fernando EM, Kurien AA, Srinivasaprasad ND, Suren S, Thirumalvalavan K.

Nov-Dec 2022

*Indian J Nephrol*.

<https://pubmed.ncbi.nlm.nih.gov/36704600/>

RSAD2: An exclusive target protein for Zika virus comparative modeling, characterization, energy minimization and stabilization.

Rangisetty PT, Kilaparthi A, Akula S, Bhardwaj M, Singh S.

Jan-Feb 2023

*Int J Health Sci (Qassim).*

<https://pubmed.ncbi.nlm.nih.gov/36704497/>

Differential Infectivity of Human Neural Cell Lines by a Dengue Virus Serotype-3 Genotype-III with a Distinct Nonstructural Protein 2A (NS2A) Amino Acid Substitution Isolated from the Cerebrospinal Fluid of a Dengue Encephalitis Patient.

Phu Ly MH, Nguyen CT, Nguyen TV, Ngan Nguyen TT, Nabeshima T, Adungo F, Takamatsu Y, Huy NT, Mai Le TQ, Morita K, Hasebe F, Moi ML.

17-01-2023

*Can J Infect Dis Med Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36704099/>

Dengue encephalitis is considered as a severe but unusual clinical presentation of dengue infection. Limited molecular information is available on the neurotropism of dengue virus (DENV), highlighting the need for further research. During a dengue outbreak in Vietnam in 2013, two DENV-3 strains were isolated, in which one was isolated from cerebrospinal fluid (CSF) samples from a dengue encephalitis patient and another strain was isolated from a patient with classical dengue fever in Hai Phong, Vietnam. DENV serotype-3 (DENV-3) isolated from these samples belonged to genotype III, marking the first report of this genotype in the country at that time. Genetic variation between both strains was elucidated by using a full genome sequencing by next-generation sequencing (NGS). The infectivity of the isolated DENV-3 strains was further characterized using human and mouse neuronal cell lines. Phylogenetic analysis of the isolates demonstrated high homogeneity between the CSF-derived and serum-derived DENV-3, in which the full genome sequences of the CSF-derived DENV-3 presented a *Thr-1339-Ile* mutation in the nonstructural 2A (NS2A) protein. The CSF-derived DENV-3 isolate grew preferentially in human neuronal cells, with a significant proportion of cells that were positive for nonstructural 1 (NS1), nonstructural 4B (NS4B), and nonstructural 5 (NS5) antigens. These results suggest that NS2A may be a crucial region in the neuropathogenesis of DENV-3 and its growth in human neuronal cells. Taken together, our results demonstrate that a CSF-derived DENV-3 has unique infectivity characteristics for human neuronal cells, which might play a crucial role in the neuropathogenesis of DENV infection.

Congenital chikungunya in a neonate with early-onset sepsis and petechiae: An unusual case report.

Bin S, Phou K, Im S.

23-01-2023

*Clin Case Rep*.

<https://pubmed.ncbi.nlm.nih.gov/36703765/>

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

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

26-01-2023

*Parasit Vectors.*

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

**Background:** Mosquitoes are vectors of various arboviruses belonging to the genera Alphavirus and Flavivirus, and Costa Rica is endemic to several of them. The aim of this study was to describe and analyze the community structure of such vectors in Costa Rica. **Methods:** Sampling was performed in two different coastal locations of Costa Rica with evidence of arboviral activity during rainy and dry seasons. Encephalitis vector surveillance traps, CDC female gravid traps and ovitraps were used. Detection of several arboviruses by Pan-Alpha and Pan-Flavi PCR was attempted. Blood meals were also identified. The Normalized Difference Vegetation Index (NDVI) was estimated for each area during the rainy and dry seasons. The Chao2 values for abundance and Shannon index for species diversity were also estimated. **Results:** A total of 1802 adult mosquitoes belonging to 55 species were captured, among which Culex quinquefasciatus was the most caught species. The differences in NDVI were higher between seasons and between regions, yielding lower Chao-Sørensen similarity index values. Venezuelan equine encephalitis virus, West Nile virus and Madariaga virus were not detected at all, and dengue virus and Zika virus were detected in two separate Cx. quinquefasciatus specimens. The primary blood-meal sources were chickens (60%) and humans (27.5%). Both sampled areas were found to have different seasonal dynamics and population turnover, as reflected in the Chao2 species richness estimation values and Shannon diversity index. **Conclusion:** Seasonal patterns in mosquito community dynamics in coastal areas of Costa Rica have strong differences despite a geographical proximity. The NDVI influences mosquito diversity at the regional scale more than at the local scale. However, year-long continuous sampling is required to better understand local dynamics.

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

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

01-01-2023

*Obstet Gynecol*.

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

Diel activity patterns of vector mosquito species in the urban environment: Implications for vector control strategies.

Wilke ABB, Mhlanga A, Kummer AG, Vasquez C, Moreno M, Petrie WD, Rodriguez A, Vitek C, Hamer GL, Mutebi JP, Ajelli M.

26-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36701264/>

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

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

31-12-2023

*Glob Health Action.*

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

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

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

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

23-01-2023

*Rev Soc Bras Med Trop*.

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

The research progress of Chikungunya fever.

Cai L, Hu X, Liu S, Wang L, Lu H, Tu H, Huang X, Tong Y.

09-01-2023

*Front Public Health*.

<https://pubmed.ncbi.nlm.nih.gov/36699921/>

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

Lu W, Ren H.

09-01-2023

*Front Public Health*.

<https://pubmed.ncbi.nlm.nih.gov/36699887/>

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

Byers NM, Burns PL, Stuchlik O, Reed MS, Ledermann JP, Pohl J, Powers AM.

25-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36696390/>

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

Zhao H, Wang K, Wang H.

25-01-2023

*J Math Biol.*

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

To explore the influence of spatial heterogeneity on mosquito-borne diseases, we formulate a reaction-diffusion model with general incidence rates. The basic reproduction ratio [Formula: see text] for this model is introduced and the threshold dynamics in terms of [Formula: see text] are obtained. In the case where the model is spatially homogeneous, the global asymptotic stability of the endemic equilibrium is proved when [Formula: see text]. Under appropriate conditions, we establish the asymptotic profiles of [Formula: see text] in the case of small or large diffusion rates, and investigate the monotonicity of [Formula: see text] with respect to the heterogeneous diffusion coefficients. Numerically, the proposed model is applied to study the dengue fever transmission. Via performing simulations on the impacts of certain factors on [Formula: see text] and disease dynamics, we find some novel and interesting phenomena which can provide valuable information for the targeted implementation of disease control measures.

CRISPR mediated transactivation in the human disease vector Aedes aegypti.

Bui M, Dalla Benetta E, Dong Y, Zhao Y, Yang T, Li M, Antoshechkin IA, Buchman A, Bottino-Rojas V, James AA, Perry MW, Dimopoulos G, Akbari OS.

19-01-2023

*PLoS Pathog.*

<https://pubmed.ncbi.nlm.nih.gov/36656895/>

Assessing dengue fever risk in Costa Rica by using climate variables and machine learning techniques.

Barboza LA, Chou-Chen SW, Vásquez P, García YE, Calvo JG, Hidalgo HG, Sanchez F.

13-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36638136/>

Exploration of novel hexahydropyrrolo[1,2-e]imidazol-1-one derivatives as antiviral agents against ZIKV and USUV.

Chen R, Francese R, Wang N, Li F, Sun X, Xu B, Liu J, Liu Z, Donalisio M, Lembo D, Zhou GC.

15-02-2023

*Eur J Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36623328/>

Zika virus (ZIKV) and Usutu virus (USUV) are two emerging flaviviruses mostly transmitted by mosquitos. ZIKV is associated with microcephaly in newborns and the less-known USUV, with its reported neurotropism and its extensive spread in Europe, represents a growing concern for human health. There is still no approved vaccine or specific antiviral against ZIKV and USUV infections. The main goal of this study is to investigate the anti-ZIKV and anti-USUV activity of a new library of compounds and to preliminarily investigate the mechanism of action of the selected hit compounds in vitro. Two potent anti-ZIKV and anti-USUV agents, namely ZDL-115 and ZDL-116, were discovered, both presenting low cytotoxicity, cell-line independent antiviral activity in the low micromolar range and ability of reducing viral progeny production. The analysis of the structure-activity relationship (SAR) revealed that introduction of 2-deoxyribose to 3-arene was fundamental to enhance the solubility and improve the antiviral action. Additionally, we demonstrated that ZDL-115 and ZDL-116 are significantly active against both viruses when added on cells for at least 24 h prior to viral inoculation or immediately post-infection. The docking analysis showed that ZDL-116 could target the host vitamin D receptor (VDR) and viral proteins. Future experiments will be focused on compound modification to discover analogues that are more potent and on the clarification of the mechanism of action and the specific drug target. The discovery and the development of a novel anti-flavivirus drug will have a significant impact in a context where there are no fully effective antiviral drugs or vaccines for most flaviviruses.

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

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

31-01-2023

*J Virol.*

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

Imidazonaphthyridine effects on Chikungunya virus replication: Antiviral activity by dependent and independent of interferon type 1 pathways.

Ruiz UEA, Santos IA, Grosche VR, Fernandes RS, de Godoy AS, Torres JDA, Freire MCLC, Mesquita NCMR, Guevara-Vega M, Nicolau-Junior N, Sabino-Silva R, Mineo TWP, Oliva G, Jardim ACG.

15-01-2023

*Virus Res*.

<https://pubmed.ncbi.nlm.nih.gov/36565816/>

The Chikungunya virus (CHIKV) causes Chikungunya fever, a disease characterized by symptoms such as arthralgia/polyarthralgia. Currently, there are no antivirals approved against CHIKV, emphasizing the need to develop novel therapies. The imidazonaphthyridine compound (RO8191), an interferon-α (IFN-α) agonist, was reported as a potent inhibitor of HCV. Here RO8191 was investigated for its potential to inhibit CHIKV replication in vitro. RO8191 inhibited CHIKV infection in BHK-21 and Vero-E6 cells with a selectivity index (SI) of 12.3 and 37.3, respectively. Additionally, RO8191 was capable to protect cells against CHIKV infection, inhibit entry by virucidal activity, and strongly impair post-entry steps of viral replication. An effect of RO8191 on CHIKV replication was demonstrated in BHK-21 through type-1 IFN production mechanism and in Vero-E6 cells which has a defective type-1 IFN production, also suggesting a type-1 IFN independent mode of action. Molecular docking calculations demonstrated interactions of RO8191 with the CHIKV E proteins, corroborated by the ATR-FTIR assay, and with non-structural proteins, supported by the CHIKV-subgenomic replicon cells assay.

Activity, Template Preference, and Compatibility of Components of RNA Replicase of Eastern Equine Encephalitis Virus.

Lello LS, Miilimäe A, Cherkashchenko L, Omler A, Skilton R, Ireland R, Ulaeto D, Merits A.

31-01-2023

*J Virol*.

<https://pubmed.ncbi.nlm.nih.gov/36533950/>

Five-Year Trend of Adolescent Hospitalizations and Deaths in Thailand: A Secondary National Data Health Situation Analysis.

Areemit RS, Manaboriboon B, In-Iw S, Arunakul J, Bongsebandhu-Phubhakdi C, Kamol N, Thunyapipat C, Leelathipkul L, Areekul W.

Feb-2023

*J Prev (2022).*

<https://pubmed.ncbi.nlm.nih.gov/36512185/>

Adolescence is a critical phase for achieving human potential, serving as the foundation for later health. In 2010, the major causes of hospital admissions and deaths in Thai adolescents were related to preventable causes, specifically engagement in high-risk behaviors such as unprotected sexual intercourse, substance use and unsafe driving. We retrieved data from 1,761,667 adolescent (10-17 years) hospital admissions and 6362 deaths between 2015 and 2019 from the National Health Security Office database. Trends of hospital admissions and deaths, length of stay and medical expenses by sex, age: early (10-13 years) and middle adolescents (14-17 years), and geographical regions were analyzed by ICD-10 disease group and single diagnosis. Hospital admissions increased in relation to the same age population from 2015 to 2019. Trends of the top 3 diagnoses shifted between disease groups from 2015 to 2019. Pregnancy retreated from the first (17.8%) to the third rank (12.2%), and arthropod-borne viral fevers advanced from the third (13.1%) to the first rank (17.1%). Injury and poisoning remained at the second rank (14.5-14.4%). Females were admitted more than males, but males had significantly longer hospital stays. Early adolescents were admitted less than middle adolescents and their hospital stay was significantly shorter. Trends of the top 3 diagnoses for deaths by disease groups remained stable: injury and poisoning (41.2%), neoplasms (10.2%), and respiratory infections (9.5%). The average direct health care cost utilized on adolescent health care was 3813 million Baht (115.54 million US Dollars) per year. Considering the top 3 disease groups, injury and poisoning had the highest average cost per hospital admission and net cost per year consuming 26.4% of the total cost. Our study highlights the cause of hospital admissions and deaths in Thai adolescents, which are mainly preventable. Adolescent health care will improve with more investment in prevention through policy, service, and education reform.

Dengue virus infection - a review of pathogenesis, vaccines, diagnosis and therapy.

Kok BH, Lim HT, Lim CP, Lai NS, Leow CY, Leow CH.

15-01-2023

*Virus Res*.

<https://pubmed.ncbi.nlm.nih.gov/36493993/>

Nucleo-Cytoplasmic Transport of ZIKV Non-Structural 3 Protein Is Mediated by Importin-α/β and Exportin CRM-1.

De Jesús-González LA, Palacios-Rápalo SN, Reyes-Ruiz JM, Osuna-Ramos JF, Farfán-Morales CN, Cordero-Rivera CD, Cisneros B, Gutiérrez-Escolano AL, Del Ángel RM.

31-01-2023

*J Virol.*

<https://pubmed.ncbi.nlm.nih.gov/36475764/>

IFITM proteins: Understanding their diverse roles in viral infection, cancer, and immunity.

Gómez-Herranz M, Taylor J, Sloan RD.

Jan-2023

*J Biol Chem.*

<https://pubmed.ncbi.nlm.nih.gov/36435199/>

No Association Between Interleukin 6 and Inducible Nitric Oxide Synthase Polymorphisms and Dengue Infection: A Case-Control Study.

Dos Santos BRC, Melo Dos Santos AC, Magalhaes Bastos D, Silva Santos LD, de Souza Praxedes FA, Sathio Bessoni Tanabe I, Fireman de Farias K, Martins de Souza Figueiredo EV.

Feb-2023

*Immunol Invest.*

<https://pubmed.ncbi.nlm.nih.gov/36394557/>

**Background:** Dengue is a life-threatening disease. The factors that lead to severe cases are not completely understood. The host immune system is involved in the response to infections and plays an important role in dengue infection. IL-6 and iNOS are components of the immune system and genetic polymorphisms in these genes may be involved in dengue virus infection. The study aimed to investigate the association of genetic polymorphisms in the *IL6* and *iNOS* genes and dengue. **Methods:** We performed a case-control study using 60 dengue-infected individuals and 119 healthy controls. Polymorphisms in the *IL6* (T15A) and *iNOS* (-1173CT) genes were amplified by Real-Time PCR. Statistical analyses were performed using BioEstat 5.0. **Results:** We identified that the frequency of T/A genotype of *IL6* was higher in dengue fever patients and C/T genotype of *iNOS* was higher in dengue hemorrhagic fever patients, however, no association was found between these polymorphisms and dengue. **Conclusion:** Polymorphisms in *iNOS* and *IL6* were not associated with dengue infection.

Weather integrated multiple machine learning models for prediction of dengue prevalence in India.

Kakarla SG, Kondeti PK, Vavilala HP, Boddeda GSB, Mopuri R, Kumaraswamy S, Kadiri MR, Mutheneni SR.

Feb-2023

*Int J Biometeorol.*

<https://pubmed.ncbi.nlm.nih.gov/36380258/>

Genetic analysis of a Fanconi anemia case revealed the presence of FANCF mutation (exon 1;469>C-T) with implications to develop acute myeloid leukemia.

Behera CK, Gyandeep G, Mishra R, Mohanty RP, Pal A, Behera J, Samal S, Das B.

Jan-2023

*Mol Biol Rep*.

<https://pubmed.ncbi.nlm.nih.gov/36369330/>

**Background:** Fanconi anemia (FA) is a rare genetic disorder and one of the most common inherited forms of aplastic anemia. FA is an autosomal recessive or X-linked genetic disorder that is characterized by typical physical malformations and haematopoietic anomalies. In most cases of FA, patients harbor homozygous or double heterozygous mutations in the FANCA (60-65%), FANCC (10-15%), FANCG (~ 10%), FANCD2 (3-6%) or FANCF (2%) genes in different ethnic populations, which leads to inherited bone marrow failure (IBMF). Hence, it is important to screen such mutations in correlation with clinical manifestations of FA in various ethnic populations. **Approach:** An 11 year old female pediatric patient of an East India family was presented with febrile illness, having thrombocytopenia with positive dengue IgM (Immunoglobulin M) and treated as a case of dengue hemorrhagic fever at the initial stage of diagnosis. Chromosomal breakage study was performed based on the abnormal physical examination, which showed 100% breaks, triradials, and quadrilaterals in mitomycin (MMC)-induced peripheral blood lymphocyte culture. Importantly, conventional cytogenetic assay in most of the bone marrow cells revealed an additional gain in chromosome 3q+ [46,XX,add(3)(q25)] and terminal loss in chr8p- [46,XX,del(8)(p23)], which might have a prognostic relevance in the outcomes of the FA patient. The bone marrow aspiration and biopsy were repeated and the results showed acute leukemia with 39% blast cells. Whole-genome sequencing analysis of the patient confirmed the presence of (exon 1; 496 > C-T) non-sense mutation leading to a truncated FANCF protein attributed to a stop codon at the amino acid position 166. **Conclusion:** The study reported the presence of a homozygous C-T exon 1 mutation in FANCF gene in the female pediatric patient from Odisha, India associated with FA. Furthermore, both parents were found to be carriers of FANCF gene mutation, as this allele was found to be in heterozygous state upon genome sequencing. The pathogenicity of the agent was robustly supported by the clinical phenotype and biochemical observations, wherein the patient eventually developed acute myeloid leukemia. The findings of the study infer the importance of early detection of FA and the associated mutations, which might lead to the development of acute myeloid leukemia.

Acute Liver Failure in Dengue: A Common but Overlooked Entity in Pediatric Patients in Tropical Countries.

Dogra S, Kumar K, Malhotra S, Jerath N, Sibal A.

01-02-2023

*J Pediatr Gastroenterol Nutr*.

<https://pubmed.ncbi.nlm.nih.gov/36302257/>

Profile of Chikungunya Patients with Ophthalmological Manifestations in a Reference Center in Brazil.

Machado MC, Moraes LA, Maia TR, Ferreira JLM, Cavalcanti LPG, Rodriguez PJY.

24-01-2023

*Jpn J Infect Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36184394/>

Clinical features and risk factors for death in acute undifferentiated fever: A prospective observational study in rural community hospitals in six states of India.

Mørch K, Manoharan A, Chandy S, Singh A, Kuriakose C, Patil S, Henry A, Chacko N, Alvarez-Uria G, Nesaraj J, Blomberg B, Kurian S, Haanshuus CG, Antony GV, Langeland N, Mathai D.

01-02-2023

*Trans R Soc Trop Med Hyg*.

<https://pubmed.ncbi.nlm.nih.gov/36130240/>

Next-generation Sequencing for Surveillance of Antimicrobial Resistance and Pathogenicity in Municipal Wastewater Treatment Plants.

Cuetero-Martínez Y, de Los Cobos-Vasconcelos D, Aguirre-Garrido JF, Lopez-Vidal Y, Noyola A.

2022

*Curr Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/35927898/>

The World Health Organization (WHO) ranks antimicrobial resistance (AMR) and various pathogens among the top 10 health threats. It is estimated that by 2050, the number of human deaths due to AMR will reach 10 million annually. On the other hand, several infectious outbreaks such as SARS, H1N1 influenza, Ebola, Zika fever, and COVID-19 have severely affected human populations worldwide in the last 20 years. These recent global diseases have generated the need to monitor outbreaks of pathogens and AMR to establish effective public health strategies. This review presents AMR and pathogenicity associated with wastewater treatment plants (WWTP), focusing on Next Generation Sequencing (NGS) monitoring as a complementary system to clinical surveillance. In this regard, WWTP may be monitored at three main points. First, at the inlet (raw wastewater or influent) to identify a broad spectrum of AMR and pathogens contained in the excretions of residents served by sewer networks, with a specific spatio-temporal location. Second, at the effluent, to ensure the elimination of AMR and pathogens in the treated water, considering the rising demand for safe wastewater reuse. Third, in sewage sludge or biosolids, their beneficial use or final disposal can represent a significant risk to public health. This review is divided into two sections to address the importance and implications of AMR and pathogen surveillance in wastewater and WWTP, based on NGS. The first section presents the fundamentals of surveillance techniques applied in WWTP (metataxonomics, metagenomics, functional metagenomics, metaviromics, and metatranscriptomics). Their scope and limitations are analyzed to show how microbiological and qPCR techniques complement NGS surveillance, overcoming its limitations. The second section discusses the contribution of 36 NGS research papers on WWTP surveillance, highlighting the current situation and perspectives. In both sections, research challenges and opportunities are presented.

An Extracorporeal Plasma Filtration Column with Specific Binding to Dengue Virions.

Thonghong S, Sinananpat P, Chatsuwan T, Srisawat N, Insin N, Salakij S, Boonyasuppayakorn S.

2023

*Blood Purif*.

<https://pubmed.ncbi.nlm.nih.gov/35512639/>

ONTdeCIPHER: an amplicon-based nanopore sequencing pipeline for tracking pathogen variants.

Cherif E, Thiam FS, Salma M, Rivera-Ingraham G, Justy F, Deremarque T, Breugnot D, Doudou JC, Gozlan RE, Combe M.

28-03-2022

*Bioinformatics.* 2022 Mar 28

<https://pubmed.ncbi.nlm.nih.gov/35080622/>

Endo-Lysosomal Cation Channels and Infectious Diseases.

Chao YK, Chang SY, Grimm C.

2023

*Rev Physiol Biochem Pharmacol*.

<https://pubmed.ncbi.nlm.nih.gov/32748124/>

Among the infectious diseases caused by pathogenic microorganisms such as bacteria, viruses, parasites, or fungi, the most prevalent ones today are malaria, tuberculosis, influenza, HIV/AIDS, Ebola, dengue fever, and methicillin-resistant Staphylococcus aureus (MRSA) infection, and most recently Covid-19 (SARS-CoV2). Others with a rather devastating history and high fatality rates such as plague, cholera, or typhus seem less threatening today but have not been eradicated, and with a declining efficacy of current antibiotics they ought to be watched carefully. Another emerging issue in this context is health-care associated infection. About 100,000 hospitalized patients in the USA ( www.cdc.gov ) and 33,000 in Europe ( https://www.ecdc.europa.eu ) die each year as a direct consequence of an infection caused by bacteria resistant to antibiotics. Among viral infections, influenza is responsible for about 3-5 million cases of severe illness, and about 250,000 to 500,000 deaths annually ( www.who.int ). About 37 million people are currently living with HIV infection and about one million die from it each year. Coronaviruses such as MERS-CoV, SARS-CoV, but in particular the recent outbreak of Covid-19 (caused by SARS-CoV2) have resulted in large numbers of infections worldwide with an estimated several hundred thousand deaths (anticipated fatality rate: <5%). With a comparatively low mortality rate dengue virus causes between 50 and 100 million infections every year, leading to 50,000 deaths. In contrast, Ebola virus is the causative agent for one of the deadliest viral diseases. The Ebola outbreak in West Africa in 2014 is considered the largest outbreak in history with more than 11,000 deaths. Many of the deadliest pathogens such as Ebola virus, influenza virus, mycobacterium tuberculosis, dengue virus, and cholera exploit the endo-lysosomal trafficking system of host cells for penetration into the cytosol and replication. Defects in endo-lysosomal maturation, trafficking, fusion, or pH homeostasis can efficiently reduce the cytotoxicity caused by these pathogens. Most of these functions critically depend on endo-lysosomal membrane proteins such as transporters and ion channels. In particular, cation channels such as the mucolipins (TRPMLs) or the two-pore channels (TPCs) are involved in all of these aspects of endo-lysosomal integrity. In this review we will discuss the correlations between pathogen toxicity and endo-lysosomal cation channel function, and their potential as drug targets for infectious disease therapy.

# Rage

Production and applications of fluorobody from redox-engineered Escherichia coli.

Srila W, Min TT, Sumphanapai T, Rangnoi K, Berkmen M, Yamabhai M.

02-02-2023

*Appl Microbiol Biotechnol.*

<https://pubmed.ncbi.nlm.nih.gov/36729226/>

Efficient selection and production of antibody fragments in microbial systems remain to be a challenging process. To optimize microbial production of single-chain variable fragments (scFvs), we have chosen five model targets, 1) a hapten, Zearalenone (ZEN) mycotoxin, along with infectious agents 2) rabies virus, 3) Propionibacterium acnes, 4) Pseudomonas aeruginosa, and a cancer cell 5) acute myeloid leukemia cell line (HL-60). The scFv binders were affinity selected from a non-immunized human phage display scFv antibody library and genetically fused to the N-terminus of emerald green fluorescent protein (EmGFP). The scFv-EmGFP fusion constructs were subcloned into an expression vector, under the control of T7 promoter, C-terminally tagged with hexa-histidine and expressed in different Escherichia coli (E. coli) hosts. This enabled the detection of cells that expressed the correct scFv-EmGFP fusion, termed fluorobody, via bright fluorescent signal in the cytoplasm. Among the three E. coli hosts tested, an engineered E. coli B strain called SHuffle B that promotes disulfide bond formation in the cytoplasm appeared to be the most appropriate host. The recombinant fluorobodies were well expressed (2-8 mg/L), possessed the fluorescence property of EmGFP, and retained the ability to bind to their cognate targets. Their specific bindings were demonstrated by ELISA, fluorescence-linked immunosorbent assay (FLISA), flow cytometry, and fluorescent microscope imaging. The fluorobody expression platform in this study could be further adopted as a one-step immunostaining technique based on scFv, isolated from phage display library to numerous desired targets. KEY POINTS: • E. coli SHuffle express T7 is a suitable expression host for scFv-EmGFP (fluorobody) • Only the clones harboring scFv-EmGFP plasmid will show bright fluorescent signal • This platform can be used to produce fluorobodies for numerous purposes.

Rabies: Reality Bites.

Fiorito TM, Krilov LR.

01-02-2023

*Pediatr Rev.*

<https://pubmed.ncbi.nlm.nih.gov/36720676/>

Nationally and locally-initiated One Health approach in controlling rabies in West Kalimantan, Indonesia.

Aptriana CD, Sudarnika E, Basri C.

Dec-2022

*Vet World*.

<https://pubmed.ncbi.nlm.nih.gov/36718315/>

**Background and aim:** Rabies is one of the prioritized zoonoses in Indonesia and West Kalimantan is one of the rabies-endemic provinces in the country. This study aimed to evaluate a locally-initiated One Health approach to implement rabies prevention and control programs in Pontianak City and Sanggau District (through a bottom-up approach), and the central government initiated a program in Ketapang District (through a top-down approach). **Materials and methods:** Data were collected using three focused group discussions involving public health and animal health/veterinary sectors from each district or city. This study collected data from the rabies control program in West Kalimantan from 2014 to 2020. **Results:** The evaluation results of the rabies prevention and control program in Pontianak City and Sanggau District that used the local initiative approach were considered effective in reducing the number of rabies cases in these areas, and they overcame the challenges, for example, limited resources, in this area. Pontianak City and Sanggau District initiatives' approach was a bottom-up policy. Thus, this program had better sustainability than the One Health approach in the Ketapang District, which used a top-down implementation. The approach in Ketapang District was also considered adequate to reduce the number of rabies cases in the area. However, the reshuffle of animal health officers and health workers in 2020, which was not followed by training on One Health for the new officers, became a challenge in implementing One Health in Ketapang District. **Conclusion:** National and local initiatives' One Health approach implemented by Ketapang District, Sanggau District, and Pontianak City involved multiple sectors and was considered effective in preventing and controlling rabies in these areas. However, the sustainability of this program in the Ketapang District requires commitment and support from the local government.

Evaluation of the immune response of dogs after a mass vaccination campaign against rabies in Tunisia.

Handous M, Turki I, Ghram A, BenMaiz S, Bensalem J, Basdouri N, Soltani M, Bassalah F, Kharmachi H.

30-01-2023

*BMC Vet Res*.

<https://pubmed.ncbi.nlm.nih.gov/36717812/>

Human rabies control in the era of post-COVID-19: a call for action.

Goel K, Sen A, Satapathy P, Kumar P, Aggarwal AK, Sah R, Padhi BK.

28-01-2023

*J Travel Med*.

<https://pubmed.ncbi.nlm.nih.gov/36715149/>

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

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

2023

*Parasite*.

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

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

# Trachome

Trachoma, the world's leading infectious cause of blindness: The remaining gap in care and access to basic handwashing facilities.

Wu TJ, Reynolds MM.

01-02-2023

*Eur J Ophthalmol*.

<https://pubmed.ncbi.nlm.nih.gov/36726295/>

**Purpose:** Trachoma, the world's leading infectious cause of blindness, has been targeted by the WHO for elimination through the SAFE strategy: surgery, antibiotics, facial cleanliness, and environmental improvement. Although significant progress has been made, there remains a gap in care. This project studied the association of geographical distribution of the remaining need for trachoma intervention and its association with access to basic handwashing facilities at home, as an indicator of water/sanitation infrastructure. We hypothesized that poor water sanitation would correspond to areas where trachoma intervention is still required. **Design:** Retrospective analysis using the WHO Global Health Observatory. Spatial, correlation, and simple and multivariable regression analyses were used. **Methods:** Using data from the WHO Global Health Observatory, a total of 194 countries were analyzed. Two choropleth maps were created, with inset maps focused on the South Pacific region, where the top 5 countries with the greatest population proportion requiring trachoma intervention are located. **Results:** Correlations and the simple regression model of total population with access to handwashing facilities as the only risk factor were insignificant. However, the multivariable regression models with access to handwashing facilities (total, urban, and rural) and population density as risk factors for trachoma intervention were significant. **Conclusion:** Poor water/sanitation infrastructure correlates with trachoma burden. Therefore, water/sanitation infrastructure improvement is a worthwhile target in the efforts toward trachoma elimination, but further research on the association between these important public health indicators is warranted.

No one left behind: how Colombia is adapting its trachoma programme to reach indigenous populations.

Trujillo-Trujillo J, Saboya M, Jesudason T.

2022

*Community Eye Health*.

<https://pubmed.ncbi.nlm.nih.gov/36704537/>

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

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

23-01-2023

*Rev Soc Bras Med Trop.*

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

Photographic grading for trachoma diagnosis within trachoma impact surveys in Amhara region, Ethiopia.

Whitson CC, Nute AW, Hailemariam B, Deathe AR, Astale T, Ayele Z, Gessese D, Sata E, Zerihun M, Melak B, Haile M, Zeru T, Getnet B, Wondimteka B, Kabtu E, Getachew H, Shibiru M, Bayecha S, Aragie S, Wittberg DM, Tadesse Z, Callahan EK, Keenan JD, Admassu F, Nash SD.

01-02-2023

*Trans R Soc Trop Med Hyg*.

<https://pubmed.ncbi.nlm.nih.gov/36162054/>

**Background:** As countries reach the trachoma elimination threshold and cases of trachomatous inflammation follicular (TF) become rare, it becomes difficult to train survey graders to recognize clinical signs. We assess the use of photography as a grading tool, the efficiency of an in-country grading center and the comparability of field and photographic grading. **Methods:** During January-February 2017 surveys in Amhara, Ethiopia, field graders assessed TF, trachomatous inflammation intense (TI) and trachomatous scarring (TS). Photographs were taken from each conjunctiva and later graded at the Gondar Grading Center (GGC) at the University of Gondar in Amhara. Two trained ophthalmology residents graded each set of photographs and a third grader provided an adjudicating grade when needed. **Results:** A total of 4953 photographs of 2477 conjunctivae from 1241 participants in 10 communities were graded over 5 d at the GGC. Six examined participants were not photographed. Agreement between field and photographic grades were for TF: percent agreement (PA) 96.7%, κ=0.70 (95% confidence interval [CI] 0.64 to 0.77; for TI: PA 94.7%, κ=0.32 (95% CI 0.20 to 0.43); and for TS: PA 83.5%, κ=0.22 (95% CI 0.15 to 0.29). **Conclusions:** Conjunctival photography may be a solution for programs near the elimination threshold where there are few available community cases for training field graders.

# Ulcère de Buruli

Complicated Mycobacterium ulcerans infection in a child in the Northern Territory.

Mahony M, Hung TY, Cox V, Sufyan W, Wallis P, Nizzero D, Francis J, Yan J.

Feb-2023

*J Paediatr Child Health.*

<https://pubmed.ncbi.nlm.nih.gov/36422163/>

# Lèpre

Giant acquired digital fibrokeratoma.

Inamadar A, Mutalik S.

02-02-2023

*BMJ Case Rep*.

<https://pubmed.ncbi.nlm.nih.gov/36731948/>

A dance that paves the way for diagnosis.

Sachan S, Shukla P, Agrawal T, Kumar S, Malhotra KP, Suvirya S.

02-02-2023

*Clin Exp Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/36730503/>

Core single nucleotide polymorphism analysis reveals transmission of Mycobacterium marinum between animal and environmental sources in two aquaria.

Komine T, Srivorakul S, Yoshida M, Tanaka Y, Sugimoto Y, Inohana M, Fukano H, Hoshino Y, Kurata O, Wada S.

02-02-2023

*J Fish Dis.*

<https://pubmed.ncbi.nlm.nih.gov/36727551/>

Atorvastatin Potentially Reduces Mycobacterial Severity through Its Action on Lipoarabinomannan and Drug Permeability in Granulomas.

Davuluri KS, Singh AK, Singh AV, Chaudhary P, Raman SK, Kushwaha S, Singh SV, Chauhan DS.

31-01-2023

*Microbiol Spectr*.

<https://pubmed.ncbi.nlm.nih.gov/36719189/>

Clinical profile of dermatitis neglecta with special emphasis on psychiatric comorbidities: A case series of 22 patients from Eastern India.

Ghosh SK, Sarkar S, Mondal S, Das S.

Nov-Dec 2022

*Indian J Psychiatry.*

<https://pubmed.ncbi.nlm.nih.gov/36714670/>

Epidemiological characteristics of leprosy during the period 2005-2020: A retrospective study based on the Chinese surveillance system.

Li X, Jin G, Yang J, Li Y, Wei P, Zhang L.

11-01-2023

*Front Public Health.*

<https://pubmed.ncbi.nlm.nih.gov/36711406/>

**Background:** Jiangsu Province is located in the Yangtze River Delta region, with a total area of 107,200 square kilometers. Since 1949, over 55,000 cases have been registered, with Taixing accounting for the highest number of patients. The proportion of new cases with MB and G2D was higher compared to other regions. As a result, Jiangsu has been considered a priority area for public health interventions in China. **Methods:** This paper mainly described the population, time, and spatial distribution of the newly detected leprosy cases in Jiangsu Province between 2005 and 2020. In this study, all the data were entered into Microsoft Excel and SPSS for the descriptive analysis. ArcGIS was applied to create statistical maps, and Geoda was used to conduct spatial autocorrelation analysis with local Moran's *I* statistics (LISA). The epidemiological data were obtained from LEPMIS. In addition, population data were obtained from the Statistical Yearbook of Jiangsu Province. **Results:** During the study period, 363 new cases were reported. Of these, 232 were men and 131 were women (1.77:1). The mean age at diagnosis was 60.56 years, and no adolescent cases were identified. Three hundred and twenty-seven (90.08%) were diagnosed with MB and 36 (9.92%) with PB. 31.68% (115/363) of the patients presented with G2D. Farmers accounted for 74.9%, and most cases were identified in skin clinics (248, 68.32%). We observed a decreasing trend in detection rate, with a higher concentration of new cases diagnosed between July and October. Spatial analysis showed that the new cases were primarily distributed in the northwest of Jiangsu province, and Suqian has the highest incidence of leprosy. Special attention should be paid to Wuzhong, a county with a potential risk of inter-provincial transmission. Furthermore, 55 new cases came from other Chinese provinces but lived in Jiangsu. **Conclusion:** The NCDR of leprosy decreased, but the new cases showed disabilities, a sign of the late diagnosis. The results indicated that some regions were still suffering from the burden of leprosy. Thus, we recommend that the government should adopt effective strategies to promote leprosy control. The main priorities for eliminating new cases were to provide sustainable financial support, improve the quality of clinical services, strengthen preventive intervention and rehabilitation services for disabilities, provide health education among high-risk populations, and explore new approaches.

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

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

23-01-2023

*Rev Soc Bras Med Trop.*

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

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

Mycobacterial mycolic acids trigger inhibitory receptor Clec12A to suppress host immune responses.

Nishimura N, Tomiyasu N, Torigoe S, Mizuno S, Fukano H, Ishikawa E, Katano H, Hoshino Y, Matsuo K, Takahashi M, Izumi Y, Bamba T, Akashi K, Yamasaki S.

Jan-2023

*Tuberculosis (Edinb).*

<https://pubmed.ncbi.nlm.nih.gov/36542980/>

Leprosy rash precipitated by immunotherapy for suspected inflammatory neuropathy.

Leung A, Arnold BJ, Hodgson TO, Cutfield NJ.

Feb-2023

*Pract Neurol.*

<https://pubmed.ncbi.nlm.nih.gov/36428101/>

Phenolic glycolipid-1 of Mycobacterium leprae is involved in human Schwann cell line ST8814 neurotoxic phenotype.

**Girardi KDCV, Mietto BS, Dos Anjos Lima K,** **Atella GC, da Silva DS, Pereira AMR, Rosa PS,** **Lara FA.**

Jan-2023

*J Neurochem.*

<https://pubmed.ncbi.nlm.nih.gov/36349509/>

Foamy histiocytes in sarcoidosis! Puzzle resolved with the aid of tattoo.

K S, Rout AN, Asati DP, Panwar H.

Jan-Feb 2023

*Indian J Dermatol Venereol Leprol*.

<https://pubmed.ncbi.nlm.nih.gov/36331865/>

An overview of mycetoma and its diagnostic dilemma: Time to move on to advanced techniques.

Husain U, Verma P, Suvirya S, Priyadarshi K, Gupta P.

2023

*Indian J Dermatol Venereol Leprol*.

<https://pubmed.ncbi.nlm.nih.gov/36331840/>

The neglected tropical disease mycetoma can become extremely devastating, and can be caused both by fungi and bacteria; these are popularly known as eumycetoma and actinomycetoma respectively. The classical triad of the disease is subcutaneous swelling, multiple discharging sinuses and the presence of macroscopic granules. The present study aims to highlight the existing diagnostic modalities and the need to incorporate newer and more advanced laboratory techniques like pan fungal/pan bacterial 16S rRNA gene polymerase chain reaction (PCR) and sequencing, Matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS), rolling circle amplification (RCA), loop-mediated isothermal amplification (LAMP) and recombinase polymerase amplification (RPA). It is important for the medical team to be aware of the various diagnostic options (both existing and future), so that diagnosis of such a debilitating disease is never missed, both by clinicians and microbiologists/pathologists. The newer diagnostic methods discussed in this article will help in rapid, accurate diagnosis thus facilitating early treatment initiation, and decreasing the overall morbidity of the disease. In the Indian context, newer technologies need to be made available more widely. Making clinicians aware and promoting research and development in mycetoma diagnostics is the need of the hour.

Impact of COVID-19 on leprosy reactions and of leprosy treatments on COVID-19 severity.

Ianhez M, Cerqueira SR, Gomes CM, Talhari CC, Criado PR, Castro CC, Ramos PM, Miot HA.

Jan-Feb 2023

*Indian J Dermatol Venereol Leprol*.

<https://pubmed.ncbi.nlm.nih.gov/36331835/>

COVID-19-associated pulmonary aspergillosis (CAPA) in Iranian patients admitted with severe COVID-19 pneumonia.

Erami M, Hashemi SJ, Raiesi O, Fattahi M, Getso MI, Momen-Heravi M, Daie Ghazvini R, Khodavaisy S, Parviz S, Mehri N, Babaei M.

Feb-2023

*Infection*.

<https://pubmed.ncbi.nlm.nih.gov/36107379/>

Ending tuberculosis in a post-COVID-19 world: a person-centred, equity-oriented approach.

Ryckman T, Robsky K, Cilloni L, Zawedde-Muyanja S, Ananthakrishnan R, Kendall EA, Shrestha S, Turyahabwe S, Katamba A, Dowdy DW.

Feb-2023

*Lancet Infect Dis*.

<https://pubmed.ncbi.nlm.nih.gov/35963272/>

The COVID-19 pandemic has disrupted systems of care for infectious diseases-including tuberculosis-and has exposed pervasive inequities that have long marred efforts to combat these diseases. The resulting health disparities often intersect at the individual and community levels in ways that heighten vulnerability to tuberculosis. Effective responses to tuberculosis (and other infectious diseases) must respond to these realities. Unfortunately, current tuberculosis programmes are generally not designed from the perspectives of affected individuals and fail to address structural determinants of health disparities. We describe a person-centred, equity-oriented response that would identify and focus on communities affected by disparities, tailor interventions to the mechanisms by which disparities worsen tuberculosis, and address upstream determinants of those disparities. We detail four key elements of the approach (data collection, programme design, implementation, and sustainability). We then illustrate how organisations at multiple levels might partner and adapt current practices to incorporate these elements. Such an approach could generate more substantial, sustainable, and equitable reductions in tuberculosis burden at the community level, highlighting the urgency of restructuring post-COVID-19 health systems in a more person-centred, equity-oriented way.

Determinants of patients' delay with disability in the diagnosed leprosy cases in the three major states of India: A case-control study.

Govindarajulu S, Muthuvel T, Lal V, Rajendran KP, Seshayyan S.

Jan-Feb 2023

*Indian J Dermatol Venereol Leprol*.

<https://pubmed.ncbi.nlm.nih.gov/35389017/>

**Background:** Skin lesions are the most common early symptoms of leprosy, often ignored by patients at an early stage and misdiagnosed as other dermatological diseases by healthcare personnel, leading to delay in diagnosis and treatment of leprosy precipitating permanent neurological deficit, deformities and serious disabilities. **Aims:** The objective is to evaluate the duration of delay and factors responsible for the delay in reporting of patients, among the newly detected leprosy cases (Grade 1 and Grade 2 disability patients). **Methods:** A case-control study was conducted during 2014-2016 in three major states of India (Delhi, Gujarat and West Bengal) in 140 randomly recruited newly registered adult leprosy patients (aged 18 years and above) with Grade 2/1 disabilities (cases) and 140 Grade 0 disability patients (controls) in each of these Indian states. **Results:** It is established that the major contributors for the delay in the early diagnosis of leprosy have been patient-related factors. The median patient delay in the three states of Delhi, Gujarat and West Bengal were five months (0.7-1.8), 2.8 months (2-14) and 12 months (2-24), respectively.

**Limitations:** The study design is case-control and has an inbuilt reporting bias due to the retrospective nature of data collection but the data collection was carried with caution to reduce the recall bias. As the study is carried out in three states, generalisation of interpretation was cautiously executed. The matching ratio of cases and controls was 1:1 in this study, but we could not increase the controls due to operational feasibility during the conduct of the study. **Conclusion:** Patient delay is a crucial factor responsible for the disability among new leprosy cases. A higher patient delay in these three states reflects that the community is not aware about the signs and symptoms of leprosy. Reducing patient delay is very important for reducing disabilities in the newly diagnosed cases.

Telltale signs of skin trespassers: Clues to superficial mycosis.

Varsha MG, Shilpa K, Revathi TN, Shanmukhappa AG, Loganathan E.

Jan-Feb 2023

*Indian J Dermatol Venereol Leprol*.

<https://pubmed.ncbi.nlm.nih.gov/35146987/>

# Trypanosomes (trypanosomiase et maladie de Chagas)

The sweet and sour sides of trypanosome social motility.

Shaw S, Roditi I.

31-01-2023

*Trends Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36732111/>

Recent studies showed that the formation of elegant geometric patterns by communities of Trypanosoma brucei on semi-solid surfaces, dubbed social motility (SoMo) by its discoverers, is a manifestation of pH taxis. This is caused by procyclic forms generating and responding to pH gradients through glucose metabolism and cAMP signalling. These findings established that trypanosomes can sense and manipulate gradients, potentially helping them to navigate through host tissues. At the same time, the host itself and bystanders such as endosymbionts have the potential to shape the environment and influence the chances of successful transmission. We postulate that the ability to sense and contribute to the gradient landscape may also underlie the tissue tropism and migration of other parasites in their hosts.

Outbreak of Chagas disease in Brazil: Validation of a molecular diagnostic method.

Costa-Oliveira CND, Paiva-Cavalcanti M, Barros MDS, Nakazawa M, Melo MGN, Pessoa-E-Silva R, Torres DJL, Oliveira KKDS, Moreira LR, Morais RCS, Goes TC, Oliveira GMA, Júnior WO, Silva MMME, Batista FP, Montenegro D, Lorena VMB.

30-01-2023

*Exp Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36731642/>

Epoxy-α-lapachone (2,2-Dimethyl-3,4-dihydro-spiro[2H-naphtho[2,3-b]pyran-10,2'-oxirane]-5(10H)-one): A promising molecule to control infections caused by protozoan parasites.

Peixoto JF, Oliveira ADS, de Oliveira LFG, da Silva FS, Alves CR.

30-01-2023

*Braz J Infect Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36731538/>

Variation of sensitivity of Trypanosoma evansi isolates from Isiolo and Marsabit counties of Kenya to locally available trypanocidal drugs.

Mdachi RE, Ogolla KO, Auma JE, Wamwiri FN, Kurgat RK, Wanjala KB, Mugunieri LG, Alusi PM, Chemuliti JK, Mukiria PW, Okoth SO.

02-02-2023

*PLoS One*.

<https://pubmed.ncbi.nlm.nih.gov/36730273/>

Detection of Babesia bovis using loop-mediated isothermal amplification (LAMP) with improved thermostability, sensitivity and alternative visualization methods.

Arnuphapprasert A, Nugraheni YR, Aung A, Asada M, Kaewthamasorn M.

01-02-2023

*Sci Rep*.

<https://pubmed.ncbi.nlm.nih.gov/36725982/>

Structural Insight into Privileged Heterocycles as Anti-Trypanosoma cruzi and brucei Agents.

Abbasi Shiran J, Ghanbari M, Mohammadnejadi E, Razzaghi-Asl N.

01-02-2023

*Curr Top Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36725826/>

Hematologic variables of free-living Leptodactylus luctator with and without hemoparasites and thrombidiform mites in southern Brazil.

Bilhalva LC, de Almeida BA, Colombo P, de Faria Valle S, Soares JF.

FEb-2023

*Vet Parasitol Reg Stud Reports*.

<https://pubmed.ncbi.nlm.nih.gov/36725158/>

It has been suggested that anuran amphibian parasites can cause clinical signs in situations of environmental imbalance. In the family Leptodactylidae, information about hematology is scarce, although these are well-known tools for the diagnosis and prognosis in clinical practice and potential bioindicators of environmental stress. The objective of this study is to describe Leptodactylus luctator hematology, to report the occurrence of hemoparasites and thrombidiform mites, and to compare the hematological variables under the presence and absence of these organisms. Ectoparasites and heparinized blood samples from 40 free-living specimens of L. luctator were collected for analysis. Hematologic variables and total plasma protein were compared between groups with and without hemoparasites and intradermal mites. As results, structures compatible with hemogregarines, Lankesterella sp., five morphotypes of Trypanosoma spp., microfilaria, Aegyptianella sp., an unidentified intraleukocytic hemoparasite, and frog erythrocytic virus (FEV) inclusion bodies were identified in the blood samples, besides Hannemania spp. intradermal mites. The hemoparasite occurrence was higher than previously reported in other anuran families and locations. Also, L. luctator has smaller red blood cells (RBCs) and white blood cells (WBCs), and a hyposegmentation of the neutrophil nucleus, when compared to many other amphibians. White blood cell, neutrophil, and monocyte counts were higher in animals parasitized by mites. There was no correlation between the number of parasitized RBCs and hematologic variables. This study provides anuran hematologic information, in addition to indicating a host reaction to infestation by Hannemania spp. mites, besides constituting the first record of the distribution of hemoparasites and intradermal mites in L. luctator of the study region.

Enzymatic synthesis of amlodipine amides and evaluation of their anti-Trypanosoma cruzi activity.

Elso OG, Bivona AE, Cenizo R, Malchiodi EL, García Liñares G.

26-01-2023

*Org Biomol Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36722938/>

Secretion of extracellular vesicles during ontogeny of the tapeworm Schistocephalus solidus.

Mazanec H, Buskova N, Gardian Z, Kuchta R.

16-01-2032

*Folia Parasitol (Praha).*

<https://pubmed.ncbi.nlm.nih.gov/36722286/>

Experimental Trypanosoma evansi infection induces pain along with oxidative stress, prevented by COX-2 inhibition.

Cipriani DS, Borges GK, Povaluk AP, Stipp MC, Casagrande RA, Vogel CIG, Miletti LC, Bastos-Pereira AL.

28-01-20323

*Exp Parasitol*.

<https://pubmed.ncbi.nlm.nih.gov/36719797/>

A trypanosome-derived immunotherapeutics platform elicits potent high-affinity antibodies, negating the effects of the synthetic opioid fentanyl.

Triller G, Vlachou EP, Hashemi H, van Straaten M, Zeelen JP, Kelemen Y, Baehr C, Marker CL, Ruf S, Svirina A, Chandra M, Urban K, Gkeka A, Kruse S, Baumann A, Miller AK, Bartel M, Pravetoni M, Stebbins CE, Papavasiliou FN, Verdi JP.

30-01-2023

*Cell Rep.*

<https://pubmed.ncbi.nlm.nih.gov/36719797/>

Statins change the cytokine profile in Trypanosoma cruzi-infected U937 macrophages and murine cardiac tissue through Rho-associated kinases inhibition.

González-Herrera F, Clayton NS, Guzmán-Rivera D, Carrillo I, Castillo C, Catalán M, Anfossi R, Quintero-Pertuz H, Quilaqueo ME, Olea-Azar C, Rivera-Meza M, Kemmerling U, Ridley AJ, Vivar R, Maya JD.

11-01-2032

*Front Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/36713380/>

**Introduction:** Chronic Chagasic cardiomyopathy (CCC), caused by the protozoan Trypanosoma cruzi, is the most severe manifestation of Chagas disease.CCC is characterized by cardiac inflammation and fibrosis caused by a persistent inflammatory response. Following infection, macrophages secrete inflammatory mediators such as IL-1β, IL-6, and TNF-α to control parasitemia. Although this response contains parasite infection, it causes damage to the heart tissue. Thus, the use of immunomodulators is a rational alternative to CCC. Rho-associated kinase (ROCK) 1 and 2 are RhoA-activated serine/threonine kinases that regulate the actomyosin cytoskeleton. Both ROCKs have been implicated in the polarization of macrophages towards an M1 (pro-inflammatory) phenotype. Statins are FDA-approved lipid-lowering drugs that reduce RhoA signaling by inhibiting geranylgeranyl pyrophosphate (GGPP) synthesis. This work aims to identify the effect of statins on U937 macrophage polarization and cardiac tissue inflammation and its relationship with ROCK activity during T. cruzi infection. **Methods:** PMA-induced, wild-type, GFP-, CA-ROCK1- and CA-ROCK2-expressing U937 macrophages were incubated with atorvastatin, or the inhibitors Y-27632, JSH-23, TAK-242, or C3 exoenzyme incubated with or without T. cruzi trypomastigotes for 30 min to evaluate the activity of ROCK and the M1 and M2 cytokine expression and secretion profiling. Also, ROCK activity was determined in T. cruzi-infected, BALB/c mice hearts. **Results:** In this study, we demonstrate for the first time in macrophages that incubation with T. cruzi leads to ROCK activation via the TLR4 pathway, which triggers NF-κB activation. Inhibition of ROCKs by Y-27632 prevents NF-κB activation and the expression and secretion of M1 markers, as does treatment with atorvastatin. Furthermore, we show that the effect of atorvastatin on the NF-kB pathway and cytokine secretion is mediated by ROCK. Finally, statin treatment decreased ROCK activation and expression, and the pro-inflammatory cytokine production, promoting anti-inflammatory cytokine expression in chronic chagasic mice hearts. **Conclusion:** These results suggest that the statin modulation of the inflammatory response due to ROCK inhibition is a potential pharmacological strategy to prevent cardiac inflammation in CCC.

Localized cardiac metabolic trajectories and post-infectious metabolic sequelae in experimental Chagas disease.

Liu Z, Ulrich R, Kendricks A, Wheeler K, Le O AC, Pollet J, Bottazzi ME, Hotez P, Gusovsky F, Jones K, McCall LI.

20-01-2023

*Res Sq.*

<https://pubmed.ncbi.nlm.nih.gov/36711878/>

Post-infectious conditions, where clinical symptoms fail to resolve even after pathogen clearance, present major health burdens. However, the mechanisms involved remain poorly understood. In Chagas disease (CD), caused by the parasite Trypanosoma cruzi, antiparasitic agents can clear T. cruzi but late-stage treatment does not improve clinical cardiac outcomes. In this study, we revealed differential metabolic trajectories of cardiac regions during T. cruzi infection, matching sites of clinical symptoms. Incomplete, region-specific, cardiac metabolic restoration was observed in animals treated with the antiparasitic benznidazole, even though parasites were successfully cleared. In contrast, superior metabolic restoration was observed for a combination treatment of reduced-dose benznidazole plus an immunotherapy (Tc24-C4 T. cruzi flagellar protein and TLR4 agonist adjuvant), even though parasite burden reduction was lower. Overall, these results provide a mechanism to explain prior clinical treatment failures in CD and to test novel candidate treatment regimens. More broadly, our results demonstrate a link between persistent metabolic perturbation and post-infectious conditions, with broad implications for our understanding of post-infectious disease sequelae.

Identification of compounds with activity against Trypanosoma cruzi within a collection of synthetic nucleoside analogs.

Barnadas-Carceller B, Martinez-Peinado N, Gómez LC, Ros-Lucas A, Gabaldón-Figueira JC, Diaz-Mochon JJ, Gascon J, Molina IJ, Pineda de Las Infantas Y Villatoro MJ, Alonso-Padilla J.

13-01-2023

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36710960/>

mTOR signaling inhibition decreases lysosome migration and impairs the success of Trypanosoma cruzi infection and replication in cardiomyocytes.

Alvim JM, Venturini G, Oliveira TG, Seidman JG, Seidman CE, Krieger JE, Pereira AC.

26-01-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/36709791/>

Chagas disease is caused by the parasite Trypanosoma cruzi (T. cruzi) and, among all the chronic manifestations of the disease, Chronic Chagas Cardiomyopathy (CCC) is the most severe outcome. Despite high burden and public health importance in Latin America, there is a gap in understanding the molecular mechanisms that results in CCC development. Previous studies showed that T. cruzi uses the host machinery for infection and replication, including the repurposing of the responses to intracellular infection such as mitochondrial activity, vacuolar membrane, and lysosomal activation in benefit of parasite infection and replication. One common signaling upstream to many responses to parasite infection is mTOR pathway, previous associated to several downstream cellular mechanisms including autophagy, mitophagy and lysosomal activation. Here, using human iPSC derived cardiomyocytes (hiPSCCM), we show the mTOR pathway is activated in hiPSCCM after T. cruzi infection, and the inhibition of mTOR with rapamycin reduced number of T. cruzi 48 h post infection (hpi). Rapamycin treatment also reduced lysosome migration from nuclei region to cell periphery resulting in less T. cruzi inside the parasitophorous vacuole (PV) in the first hour of infection. In addition, the number of parasites leaving the PV to the cytoplasm to replicate in later times of infection was also lower after rapamycin treatment. Altogether, our data suggest that host's mTOR activation concomitant with parasite infection modulates lysosome migration and that T. cruzi uses this mechanism to achieve infection and replication. Modulating this mechanism with rapamycin impaired the success of T. cruzi life cycle independent of mitophagy.

Synthesis and Testing of Analogs of the Tuberculosis Drug Candidate SQ109 against Bacteria and Protozoa: Identification of Lead Compounds against Mycobacterium abscessus and Malaria Parasites.

Stampolaki M, Malwal SR, Alvarez-Cabrera N, Gao Z, Moniruzzaman M, Babii SO, Naziris N, Rey-Cibati A, Valladares-Delgado M, Turcu AL, Baek KH, Phan TN, Lee H, Alcaraz M, Watson S, van der Watt M, Coertzen D, Efstathiou N, Chountoulesi M, Shoen CM, Papanastasiou IP, Brea J, Cynamon MH, Birkholtz LM, Kremer L, No JH, Vázquez S, Benaim G, Demetzos C, Zgurskaya HI, Dick T, Oldfield E, Kolocouris AD.

27-01-2023

*ACS Infect Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36706233/>

Steroid and triterpenoid compounds with antiparasitic properties.

Kuzminac IZ, Savić MP, Ajduković JJ, Nikolić AR.

26-01-2032

*Curr Top Med Chem.*

<https://pubmed.ncbi.nlm.nih.gov/36703585/>

Tolerance and Adherence of Patients with Chronic Chagas Disease Treated with Benznidazole.

Vázquez C, García-Vázquez E, Carrilero B, Simón M, Franco F, Iborra MA, Gil-Gallardo LJ, Segovia M.

23-01-2023

*Rev Soc Bras Med Trop*.

<https://pubmed.ncbi.nlm.nih.gov/36700605/>

Identification of inhibitors as drug candidates against Chagas disease.

Araujo SC, de Angelo RM, Barbosa H, Costa-Silva TA, Tempone AG, Lago JHG, Honorio KM.

15-02-2023

*Eur J Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36623331/>

Chagas disease, after more than a century after its discovery, is still a major public health problem. It is estimated that approximately 10 million people worldwide are infected with T. cruzi. However, the situation is more critical in Latin America and other regions where the disease is endemic. The largest number of cases occurs in Brazil, Argentina, and Mexico as more than 100 million people in these regions are located in areas with a high risk of contamination by the vector. The need for new therapeutic alternatives is urgent, as the available drugs have severe limitations such as low efficacy and high toxicity. From this scenario, in this work, we employed the virtual screening technique using cruzain and BDF2 as key biological targets for the survival of the parasite. Our objective was to identify potential inhibitors of T. cruzi trypomastigotes, which could be considered drug candidates against Chagas disease. For this, we employed different in silico methodologies and the obtained results were corroborated using in vitro biological assays. For the VS studies, a database containing synthetic compounds was simulated at the binding site of cruzain and BDF2. In addition, pharmacophoric models were constructed in the initial phases of VS, as well as other advanced analyses (molecular dynamics simulations, calculations of binding free energy, and ADME prediction) were carried out and the results allowed the selection of potential inhibitors of T. cruzi. Based on the obtained data, 32 different compounds commercially available were subjected to biological tests against the trypomastigote form of T. cruzi. As result, 11 of those compounds displayed significant activity against T. cruzi and can be considered potential candidates for the treatment of Chagas disease.

# Leishmaniose

Role of Treg, Breg and other cytokine sets in host protection and immunopathology during human leishmaniasis: are they potential valuable markers in clinical settings and vaccine evaluation?

Divenuto F, Pavia G, Marascio N, Barreca GS, Quirino A, Matera G.

30-01-2023

*Acta Trop.*

<https://pubmed.ncbi.nlm.nih.gov/36731621/>

Leishmaniasis is a vector-borne disease caused by obligate intracellular protozoan parasites that can infect humans and other mammals. Pro- and anti-inflammatory cytokines are important regulators of innate and specific responses in Leishmania infection. Resistance to leishmaniasis is related to T helper 1 (Th1) response with the production of pro-inflammatory cytokines: IL-12, IL-1β, IFN-γ, TNF-α, IL-2 leading to activation of macrophages and parasite killing. Instead, a more intense Th2 (IL-4, IL-5, IL-13), Treg (IL-10 and TGF-β) and Breg response (IL-10 and IL-35) are related to parasite persistence through the inhibition of macrophage activation, which promotes the escape from host immune system. Interestingly, a cytokine involved in the parasite killing in one form of leishmaniasis may be "pathogen friendly" in another form of the disease. To date, few studies are focusing on the role of Treg and Breg cytokines in human models of leishmaniasis; therefore, further investigations are needed to clarify their potential role in the diagnosis and prognosis of such protozoan infections, as well as in the development of vaccines against leishmaniasis. This review summarizes the current knowledge about the role of cytokines produced by Th1, Th2, Treg, and Breg cells involved in Leishmania disease progression and host protection. Some cytokines might play a role as diagnostic and prognostic clinical markers, or they could represent a novel approach leading to new anti-leishmaniasis therapies. Overall, advances in knowledge of the complex network of cytokines secreted by immune cells could help to better understand signalling pathways and host immune responses during Leishmania infection. This approach would allow these mediators to be used as therapeutic strategies against leishmaniasis.

Epoxy-α-lapachone (2,2-Dimethyl-3,4-dihydro-spiro[2H-naphtho[2,3-b]pyran-10,2'-oxirane]-5(10H)-one): A promising molecule to control infections caused by protozoan parasites.

Peixoto JF, Oliveira ADS, de Oliveira LFG, da Silva FS, Alves CR.

30-01-2023

*Braz J Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/36731538/>

Recombinant endonuclease III protein from Leishmania infantum associated with Th1-type adjuvants is immunogenic and induces protection against visceral leishmaniasis.

Lage DP, Machado AS, Freitas CS, Vale DL, Linhares FP, Cardoso JMO, Oliveira-da-Silva JA, Ramos FF, Pereira IAG, Ludolf F, Tavares GSV, Bandeira RS, Oliveira JS, Menezes-Souza D, Duarte MC, Galdino AS, Christodoulides M, Chávez-Fumagalli MA, Roatt BM, Martins VT, Coelho EAF.

31-01-2023

*Mol Immunol*.

<https://pubmed.ncbi.nlm.nih.gov/36731193/>

Vaccination against visceral leishmaniasis (VL) should be considered as a safe and effective measure to disease control; however, few vaccines are available against canine VL and there is no an approved human vaccine. In this context, in the present study, we evaluated the endonuclease III (ENDO) protein, which was recently showed to be antigenic for human disease, as a vaccine candidate against Leishmania infantum infection. The recombinant protein (rENDO) was administered in BALB/c mice alone or associated with saponin (rENDO/Sap) or micelles (rENDO/Mic) as adjuvants. Controls received saline, saponin or empty micelles. Results showed that both rENDO/Sap and rENDO/Mic compositions induced higher levels of IFN-γ, IL-12, TNF-α, and GM-CSF cytokines, besides nitrite and IgG2a isotype antibodies, before and after challenge infection, which were related to both CD4+ and CD8+ T cell subtypes. The immunological results contributed to significant reductions in the parasite load found in the spleens, livers, bone marrows and draining lymph nodes of the vaccinated animals. In general, mice immunized with rENDO/Mic presented a slightly higher Th1-type cellular and humoral immune response, as compared to those receiving rENDO/Sap. In addition, saponin caused a slight to moderate inflammatory edema in their vaccinated footpads, which was not observed when micelles were used with rENDO. In addition, a preliminary analysis showed that the recombinant protein was immunogenic to human cells cultures, since PBMCs from treated VL patients and healthy subjects showed higher lymphoproliferation and IFN-γ production in the culture supernatants. In conclusion, data suggest that rENDO could be considered as a candidate to be evaluated in future studies as vaccine to protect against VL.

DNA barcoding of sand flies (Diptera, Psychodidae, Phlebotominae) from the western Brazilian Amazon.

Pinto IS, Rodrigues BL, de Araujo-Pereira T, Shimabukuro PHF, de Pita-Pereira D, Britto C, Brazil RP.

02-02-2023

*PLoS One*.

<https://pubmed.ncbi.nlm.nih.gov/36730314/>

The subfamily Phlebotominae comprises important insects for public health. The use of complementary tools such as molecular taxonomy is necessary for interspecific delimitation and/or discovery of cryptic species. Here, we evaluated the DNA barcoding tool to identify different species in the southwestern Brazilian Amazon. For this, we collected sand flies in forest fragments along the highway BR-317, in the municipality of Brasiléia, state of Acre, Brazil. The specimens were DNA-barcoded using a fragment of the cytochrome c oxidase subunit I (COI) gene. The sequences were analyzed to generate K2P pairwise genetic distances and a Neighbour-joining tree. The sand fly barcodes were also clustered into Molecular Operation Taxonomic Units (MOTU) using Automatic Barcode Gap Discovery (ABGD) approach. A total of 59 COI sequences comprising 22 nominal species and ten genera were generated. Of these, 11 species had not been sequenced before, thus being new COI sequences to science. Intraspecific genetic distances ranged between 0 and 4.9%, with Pintomyia serrana presenting the highest values of genetic distance, in addition to having been partitioned into three MOTUs. Regarding the distances to the nearest neighbour, all species present higher values in relation to the maximum intraspecific distance, in addition to forming well supported clusters in the neighbour-joining analysis. The DNA barcoding approach is useful for the molecular identification of sand flies from Brasiléia, state of Acre, and was efficient in detecting cryptic diversity of five species which can be confirmed in future studies using an integrative approach. We also generated new COI barcodes for Trichophoromyia auraensis, Nyssomyia shawi, and Psychodopygus paraensis, which may play a role in the transmission of Leishmania spp. in the Brazilian Amazon.

An overview of the sand fly salivary proteins in vaccine development against leishmaniases.

Fayaz S, Bahrami F, Parvizi P, Fard-Esfahani P, Ajdary S.

DEc-2022

*Iran J Microbiol*.

<https://pubmed.ncbi.nlm.nih.gov/36721440/>

miR-148a regulation interferes in inflammatory cytokine and parasitic load in canine leishmaniasis.

Rebech GT, Bragato JP, Costa SF, de Freitas JH, Dos Santos MO, Soares MF, Eugênio FR, Dos Santos PSP, de Lima VMF.

31-01-2023

*PLoS Negl Trop Dis.*

<https://pubmed.ncbi.nlm.nih.gov/36719867/>

Leishmania RNA Virus Is Not Detected in All Species of the Leishmania Viannia Subgenus: The Case of L. (V.) panamensis in Colombia.

Rosales-Chilama M, Y Oviedo M, K Quintero Y, L Fernández O, Gómez MA.

30-01-2023

*Am J Trop Med Hyg*.

<https://pubmed.ncbi.nlm.nih.gov/36716739/>

High levels of infectiousness of asymptomatic Leishmania (Viannia) braziliensis infections in wild rodents highlights their importance in the epidemiology of American Tegumentary Leishmaniasis in Brazil.

Marinho-Júnior JF, Monteiro JFCLS, Sales de Carvalho AW, de Carvalho FG, de Paiva Cavalcanti M, Shaw J, Courtenay O, Brandão-Filho SP.

30-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36716345/>

**Background:** The epidemiological significance of wildlife infections with aetiological agents causing human infectious diseases is largely determined by their infection status, contact potential with humans (via vectors for vector-borne diseases), and their infectiousness to maintain onward transmission. This study quantified these parameters in wild and synanthropic naturally infected rodent populations in an endemic region of tegumentary leishmaniasis in northeast Brazil. **Methods:** Capture-mark-recapture (CMR) of rodents was conducted over 27 months in domestic/peri domestic environs, household plantations and nearby Atlantic Forest (9,920 single trap nights). Rodent clinical samples (blood and ear tissue) were tested for infection by conventional PCR and quantitative PCR (qPCR) for L. (Viannia) braziliensis, and xenodiagnosis to measure infectiousness to the local sand fly vector. **Results:** A total 603 individuals of 8 rodent species were (re)captured on 1,051 occasions. The most abundant species were Nectomys squamipes (245 individuals, 41% of the total catch), Rattus rattus (148, 25%), and Necromys lasiurus (83, 14%). All species were captured in greater relative frequencies in plantations; R. rattus was the only species captured in all three habitats including in and around houses. Four species, comprising 22.6% of individuals captured at least twice, were geolocated in more than one habitat type; 78.6% were infected with L. (V.) braziliensis, facilitating inter-species and inter-habitat transmission. Species specific period prevalence ranged between 0%-62% being significantly higher in N. squamipes (54-62%) and H. sciureus (43-47%). Xenodiagnosis was performed on 41 occasions exposing 1,879 Nyssomyia whitmani sand flies to five rodent species (37 individuals). Similar mean levels of infectiousness amongst the more common rodent species were observed. Longitudinal xenodiagnosis of the N. squamipes population revealed a persistent level of infectiousness over 13 months follow-up, infecting a median 48% (IQR: 30.1%-64.2%) of exposed blood-fed vectors. The proportion of exposed flies infected was greater in the low comparted to in the high seasonal period of vector abundance. L. (V.) braziliensis parasite loads in rodent blood quantified by qPCR were similar across rodent species but did not represent a reliable quantitative marker of infectiousness to sand flies. The standardised risk of rodent infection in plantations was 70.3% relative to 11.3% and 18.4% in peri domestic and forest habitats respectively. R. rattus was the only exception to this trend indicating greatest risk in the peri domestic environment. **Conclusions:** The results support the view that a collective assemblage of wild and synanthropic rodent species is an important wild reservoir of L. (V.) braziliensis in this region, with N. squamipes and R. rattus probably playing a key role in transmission within and between habitat types and rodent species. Rodents, and by implication humans, are at risk of infection in all sampled habitats, but more so in homestead plantations. These conclusions are based on one of the longest CMR study of small rodents in an American Tegumentary Leishmaniasis (ATL) foci.

Forty years (1980-2019) of visceral leishmaniasis in Nepal: trends and elimination challenges.

Pandey K, Dumre SP, Shah Y, Acharya BK, Khanal L, Pyakurel UR, Kaneko O, Pandey BD.

28-01-2023

*Trans R Soc Trop Med Hyg*.

<https://pubmed.ncbi.nlm.nih.gov/36715092/>

Case report: Application of metagenomic next-generation sequencing in the diagnosis of visceral leishmaniasis and its treatment evaluation.

Liang Q, Liang X, Hong D, Fang Y, Tang L, Mu J, Tan X, Chen F.

13-01-2023

*Front Med (Lausanne).*

<https://pubmed.ncbi.nlm.nih.gov/36714105/>

Ethanolaminephosphate cytidyltransferase is essential for survival, lipid homeostasis and stress tolerance in Leishmania major.

Basu S, Pawlowic M, Hsu FF, Thomas G, Zhang K.

11-01-2023

*bioRxiv.*

<https://pubmed.ncbi.nlm.nih.gov/36712124/>

Glycerophospholipids including phosphatidylethanolamine (PE) and phosphatidylcholine (PC) are vital components of biological membranes. Trypanosomatid parasites of the genus *Leishmania* can acquire PE and PC via *de novo* synthesis and the uptake/remodeling of host lipids. In this study, we investigated the ethanolaminephosphate cytidyltransferase (EPCT) in *Leishmania major* , which is the causative agent for cutaneous leishmaniasis. EPCT is a key enzyme in the ethanolamine branch of the Kennedy pathway which is responsible for the *de novo* synthesis of PE. Our results demonstrate that *L. major* EPCT is a cytosolic protein capable of catalyzing the formation of CDP-ethanolamine from ethanolamine-phosphate and cytidine triphosphate. Genetic manipulation experiments indicate that EPCT is essential in both the promastigote and amastigote stages of *L. major* as the chromosomal null mutants cannot survive without the episomal expression of EPCT. This differs from our previous findings on the choline branch of the Kennedy pathway (responsible for PC synthesis) which is required only in promastigotes but not amastigotes. While episomal EPCT expression does not affect promastigote proliferation under normal conditions, it leads to reduced production of ethanolamine plasmalogen or plasmenylethanolamine, the dominant PE subtype in *Leishmania* . In addition, parasites with epsiomal EPCT exhibit heightened sensitivity to acidic pH and starvation stress, and significant reduction in virulence. In summary, our investigation demonstrates that proper regulation of EPCT expression is crucial for PE synthesis, stress response, and survival of *Leishmania* parasites throughout their life cycle.

Therapeutic effect of oral quercetin in hamsters infected with Leishmania Viannia braziliensis.

Dos Santos RF, Da Silva T, Brito ACS, Inácio JD, Ventura BD, Mendes MAP, Azevedo BF, Siqueira LM, Almeida-Amaral EE, Dutra PML, Da-Silva SAG.

13-01-2023

*Front Cell Infect Microbiol*.

<https://pubmed.ncbi.nlm.nih.gov/36710981/>

Leishmania infantum infecting the carnivore Nasua nasua from urban forest fragments in an endemic area of visceral leishmaniasis in Brazilian Midwest.

de Macedo GC, Barreto WTG, de Oliveira CE, Santos FM, Porfírio GEO, Xavier SCDC, Alves FM, da Silva AR, de Andrade GB, Rucco AC, de Assis WO, Jansen AM, Roque ALR, Herrera HM.

13-01-2023

*Front Cell Infect Microbiol*.

<https://pubmed.ncbi.nlm.nih.gov/36710973/>

**Introduction:** The aim of the present study was to investigate the occurrence of *Leishmania infantum* in South American coatis inhabiting two forest fragments in Campo Grande, Mato Grosso do Sul, Midwest region of Brazil, an endemic area of human and canine visceral leishmaniasis (VL). **Material and methods:** A total of 110 South American coatis were sampled in the conservation unit "*Parque Estadual do Prosa*" (PEP) and in the residential area "*Vila da Base Aérea*" (VBA) from March 2018 to April 2019. As a longitudinal study that include up to six recaptures of the same individual, a total of 190 capture events were obtained. Blood, bone marrow and skin samples were obtained for parasitological (axenic culture), serological (Enzyme Linked Immunosorbent Assay - ELISA and Dual-path Platform immunoassay - DPP® CVL) and molecular diagnostic assays (targeting kDNA for *Leishmania* spp. and *L. infantum*; and HSP70 followed by sequence analysis). **Results:** Seropositivity for *L. infantum* was found in 33 individuals, six in PEP and 27 in VBA. Furthermore, *L. infantum* was detected by molecular analysis in 16 individuals, seven from PEP and nine from VBA. We also isolated *L. infantum* from bone marrow of one individual and detected a single positive skin sample in molecular assay from other individual, both from VBA. **Discussion:** An overall infection rate of 36.4% (40/110) was observed, significantly higher in the VBA (49.1%) than in the PEP (21.6%), probably because VBA presents: (i) a large number of resident dogs and chickens that would be attracting sandflies; (ii) a denser population of this wild mammal species; and (iii) physical barriers and a lack of functional connectivity in the surroundings, preventing these animals to disperse out. We conclude that South American coati populations living in urban forest fragments of Campo Grande are affected by the epidemiological scenario of VL, known to involve dogs, vectors and humans. We highlight the importance of investigate the parasitism by *L. infantum* in this and other potential *L. infantum* reservoirs that inhabit urbanized regions endemic to VL.

Diversity and antibiograms of bacteria isolated from cutaneous leishmaniasis wounds in the Nkwanta South District of Ghana.

Yeboaa C, Odoi H, Owusu Ntim R, Boakye YD, Kwakye-Nuako G, Agyare C, Boamah VE, Badu K.

28-01-2023

*Arch Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36707480/>

Synthesis and Testing of Analogs of the Tuberculosis Drug Candidate SQ109 against Bacteria and Protozoa: Identification of Lead Compounds against Mycobacterium abscessus and Malaria Parasites.

**Stampolaki M, Malwal SR, Alvarez-Cabrera N, Gao Z, Moniruzzaman M, Babii SO, Naziris N,** **Rey-Cibati A, Valladares-Delgado M, Turcu AL, Baek KH, Phan TN, Lee H, Alcaraz M, Watson S, van der Watt M, Coertzen D, Efstathiou N, Chountoulesi M, Shoen CM, Papanastasiou IP, Brea J, Cynamon MH, Birkholtz LM, Kremer L, No JH, Vázquez S, Benaim G, Demetzos C, Zgurskaya HI, Dick T, Oldfield E, Kolocouris AD.**

27-01-2023

*ACS Infect Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36706233/>

Molecular targets for chalcones in antileishmanial drug discovery.

de Santiago-Silva KM, da Silva Gomes GF, Perez CC, da Silva Lima CH, de Lima Ferreira Bispo M.

27-01-2023

*Mini Rev Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36705240/>

In vitro leishmanicidal effect of Yangambin and Epi-yangambin lignans isolated from Ocotea fasciculata (Nees) Mez.

Rebouças-Silva J, Santos GF, Filho JMB, Berretta AA, Marquele-Oliveira F, Borges VM.

01-10-2023

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36704104/>

**Introduction:** Yangambin and epi-yangambin are the main lignans found in Louro-de-Cheiro [*Ocotea fasciculata* (Nees) Mez], a tree native to the Atlantic forests of northeastern Brazil whose leaves and bark are widely used in folk medicine. The present study investigated the leishmanicidal and immunomodulatory effects of both lignans in *in vitro* models of infection by *Leishmania amazonensis* or *Leishmania braziliensis*, both etiological agents of Cutaneous Leishmaniasis in Brazil. **Methods:** Bone marrow-derived mouse macrophages were infected with *L. amazonensis* or *L. braziliensis* and then treated for 48 h at varying concentrations of yangambin or epi-yangambin. **Results:** Yangambin and epi-yangambin were found to reduce the intracellular viability of either *Leishmania* species in a concentration-dependent manner, with respective IC50 values of: 43.9 ± 5 and 22.6 ± 4.9 µM for *L. amazonensis*, compared to IC50 values of 76 ± 17 and 74.4 ± 9.8 µM for *L. braziliensis*. In this context, epi-yangambin proved more selective and effective against *in vitro* infection by *L. amazonensis*. However, both lignans were found to distinctly modulate the production of inflammatory mediators and other cytokines by macrophages infected by either of the *Leishmania* species evaluated. While yangambin increased the production of IL-10 by *L. braziliensis-*infected macrophages, both compounds were observed to lower the production of NO, PGE2, IL-6 and TNF-α in both *Leishmania* species. **Discussion:** The present results serve to encourage the development of novel studies aimed at screening natural bioactive compounds with the hope of discovering new therapeutic options for the treatment of Cutaneous Leishmaniasis.

Steroid and triterpenoid compounds with antiparasitic properties.

Kuzminac IZ, Savić MP, Ajduković JJ, Nikolić AR.

26-01-2023

*Curr Top Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/36703585/>

Intracellular IFN-γ and IL-4 levels of CD4 + and CD8 + T cells in the peripheral blood of naturally infected (Leishmania infantum) symptomatic dogs before and following a 4-week treatment with miltefosine and allopurinol: a double-blinded, controlled and cross-sectional study.

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

26-01-2023

*Acta Vet Scand*.

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

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

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

26-01-2023

*Parasit Vectors*.

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

Parasites of the genus Leishmania are unusual unicellular microorganisms in that they are characterized by the capability to subvert in their favor the immune response of mammalian phagocytes, including dendritic cells. Thus, in overt leishmaniasis, dendritic cells and macrophages are converted into a niche for Leishmania spp. in which the parasite, rather than being inactivated and disassembled, survives and replicates. In addition, Leishmania parasites hitchhike onto phagocytic cells, exploiting them as a mode of transport to lymphoid tissues where other phagocytic cells are potentially amenable to parasite colonization. This propensity of Leishmania spp. to target dendritic cells has led some researchers to consider the possibility that the non-pathogenic, reptile-associated Leishmania tarentolae could be exploited as a vaccine platform and vehicle for the production of antigens from different viruses and for the delivery of the antigens to dendritic cells and lymph nodes. In addition, as L. tarentolae can also be regarded as a surrogate of pathogenic Leishmania parasites, this parasite of reptiles could possibly be developed into a vaccine against human and canine leishmaniases, exploiting its immunological cross-reactivity with other Leishmania species, or, after its engineering, for the expression of antigens from pathogenic species. In this article we review published studies on the use of L. tarentolae as a vaccine platform and vehicle, mainly in the areas of leishmaniases and viral infections. In addition, a short summary of available knowledge on the biology of L. tarentolae is presented, together with information on the use of this microorganism as a micro-factory to produce antigens suitable for the serodiagnosis of viral and parasitic infections.

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

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

26-01-2023

*AAPS PharmSciTech.*

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

Unraveling the role of natural killer cells in leishmaniasis.

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

Jan-2023

*Int Immunopharmacol.*

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

Insights into the drug screening approaches in leishmaniasis.

Gopu B, Kour P, Pandian R, Singh K.

Jan-2023

*Int Immunopharmacol.*

<https://pubmed.ncbi.nlm.nih.gov/36700771/>

Leishmaniasis, a tropically neglected disease, is responsible for the high mortality and morbidity ratio in poverty-stricken areas. Currently, no vaccine is available for the complete cure of the disease. Current chemotherapeutic regimens face the limitations of drug resistance and toxicity concerns indicating a great need to develop better chemotherapeutic leads that are orally administrable, potent, non-toxic, and cost-effective. The anti-leishmanial drug discovery process accelerated the desire for large-scale drug screening assays and high-throughput screening (HTS) technology to identify new chemo-types that can be used as potential drug molecules to control infection. Using the HTS approach, about one million compounds can be screened daily within the shortest possible time for biological activity using automation tools, miniaturized assay formats, and large-scale data analysis. Classical and modern in vitro screening assays have led to the progression of active compounds further to ex vivo and in vivo studies. In the present review, we emphasized on the HTS approaches employed in the leishmanial drug discovery program. Recent in vitro screening assays are widely explored to discover new chemical scaffolds. Developing appropriate experimental animal models and their related techniques is necessary to understand the pathophysiological processes and disease host responses, paving the way for unraveling novel therapies against leishmaniasis.

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

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

09-01-2023

*Front Cell Infect Microbiol*.

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

TriTrypDB: An integrated functional genomics resource for kinetoplastida.

Shanmugasundram A, Starns D, Böhme U, Amos B, Wilkinson PA, Harb OS, Warrenfeltz S, Kissinger JC, McDowell MA, Roos DS, Crouch K, Jones AR.

19-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36656904/>

Parasitic diseases caused by kinetoplastid parasites are a burden to public health throughout tropical and subtropical regions of the world. TriTrypDB (https://tritrypdb.org) is a free online resource for data mining of genomic and functional data from these kinetoplastid parasites and is part of the VEuPathDB Bioinformatics Resource Center (https://veupathdb.org). As of release 59, TriTrypDB hosts 83 kinetoplastid genomes, nine of which, including Trypanosoma brucei brucei TREU927, Trypanosoma cruzi CL Brener and Leishmania major Friedlin, undergo manual curation by integrating information from scientific publications, high-throughput assays and user submitted comments. TriTrypDB also integrates transcriptomic, proteomic, epigenomic, population-level and isolate data, functional information from genome-wide RNAi knock-down and fluorescent tagging, and results from automated bioinformatics analysis pipelines. TriTrypDB offers a user-friendly web interface embedded with a genome browser, search strategy system and bioinformatics tools to support custom in silico experiments that leverage integrated data. A Galaxy workspace enables users to analyze their private data (e.g., RNA-sequencing, variant calling, etc.) and explore their results privately in the context of publicly available information in the database. The recent addition of an annotation platform based on Apollo enables users to provide both functional and structural changes that will appear as 'community annotations' immediately and, pending curatorial review, will be integrated into the official genome annotation.

In vitro anti-Leishmania activity of new isomeric cobalt(II)complexes and in silico insights: Mitochondria impairment and apoptosis-like cell death of the parasite.

Rocha SM, Horn A Jr, R de M L Terra A, Rezende LM, Moreira FF, DaMatta RA, Xavier FR, Cervo R, Cargnelutti R, Moorkkannur SN, Owenby G, Prabhakar R, Seabra SH, Fernandes C.

Mar-2023

*J Inorg Biochem*.

<https://pubmed.ncbi.nlm.nih.gov/36630792/>

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

Antinarelli LMR, Midlej V, da Silva EDS, Coelho EAF, da Silva AD, Coimbra ES.

01-02-2023

*Chem Biol Interact.*

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

Visceral leishmaniasis (VL) is a progressive, debilitating, and potentially fatal disease if left untreated. As a neglected tropical disease (NTD), the available treatment is restricted to a few drugs, which typically must be administered over a long period but are associated with serious adverse effects and have variability in efficacy. In this sense, drug repositioning has been considered an excellent strategy in the search for alternative treatments, especially in reducing the time and cost of the research. In this work, the repositioning potential of amodiaquine (AQ), a well-known antimalarial drug, was investigated for the treatment of VL. AQ showed significant and selective activity against promastigotes (IC50 = 11.6 μg/mL) and intracellular amastigotes (IC50 = 2.4 μg/mL) of L. infantum, being 10 times more destructive to the intracellular parasites than the host cell. In addition, pre-treatment of macrophages with AQ caused a significant reduction in the infection index, indicating a prophylactic effect of this drug. SEM images showed that AQ induces strong shape alterations of the promastigotes with an increase in cell volume with rounding and ribbing (vertical ridges), as well as a shortened flagellum. In addition, AQ induced depolarization of the ΔΨm, an increase in ROS and neutral lipids levels, and changes in the cell cycle in promastigotes, without alterations to the permeability of the parasite plasma membrane. L. infantum-infected macrophages treated with AQ induced the activation of oxidative mechanisms by infected host cells, with an increase in ROS and NO levels. Finally, in vitro interactions between AQ and miltefosine were found to have an additive effect in both biological stages of the parasite, with the ∑FIC50 values ranging from 0.74 to 1.16 μg/mL and 0.54-1.11 μg/mL for promastigotes and intracellular amastigotes, respectively. Overall, these data highlight the utility of drug repurposing and indicate future preclinical testing for AQ itself or in combination as a potential VL treatment.

First Record of Forcipomyia (Lasiohelea) Kieffer (Diptera: Ceratopogonidae) in Uruguay.

Canneva B.

Feb-2023

*Neotrop Entomol.*

<https://pubmed.ncbi.nlm.nih.gov/36459344/>

In Silico Analysis of Potential Drug Targets for Protozoan Infections.

Juárez-Saldivar A, Campillo NE, Ortiz-Perez E, Paz-Gonzalez AD, Saavedra E, Rivera G.

2022

*Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/35975866/>

Promising Molecular Targets Related to Polyamine Biosynthesis in Drug Discovery against Leishmaniasis.

Santiago-Silva KM, Camargo PG, Bispo MLF.

2022

*Med Chem*.

<https://pubmed.ncbi.nlm.nih.gov/35838221/>

Leishmaniasis is a neglected tropical disease widely distributed worldwide, caused by parasitic protozoa of the genus Leishmania. Despite representing a significant public health problem, the therapeutic options are old, with several reported adverse effects, have high costs, with administration mainly by parenteral route, which makes treatment difficult, increasing dropout and, consequently, the emergence of resistant strains. Thus, the research and development of new antileishmanial therapies become necessary. In this field, inhibiting essential targets that affect the parasite's growth, survival, and infectivity represents an attractive therapeutic strategy. With this in mind, this review addresses the main structural, functional characteristics and recent reports of the discovery of promising inhibitors of the enzymes Arginase (ARG) and trypanothione synthase (TryS), which are involved in the biosynthesis of polyamines and trypanothione and Trypanothione Reductase (TR), responsible for the reduction of trypanothione thiol.

N-acetylglucosamine-phosphatidylinositol de-N-acetylase as a novel target for probing potential inhibitor against Leishmania donovani.

Kumar M, Tripathi MK, Gupta D, Kumar S, Biswas NR, Ethayathulla AS, Kaur P.

Mar-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35014594/>

# Cysticercose

Disseminated cysticercosis with multi-system involvement in a child.

Kaur L, Bansal A, Dayal S, Karwal A, Singh S.

01-02-2023

*Pediatr Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/36724898/>

We report a rare case of disseminated cysticercosis in a 7-year-old Indian girl with recent onset seizures treated with antiepileptics for 2 months. When she presented to dermatology clinic, she had multifocal subcutaneous and submucosal nodules. The subsequent diagnostic workup revealed extensive neurocysticercosis as well as orbital and myocysticercosis.

Cerebral Cystic Echinococcosis.

Thakar S, Sunil A.

02-02-2023

*N Engl J Med*.

<https://pubmed.ncbi.nlm.nih.gov/36724331/>

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

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

2023

*Parasite*.

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

Cerebral Taenia crassiceps larvae infection in a 71-year-old immunocompetent male.

Floß N, Dolff S, Junker A, Blau T, Rauschenbach L, Sure U, Witzke O, Tappe D, Schönfeld A.

Feb-2023

*Infection.*

<https://pubmed.ncbi.nlm.nih.gov/36083404/>

# Dracunculose

Studying Whole-Genome Duplication Using Experimental Evolution of Spirodela polyrhiza.

Wu T, Natran A, Prost L, Aydogdu E, Van de Peer Y, Bafort Q.

2023

*Methods Mol Biol*.

<https://pubmed.ncbi.nlm.nih.gov/36720823/>

Diversity, antibacterial and phytotoxic activities of culturable endophytic fungi from Pinellia pedatisecta and Pinellia ternata.

Kong K, Huang Z, Shi S, Pan W, Zhang Y.

28-01-2023

*BMC Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36707757/>

**Background:** Endophytic fungi of medicinal plants, as special microorganisms, are important sources of antibacterial compounds. However, the diversity and antibacterial activity of endophytic fungi from Pinellia Tenore have not been systematically studied. **Results:** A total of 77 fungi were isolated from roots, stems, leaves, and tubers of Pinellia ternata and P. pedatisecta. All fungi were belonged to five classes and twenty-five different genera. Biological activities tests indicated that 21 extracts of endophytic fungi exhibited antibacterial activities against at least one of the tested bacteria, and 22 fermentation broth of endophytic fungi showed strong phytotoxic activity against Echinochloa crusgalli with the inhibition rate of 100%. Furthermore, four compounds, including alternariol monomethyl ether (1), alternariol (2), dehydroaltenusin (3) and altertoxin II (4), and three compounds, including terreic acid (5), terremutin (6), citrinin (7), were isolated from Alternaria angustiovoidea PT09 of P. ternata and Aspergillus floccosus PP39 of P. pedatisecta, respectively. Compound 5 exhibited strong antibacterial activities against Escherichia coli, Micrococcus tetragenus, Staphylococcus aureus, and Pseudomonas syringae pv. actinidiae with the inhibition zone diameter (IZD) of 36.0, 31.0, 33.7, 40.2 mm and minimum inhibitory concentration (MIC) values of 1.56, 3.13, 1.56, 1.56 μg/mL respectively, which were better than or equal to those of positive gentamicin sulfate. The metabolite 7 also exhibited strong antibacterial activity against P. syringae pv. actinidiae with the IZD of 26.0 mm and MIC value of 6.25 μg/mL. In addition, the compound 7 had potent phytotoxic activity against E. crusgalli with the inhibition rate of 73.4% at the concentration of 100 μg/mL. **Conclusions:** Hence, this study showed that endophytic fungi of P. ternata and P. pedatisecta held promise for the development of new antibiotic and herbicide resources.

Engineering triacylglycerol accumulation in duckweed (Lemna japonica).

Liang Y, Yu XH, Anaokar S, Shi H, Dahl WB, Cai Y, Luo G, Chai J, Cai Y, Mollá-Morales A, Altpeter F, Ernst E, Schwender J, Martienssen RA, Shanklin J.

Feb-2023

*Plant Biotechnol J*.

<https://pubmed.ncbi.nlm.nih.gov/36209479/>

Duckweeds are amongst the fastest growing of higher plants, making them attractive high-biomass targets for biofuel feedstock production. Their fronds have high rates of fatty acid synthesis to meet the demand for new membranes, but triacylglycerols (TAG) only accumulate to very low levels. Here we report on the engineering of Lemna japonica for the synthesis and accumulation of TAG in its fronds. This was achieved by expression of an estradiol-inducible cyan fluorescent protein-Arabidopsis WRINKLED1 fusion protein (CFP-AtWRI1), strong constitutive expression of a mouse diacylglycerol:acyl-CoA acyltransferase2 (MmDGAT), and a sesame oleosin variant (SiOLE(\*)). Individual expression of each gene increased TAG accumulation by 1- to 7-fold relative to controls, while expression of pairs of these genes increased TAG by 7- to 45-fold. In uninduced transgenics containing all three genes, TAG accumulation increased by 45-fold to 3.6% of dry weight (DW) without severely impacting growth, and by 108-fold to 8.7% of DW after incubation on medium containing 100 μm estradiol for 4 days. TAG accumulation was accompanied by an increase in total fatty acids of up to three-fold to approximately 15% of DW. Lipid droplets from fronds of all transgenic lines were visible by confocal microscopy of BODIPY-stained fronds. At a conservative 12 tonnes (dry matter) per acre and 10% (DW) TAG, duckweed could produce 350 gallons of oil/acre/year, approximately seven-fold the yield of soybean, and similar to that of oil palm. These findings provide the foundation for optimizing TAG accumulation in duckweed and present a new opportunity for producing biofuels and lipidic bioproducts.

# Echinococcose

Body Imaging of Bacterial and Parasitic Zoonoses: Keys to Diagnosis.

Kraft DC, Naeem M, Mansour J, Beal MA, Bailey TC, Bhalla S.

Mar-2023

*Radiographics.*

<https://pubmed.ncbi.nlm.nih.gov/36729948/>

Zoonotic infections, which are transmitted from animals to humans, have been a substantial source of human disease since antiquity. As the human population continues to grow and human influence on the planet expands, humans frequently encounter both domestic and wild animals. This has only increased as deforestation, urbanization, agriculture, habitat fragmentation, outdoor recreation, and international travel evolve in modern society, all of which have resulted in the emergence and reemergence of zoonotic infections. Zoonotic infections pose a diagnostic challenge because of their nonspecific clinical manifestations and the need for specialized testing procedures to confirm these diagnoses. Affected patients often undergo imaging during their evaluation, and a radiologist familiar with the specific and often subtle imaging patterns of these infections can add important clinical value. The authors review the multimodality thoracic, abdominal, and musculoskeletal imaging findings of zoonotic bacterial (eg, *Bartonella henselae, Pasteurella multocida, Francisella tularensis, Coxiella burnetii*, and *Brucella* species), spirochetal (eg, *Leptospira* species), and parasitic (eg, *Echinococcus, Paragonimus, Toxocara*, and *Dirofilaria* species) infections that are among the more commonly encountered zoonoses in the United States. Relevant clinical, epidemiologic, and pathophysiologic clues such as exposure history, occupational risk factors, and organism life cycles are also reviewed. Although many of the imaging findings of zoonotic infections overlap with those of nonzoonotic infections, granulomatous diseases, and malignancies, radiologists' familiarity with the imaging patterns can aid in the differential diagnosis in a patient with a suspected or unsuspected zoonotic infection. © RSNA, 2023 Quiz questions for this article are available through the Online Learning Center.

The potential role of roaming dogs in establishing a geographically novel life cycle of taeniids (Echinococcus spp. and Taenia spp.) in a non-endemic area.

Mutwiri T, Muigai AWT, Magambo J, Mulinge E, Gitau L, Muinde P, Bettridge JM, Rogan M, Fèvre EM, Falzon LC.

Feb-2023

*Vet Parasitol Reg Stud Reports*.

<https://pubmed.ncbi.nlm.nih.gov/36725161/>

Case Report: Amphotericin B and Mefloquine as a Salvage Treatment of Alveolar Echinococcosis.

**Jelicic K, Papic N, Viskovic K, Vince A.**

30-01-2023

*Am J Trop Med Hyg*.

<https://pubmed.ncbi.nlm.nih.gov/36716742/>

Comparing copromicroscopy to intestinal scraping to monitor red fox intestinal helminths with zoonotic and veterinary importance.

Marchiori E, Obber F, Celva R, Marcer F, Danesi P, Maurizio A, Cenni L, Massolo A, Citterio CV, Cassini R.

12-01-2023

*Front Vet Sci*.

<https://pubmed.ncbi.nlm.nih.gov/36713854/>

The red fox acts as reservoir for several helminthic infections which are of interest for both public and animal health. Huge efforts have been made for the assessment of the sensitivity of coprological tests for the detection of *Echinococcus multilocularis*, while less attention has been paid to other helminthic species. This study aimed at assessing the performance of two copromicroscopic techniques in the detection and prevalence estimation of gastrointestinal helminths in the red fox. Helminths were isolated from the small intestines of 150 red foxes from Bolzano province, Italy, with a scraping, filtration and counting technique (SFCT) and morphologically identified. Rectal contents were collected and submitted to simple flotation (FT) and, only for Taenids, a method based on the concentration of eggs and identification with multiplex PCR (CMPCR). Using SFCT as a reference standard, we estimated the sensitivity of the copromicroscopic tests. Three species of nematodes (namely, *Toxocara canis, Uncinaria stenocephala* and *Pterygodermatites* sp.) and five species of cestodes (*E*. *multilocularis, Taenia crassiceps, T. polycantha, Hydatigera taeniaeformis, Mesocestoides* sp.) were identified with SFCT, whereas eggs referable to the same taxa were detected with fecal diagnostics, except for *Pterygodermatites* sp. and *Mesocestoides* sp. The sensitivity of FT was low for all taxa, ranging from 9.8 to 36.3%, with lower values for Taeniidae. CMPCR was confirmed to perform better for the detection of Taeniidae eggs (23.5%) and the multiplex PCR on retrieved eggs was effective in the identification of the species. A meta-analysis of literature also suggested that our results are consistent with existing data, indicating that copromicroscopy tends to underestimate the prevalence of helminthic infections. The extent of such underestimation varies with taxon, being higher at high prevalence levels, in particular for cestodes. Irregular dynamics of egg shedding, and routine deep freezing of red fox feces may explain the frequency of false negatives with copromicroscopy. Low sensitivity of copromicroscopic tests should be accounted for when estimating prevalence and when defining the correct sample size for the detection of the parasites.

The non-oral infection of larval Echinococcus granulosus induces immune and metabolic reprogramming in the colon of mice.

Zhou Y, Luo T, Gong Y, Guo Y, Wang D, Gao Z, Sun F, Fu L, Liu H, Pan W, Yang X.

13-01-2023

*Front Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/36713407/>

Rapid and accurate screening of cystic echinococcosis in sheep based on serum Fourier-transform infrared spectroscopy combined with machine learning algorithms.

Dawuti W, Dou J, Zheng X, Lv X, Zhao H, Yang L, Lin R, Lü G.

27-01-2023

*J Biophotonics.*

<https://pubmed.ncbi.nlm.nih.gov/36707914/>

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

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

2023

*Parasite*.

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

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

Differentiation of hepatic alveolar echinococcosis with a hemangioma-like pattern compared to typical liver hemangioma using contrast-enhanced ultrasound: a pilot study.

Philipp J, Schmidberger J, Schlingeloff P, Kratzer W.

Feb-2023

*Infection*.

<https://pubmed.ncbi.nlm.nih.gov/35776381/>

An accidental finding of a giant intra-abdominal mass.

Mertens J, Driessen A, Komen N.

Feb-2023

*Acta Chir Belg*.

<https://pubmed.ncbi.nlm.nih.gov/33905308/>

A giant solitary fibrous tumour of the liver: a case report.

Roman J, Vávra P, Vávrová M, Židlík V, Pelikán A.

Feb-2023

*Acta Chir Belg*.

<https://pubmed.ncbi.nlm.nih.gov/34006182/>

**Background:** Solitary fibrous tumour of the liver is a rare mesenchymal tumour, occurring usually in women and with various symptomatology. The symptoms mostly result from pressure of the tumour mass on surrounding organs. Due to unknown biological behaviour and gradual increase of tumour volume, surgical resection is mostly the preferred treatment option. **Case:** A 75-year-old woman with a history of endometrial cancer, presenting with an incidental finding of a liver mass, initially considered of infectious origin (either echinococcosis or cysticercosis). Further diagnostics did not clarify the aetiology, a surgical revision was rejected at the time. The subsequent follow-up was interrupted by the development of symptoms of gastrointestinal and renal obstruction, which led to a complete surgical removal of the tumour, sized 30 × 25 × 20 cm. A histopathological examination showed a *CD34* and *STAT6* positivity, leading to a diagnosis of a giant solitary fibrous tumour of the liver. The patient recovered well, without any signs of recurrence. **Conclusion:** The solitary fibrous tumour of the liver is a rare, often incidental finding. It is considered benign, but malignant growth was also reported. A gradual growth mostly results in pressure on other organs. A surgical resection is the treatment of choice. Transarterial embolization is another treatment possibility. Due to indeterminate malignant potential a regular follow-up is necessary, including tumour markers and imaging methods.

# Trématodoses d’origine alimentaire (clonorchiase, opisthorchiase, fasciolase et paragonimose

Body Imaging of Bacterial and Parasitic Zoonoses: Keys to Diagnosis.

Kraft DC, Naeem M, Mansour J, Beal MA, Bailey TC, Bhalla S.

Mar-2023

*Radiographics.*

<https://pubmed.ncbi.nlm.nih.gov/36729948/>

Zoonotic infections, which are transmitted from animals to humans, have been a substantial source of human disease since antiquity. As the human population continues to grow and human influence on the planet expands, humans frequently encounter both domestic and wild animals. This has only increased as deforestation, urbanization, agriculture, habitat fragmentation, outdoor recreation, and international travel evolve in modern society, all of which have resulted in the emergence and reemergence of zoonotic infections. Zoonotic infections pose a diagnostic challenge because of their nonspecific clinical manifestations and the need for specialized testing procedures to confirm these diagnoses. Affected patients often undergo imaging during their evaluation, and a radiologist familiar with the specific and often subtle imaging patterns of these infections can add important clinical value. The authors review the multimodality thoracic, abdominal, and musculoskeletal imaging findings of zoonotic bacterial (eg, *Bartonella henselae, Pasteurella multocida, Francisella tularensis, Coxiella burnetii*, and *Brucella* species), spirochetal (eg, *Leptospira* species), and parasitic (eg, *Echinococcus, Paragonimus, Toxocara*, and *Dirofilaria* species) infections that are among the more commonly encountered zoonoses in the United States. Relevant clinical, epidemiologic, and pathophysiologic clues such as exposure history, occupational risk factors, and organism life cycles are also reviewed. Although many of the imaging findings of zoonotic infections overlap with those of nonzoonotic infections, granulomatous diseases, and malignancies, radiologists' familiarity with the imaging patterns can aid in the differential diagnosis in a patient with a suspected or unsuspected zoonotic infection.

Genome-wide exploration reveals distinctive northern and southern variants of Clonorchis sinensis in the Far East.

Kinkar L, Korhonen PK, Saarma U, Wang T, Zhu XQ, Harliwong I, Yang B, Fink JL, Wang D, Chang BCH, Chelomina GN, Koehler AV, Young ND, Gasser RB.

02-02-2023

*Mol Ecol Resour*.

<https://pubmed.ncbi.nlm.nih.gov/36727564/>

Prevalence of intestinal parasites in animal hosts and potential implications to animal and human health in Edo, Nigeria.

Inegbenosun CU, Isaac C, Anika FU, Aihebholoria OP.

Jan-2023

*J Vet Sci*.

<https://pubmed.ncbi.nlm.nih.gov/36726275/>

Comparison of the therapeutic efficacy of five anthelmintics against natural Fasciola hepatica infections in dairy cattle from the Mantaro Valley, Peru.

Zárate-Rendón DA, Briones-Montero A, Huaraca-Oré NA, Veirano GS, Levecke B, Geldhof P.

Feb-2023

*Vet Parasitol Reg Stud Reports.*

<https://pubmed.ncbi.nlm.nih.gov/36725157/>

The intensive use of anthelmintic drugs to control Fasciola hepatica infections in dairy cattle has resulted in the emergence of anthelmintic resistance. Cases of resistance to triclabendazole (TCBZ) have been reported worldwide. The main goal of this research was to evaluate the main five fasciolicides to control fasciolosis in dairy cattle in the Mantaro Valley, Peru. Two fecal egg count reduction tests were performed. In a first study, 24 naturally F. hepatica infected cattle were randomly grouped into three experimental groups (n = 8). Groups were treated with either TCBZ, nitroxynil (NTX) or closantel (CLOS). In a second experiment, 55 naturally infected cows were grouped into three experimental groups and treated with either TCBZ (n = 18), rafoxanide (RFX) + albendazole (ABZ) (n = 19) or clorsulon (CLN) + ivermectin (IVM) (n = 18). Therapeutic efficacy was determined following the WAAVP guidelines by measuring reduction in fluke egg output at days 15 and 30 post-treatment. Bootstrapping method was used to obtain the 95% confidence intervals. The efficacy of TCBZ was inadequate in both studies (≤80.8%). Closantel showed high efficacy (≥ 90%) at both days, while NTX showed 92.9% (83-100) and 82.1% (53.6-100), efficacy, at days 15 and 30, respectively. Efficacy for RFX were 92.1% (79.6-98.9) and 97.4% (94.1-99.4); and for CLN, 98.8% (97.6-100) and 80.1% (44.7-99.4), at days 15 and 30, respectively. The outcome of this study indicates reduced therapeutic efficacy of TCBZ against F. hepatica in an important dairy area of the Peruvian central highlands but also demonstrates the validity of four alternatives.

Secretion of extracellular vesicles during ontogeny of the tapeworm Schistocephalus solidus.

Mazanec H, Buskova N, Gardian Z, Kuchta R.

16-01-2023

*Folia Parasitol (Praha).*

<https://pubmed.ncbi.nlm.nih.gov/36722286/>

We provide the first ultrastructural evidence of the secretion of extracellular vesicles (EVs) across all parasitic stages of the tapeworm Schistocephalus solidus (Müller, 1776) (Cestoda: Diphyllobothriidea) using a laboratory life cycle model. We confirmed the presence of EV-like bodies in all stages examined, including the hexacanth, procercoids in the copepod, Macrocyclops albidus (Jurine, 1820), plerocercoids from the body cavity of the three-spined stickleback, Gasterosteus aculeatus Linnaeus, and adults cultivated in artificial medium. In addition, we provide description of novel tegumental structures potentially involved in EV biogenesis and the presence of unique elongated EVs similar to those previously described only in Fasciola hepatica Linnaeus, 1758 (Trematoda), Hymenolepis diminuta (Rudolphi, 1819) (Cestoda), and Trypanosoma brucei Plimmer et Bradford, 1899 (Kinetoplastida).

Fasciolosis in the Mediterranean island of Corsica (France): Insights from epidemiological and malacological investigations.

Alba A, Grech-Angelini S, Vázquez AA, Alda P, Blin Q, Lemmonier L, Chauvin A, Chartier C, Douchet P, Hurtrez-Boussès S, Rey O, Foata J, Boissier J, Quilichini Y.

19-01-2023

*Food Waterborne Parasitol.*

<https://pubmed.ncbi.nlm.nih.gov/36718346/>

The giant liver fluke in Europe: A review of Fascioloides magna within cervids and livestock with considerations on an expanding snail-fluke transmission risk.

Juhász A, Stothard JR.

2023

*Adv Parasitol*.

<https://pubmed.ncbi.nlm.nih.gov/36707174/>

The giant liver fluke, Fascioloides magna, common in North America and introduced into Europe in the 19th century, is an underappreciated model system for epidemiological studies on biological invasions, interactions with other native parasites and for health impact assessments within both definitive and intermediate snail host populations. Owing to its first contemporary appearance in Europe and then its subsequent spread, fascioloidosis has become a fluke-livestock/wildlife-snail combination of increasing interest for veterinarians, parasitologists and population geneticists. Here, we present a description of its recent epidemiology, biogeography and biology, inclusive of host species lists. Special emphasis is placed upon known definitive hosts of F. magna within Europe and considerations upon this fluke's local intermediate snail hosts. This helps us envisage plausible future epidemiological scenarios for further expansion across Europe, potentially even invasion into the UK. In line with others who draw attention upon needs for better systematic monitoring of putative risk-areas of fluke transmission, we close by highlighting why better surveillance of F. magna across continental Europe, and neighbouring territories, is justified.

Effects of Clonorchis sinensis combined with Hepatitis B virus infection on the prognosis of patients with Hepatocellular Carcinoma following Hepatectomy.

Li YK, Zhao JF, Yang CL, Zhan GH, Zhang J, Qin SD, Zhou M, Li MJ, Huang JT, Kong FY, Huang H, Chen JH, Xiang BD.

13-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36638133/>

# Filariose lymphatique

Detection of Wuchereria bancrofti in the city of São Luís, state of Maranhão, Brazil: New incursion or persisting problem?

Araújo TA, Lima de Albuquerque A, Melo DCTV, Santos EMM, Oliveira ALS, Ayres CFJ, Oliveira CMF.

30-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36716339/>

**Background:** The elimination of lymphatic filariasis (LF) from Brazil by 2020 was not accomplished; however, this goal can be achieved in the upcoming years with the assistance of specific strategies. The surveillance of LF can be performed using molecular xenomonitoring (MX), a noninvasive method used to infer the presence of the parasite in the human population. Herein, São Luís (state of Maranhão) was the first city to be investigated to identify whether LF transmission in Brazil has been interrupted and if there were any new incursions. **Methodology/principal findings:** Mosquitoes were collected by aspiration at 901 points distributed among 11 neighborhoods in São Luís with records of patients with microfilaremia. Pools of engorged or gravid Culex quinquefasciatus females were evaluated by WbCx duplex PCR with endogenous control for mosquitoes and target for W. bancrofti for determining the vector infection rate. Among the 10,428 collected mosquitoes, the most abundant species were C. quinquefasciatus (85%) and Aedes aegypti (12%). Significantly larger numbers of mosquitoes were collected from the neighborhoods of Areinha and Coreia (p<0.05). MX performed using PCR validated 705 pools of engorged or gravid females, fifteen of which were positive for Wuchereria bancrofti in two neighborhoods. **Conclusions:** The high density of engorged C. quinquefasciatus females per home, inadequate sanitation, and detection of W. bancrofti-infected mosquitoes in the city of São Luís represent a warning of the possible upsurge of LF, a disease that is still neglected; this underscores the need for the ostensive monitoring of LF in Brazil.

The Impact of the COVID-19 Pandemic on People With Lymphedema in an Endemic Area for Lymphatic Filariasis in Brazil.

de Aquino LT, Aguiar-Santos AM, Rocha A, Coutinho AVA, do Nascimento MSB, Moretti EC, da Silva FL, Lima FM, Bonfim C, Medeiros Z.

12-01-2023

*Int J Public Health.*

<https://pubmed.ncbi.nlm.nih.gov/36712817/>

**Objectives:** To investigate the repercussions of the COVID-19 pandemic on lymphedema patients from an endemic area of lymphatic filariasis. **Methods:** The study descriptive compared sociodemographic and clinical aspects, risk of falling and quality of life, prior and during the COVID-19 pandemic in 28 lymphedema patients, older than 18 years old and under investigation of filarial infection. For the evaluation of functional mobility, the *Time Up and Go* test and *The Medical Outcome Study Short Form-36 Health* for quality of life, was used. **Results:** An increase in interdigital and dermal lesions, a higher frequency of acute dermatolymphangioadenitis crises and risk of falling, worsening of quality of life in the domains of physical functioning, general health, vitality, and mental health during the pandemic was observed. **Conclusion:** Our findings of clinical worsening and quality of life of patients during the COVID-19 pandemic indicate the need to reinforce the goal of the Lymphatic Filariasis Program regarding the follow-up of these patients in the actions of the Global Program for the Elimination of Lymphatic Filariasis, due to the discontinuity in the care during the pandemic.

# Mycétome

An overview of mycetoma and its diagnostic dilemma: Time to move on to advanced techniques.

Husain U, Verma P, Suvirya S, Priyadarshi K, Gupta P.

Jan-Feb 2023

*Indian J Dermatol Venereol Leprol.*

<https://pubmed.ncbi.nlm.nih.gov/36331840/>

The neglected tropical disease mycetoma can become extremely devastating, and can be caused both by fungi and bacteria; these are popularly known as eumycetoma and actinomycetoma respectively. The classical triad of the disease is subcutaneous swelling, multiple discharging sinuses and the presence of macroscopic granules. The present study aims to highlight the existing diagnostic modalities and the need to incorporate newer and more advanced laboratory techniques like pan fungal/pan bacterial 16S rRNA gene polymerase chain reaction (PCR) and sequencing, Matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS), rolling circle amplification (RCA), loop-mediated isothermal amplification (LAMP) and recombinase polymerase amplification (RPA). It is important for the medical team to be aware of the various diagnostic options (both existing and future), so that diagnosis of such a debilitating disease is never missed, both by clinicians and microbiologists/pathologists. The newer diagnostic methods discussed in this article will help in rapid, accurate diagnosis thus facilitating early treatment initiation, and decreasing the overall morbidity of the disease. In the Indian context, newer technologies need to be made available more widely. Making clinicians aware and promoting research and development in mycetoma diagnostics is the need of the hour.

Stereotactic body radiotherapy for recurrent hemoptysis due to chronic pulmonary aspergillosis: a case report and systematic review of the literature.

Koch A, Schanne DH, Günther G, Aebersold DM, Elicin O.

Feb-2023

*Strahlenther Onkol*.

<https://pubmed.ncbi.nlm.nih.gov/36264357/>

**Purpose:** Chronic pulmonary aspergillosis (CPA) can manifest as fungus balls in preexisting cavities of lung parenchyma and recurrent hemoptysis is among the most frequent complications. Radiotherapy can be considered for treatment-refractory aspergilloma and severe hemoptysis. To the best of our knowledge, we present the first application of stereotactic body radiotherapy (SBRT) for a pulmonary aspergilloma in a patient with limited functional lung capacity. The topic was further expanded on with a systematic review of the literature addressing the implementation of radiotherapy in CPA patients. **Case report:** A 52-year-old man presented with recurring and treatment-refractory hemoptysis caused by chronic cavitary aspergillosis localized in the left lower lobe. We applied SBRT on two consecutive days with a total dose of 16 Gy. Hemoptysis frequency decreased to a clinically insignificant level. **Systematic review:** We performed a systematic search of the literature in line with the PRISMA statement. The initial PubMed search resulted in 230 articles, of which 9 were included. **Results:** The available literature contained 35 patients with CPA who received radiotherapy. Dose fractionation usually ranged from 2 to 4 Gy per fraction, applied almost exclusively in conventional two-dimensional (2D) techniques. There is no report of SBRT usage in such a scenario. Most cases report a positive treatment response after irradiation. **Conclusion:** The presented case demonstrates long-term clinical stability after SBRT for recurrent hemoptysis due to pulmonary aspergilloma. The systematic literature search revealed that concept definition is still uncertain, and further work is necessary to establish radiotherapy in clinical practice.

# Onchocercose

Autochthonous Onchocerca lupi infection of a domestic dog in Austria.

Unterköfler MS, Huck A, Silbermayr K, Fuehrer HP.

01-02-2023

*Parasit Vectors.*

<https://pubmed.ncbi.nlm.nih.gov/36726184/>

# Schistosomiase

A cercarial invadolysin interferes with the host immune response and facilitates infection establishment of Schistosoma mansoni.

Hambrook JR, Hanington PC.

02-02-2023

*PLoS Pathog.*

<https://pubmed.ncbi.nlm.nih.gov/36730464/>

Schistosoma mansoni employs immune evasion and immunosuppression to overcome immune responses mounted by its snail and human hosts. Myriad immunomodulating factors underlie this process, some of which are proteases. Here, we demonstrate that one protease, an invadolysin we have termed SmCI-1, is released from the acetabular glands of S. mansoni cercaria and is involved in creating an immunological milieu favorable for survival of the parasite. The presence of SmCI-1 in the cercarial stage of S. mansoni is released during transformation into the schistosomula. SmCI-1 functions as a metalloprotease with the capacity to cleave collagen type IV, gelatin and fibrinogen. Additionally, complement component C3b is cleaved by this protease, resulting in inhibition of the classical and alternative complement pathways. Using SmCI-1 knockdown cercariae, we demonstrate that SmCI-1 protects schistosomula from complement-mediated lysis in human plasma. We also assess the effect of SmCI-1 on cytokine release from human peripheral blood mononuclear cells, providing compelling evidence that SmCI-1 promotes an anti-inflammatory microenvironment by enhancing production of IL-10 and suppressing the production of inflammatory cytokines like IL-1B and IL-12p70 and those involved in eosinophil recruitment and activation, like Eotaxin-1 and IL-5. Finally, we utilize the SmCI-1 knockdown cercaria in a mouse model of infection, revealing a role for SmCI-1 in S. mansoni survival.

Molecular diagnosis of urogenital schistosomiasis in pre-school children, school-aged children and women of reproductive age at community level in central Senegal.

Sow D, Sylla K, Dieng NM, Senghor B, Gaye PM, Fall CB, Goumballa N, Diallo A, Ndiaye JLA, Parola P, Sokhna C, Doucouré S, Faye B.

31-01-2023

*Parasit Vectors.*

<https://pubmed.ncbi.nlm.nih.gov/36717835/>

CRISPR interference for sequence-specific regulation of fibroblast growth factor receptor A in Schistosoma mansoni.

Du X, McManus DP, French JD, Collinson N, Sivakumaran H, MacGregor SR, Fogarty CE, Jones MK, You H.

13-01-2023

*Front Immunol.*

<https://pubmed.ncbi.nlm.nih.gov/36713455/>

Annotation of G-Protein Coupled Receptors in the Genomes of Parasitic Blood Flukes.

Kamara IK, Thao JT, Kaur K, Wheeler NJ, Chan JD.

11-01-2023

*MicroPubl Biol.*

<https://pubmed.ncbi.nlm.nih.gov/36713056/>

Schistosomes contain divergent ligand-gated ion channels with an atypical Cys-loop motif.

Johnson H, VanHooreweghe M, Satori JA, Chan JD.

11-01-2023

*MicroPubl Biol.*

<https://pubmed.ncbi.nlm.nih.gov/36713055/>

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

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

01-11-2022

*Front Cell Infect Microbiol.*

<https://pubmed.ncbi.nlm.nih.gov/36710964/>

Schistosomiasis is a tropical parasitic disease that seriously endangers humans and animals. In this study, two *Oncomelania* snails, *Oncomelania hupensis* (*O. hupensis*) and *Oncomelania weishan* (*O. weishan*), were infected with *Schistosoma japonicum* (*S. japonicum*) cercariae during the early period, and ICR mice were subsequently infected with two kinds of miracidia that developed in male and female adult worms. In this study, isobaric tags for relative and absolute quantification (iTRAQ) were used to identify four channels: 113, 115, 117, and 119. A total of 2364 adult schistosome proteins were identified, and 1901 proteins were quantitative. Our results revealed 68 differentially expressed proteins (DEPs) in female adult worms, including 24 upregulated proteins and 44 downregulated proteins, and 55 DEPs in male adult worms, including 25 upregulated proteins and 30 downregulated proteins. LC-MS/MS and bioinformatics analysis indicated that these DEPs are mainly concentrated in cellular composition, molecular function, biological function and catabolism pathways. In summary, this proteomics analysis of adult schistosomes that hatched in two intermediate hosts helps to improve our understanding of the growth and developmental mechanisms of *S. japonicum*.

Risk factors affecting the occurrence of urinary schistosomiasis and urinary tract infections in some communities of Ondo State, Nigeria.

Kone KJ, Onifade AK, Dada EO.

Jan-2023

*J Water Health*.

<https://pubmed.ncbi.nlm.nih.gov/36705495/>

Accuracy of the urine point-of-care circulating cathodic antigen assay for diagnosing Schistosomiasis mansoni infection in Brazil: A multicenter study.

Pieri OS, Bezerra FSM, Coelho PMZ, Enk MJ, Favre TC, Graeff-Teixeira C, Oliveira RR, Reis MGD, Andrade LSA, Beck LCNH, Favero V, Fialho TRS, Guimarães RJPSE, Oliveira BSS, Pascoal VF, Pinheiro MCC, Santos RAD, Silva LK, Siqueira IC, Souza RP, Katz N.

23-01-2023

*Rev Soc Bras Med Trop*.

<https://pubmed.ncbi.nlm.nih.gov/36700600/>

Understanding perceptions of schistosomiasis and its control among highly endemic lakeshore communities in Mayuge, Uganda.

Mujumbusi L, Nalwadda E, Ssali A, Pickering L, Seeley J, Meginnis K, Lamberton PHL.

19-01-2023

*PLoS Negl Trop Dis*.

<https://pubmed.ncbi.nlm.nih.gov/36656869/>

Immunoinformatics analysis for design of multi-epitope subunit vaccine by using heat shock proteins against Schistosoma mansoni.

Pandya N, Kumar A.

Mar-2023

*J Biomol Struct Dyn.*

<https://pubmed.ncbi.nlm.nih.gov/35040367/>

The development of T cell and B cell that able provide long-term immune response against the schistosomiasisis to the people belongs to the epidemic area. Heat Shock Proteins (HSPs) are up-regulated in schistosomes as their environment changes owing to the developmental cycle, assisting the parasite in living with the adverse circumstances related with its life cycle. Schistosomiasis is still a severe health problem in the people of many countries in worldwide. In this work, to develop a chimeric antigen, we used an advanced and powerful immunoinformatics technique that targeted *Schistosoma mansoni* (*S. mansoni*) Heat shock protein (HSPs). Antigenicity, immunogenicity, allergenicity, and physicochemical characteristics were all assessed *in silico* for the developed subunit vaccine. The 3D structure of the vaccine was constructed and the stability of the vaccine construct was increased by using disulphide engineering. The protein-protein docking and simulation were performed between the vaccine construct and Toll-like receptor-4. The antigenicity probability value obtained for the vaccine construct was 0.93, which indicates that vaccine is non-allergenic and safe for human consumption. Communicated by Ramaswamy H. Sarma.

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

Biliary parascarosis in a foal.

Sazmand A, Yavari M, Babaei M, Nourian A, Otranto D.

01-02-2023

*Vet Med Sci*.

<https://pubmed.ncbi.nlm.nih.gov/36723790/>

Migration of Ascaris lumbricoides through the papilla of Vater in humans, and entry into the biliary tree, is well-recognised. Ascaris suum and Toxocara vitulorum have been recovered from the liver of swine and buffalo. We necropsied a Persian Kurdish filly at age 6 months, weighing ∼100 kg. Death evidently was caused by oleander (Nerium oleander) intoxication. An 8-cm adult male Parascaris was found at the lobar-left hepatic bile duct junction. We suggest that the nematode entered anteriorly into the hepatic tree, via the duodenum, major duodenal papilla, bile duct, left hepatic duct and finally the lobar duct. Considering the brief 4-h elapsed time between death and necropsy, and the 18-cm distance from the major duodenal papilla to the location of the parasite, we conclude that entry into the biliary tree likely occurred ante-mortem. We advise consideration of Parascaris infection in differential diagnosis of equine hepatic and pancreatic dysfunction.

Epidemiological studies of gastrointestinal parasites infecting dogs in Kwara Central, North Central, Nigeria.

Ola-Fadunsin SD, Abdulrauf AB, Abdullah DA, Ganiyu IA, Hussain K, Sanda IM, Rabiu M, Akanbi OB.

Feb-2023

*Comp Immunol Microbiol Infect Dis.*

<https://pubmed.ncbi.nlm.nih.gov/36610227/>

Dogs are the most cosmopolitan pets of humans and as such a means of transmitting zoonotic parasites to their owners. This study was designed to investigate the diversity, prevalence, pattern of infection, intensity of infections, and the risk factors associated with gastrointestinal parasites of dogs in Kwara Central, North Central, Nigeria. Three hundred and five clinically healthy dogs were sampled. Faecal samples were subjected to the direct smear, simple faecal centrifugation flotation, formol-ether concentration, and the Modified Ziehl-Neelsen staining techniques. Oocysts/eggs per gram of faeces were counted using the modified McMaster technique. Data were analysed using univariate logistic regression, multivariate logistic regression, and the one-way analysis of variance (ANOVA). A p -value of < 0.05 was considered significant for all analyses. One hundred and sixty-six dogs were positive for at least one species of gastrointestinal parasite, representing 54.43% (95% CI: 44.81 - 59.96) of the sampled population. The study identified Cystoisospora species (15.41%), Cryptosporidium species (25.25%), Ancylostoma species (25.25%), Toxocara canis (19.02%), Strongyloides stercoralis (7.54%), Uncinaria stenocephala (6.89%), and Dipylidium caninum (2.30%) as the gastrointestinal parasites infecting dogs in the study area. Coinfection with more than one species of gastrointestinal parasites was a common finding in dogs. The intensity of Cystoisospora spp. among infected dogs ranged between 40 and 980 oocysts per gram of faeces, while that of helminth parasites was 40 - 1560 eggs per gram of faeces. Age, sex, breeds, body condition score, presence of ticks on dogs, the purpose of keeping dog(s), types of housing, types of feed consumed, vaccination status, and treatment with antiparasitics were predators associated with the prevalence and intensity of gastrointestinal parasites infections. Due to the zoonotic nature of most of the encountered gastrointestinal parasites, there is need for regular antiparasitic treatment, proper dog management, and adequate personal hygiene to prevent zoonosis.

# Gale

Use of complementary and alternative medicine in children with scabies.

Akca G, Sen NO, Akca U.

02-02-2023

*Complement Med Res*.

<https://pubmed.ncbi.nlm.nih.gov/36731431/>

Permethrin steal effect by unmasked corneocytic keratin in topical therapy of scabies.

Scholz L, Fritz C, Chuttke J, Eichner A, Wohlrab J.

30-01-2023

*Skin Pharmacol Physiol.*

<https://pubmed.ncbi.nlm.nih.gov/36716721/>

**Introduction:** The use of epicutaneously applied permethrin in the treatment of common scabies is considered to be the first-line therapy. Due to increasing clinical treatment failure, the development of genetic resistance to permethrin in Sarcoptes scabiei var. hominis has been postulated. In addition, metabolic resistance and pharmacokinetic limitations by parasitic digestion and reactive thickening of stratum corneum are suspected to cause a reduction in cutaneous bioavailability. **Methods:** Since lipophilic permethrin is known to form hydrophobic interactions with proteins via van der Waals interactions, a similar interaction was assumed and investigated for permethrin and the protein keratin. Using keratin particles extracted from animal material, a model for hyperkeratotic and parasitic digested scabies skin was developed. Using fluorescence-labeled keratin and ³H-permethrin, their interaction potential was validated by loading and unloading experiments. Additionally, the impact of keratin to permethrin penetration was investigated based on an in vitro model using Franz diffusion cells. **Results:** For the first time, keratin particles were introduced as a model for dyskeratotic skin, as we were able to show, the keratin particles´ interaction potential with permethrin but no penetration behavior into the stratum corneum. Moreover, comparative penetration experiments of a reference formulation with and without added keratin or keratin-adherent permethrin showed that keratin causes a steal effect for permethrin, leading to a relevant reduction in cutaneous bioavailability in the target compartment. **Conclusion:** The results provide further evidence for a relevant pharmacokinetic influencing factor in the epicutaneous application of permethrin and a rationale for the necessity of keratolytic pretreatment in hyperkeratotic skin for the effective use of topical permethrin application in scabies.

Standardized cotton swab sampling with nested quantitative polymerase chain reaction is effective for diagnosing ordinary scabies.

Chung HC, Chun EJ, Kim JK, Kim SS, Kim CW.

30-01-2023

*Clin Exp Dermatol.*

<https://pubmed.ncbi.nlm.nih.gov/36715503/>

The impact of the COVID-19 pandemic on fungal and parasitic skin infections in a Swedish health region without lockdown: Focus on scabies and tinea capitis/ tinea barbae.

Pissa M, Seifert O, Gulin SJ.

Mai-2023

*Parasite Epidemiol Control.*

<https://pubmed.ncbi.nlm.nih.gov/36714885/>

Leukemia Cutis As the Initial Manifestation of Chronic Lymphocytic Leukemia Progression.

Pedreira-García WM, Nieves D, Montesinos-Cartagena M, Cortés CA, Cáceres-Perkins W, Rabelo-Cartagena J.

27-12-2023

*Cureus.*

<https://pubmed.ncbi.nlm.nih.gov/36712707/>

Chronic lymphocytic leukemia (CLL) is a malignant proliferation of monoclonal mature B-cells in peripheral blood. Leukemia cells can commonly spread from the blood to other sites such as the lymph nodes, liver, and spleen. However, contrary to T-cell lymphomas that can involve the skin, CLL metastasis to the skin is unusual and is rarely the first manifestation of systemic disease. When leukemia cells invade the skin, it is termed leukemia cutis. Furthermore, multiple skin morphologies can be present in leukemia cutis making diagnosis challenging. Likewise, it can be mistaken for other common etiologies such as drug or substance allergy, infection, and scabies, among others. We herein present a case of CLL with leukemia cutis as the initial manifestation of systemic disease. The initial punch biopsy results were non-specific for inflammatory changes, but a subsequent biopsy revealed findings confirming leukemia cutis. This case not only demonstrates that identifying malignant skin manifestations in a timely manner and treating them is essential, as it improves the quality of life and survival, but also demonstrates that leukemia cutis can be a dynamic disease where multiple biopsies may be needed to confirm the diagnosis, as histopathology can change over time.

# Morsures de serpent

Polyphyllin I Effects Candida albicans via Inhibition of Virulence Factors.

Sun AM, Wang YX, Hu GX, Li L, Wang RR.

23-01-2023

*Evid Based Complement Alternat Med*.

<https://pubmed.ncbi.nlm.nih.gov/36726525/>

*Paris polyphylla* is often used in Chinese medicine to treat conditions such as carbuncles, trauma, snake bites, and mosquito bites. In the present study, we investigated the effect and mechanism of the morphological transition and extracellular phospholipase activity of *Candida albicans* treated with polyphyllin I (PPI). First, the minimum inhibitory concentration and antifungal activity of PPI were evaluated using the multiple microdilution method and time-killing assays. Then, the effect of PPI on the morphological transition of *Candida albicans* in Spider liquid medium and Sabouraud-dextrose liquid medium containing 10% fetal bovine serum was observed under an inverted microscope and by scanning electron microscopy. Finally, egg yolk agar plates were used to evaluate extracellular phospholipase activity. Gene expression was detected by real-time quantitative polymerase chain reaction analysis. Our results suggest that PPI inhibited the transition from the yeast to the hyphal stage and decreased secreted aspartyl proteinase activity. We further confirmed that PPI significantly downregulated the expression of extracellular phospholipase genes and cAMP-PKA signaling pathway-related genes. Taken together, our results suggest that PPI exerts anti-*Candida albicans* activity by inhibiting virulence characteristics, including the yeast-to-hyphal transition and the secretion of aspartyl proteases and phospholipases. The study results also indicated that PPI could be a promising therapeutic strategy for *Candida albicans*.

The use of serum protein analysis in the diagnosis of fatal envenomation via Crotalus horridus (timber rattlesnake).

Gallagher T, Roberts S, Silva-Sanchez C, Sutton L, Laventure K.

30-01-2023

*J Forensic Sci.*

<https://pubmed.ncbi.nlm.nih.gov/36715131/>

Takotsubo cardiomyopathy following envenomation: An updated review.

Mishra AK, George AA, John KJ, Arun Kumar P, Dasari M, Afraz Pasha M, Hadley M.

26-01-2023

*World J Cardiol.*

<https://pubmed.ncbi.nlm.nih.gov/36714368/>

Envenomation by Micrurus hemprichii in Brazilian Amazonia: A report of three cases.

Bisneto PF, Silva Pereira H, de Almeida Gonçalves Sachett J, Kaefer IL, Monteiro WM.

26-01-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/36709049/>

Morbidity survey of the history of snakebites in different communities in the alto Juruá, western Brazilian Amazon.

Rodrigues TDSN, Mota-da-Silva A, Gomes da Costa J, de Souza Dutra J, de Oliveira Gomes M, Gurgel do Amaral GL, Ortega GP, Lima da Silva J, Monteiro WM, Bernarde PS.

26-01-2023

*Toxicon.*

<https://pubmed.ncbi.nlm.nih.gov/36709048/>

The secretory phenotypes of envenomed cells: Insights into venom cytotoxicity.

Yong Y, Hiu JJ, Yap MKK.

2023

*Adv Protein Chem Struct Biol*.

<https://pubmed.ncbi.nlm.nih.gov/36707202/>

Snake envenomation is listed as Category A Neglected Tropical Diseases (NTD) by World Health Organization, indicates a severe public health problem. The global figures for envenomation cases are estimated to be more than 1.8 million annually. Even if the affected victims survive the envenomation, they might suffer from permanent morbidity due to local envenomation. One of the most prominent local envenomation is dermonecrosis. Dermonecrosis is a pathophysiological outcome of envenomation that often causes disability in the victims due to surgical amputations, deformities, contracture, and chronic ulceration. The key venom toxins associated with this local symptom are mainly attributed to substantial levels of enzymatic and non-enzymatic toxins as well as their possible synergistic actions. Despite so, the severity of the local tissue damage is based on macroscopic observation of the bite areas. Furthermore, limited knowledge is known about the key biomarkers involved in the pathogenesis of dermonecrosis. The current immunotherapy with antivenom is also ineffective against dermonecrosis. These local effects eventually end up as sequelae. There is also a global shortage of toxins-targeted therapeutics attributed to inadequate knowledge of the actual molecular mechanisms of cytotoxicity. This chapter discusses the characterization of secretory phenotypes of dermonecrosis as an advanced tool to indicate its severity and pathogenesis in envenomation. Altogether, the secretory phenotypes of envenomed cells and tissues represent the precise characteristics of dermonecrosis caused by venom toxins.

Online Microextraction Coupled with HPLC-ABTS for Rapid Analysis of Antioxidants from the Root of Polygonum bistorta.

Yang WQ, Qian ZM, Wu MQ, Gao JL, Huang Q, Zou YS, Tang D.

17-01-2023

*Evid Based Complement Alternat Med*.

<https://pubmed.ncbi.nlm.nih.gov/36704212/>

Bothrops atrox mice experimental envenoming treatment using light-emitting diode (led) as an adjunct therapy to conventional serum therapy.

**Ferreira E Ferreira AA, Dos Reis VP, Santana HM, Nery NM, Evangelista JR, Serrath SN, da Silva Dutra RS, Rego CMA, Tavares MNM, Silva** **MDS, Soares AM, Rodrigues MMS, Zamuner SR, Zuliani JP.**

25-01-2023

*Lasers Med Sci*.

<https://pubmed.ncbi.nlm.nih.gov/36695923/>

Snakebite in the Hills and Mountains of Nepal.

Bogati S, Bhatt N, Nepal S, Nepali P, Sharma SK.

01-12-2022

*JNMA J Nepal Med Assoc.*

<https://pubmed.ncbi.nlm.nih.gov/36705115/>

Snakebite is an important public health issue around the world. In Nepal, it affects a huge number of people mostly belonging to low-income households who are involved in agriculture. Although snakebite has a serious impact on the Terai population, a few studies suggest that snakebite also occurs frequently in hills and mountains. In the absence of sufficient studies related to snakebites in these geographical regions, it is tough to sketch a true picture and estimate the magnitude of snakebites in those areas. Because of this, the healthcare system is probably not prepared enough to handle the victims of snakebites. This demands a proper study of the burden of the issue in these regions and appropriate initiatives for addressing it.

Platelet aggregation inhibitors from Bothrops alternatus snake venom.

Echeverría SM, Van de Velde AC, Luque DE, Cardozo CM, Kraemer S, Gauna Pereira MDC, Gay CC.

Feb-2023

*Toxicon*.

<https://pubmed.ncbi.nlm.nih.gov/36610603/>

A case of envenoming by a Persian false-horned viper Pseudocerastes persicus (Duméril, Bibron & Duméril, 1854) (Serpentes: Viperidae) in Southeastern Iran.

Kazemi SM, Jahan-Mahin MH, Zangi B, Khozani RS, Warrell DA.

Feb-2023

*Toxicon*.

<https://pubmed.ncbi.nlm.nih.gov/36586490/>

Perceptions of nurses regarding the management of snakebite envenomations: Limits and possibilities.

Rocha GDS, Souza Rodrigues MF, Rocha YV, Beckman de Lima H, Ramos FR, Teixeira E, Monteiro W, Sachett JAG.

Feb-2023

*Toxicon*.

<https://pubmed.ncbi.nlm.nih.gov/36566992/>

Snakebites can be caused by harmless or venomous snakes and, according to their severity and frequency, can be considered events of medical importance. In health facilities in remote areas, nurses work in the first line of care of patients that are victims of these envenomations. The aim was to discover the perception of nurses regarding the management of snakebites, its limitations and possibilities, with a view to professional empowerment in the context of primary health care. This is exploratory and descriptive research, with a qualitative approach, developed at FMT-HVD in Manaus, Amazonas state, Brazil, in the year 2021. The participants were nurses who work in basic health units in the municipalities of Careiro da Várzea, Ipixuna and Boa Vista do Ramos in the state of Amazonas. For data collection, the focus group strategy was adopted. Thematic content analysis was employed, which was carried out in the stages of pre-analysis; exploration or coding of the material; treatment of the results, inference and interpretation. After processing the data obtained, four topics emerged from the coding: Topic 1 - limitations in the primary care. Topic 2 - the need for infrastructure and personnel. Topic 3 - the need for continuing education. Topic 4 - the perception of training regarding the management of snakebite envenomations. The results showed a lack of antivenom in the healthcare units where nurses work. Another aspect highlighted by the nurses is the absence of a doctor in situ to perform the primary care or out of hours care in the units. The nurses' perceptions regarding the management of snakebite envenomations revealed the existence of failures in relation to the subject, such as the lack of antivenom, poor infrastructure in the units and the lack of a doctor, which must be solved, since the nurses are the most active professionals in primary health care, in addition to the high incidence of snakebite envenomations in the Brazilian Amazon.

A case series of samar cobra, Naja samarensis Peters, 1861 (Elapidae) envenomation.

Paghubasan J, Aoki Y, Tiglao PJG, Sarmiento MJ, Tan MA, Sarsalijo MS, Aquino GJB, Comandante JDL, Santamaria EB, Takahashi K, Smith C, Ariyoshi K, Agosto LC, Warrell DA.

Feb-2023

*Toxicon*.

<https://pubmed.ncbi.nlm.nih.gov/36563861/>

A retrospective study of clinical and epidemiological characteristics of snakebite in Napo Province, Ecuadorian Amazon.

Patiño RSP, Salazar-Valenzuela D, Robles-Loaiza AA, Santacruz-Ortega P, Almeida JR.

01-02-2023

*Trans R Soc Trop Med Hyg.*

<https://pubmed.ncbi.nlm.nih.gov/35917814/>

**Background:** Snakebite envenoming remains a relevant public health problem in tropical and subtropical countries. In Ecuador, this is particularly true in an area of great diversity like the Amazon region. Nevertheless, there is scarce information about epidemiological and clinical characteristics of these accidents in this area. **Methods:** This was a descriptive and retrospective study of snakebite cases treated at a tertiary hospital in the Napo Province, Ecuadorian Amazon, from 2015 to 2019. We collected sociodemographic and snakebite-related information, clinical aspects and the use of antivenom and antibiotics from medical records. **Results:** Information from 133 snakebite accidents was reviewed in this time period. Reports of snakebite envenoming decreased over the years. In total, 67% of those bitten were from nearby indigenous communities, which were the most affected groups. When a species was identified, Bothrops atrox was responsible for the highest number of cases registered. Local clinical manifestations were more frequent than systemic signs, in keeping with the typical effects produced by bothropic venoms. Additionally, data showed that more antivenom vials were given than those suggested by the protocol of the Ecuadorian Ministry of Health, in proportion to the grade of severity. Finally, we identified a low incidence of adverse reactions with antivenom administration, as well as a frequent use of antibiotics. **Conclusions:** The profile of snakebite accidents in the Napo Province is very similar to that described for other localities in the Amazon region of Ecuador and neighboring countries, with its challenges and limitations. Such aspects underlie the importance of establishing a robust and science-based public health program to respond to this frequent, but neglected, tropical disease.