



Veille scientifique

Maladies tropicales négligées

Semaine 19
08 au 14 mai 2023

Cysticercose	2
Dengue, chikungunya et maladie à virus Zika	2
Dracunculose	15
Echinococcose	16
Filariose lymphatique	18
Gale	20
Helminthiases transmises par le sol (ascaridiose, trichuriase, ankylostomiase)	20
Leishmaniose	21
Lèpre	26
Morsures de serpent	30
Mycétome	32
Onchocercose	33
Pian	34
Rage	34
Schistosomiase	36
Trachome	38
Trématodoses d'origine alimentaire (clonorchiose, opisthorchiase, fasciolase et paragonimose)	39
Trypanosomes (trypanosomiase et maladie de Chagas)	41
Ulcère de Buruli	43

Cysticercose

From (Cat) Scratch: A Unique Presentation of Central Nervous System Bartonella Infection.

Rodriguez W, Fedorova M, Rukmangadachar L.

02-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37153245/>

Neuropsychiatric Aspects of Parasitic Infections-A Review.

Goyal G, Kaur U, Sharma M, Sehgal R.

Mars-Avril 2023

Neurol India.

<https://pubmed.ncbi.nlm.nih.gov/37148042/>

Dengue, chikungunya et maladie à virus Zika

Association between rapid renal function deterioration and cancer mortality in the elderly: A retrospective cohort study.

Kuo IC, Chu YC, Chen YH, Chan TC.

Avr-2023

Cancer Med.

<https://pubmed.ncbi.nlm.nih.gov/36880220/>

Re-mining serum proteomics data reveals extensive post-translational modifications upon Zika and dengue infection.

Allgoewer K, Wu S, Choi H, Vogel C.

09-05-2023

Mol Omics.

<https://pubmed.ncbi.nlm.nih.gov/36810580/>

Zika virus (ZIKV) and dengue virus (DENV) are two closely related flaviviruses with similar symptoms. However, due to the implications of ZIKV infections for pregnancy outcomes, understanding differences in their molecular impact on the host is of high interest. Viral infections change the host proteome, including post-translational modifications. As modifications are diverse and of low abundance, they typically require additional sample processing which is not feasible for large cohort studies. Therefore, we tested the potential of next-generation proteomics data in its ability to prioritize specific modifications for later analysis. We re-mined published mass spectra from 122 serum samples from ZIKV and DENV patients for the presence of phosphorylated, methylated, oxidized, glycosylated/glycated, sulfated, and carboxylated peptides. We identified 246 modified peptides with significantly differential abundance in ZIKV and DENV patients. Amongst these, methionine-oxidized peptides from apolipoproteins and glycosylated peptides from immunoglobulin proteins were more abundant in ZIKV patient serum and generate hypotheses on the

potential roles of the modification in the infection. The results demonstrate how data-independent acquisition techniques can help prioritize future analyses of peptide modifications.

Development and Validation of a Bedside Dengue Severity Score for Predicting Severe Dengue in Children.

Gayathri V, Lakshmi SV, Murugan SS, Poovazhagi V, Kalpana S.

15-05-2023

Indian Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36757000/>

Objective: To develop and validate a bedside dengue severity score in children less than 12 years for predicting severe dengue disease. **Methods:** We carried out an analysis of data on the clinical and laboratory parameters of patients with confirmed dengue, hospitalized in October, 2019 at our center. A comprehensive patient's score was developed. Predictive models for severity were built using a forward step-wise method. This model was validated on the data of 312 children with dengue admitted during September- October, 2021. **Results:** Severe dengue was predicted by the dengue severity score with a sensitivity of 86.75% (95% CI 77.52%-93.19%), specificity of 98.25% (95% CI 95.56-99.52%), a positive predictive value of 95.34% (95% CI 92.18%-97.26%) and a negative predictive value of 94.74% (95% CI 87.16%-97.95%). The overall predictive accuracy was 95.2% (95% CI 92.19%-97.28%). **Conclusion:** The proposed bedside dengue severity scoring system was found to have good validity. Validating the score in different settings and patient populations is suggested.

The Hip of Children with Congenital Zika Syndrome: A Prospective Observational Study.

da Fonseca JO, de Oliveira Vianna RA, Carvalho FR, Velarde LGC, de Oliveira SA, Cardoso CAA, Gameiro VS.

Mai-2023

Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36470461/>

Design of a multi-epitope Zika virus vaccine candidate - an in-silico study.

Ezzemani W, Windisch MP, Altawalrah H, Guessous F, Saile R, Benjelloun S, Kettani A, Ezzikouri S.

Juin-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/35318896/>

Electromyography in Congenital Zika Syndrome.

Gouveia de Melo ACM, van der Linden V, Serpa SC, Rolim Filho EL, Lins OG.

01-05-2023

J Clin Neurophysiol.

<https://pubmed.ncbi.nlm.nih.gov/34510092/>

Introduction: Congenital Zika virus syndrome is a distinct pattern of birth defects in fetuses infected by the Zika

virus. It presents a broad clinical spectrum that includes occurrences of microcephaly, hypertonia, dysphagia, hyperexcitability, seizures, and arthrogryposis. Imaging findings show neuronal migration disorders. **Methodology:** Case reports have suggested that arthrogryposis has a neurogenic cause. We analyzed needle electromyography and nerve conduction examinations on 77 patients aged 2-24 months presenting highly probable congenital Zika virus syndrome, with or without arthrogryposis. **Results:** All those with arthrogryposis presented with chronic muscle denervation in the electromyography examination. Similarly, children with single or reversible joint abnormalities at birth showed the same findings. Denervation in the paravertebral musculature was found in all of the children with diaphragmatic paralysis or thoracic deformities. **Conclusions:** We propose that congenital contractures associated with congenital Zika virus syndrome are caused by the malformation of upper and lower motor neurons during embryogenesis.

Differentiating Multisystem Inflammatory Syndrome in Children (MIS-C) and Its Mimics - A Single-Center Experience From a Tropical Setting.

Balasubramanian S, Sankar J, Dhanalakshmi K, Raj SL, Nandakumar D, Ramanan AV, Chandy S.
15-05-2023

Indian Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36896750/>

Objective: Identifying clinical and laboratory indicators that differentiate multisystem inflammatory syndrome in children (MIS-C) apart from other febrile diseases in a tropical hospital setting. **Methods:** Review of hospital records done in a tertiary care exclusive children's hospital for children admitted from April, 2020 till June, 2021. Laboratory values, severe acute respiratory syndrome coronavirus (SARS-CoV-2) serological status, and clinical signs and symptoms of patients with MIS-C, and those with similar presentations were analyzed. **Results:** 114 children fulfilled the inclusion criteria (age group of 1 mo-18 y) for whom a diagnosis of MIS-C was considered in the emergency room based on the clinical features. Among them, 64 children had the final diagnosis of MIS-C, and the remaining 50 children had confirmatory evidence of infections mimicking MIS-C such as enteric fever, scrub typhus, dengue and appendicitis.

Conclusion: Older age group, presence of muco-cutaneous symptoms, very high C-reactive protein, neutrophilic leukocytosis, abdominal pain and absence of hepatosplenomegaly favor a diagnosis of MIS-C.

Spatiotemporal dynamics and recurrence of chikungunya virus in Brazil: an epidemiological study.

de Souza WM, de Lima STS, Simões Mello LM, Candido DS, Buss L, Whittaker C, Claro IM, Chandradeva N, Granja F, de Jesus R, Lemos PS, Toledo-Teixeira DA, Barbosa PP, Firmino ACL, Amorim MR, Duarte LMF, Pessoa IB Jr, Forato J, Vasconcelos IL, Maximo ACBM, Araújo ELL, Perdigão Mello L, Sabino EC, Proença-Módena JL, Faria NR, Weaver SC.

Mai-2023

Lancet Microbe.

<https://pubmed.ncbi.nlm.nih.gov/37031687/>

DENV inhibitor effective in non-human primates.

Crunkhorn S.

Mai-2023

Nat Rev Drug Discov.

<https://pubmed.ncbi.nlm.nih.gov/37020012/>

Genetic polymorphisms rs1800871 and rs1800872 of IL-10 gene are associated with dengue infection, especially with serotype 1 and DwoWS in Mexican population.

Eloisa Monroy-Muñoz I, Esteban Muñoz-Medina J, Manuel Fragoso J, Esperanza Santacruz-Tinoco C, Sevilla-Montoya R, Hidalgo-Bravo A, Montes-Herrera D, Bravo-Flores E, Angeles-Martínez J.

Juin-2023

Cytokine.

<https://pubmed.ncbi.nlm.nih.gov/37015157/>

Introduction: Dengue infection is generated by a complex interaction between DENV (Dengue Virus) and the host's immune response. Interleukin-10 is an immunoregulatory cytokine during DENV infection. The objective of this study was to investigate whether genetic variants in IL-10 could be useful as a predictive and susceptibility marker in the prognosis of DENV infection, particularly with serotype 1, and in participants with dengue without warning signs. **Material and methods:** A study of cases (n = 365) and controls (n = 364) was carried out. Genotyping was performed by real-time PCR using TaqMan probes. Sample size power was calculated using Quanto software. **RESULTS:** This is the first report showing the independent association of the T allele of rs1800871 (P = 0.023) and the A allele of rs1800872 (P = 0.010) with the risk of dengue infection. Statistical analysis established the genotypic association of IL-10 SNPs with DENV infection under different inheritance models. Our results also showed the association of the CC, TC, and CA haplotypes (P = 0.0064, P = 0.0032, and P = 0.0010 respectively) with infection. Furthermore, both polymorphic sites were associated with the risk of DwoWS and serotype 1 (Den-1) under different inheritance models. Finally, under the dominant model, we identified a positive correlation between IL-10 levels vs. IFN-γ and IL-8. **Conclusion:** Our results show the first independent association of the T and A alleles of the polymorphic sites rs1800871 and rs1800872, with dengue infection, particularly with Den-1, and in participants with DwoWs.

Potential use of the cholesterol transfer inhibitor U18666A as an antiviral drug for research on various viral infections.

Assefi M, Bijan Rostami R, Ebrahimi M, Altafi M, Tehrani PM, Zaidan HK, Talib Al-Naqeeb BZ, Hadi M, Yasamineh S, Gholizadeh O.

Juin-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37011734/>

Hemocup blood feeder: An affordable and simplified blood-feeding device for maintenance of *Aedes aegypti* mosquito colonies in Sri Lanka.

Dilani PVD, Wickramasinghe PDSU, Lakshman GVCP, Ranathunge T, Dassanayake RS, Silva Gunawardene YIN.
Juin-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37003431/>

Biosynthesis of zinc oxide nanoparticles using *Indigofera tinctoria* and their efficacy against dengue vector, *Aedes aegypti* (Diptera: Culicidae).

Chithiga A, Manimegalai K.

Juin-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36997017/>

Bio-efficacy of insecticidal molecule emodin against dengue, filariasis, and malaria vectors.

Chinnasamy R, Govindasamy B, Venkatesh M, Magudeeswaran S, Dhanarajan A, Devarajan N, Willie P, Perumal V, Mekchay S, Krutmuang P.

Mai-2023

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/36934179/>

Emodin, a compound isolated from *Aspergillus terreus*, was studied using chromatographic and spectroscopic methods and compound purity (96%) was assessed by TLC. Furthermore, high larvicidal activity against *Aedes aegypti*-AeA (LC₅₀ 6.156 and LC₉₀ 12.450 mg/L), *Culex quinquefasciatus*-CuQ (8.216 and 14.816 mg/L), and *Anopheles stephensi*-AnS larvae (6.895 and 15.24 mg/L) was recorded. The first isolated fraction (emodin) showed higher pupicidal activity against AeA (15.449 and 20.752 mg/L). Most emodin-treated larvae (ETL) showed variations in acetylcholine esterase, α and β -carboxylesterases, and phosphatase activities in the 4th instar, indicating the intrinsic differences in their biochemical changes. ETL had numerous altered tissues, including muscle, gastric caeca, hindgut, midgut, nerve ganglia, and midgut epithelium. Acute toxicity of emodin on brine shrimp *Artemia nauplii* (54.0 and 84.5 mg/L) and the zebrafish *Danio rerio* (less toxicity observed) was recorded. In docking studies, Emodin interacted well with odorant-binding-proteins of AeA, AnS, and CuQ with docking scores of - 8.89, - 6.53, and - 8.09 kcal mol⁻¹, respectively. Therefore, *A. terreus* is likely to be effective against mosquito larvicides.

Where boundaries become bridges: Mosquito community composition, key vectors, and environmental associations at forest edges in the central Brazilian Amazon.

Hendy A, Hernandez-Acosta E, Valério D, Fé NF, Mendonça CR, Costa ER, Andrade ES, Andes Júnior JT, Assunção FP, Scarpassa VM, Lacerda MVG, Buenemann M, Vasilakis N, Hanley KA.

26-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37099599/>

Molecular Characterization and Phylogenetic Analysis of Dengue Fever Viruses in Three Outbreaks in Tanzania Between 2017 and 2019.

Kelly ME, Msafiri F, Affara M, Gehre F, Moremi N, Mghamba J, Misinzo G, Thye T, Gatei W, Whistler T, Joachim A, Lema N, Santiago GA.

26-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37099594/>

Background: Dengue is a disease of public health interest, and Tanzania experienced major outbreaks in 2014 and 2019. Here, we report our findings on the molecular characterization of dengue viruses (DENV) that circulated during two smaller outbreaks (2017 and 2018) and one major epidemic (2019) in Tanzania. **Methodology/principal findings:** We tested archived serum samples from 1,381 suspected dengue fever patients, with a median age of 29 (IQR:22-40) years, referred to the National Public Health Laboratory for confirmation of DENV infection. DENV serotypes were identified by reverse transcription polymerase chain reaction (RT-PCR), and specific genotypes were identified by sequencing the envelope glycoprotein gene and phylogenetic inference methods. DENV was confirmed in 823 (59.6%) cases. More than half (54.7%) of patients with dengue fever infection were males, and nearly three-quarters (73%) of the infected individuals were living in Kinondoni district, Dar es Salaam. DENV-3 Genotype III caused the two smaller outbreaks in 2017 and 2018, while DENV-1 Genotype V caused the 2019 epidemic. DENV-1 Genotype I was also detected in one patient in 2019. **Conclusion/significance:** This study has demonstrated the molecular diversity of dengue viruses circulating in Tanzania. We found that contemporary circulating serotypes did not cause the major epidemic of 2019 but rather due to a serotype shift from DENV-3 (2017/2018) to DENV-1 in 2019. Such a change increases the risk for patients previously infected with a particular serotype to develop severe symptoms upon potential re-infection with a heterologous serotype due to antibody-dependent enhancement of infection. Therefore, the circulation of serotypes emphasizes the need to strengthen the country's dengue surveillance system for better management of patients, early detection of outbreaks, and vaccine development.

Structure-Activity Relationships Reveal Beneficial Selectivity Profiles of Inhibitors Targeting Acetylcholinesterase of Disease-Transmitting Mosquitoes.

Vidal-Albalat A, Kindahl T, Rajeshwari R, Lindgren C, Forsgren N, Kitur S, Tengo LS, Ekström F, Kamau L, Linusson A.

11-05-2023

J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37094110/>

Insecticide resistance jeopardizes the prevention of infectious diseases such as malaria and dengue fever by vector control of disease-transmitting mosquitoes. Effective new insecticidal compounds with minimal adverse effects on humans and the environment are therefore urgently needed. Here, we explore noncovalent inhibitors of the well-validated insecticidal target acetylcholinesterase (AChE) based on a 4-thiazolidinone scaffold. The 4-thiazolidinones inhibit AChE1 from the mosquitoes *Anopheles gambiae* and *Aedes aegypti* at low micromolar concentrations. Their selectivity depends primarily on the substitution pattern of the phenyl ring; halogen substituents have complex effects. The compounds also feature a pendant aliphatic amine that was important for activity; little variation of this group is tolerated. Molecular docking studies suggested that the tight selectivity profiles of these compounds are due to competition between two binding sites. Three 4-thiazolidinones tested for in vivo insecticidal activity had similar effects on disease-transmitting mosquitoes despite a 10-fold difference in their in vitro activity.

A universal fluorescence polarization high throughput screening assay to target the SAM-binding sites of SARS-CoV-2 and other viral methyltransferases.

Samrat SK, Bashir Q, Zhang R, Huang Y, Liu Y, Wu X, Brown T, Wang W, Zheng YG, Zhang QY, Chen Y, Li Z, Li H.

Dec-2023

Emerg Microbes Infect.

<https://pubmed.ncbi.nlm.nih.gov/37060263/>

Maternal respiratory viral infections during pregnancy and offspring's neurodevelopmental outcomes: A systematic review.

San Martín-González N, Castro-Quintas Á, Marques-Feixa L, Ayesa-Arriola R, López M, Fañanás L.

Juin-2023

Neurosci Biobehav Rev.

<https://pubmed.ncbi.nlm.nih.gov/37059407/>

Fusing an agent-based model of mosquito population dynamics with a statistical reconstruction of spatio-temporal abundance patterns.

Cavany SM, España G, Lloyd AL, Vazquez-Prokopec GM, Astete H, Waller LA, Kitron U, Scott TW, Morrison AC, Reiner RC Jr, Perkins TA.

27-04-2023

PLoS Comput Biol.

<https://pubmed.ncbi.nlm.nih.gov/37104528/>

The mosquito *Aedes aegypti* is the vector of a number of medically-important viruses, including dengue virus, yellow fever virus, chikungunya virus, and Zika virus, and as such vector control is a key approach to managing the diseases they cause. Understanding the impact of vector control on these diseases is aided by first understanding its impact on *Ae. aegypti* population dynamics. A number of detail-rich models have been developed to couple the dynamics of the immature and adult stages of *Ae. aegypti*. The numerous assumptions of these models enable them to realistically characterize impacts of mosquito control, but they also constrain the ability of such models to reproduce empirical patterns that do not conform to the models' behavior. In contrast, statistical models afford sufficient flexibility to extract nuanced signals from noisy data, yet they have limited ability to make predictions about impacts of mosquito control on disease caused by pathogens that the mosquitoes transmit without extensive data on mosquitoes and disease. Here, we demonstrate how the differing strengths of mechanistic realism and statistical flexibility can be fused into a single model. Our analysis utilizes data from 176,352 household-level *Ae. aegypti* aspirator collections conducted during 1999-2011 in Iquitos, Peru. The key step in our approach is to calibrate a single parameter of the model to spatio-temporal abundance patterns predicted by a generalized additive model (GAM). In effect, this calibrated parameter absorbs residual variation in the abundance time-series not captured by other features of the mechanistic model. We then used this calibrated parameter and the literature-derived parameters in the agent-based model to explore *Ae. aegypti* population dynamics and the impact of insecticide spraying to kill adult mosquitoes. The baseline abundance predicted by the agent-based model closely matched that predicted by the GAM. Following spraying, the agent-based model predicted that mosquito abundance rebounds within about two months, commensurate with recent experimental data from Iquitos. Our approach was able to accurately reproduce abundance patterns in Iquitos and produce a realistic response to adulticide spraying, while retaining sufficient flexibility to be applied across a range of settings.

Risk of adverse pregnancy and infant outcomes associated with prenatal Zika virus infection: a post-epidemic cohort in Central-West Brazil.

Rosado LEP, Martelli CMT, Brickley EB, Gomes MBF, de Toledo Lima T, da Costa PSS, de Ávila MP, Viggiano MB, do Amaral WN, de Rezende Feres VC, Fiaccadori FS, de Sene Amancio Zara AL, Ferreira-Lopes A, Turchi MD.

05-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37147405/>

Effects of rIL2/anti-IL2 antibody complex on chikungunya virus-induced chronic arthritis in a mouse model.

Tritsch SR, Porzucek AJ, Schwartz AM, Proctor AM, Amdur RL, Latham PS, Simon GL, Mores CN, Chang AY.

05-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37147383/>

Chikungunya virus (CHIKV) is characterized by disabling joint pain that can cause persistent arthritis in approximately one-fourth of patients. Currently, no standard treatments are available for chronic CHIKV arthritis. Our preliminary data suggest that decreases in interleukin-2 (IL2) levels and regulatory T cell (Treg) function may play a role in CHIKV arthritis pathogenesis. Low-dose IL2-based therapies for autoimmune diseases have been shown to up-regulate Tregs, and complexing IL2 with anti-IL2 antibodies can prolong the half-life of IL2. A mouse model for post-CHIKV arthritis was used to test the effects of recombinant IL2 (rIL2), an anti-IL2 monoclonal antibody (mAb), and the complex on tarsal joint inflammation, peripheral IL2 levels, Tregs, CD4 + effector T cells (Teff), and histological disease scoring. The complex treatment resulted in the highest levels of IL2 and Tregs, but also increased Teffs, and therefore did not significantly reduce inflammation or disease scores. However, the antibody group, which had moderately increased levels of IL2 and activated Tregs, resulted in a decreased average disease score. These results suggest the rIL2/anti-IL2 complex stimulates both Tregs and Teffs in post-CHIKV arthritis, while the anti-IL2 mAb increases IL2 availability enough to shift the immune environment towards a tolerogenic one.

Zika Virus affects neurobehavioral development, and causes oxidative stress associated to blood-brain barrier disruption in a rat model of congenital infection.

de Almeida W, Deniz BF, Souza Dos Santos A, Faustino AM, Ramires Junior OV, Schmitz F, Varela APM, Teixeira TF, Sesterheim P, Marques da Silva F, Roehe PM, Wyse AT, Pereira LO.

03-05-2023

Brain Behav Immun.

<https://pubmed.ncbi.nlm.nih.gov/37146656/>

In silico design and validation of a novel multi-epitope vaccine candidate against structural proteins of Chikungunya virus using comprehensive immunoinformatics analyses.

Mahmoodi S, Amirzakaria JZ, Ghasemian A.

05-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37146081/>

Chikungunya virus (CHIKV) is an emerging viral infectious agent with the potential of causing pandemic. There is neither a protective vaccine nor an approved drug against the virus. The aim of this study was design of a novel multi-epitope vaccine (MEV) candidate against the CHIKV structural proteins using comprehensive immunoinformatics and immune simulation analyses. In this study, using comprehensive immunoinformatics approaches, we developed a novel MEV candidate using the CHIKV structural proteins (E1, E2, 6 K, and E3). The polyprotein sequence was obtained from the UniProt

Knowledgebase and saved in FASTA format. The helper and cytotoxic T lymphocytes (HTLs and CTLs respectively) and B cell epitopes were predicted. The toll-like receptor 4 (TLR4) agonist RS09 and PADRE epitope were employed as promising immunostimulatory adjuvant proteins. All vaccine components were fused using proper linkers. The MEV construct was checked in terms of antigenicity, allergenicity, immunogenicity, and physicochemical features. The docking of the MEV construct and the TLR4 and molecular dynamics (MD) simulation were also performed to assess the binding stability. The designed construct was non-allergen and was immunogen which efficiently stimulated immune responses using the proper synthetic adjuvant. The MEV candidate exhibited acceptable physicochemical features. Immune provocation included prediction of HTL, B cell, and CTL epitopes. The docking and MD simulation confirmed the stability of the docked TLR4-MEV complex. The high-level protein expression in the *Escherichia coli* (*E. coli*) host was observed through in silico cloning. The in vitro, in vivo, and clinical trial investigations are required to verify the findings of the current study.

Development of immortalized rhesus macaque kidney cells supporting infection with a panel of viruses.

Reiter S, Gärtner S, Decker K, Pöhlmann S, Winkler M.

05-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37146034/>

Non-human primate (NHP)-based model systems faithfully reproduce various viral diseases including Ebola, influenza, AIDS and Zika. However, only a small number of NHP cell lines are available and generation of additional cell lines could help to refine these models. We immortalized rhesus macaque kidney cells by lentiviral transduction with a vector encoding telomerase reverse transcriptase (TERT) and report the generation of three TERT-immortalized cell lines derived from rhesus macaque kidney. Expression of the kidney podocyte marker podoplanin on these cells was demonstrated by flow cytometry. Quantitative real-time PCR (qRT-PCR) was employed to demonstrate induction of MX1 expression upon stimulation with interferon (IFN) or viral infection, suggesting a functional IFN system. Further, the cell lines were susceptible to entry driven by the glycoproteins of vesicular stomatitis virus, influenza A virus, Ebola virus, Nipah virus and Lassa virus as assessed by infection with retroviral pseudotypes. Finally, these cells supported growth of Zika virus and the primate simplexviruses Cercopithecine alphaherpesvirus 2 and Papiine alphaherpesvirus 2. In summary, we developed IFN-responsive rhesus macaque kidney cell lines that allowed entry driven by diverse viral glycoproteins and were permissive to infection with Zika virus and primate simplexviruses. These cell lines will be useful for efforts to analyze viral infections of the kidney in macaque models.

A pH-dependent cluster of charges in a conserved cryptic pocket on flaviviral envelopes.

Zuzic L, Marzinek JK, Anand GS, Warwicker J, Bond PJ.

Mai-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37144875/>

Twist1-IRF9 Interaction Is Necessary for IFN-Stimulated Gene Anti-Zika Viral Infection.

You Y, Grasso E, Alvero A, Condon J, Dimova T, Hu A, Ding J, Alexandrova M, Manchorova D, Dimitrova V, Liao A, Mor G.

05-05-2023

J Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37144865/>

An efficient immune defense against pathogens requires sufficient basal sensing mechanisms that can deliver prompt responses. Type I IFNs are protective against acute viral infections and respond to viral and bacterial infections, but their efficacy depends on constitutive basal activity that promotes the expression of downstream genes known as IFN-stimulated genes (ISGs). Type I IFNs and ISGs are constitutively produced at low quantities and yet exert profound effects essential for numerous physiological processes beyond antiviral and antimicrobial defense, including immunomodulation, cell cycle regulation, cell survival, and cell differentiation. Although the canonical response pathway for type I IFNs has been extensively characterized, less is known regarding the transcriptional regulation of constitutive ISG expression. Zika virus (ZIKV) infection is a major risk for human pregnancy complications and fetal development and depends on an appropriate IFN- β response. However, it is poorly understood how ZIKV, despite an IFN- β response, causes miscarriages. We have uncovered a mechanism for this function specifically in the context of the early antiviral response. Our results demonstrate that IFN regulatory factor (IRF9) is critical in the early response to ZIKV infection in human trophoblast. This function is contingent on IRF9 binding to Twist1. In this signaling cascade, Twist1 was not only a required partner that promotes IRF9 binding to the IFN-stimulated response element but also an upstream regulator that controls basal levels of IRF9. The absence of Twist1 renders human trophoblast cells susceptible to ZIKV infection.

Contributions of musculoskeletal rehabilitation in patients after chikungunya fever: a systematic review.

Sales WB, Leite DG, Truta Ramalho CS, Macêdo SGGF, de Souza GF, Cavalcanti Maciel AC.

04-05-2023

BMC Musculoskelet Disord.

<https://pubmed.ncbi.nlm.nih.gov/37143009/>

Infection of the maternal-fetal interface and vertical transmission following low-dose inoculation of pregnant rhesus macaques (*Macaca mulatta*) with an African-lineage Zika virus.

Koenig MR, Mitzey AM, Morgan TK, Zeng X, Simmons HA, Mejia A, Leyva Jaimes F, Keding LT, Crooks CM,

Weiler AM, Bohm EK, Aliota MT, Friedrich TC, Mohr EL, Golos TG.

04-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37141276/>

Background: Congenital Zika virus (ZIKV) infection can result in birth defects, including malformations in the fetal brain and visual system. There are two distinct genetic lineages of ZIKV: African and Asian. Asian-lineage ZIKVs have been associated with adverse pregnancy outcomes in humans; however, recent evidence from experimental models suggests that African-lineage viruses can also be vertically transmitted and cause fetal harm.

Methodology/principal findings: To evaluate the pathway of vertical transmission of African-lineage ZIKV, we inoculated nine pregnant rhesus macaques (*Macaca mulatta*) subcutaneously with 44 plaque-forming units of a ZIKV strain from Senegal, (ZIKV-DAK). Dams were inoculated either at gestational day 30 or 45. Following maternal inoculation, pregnancies were surgically terminated seven or 14 days later and fetal and maternal-fetal interface tissues were collected and evaluated. Infection in the dams was evaluated via plasma viremia and neutralizing antibody titers pre- and post- ZIKV inoculation. All dams became productively infected and developed strong neutralizing antibody responses. ZIKV RNA was detected in maternal-fetal interface tissues (placenta, decidua, and fetal membranes) by RT-qPCR and in situ hybridization. In situ hybridization detected ZIKV predominantly in the decidua and revealed that the fetal membranes may play a role in ZIKV vertical transmission. Infectious ZIKV was detected in the amniotic fluid of three pregnancies and one fetus had ZIKV RNA detected in multiple tissues. No significant pathology was observed in any fetus; and ZIKV did not have a substantial effect on the placenta.

Conclusions/significance: This study demonstrates that a very low dose of African-lineage ZIKV can be vertically transmitted to the macaque fetus during pregnancy. The low inoculating dose used in this study suggests a low minimal infectious dose for rhesus macaques. Vertical transmission with a low dose in macaques further supports the high epidemic potential of African ZIKV strains.

Potential risk sites and their relationship with dengue cases, Campinas municipality, Southeast Brazil.

Mendes JA, Vanwambeke SO.

27-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37104540/>

Self-care practices and health-seeking behaviours in patients with dengue fever: A qualitative study from patients' and physicians' perspectives.

Ng WL, Toh JY, Ng CJ, Teo CH, Lee YK, Loo KK, Abdul Hadi H, Noor Azhar AM.

27-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37104529/>

TLR4 is one of the receptors for Chikungunya virus envelope protein E2 and regulates virus induced pro-inflammatory responses in host macrophages.

Mahish C, De S, Chatterjee S, Ghosh S, Keshry SS, Mukherjee T, Khamaru S, Tung KS, Subudhi BB, Chattopadhyay S, Chattopadhyay S.

Avr-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37153546/>

Toll like receptor 4 (TLR4), a pathogen-associated molecular pattern (PAMP) receptor, is known to exert inflammation in various cases of microbial infection, cancer and autoimmune disorders. However, any such involvement of TLR4 in Chikungunya virus (CHIKV) infection is yet to be explored. Accordingly, the role of TLR4 was investigated towards CHIKV infection and modulation of host immune responses in the current study using mice macrophage cell line RAW264.7, primary macrophage cells of different origins and *in vivo* mice model. The findings suggest that TLR4 inhibition using TAK-242 (a specific pharmacological inhibitor) reduces viral copy number as well as reduces the CHIKV-E2 protein level significantly using p38 and JNK-MAPK pathways. Moreover, this led to reduced expression of macrophage activation markers like CD14, CD86, MHC-II and pro-inflammatory cytokines (TNF, IL-6, MCP-1) significantly in both the mouse primary macrophages and RAW264.7 cell line, *in vitro*. Additionally, TAK-242-directed TLR4 inhibition demonstrated a significant reduction of percent E2-positive cells, viral titre and TNF expression in hPBMC-derived macrophages, *in vitro*. These observations were further validated in TLR4-knockout (KO) RAW cells. Furthermore, the interaction between CHIKV-E2 and TLR4 was demonstrated by immuno-precipitation studies, *in vitro* and supported by molecular docking analysis, *in silico*. TLR4-dependent viral entry was further validated by an anti-TLR4 antibody-mediated blocking experiment. It was noticed that TLR4 is necessary for the early events of viral infection, especially during the attachment and entry stages. Interestingly, it was also observed that TLR4 is not involved in the post-entry stages of CHIKV infection in host macrophages. The administration of TAK-242 decreased CHIKV infection significantly by reducing disease manifestations, improving survivability (around 75%) and reducing inflammation in mice model. Collectively, for the first time, this study reports TLR4 as one of the novel receptors to facilitate the attachment and entry of CHIKV in host macrophages, the TLR4-CHIKV-E2 interactions are essential for efficient viral entry and modulation of infection-induced pro-inflammatory responses in host macrophages, which might have translational implication for designing future therapeutics to regulate the CHIKV infection.

Perimyocarditis: An Unusual Manifestation of Dengue Virus Infection.

Ullah A, Khan S, Ahmad A, Irfan M, Majeed I.

04-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37153319/>

(R)-(+)-Rosmarinic Acid as an Inhibitor of Herpes and Dengue Virus Replication: an In Silico Assessment.

Samy CRA, Karunanithi K, Sheshadhri J, Rengarajan M, Srinivasan P, Cherian P.

2023

Rev Bras Farmacogn.

<https://pubmed.ncbi.nlm.nih.gov/37151219/>

Since ancient times, viruses such as dengue, herpes, Ebola, AIDS, influenza, chicken meat, and SARS have been roaming around causing great health burdens. Currently, the prescribed antiviral drugs have not cured the complications caused by viruses, whereas viral replication was not controlled by them. The treatments suggested are not only ineffectual, but also sometimes inefficient against viruses at all stages of the viral cycle as well. To fight against these contagious viruses, people rely heavily on medicinal plants to enhance their innate and adaptive immune systems. In this research, the preparation of ligands and proteins was performed using the Maestro V.13.2 module tool. This software, consisting of LigPrep, Grid Generation, SiteMap, and Glide XP, has each contributed significantly to the preparation of ligands and proteins. Ultimately, the research found that (R)-(+)-rosmarinic acid was found to have significant docking scores of - 10.847 for herpes virus, of - 10.033 for NS5, and - 7.259 for NS1. In addition, the Prediction of Activity Spectra for Substances (PASS) server indicates that rosmarinic acid possesses a diverse spectrum of enzymatic activities, as probability active (Pa) values start at > 0.751, whereas it has fewer adverse effects than the drugs prescribed for viruses. Accordingly, it was found the rate of acute toxicity values of (R)-(+)-rosmarinic acid at doses LD₅₀ log10 (mmol/g) and LD₅₀ (mg/g) in different routes of administration, such as intraperitoneal, intravenous, oral, and subcutaneous. Ultimately, the present study concluded that (R)-(+)-rosmarinic acid would expose significant antiviral effects in *in vitro* and *in vivo* experiments, and this research would be a valuable asset for the future, especially for those who wish to discover a drug molecule for a variety of viruses.

A Review of the Therapeutic Importance of Indole Scaffold in Drug Discovery.

Teraiya N, Agrawal K, Patel TM, Patel A, Patel S, Shah U, Shah S, Rathod K, Patel K.

05-05-2023

Curr Drug Discov Technol.

<https://pubmed.ncbi.nlm.nih.gov/37151073/>

Indole is known as a versatile heterocyclic building block for its multiple pharmacological activities and has a high probability of success in the race for drug candidates. Many natural products, alkaloids, and bioactive heterocycles contain indole as the active principle pharmacophore. These encourage the researchers to explore it as a lead in the drug development process. The current manuscript will serve as a torchbearer for understanding the structurally diverse class of indole derivatives with extensive pharmacological activity. The

current manuscript describes the intermediates and their functional groups responsible for superior biological activity compared to the standard. The review is written to help researchers to choose leads against their target but also to provide crucial insight into the design of a hybrid pharmacophore-based approach in drug design with enhanced potential. The present reviews on the indole derivatives correlate the structures with biological activities as well as essential pharmacophores, which were highlighted. The discussion was explored under challenging targets like dengue, chikungunya (anti-viral), antihypertensive, diuretic, immunomodulator, CNS stimulant, antihyperlipidemic, antiarrhythmic, anti-Alzheimer's, and neuroprotective, along with anticancer, antitubercular, antimicrobial, anti-HIV, antimalarial, anti-inflammatory, antileishmanial, anti-anthelmintic, and enzyme inhibitors. So, this review includes a discussion of 19 different pharmacological targets for indole derivatives that could be utilized to derive extensive information needed for ligand-based drug design. The article will guide the researchers in the selection, design of lead and pharmacophore, and ligand-based drug design using indole moiety.

Vitamin D modulates expression of antimicrobial peptides and proinflammatory cytokines to restrict Zika virus infection in macrophages.

Fernandez GJ, Ramírez-Mejía JM, Castillo JA, Urcuqui-Inchima S.

05-05-2023

Int Immunopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37150017/>

Density of *Aedes aegypti* (Diptera: Culicidae) in a low-income Brazilian urban community where dengue, Zika, and chikungunya viruses co-circulate.

Souza RL, Nazare RJ, Argibay HD, Pellizzaro M, Anjos RO, Portilho MM, Jacob-Nascimento LC, Reis MG, Kitron UD, Ribeiro GS.

06-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37149611/>

Host factor DUSP5 potently inhibits dengue virus infection by modulating cytoskeleton rearrangement.

Liang M, Li Y, Zhang K, Zhu Y, Liang J, Liu M, Zhang S, Chen D, Liang H, Liang L, An S, Zhu X, He Z.

04-05-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/37149044/>

Cytoskeleton has been reported to play an essential role in facilitating the viral life cycle. However, whether the host can exert its antiviral effects by modulating the cytoskeleton is not fully understood. In this study, we identified that host factor DUSP5 was upregulated after dengue virus (DENV) infection. In addition, we demonstrated that overexpression of DUSP5 remarkably inhibited DENV replication. Conversely, the depletion of

DUSP5 led to an increase in viral replication. Moreover, DUSP5 was found to restrain viral entry into host cells by suppressing F-actin rearrangement via negatively regulating the ERK-MLCK-Myosin IIB signaling axis. Depletion of dephosphorylase activity of DUSP5 abolished its above inhibitory effects. Furthermore, we also revealed that DUSP5 exhibited broad-spectrum antiviral effects against DENV and Zika virus. Taken together, our studies identified DUSP5 as a key host defense factor against viral infection and uncovered an intriguing mechanism by which the host exerts its antiviral effects through targeting cytoskeleton rearrangement.

Chikungunya in Brazil ... and beyond?

The Lancet Microbe.

Mai-2023

Lancet Microbe.

<https://pubmed.ncbi.nlm.nih.gov/37148895/>

The tick saliva peptide HIDfsin2 promotes the tick-borne virus SFTSV replication in vitro by enhancing p38 signal pathway.

Wang L, Sun F, Hu J, Zuo W, Zheng Y, Wu Y, Kwok HF, Cao Z.

06-05-2023

Arch Toxicol.

<https://pubmed.ncbi.nlm.nih.gov/37148319/>

Genetic structure of *Aedes albopictus* (Diptera: Culicidae) populations in China and relationship with the knockdown resistance mutations.

Shan W, Yuan H, Chen H, Dong H, Zhou Q, Tao F, Bai J, Chen H, Ma Y, Peng H.

05-05-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/37147696/>

Genetic characterization of dengue virus serotype 1 circulating in Reunion Island, 2019-2021, and the Seychelles, 2015-2016.

Hafsia S, Barbar T, Wilkinson DA, Atyame C, Biscornet L, Bibi J, Louange M, Gedeon J, De Santis O, Flahault A, Cabie A, Bertolotti A, Mavingui P.

05-05-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37147570/>

Background: An unprecedented increase in the number of cases and deaths reported from dengue virus (DENV) infection has occurred in the southwestern Indian ocean in recent years. From 2017 to mid-2021 more than 70,000 confirmed dengue cases were reported in Reunion Island, and 1967 cases were recorded in the Seychelles from 2015 to 2016. Both these outbreaks displayed similar trends, with the initial circulation of DENV-2 which was replaced by DENV-1. Here, we aim to determine the origin of the DENV-1 epidemic strains and to explore their genetic characteristics along the uninterrupted circulation,

particularly in Reunion. **Methods:** Nucleic acids were extracted from blood samples collected from dengue positive patients; DENV-1 was identified by RT-qPCR. Positive samples were used to infect VERO cells. Genome sequences were obtained from either blood samples or infected-cell supernatants through a combination of both Illumina or MinION technologies. **Results:** Phylogenetic analyses of partial or whole genome sequences revealed that all DENV-1 sequences from Reunion formed a monophyletic cluster that belonged to genotype I and were closely related to one isolate from Sri Lanka (OL752439.1, 2020). Sequences from the Seychelles belonged to the same major phylogenetic branch of genotype V, but fell into two paraphyletic clusters, with greatest similarity for one cluster to 2016-2017 isolate from Bangladesh, Singapore and China, and for the other cluster to ancestral isolates from Singapore, dating back to 2012. Compared to publicly available DENV-1 genotype I sequences, fifteen non-synonymous mutations were identified in the Reunion strains, including one in the capsid and the others in nonstructural proteins (NS) (three in NS1, two in NS2B, one in NS3, one in NS4B, and seven in NS5). **Conclusion:** In contrast to what was seen in previous outbreaks, recent DENV-1 outbreaks in Reunion and the Seychelles were caused by distinct genotypes, all likely originating from Asia where dengue is (hyper)endemic in many countries. Epidemic DENV-1 strains from Reunion harbored specific non-synonymous mutations whose biological significance needs to be further investigated.

The cytoplasmic N-terminal tail of Zika virus NS4A protein forms oligomers in the absence of detergent or lipids.

Surya W, Liu Y, Torres J.

05-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37147499/>

Molecular mimicry between Zika virus and central nervous system inflammatory demyelinating disorders: the role of NS5 Zika virus epitope and PLP autoantigens.

França LC, Fontes-Dantas FL, Garcia DG, de Araújo AD, da Costa Gonçalves JP, Rêgo CCDS, da Silva EV, do Nascimento OJM, Lopes FCR, Herlinger AL, de Aguiar RS, da Costa Ferreira Junior O, Figueira FFA, de Souza JPB, De Mesquita JF, Alves-Leon SV.

Avr-2023

Arq Neuropsiquiatr.

<https://pubmed.ncbi.nlm.nih.gov/37160141/>

Background: Evidence indicates a strong link between Zika virus (ZikV) and neurological complications. Acute myelitis, optic neuritis, polyneuropathy, and encephalomyelitis that mimic inflammatory idiopathic demyelination disorders (IIDD) after ZikV infection have been reported in Brazil.

Objective: The present study aims to investigate the possible occurrence of molecular mimicry between ZikV antigens and Multiple Sclerosis (MS) autoantigens, the most frequent IIDD of the central nervous system (CNS).

Methods: A retrospective cohort study with 305 patients

admitted due to suspected arbovirus infection in Rio de Janeiro was performed, all subjects were submitted to neurological examination, and a biological sample was collected for serologic and molecular diagnostic. Bioinformatics tools were used to analyze the peptides shared between ZikV antigens and MS autoantigens. **Results:** Of 305 patients, twenty-six were positive for ZikV and 4 presented IIDD patterns found in MS cases. Sequence homology comparisons by bioinformatics approach between NS5 ZikV and PLP MS protein revealed a homology of 5/6 consecutive amino acids (CSSVPV/CSAVPV) with 83% identity, deducing a molecular mimicry. Analysis of the 3D structures revealed a similar conformation with alpha helix presentation. **Conclusions:** Molecular mimicry between NS5 Zika virus antigen and PLP MS autoantigens emerge as a possible mechanism for IIDD spectrum in genetically susceptible individuals.

Perspectives on the current antiviral developments towards RNA-dependent RNA polymerase (RdRp) and methyltransferase (MTase) domains of dengue virus non-structural protein 5 (DENV-NS5).

Sreekanth GP.

28-04-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37159959/>

Dengue virus (DENV) infection is one of the most emerging arboviral infections in humans. DENV is a positive-stranded RNA virus in the Flaviviridae family consisting of an 11 kb genome. DENV non-structural protein 5 (DENV-NS5) constitutes the largest among the non-structural proteins, which act as two domains, the RNA-dependent RNA polymerase (RdRp) and RNA methyltransferase enzyme (MTase). The DENV-NS5 RdRp domain contributes to the viral replication stages, whereas the MTase initiates viral RNA capping and facilitates polyprotein translation. Given the functions of both DENV-NS5 domains have made them an important druggable target. Possible therapeutic interventions and drug discoveries against DENV infection were thoroughly reviewed; however, a current update on the therapeutic strategies specific to DENV-NS5 or its active domains was not attempted. Since most potential compounds and drugs targeting the DENV-NS5 were evaluated in both in vitro cultures and animal models, a more detailed evaluation of molecules/drug candidates still requires investigation in randomized controlled clinical trials. This review summarizes current perspectives on the therapeutic strategies adopted to target the DENV-NS5 (RdRp and MTase domains) at the host-pathogen interface and further discusses the directions to identify candidate drugs to combat DENV infection.

Zika Virus from the Perspective of Observational Studies: a Review.

Saleem T, Akhtar H, Jamal SB, Maryam F, Faheem M.

31-12-2022

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37159602/>

Background: Since 1952 when Zika Virus (ZIKV): a *Flavivirus*, was first discovered in humans, it has not received enough scientific research compared to some of the other members of the family *Flaviviridae*; like Dengue Virus (DENV). However, this has not stopped the virus from infecting the human population globally. In particular, the global spread of ZIKV has led to a surge in observational studies. **Methods:** Regarding recently published ZIKV-related literature, we are not aware of any reviews strictly focusing on ZIKV from the perspective of observational studies. Therefore, we reviewed recently published observational studies exploring the global spread of ZIKV and its association with Congenital ZIKV Infection (CZI) and clinical manifestations in adults. Online databases including google scholar, PubMed and Elsevier were used for retrieving relevant studies. **Results:** ZIKV cases have been reported in different parts of the world, with certain regions reporting more cases than the rest, like Brazil. ZIKV causes a wide spectrum of diseases and disorders including microcephaly, developmental disorders, and Guillain-Barre syndrome to name a few. Furthermore, CZI in neonates mainly manifests into neurological disorders and diseases, whereas ZIKV in adults' targets various organs. **Conclusion:** ZIKV poses a serious threat to human population and observational studies provide a different perspective on the damaging capabilities of ZIKV in real-life settings. Moreover, there are gaps in the literature regarding ZIKV-related-complications that future experimental studies need to address. These complications include in-utero transmission, Guillain-Barre syndrome, cross-reactivity, sexual transmission, along with its persistence in the male reproductive tract.

Predictors of Dengue Preventive Practices Based on Precaution Adoption Process Model among Health Care Professionals in Northwest of Iran.

Firoozian S, Sadeghi R, Sabouri M, Tol A, Rikhtehgar E, Fathi B, Sedaghat MM.

31-12-2022

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37159598/>

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

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

08-05-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37158835/>

El Niño Southern Oscillation (ENSO) effects on local weather, arboviral diseases, and dynamics of managed and unmanaged populations of *Aedes aegypti* (Diptera: Culicidae) in Puerto Rico.

Barrera R, Acevedo V, Amador M, Marzan M, Adams LE, Paz-Bailey G.

08-05-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37156093/>

We investigated the effects of interannual El Niño Southern Oscillation (ENSO) events on local weather, *Aedes aegypti* populations, and combined cases of dengue (DENV), chikungunya (CHIKV), and Zika (ZIKV) viruses in 2 communities with mass mosquito trapping and 2 communities without mosquito control in southern Puerto Rico (2013-2019). Gravid adult *Ae. aegypti* populations were monitored weekly using Autocidal Gravid Ovitrap (AGO traps). Managing *Ae. aegypti* populations was done using 3 AGO traps per home in most homes. There were drought conditions in 2014-2015 concurrent with the emergence of a strong El Niño (2014-2016), wetter conditions during La Niña (2016-2018), a major hurricane (2017), and a weaker El Niño (2018-2019). The main factor explaining differences in *Ae. aegypti* abundance across sites was mass trapping. Populations of *Ae. aegypti* reached maximum seasonal values during the wetter and warmer months of the year when arbovirus epidemics occurred. El Niño was significantly associated with severe droughts that did not impact the populations of *Ae. aegypti*. Arbovirus cases at the municipality level were positively correlated with lagged values (5-12 mo.) of the Oceanic El Niño Index (ONI), droughts, and abundance of *Ae. aegypti*. The onset of strong El Niño conditions in Puerto Rico may be useful as an early warning signal for arboviral epidemics in areas where the abundance of *Ae. aegypti* exceeds the mosquito density threshold value.

Viral Protein Accumulation of Zika Virus Variants Links with Regulation of Innate Immunity for Differential Control of Viral Replication, Spread, and Response to Interferon.

Lu AY, Gustin A, Newhouse D, Gale M Jr.

10-05-2023

J Virol.

<https://pubmed.ncbi.nlm.nih.gov/37162358/>

Primary infection of BALB/c mice with a dengue virus type 4 strain leads to kidney injury.

Rasinha ADC, Jácome FC, Caldas GC, de Almeida ALT, de Souza DDC, Dos Santos JPR, Dias HG, Araujo EL, Mohana-Borges R, Barth OM, Dos Santos FB, Barreto-Vieira DF.

08-05-2023

Mem Inst Oswaldo Cruz.

<https://pubmed.ncbi.nlm.nih.gov/37162062/>

Background: Dengue is a disease caused by dengue virus (DENV-1 through -4). Among the four serotypes, DENV-4 remains the least studied. Acute kidney injury is a potential complication of dengue generally associated with severe dengue infection. **Objectives:** The goal of this study was to investigate the alterations caused by experimental dengue infection in the kidney of adult BALB/c mice. **Methods:** In this study, BALB/c mice were infected through the intravenous route with a DENV-4 strain, isolated from a

human patient. The kidneys of the mice were procured and subject to histopathological and ultrastructural analysis. **Findings:** The presence of the viral antigen was confirmed through immunohistochemistry. Analysis of tissue sections revealed the presence of inflammatory cell infiltrate throughout the parenchyma. Glomerular enlargement was a common find. Necrosis of tubular cells and haemorrhage were also observed. Analysis of the kidney on a transmission electron microscope allowed a closer look into the necrotic tubular cells, which presented nuclei with condensed chromatin, and loss of cytoplasm. **Main conclusions:** Even though the kidney is probably not a primary target of dengue infection in mice, the inoculation of the virus in the blood appears to damage the renal tissue through local inflammation.

Bedside Severity Prediction Score for Predicting Severe Dengue in Children: A Shot in the Arm for Triaging Dengue Positive Children?

Dash N, Rose W.

15-05-2023

Indian Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37161953/>

Safety, tolerability and pharmacokinetics of JNJ-1802, a pan-serotype dengue direct antiviral small molecule, in a Phase 1, double-blind, randomized, dose-escalation study in healthy volunteers.

Ackaert O, Vanhoutte F, Verpoorten N, Buelens A, Lachau-Durand S, Lammens L, Hoetelmans R, Van Look M, Herrera-Taracena G.

10-05-2023

Clin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37161721/>

Mosquito densovirus significantly reduces the vector susceptibility to dengue virus serotype 2 in Aedes albopictus mosquitoes (Diptera: Culicidae).

Kong L, Xiao J, Yang L, Sui Y, Wang D, Chen S, Liu P, Chen XG, Gu J.

09-05-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/37161462/>

Background: Dengue virus (DENV) is a major public health threat, with Aedes albopictus being the confirmed vector responsible for dengue epidemics in Guangzhou, China. Mosquito densoviruses (MDVs) are pathogenic mosquito-specific viruses, and a novel MDV was previously isolated from Ae. albopictus in Guangzhou. This study aims to determine the prevalence of MDVs in wild Ae. albopictus populations and investigate their potential interactions with DENV and impact on vector susceptibility for DENV. **Methods:** The prevalence of MDV in wild mosquitoes in China was investigated using open access sequencing data and PCR detection in Ae. albopictus in Guangzhou. The

viral infection rate and titers in MDV-persistent C6/36 cells were evaluated at 12, 24, 48, 72, 96, and 120 h post infection (hpi) by indirect immunofluorescence assay (IFA) and real time quantitative PCR (RT-qPCR). The midgut infection rate (MIR), dissemination rate (DR), and salivary gland infection rate (SGIR) in various tissues of MDV-infected mosquitoes were detected and quantified at 0, 5, 10, and 15 days post infection (dpi) by RT-PCR and RT-qPCR. The chi-square test evaluated dengue virus serotype 2 (DENV-2) and Aedes aegypti densovirus (AaeDV) infection rates and related indices in mosquitoes, while Tukey's LSD and t-tests compared viral titers in C6/36 cells and tissues over time. **Results:** The results revealed a relatively wide distribution of MDVs in Aedes, Culex, and Anopheles mosquitoes in China and an over 68% positive rate. In vitro, significant reductions in DENV-2 titers in supernatant at 120 hpi, and an apparent decrease in DENV-2-positive cells at 96 and 120 hpi were observed. In vivo, DENV-2 in the ovaries and salivary glands was first detected at 10 dpi in both monoinfected and superinfected Ae. albopictus females, while MDV superinfection with DENV-2 suppressed the salivary gland infection rate at 15 dpi. DENV-2 titer in the ovary and salivary glands of Ae. albopictus was reduced in superinfected mosquitoes at 15 dpi. **Conclusions:** MDVs is widespread in natural mosquito populations, and replication of DENV-2 is suppressed in MDV-infected Ae. albopictus, thus reducing vector susceptibility to DENV-2. Our study supports the hypothesis that MDVs may contribute to reducing transmission of DENV and provides an alternative strategy for mosquito-transmitted disease control.

Dynamics and optimal control of a Zika model with sexual and vertical transmissions.

Huo HF, Fu T, Xiang H.

28-02-2023

Math Biosci Eng.

<https://pubmed.ncbi.nlm.nih.gov/37161197/>

Analysis of the correlation between climatic variables and Dengue cases in the city of Alagoinhas/BA.

Figueredo MB, Monteiro RLS, do Nascimento Silva A, de Araújo Fontoura JR, da Silva AR, Alves CAP.

09-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37160928/>

SARS-CoV-2 N protein enhances the anti-apoptotic activity of MCL-1 to promote viral replication.

Pan P, Ge W, Lei Z, Luo W, Liu Y, Guan Z, Chen L, Yu Z, Shen M, Hu D, Xiang Q, Wang W, Wan P, Tian M, Yu Y, Luo Z, Chen X, Xiao H, Zhang Q, Liang X, Chen X, Li Y, Wu J.

09-05-2023

Signal Transduct Target Ther.

<https://pubmed.ncbi.nlm.nih.gov/37160897/>

Viral infection in respiratory tract usually leads to cell death, impairing respiratory function to cause severe disease. However, the diversity of clinical manifestations of SARS-CoV-2 infection increases the complexity and difficulty of viral infection prevention, and especially the high-frequency asymptomatic infection increases the risk of virus transmission. Studying how SARS-CoV-2 affects apoptotic pathway may help to understand the pathological process of its infection. Here, we uncovered SARS-CoV-2 employed a distinct anti-apoptotic mechanism via its N protein. We found SARS-CoV-2 virus-like particles (trVLP) suppressed cell apoptosis, but the trVLP lacking N protein didn't. Further study verified that N protein repressed cell apoptosis in cultured cells, human lung organoids and mice. Mechanistically, N protein specifically interacted with anti-apoptotic protein MCL-1, and recruited a deubiquitinating enzyme USP15 to remove the K63-linked ubiquitination of MCL-1, which stabilized this protein and promoted it to hijack Bak in mitochondria. Importantly, N protein promoted the replications of IAV, DENV and ZIKV, and exacerbated death of IAV-infected mice, all of which could be blocked by a MCL-1 specific inhibitor, S63845. Altogether, we identified a distinct anti-apoptotic function of the N protein, through which it promoted viral replication. These may explain how SARS-CoV-2 effectively replicates in asymptomatic individuals without causing respiratory dysfunction, and indicate a risk of enhanced coinfection with other viruses. We anticipate that abrogating the N/MCL-1-dominated apoptosis repression is conducive to the treatments of SARS-CoV-2 infection as well as coinfections with other viruses.

Author Correction: The 8-bromobaicalein inhibited the replication of dengue, and Zika viruses and targeted the dengue polymerase.

Boonyasuppayakorn S, Saelee T, Huynh TNT, Hairani R, Hengphasatporn K, Loeanurit N, Cao V, Vibulakhaophan V, Siripitakpong P, Kaur P, Chu JJH, Tunghirun C, Choksupmanee O, Chimnaronk S, Shigeta Y, Rungrotmongkol T, Chavasiri W.

11-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37169861/>

Dataset on biochemical inhibiting activities of selected phytochemicals in *Azadirachta indica* L as potential NS2B-NS3 proteases inhibitors.

Oyebamiji AK, Akintelu SA, Akande IO, Aworinde HO, Adepegba OA, Akintayo ET, Akintayo CO, Semire B, Babalola JO.

18-04-2023

Data Brief.

<https://pubmed.ncbi.nlm.nih.gov/37168603/>

The anti-NS2B-NS3 proteases activities of *Azadirachta indica* L. were investigated via the data obtained from selected bioactive compounds from *Azadirachta indica* L. The work was investigated using *insilico* approach and the series of computational software were used to execute the

task. The software used were Spartan 14, material studio, Padel, Pymol, Autodock tool, Autodock vina and discovery studio. The obtained descriptors from 2D and 3D of the optimized compounds were screened and they were used to develop QSAR model using material studio software. Also, biological interaction between the selected bioactive compounds from *Azadirachta indica* L. and NS2B-NS3 proteases (PDB ID: 2fom) were accomplished using docking method and the calculated binding affinity as well as the residues involved in the interaction were reported. More so, the ADMET features for [(5S,6R,7S,8R,9S,10R,11S,12R,13S,17R)-17-(2,5-dihydroxy-2,5-dihydrofuran-3-yl)-11,12-dihydroxy-6-methoxy-4,4,8,10,13-pentamethyl-1,16-dioxo-6,7,9,11,12,17-hexahydro-5H-cyclopenta[a]phenanthren-7-yl] 3-methylbut-2-enoate (Compound 6) and (10R,13S,14S,17S)-17-[1-(3,4-dihydroxy-5,5-dimethyloxolan-2-yl)ethyl]-4,4,10,13,14-pentamethyl-1,2,5,6,9,11,12,15,16,17-decahydrocyclopenta[a]phenanthren-3-one (compound 12) with lowest binding affinity were investigated and reported.

First introduction of dengue virus type 3 in Niger, 2022.

Lagare A, Faye M, Fintan G, Fall G, Ousmane H, Ibrahim ET, Diagne MM, Amadou S, Sankhe S, Ibrahim L, Seini H, Faye O, Jambou R.

07-04-2023

IJID Reg.

<https://pubmed.ncbi.nlm.nih.gov/37168517/>

Age-dependence of susceptibility to single and repeated deltamethrin exposure in pyrethroid-resistant *Aedes aegypti* strains.

Al Nazawi AM, Weetman D.

14-04-2023

Curr Res Parasitol Vector Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37168454/>

Spatial repellency and attractancy responses of some chemical lures against *Aedes albopictus* (Diptera: Culicidae) and *Anopheles minimus* (Diptera: Culicidae) using the high-throughput screening system.

Boonyuan W, Tisgratog R, Ahebwa A, Leepasert T, Thanispong K, Chareonviriyaphap T.

11-05-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37167551/>

We evaluated the behavioral responses of *Aedes albopictus* and *Anopheles minimus* to 3 isovaleric acid and lactic acid-based chemical lure blends and 2 individual alcohols, using Spatial Repellency Assay in a high-throughput screening system (HITSS). Five doses of 0.0002, 0.001, 0.0025, 0.005, and 0.01 g were tested per lure. A BG-lure was used as a reference standard. After 10-min exposure, the number of mosquitoes moving toward or away from the treated chamber was calculated. The

results showed that all lures were repellent against *Ae. albopictus* except for Lure-4 (4% w/v isovaleric acid + 2% w/v lactic acid + 0.0025% w/v myristic acid + 2.5% w/v ammonium hydroxide) which showed a nonsignificant attractancy at the lowest dose. Significantly high spatial repellency was observed at the highest dose of all the tested lures including BG-lure. Lure-2 (isoamyl alcohol) was significantly repellent at all the tested doses. Against *An. minimus*, Lure-5 (0.02% w/v isovaleric acid + 2% w/v lactic acid) showed significant spatial repellency while Lure-4 was significantly attractant, at all the tested doses. All lures, except Lure-4, showed strong spatial repellency at high doses and attractancy or weak spatial repellency at the lowest dose of 0.0002 g. In summary, our study demonstrated that spatial repellency and attractancy of the tested lures were influenced by both the dose tested and the mosquito species. Lure-2 and Lure-4 are potential spatial repellents and attractants, respectively, for malaria and dengue vectors. However, further studies are necessary to confirm these results at a semifield and open field level.

Mapping the distribution and trends of co-circulating dengue virus serotypes in Odisha, India: A retrospective facility-based analysis.

Labala S, Sinha A, Panda S, Turuk J, Pati S, Sahoo PK.

Nov-Dec 2023

Natl Med J India.

<https://pubmed.ncbi.nlm.nih.gov/37167511/>

Background Dengue, caused by mosquito bite, is an emerging disease of international concern. Evidence regarding the prevalent dengue serotypes is scarce, but essential for its management during the outbreaks. Hence, we mapped the distribution and trends of currently prevalent dengue virus (DENV) serotypes in Odisha. **Methods** We conducted a facility-based retrospective study from referral samples sent for the diagnosis/confirmation of dengue in 2018. The samples were serologically tested for enzyme-linked immunosorbent assay (ELISA) IgM antibody and NS1. Only NS1-positive samples were chosen for sero-typing. A pool of 8-10 NS1-positive samples were analysed for district-wise serotypes. Ribonucleic acid extraction and nested polymerase chain reaction (PCR) was done from NS1-positive samples. The PCR products were then subjected to gel electrophoresis. **Results** A total of 2892 samples were screened for dengue virus across various districts of Odisha where 763 samples were found to be NS1-positive. Thirteen of 18 districts covering all topographies of Odisha predominantly had DENV2 serotype. Only few districts such as Balangir, Kalahandi and Rayagada had mixed serotypes. **Conclusion** Although DENV2 is predominantly prevalent, mixed serotypes too exist in Odisha. Evidence based on variations of dengue serotypes across topographies, seasons, gender and age groups may support public health efforts in preventing the disease.

[El programa del manejo integrado de vectores en el marco de la pandemia por COVID-19 en Medellín, Colombia].

Rojo-Ospina RA, Quimbayo-Forero M, Calle-Tobón A, Bedoya-Patiño SC, Gómez M, Ramírez A, Sánchez J, Silva-Alzate JF, Montes-Zuluaga CJ, Cadavid JM, Henao-Correa EA.

30-03-2023

Biomedica.

<https://pubmed.ncbi.nlm.nih.gov/37167464/>

[The experience in treatment of dengue fever using antiviral drug riamilovir in the Republic of Guinea (case report)].

Maltsev OV, Kasyanenko KV, Zhdanov KV, Malyshev NA, Kolomoets EV, Konomou VK.

24-02-2023

Ter Arkh.

<https://pubmed.ncbi.nlm.nih.gov/37167119/>

Dengue fever is classified as one of the most common viral diseases with a transmission mechanism implemented through arthropod vectors. The expansion of the *Aedes aegypti* mosquito is leading to a significant increase in the number of cases of dengue fever in more than 100 countries, highlighting the importance of developing and implementing specific prevention and treatment measures. Etiotropic drugs with proven efficacy against the pathogen are not registered, and the use of the vaccine is approved only among seropositive individuals. In this regard, pathogenetic treatment remains the main therapeutic strategy, however, work on the synthesis of antiviral drugs is being actively carried out. Due to the unique functions of non-structural proteins NS3 and NS5 in the viral replication cycle, they have become the main targets for studying the antiviral activity of a number of chemotherapy drugs. Of these proteins, due to the most conserved structure, the NS5 protein is a promising target for inhibition, however, success in obtaining a clinical effect using a number of available antiviral drugs has not been reached. This study describes the positive experience of using the nucleoside analogue riamilovir in the treatment of a patient with dengue fever in the Republic of Guinea.

Co-infection of dengue and Zika viruses mutually enhances viral replication in the mosquito *Aedes aegypti*.

Lin DC, Weng SC, Tsao PN, Chu JH, Shiao SH.

11-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37165438/>

Background: The mosquito *Aedes aegypti* transmits two of the most serious mosquito-borne viruses, dengue virus (DENV) and Zika virus (ZIKV), which results in significant human morbidity and mortality worldwide. The quickly shifting landscapes of DENV and ZIKV endemicity worldwide raise concerns that their co-circulation through the *Ae. aegypti* mosquito vector could greatly exacerbate the disease burden in humans. Recent reports have indicated an increase in the number of co-infection cases in expanding co-endemic regions; however, the impact of co-infection on viral infection and the detailed molecular mechanisms remain to be defined. **Methods:** C6/36 (*Aedes albopictus*) cells were cultured in Dulbecco's modified

Eagle medium/Mitsubishi and Maramorosch Insect Medium (DMEM/MM) (1:1) containing 2% heat-inactivated fetal bovine serum and 1x penicillin/streptomycin solution. For virus propagation, the cells were infected with either DENV serotype 2 (DENV2) strain 16681 or ZIKV isolate Thailand/1610acTw (MF692778.1). Mosquitoes (*Ae. aegypti* UGAL [University of Georgia Laboratory]/Rockefeller strain) were orally infected with DENV2 and ZIKV through infectious blood-feeding. **Results:** We first examined viral replication activity in cells infected simultaneously, or sequentially, with DENV and ZIKV, and found interspecies binding of viral genomic transcripts to the non-structural protein 5 (NS5). When we challenged *Ae. aegypti* mosquitoes with both DENV2 and ZIKV sequentially to probe similar interactions, virus production and vector susceptibility to infection were significantly enhanced. **Conclusions:** Our results suggest that DENV2 and ZIKV simultaneously establishing infection in the *Ae. aegypti* mosquito vector may augment one another during replication. The data also implicate the homologous NS5 protein as a key intersection between the flaviviruses in co-infection, highlighting it as a potential target for vector control.

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

Singhal T.

11-05-2023

Indian J Pediatr.

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

Projecting future risk of dengue related to hydrometeorological conditions in mainland China under climate change scenarios: a modelling study.

Li C, Liu Z, Li W, Lin Y, Hou L, Niu S, Xing Y, Huang J, Chen Y, Zhang S, Gao X, Xu Y, Wang C, Zhao Q, Liu Q, Ma W, Cai W, Gong P, Luo Y.

Mai-2023

Lancet Planet Health.

<https://pubmed.ncbi.nlm.nih.gov/37164516/>

RNA interference to combat the Asian tiger mosquito in Europe: A pathway from design of an innovative vector control tool to its application.

Müller R, Bálint M, Hards K, Hollert H, Klimpel S, Knorr E, Kochmann J, Lee KZ, Mehring M, Pauls SU, Smets G, Steinbrink A, Vilcinskis A.

08-05-2023

Biotechnol Adv.

<https://pubmed.ncbi.nlm.nih.gov/37164239/>

A Zika virus protein expression screen in *Drosophila* to investigate targeted host pathways during development.

Link N, Harnish JM, Hull B, Gibson S, Dietze M, Mgbike UE, Medina-Balcazar S, Shah PS, Yamamoto S.

29-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37163061/>

In the past decade, Zika virus (ZIKV) emerged as a global public health concern. While adult infections are typically mild, maternal infection can lead to adverse fetal outcomes. Understanding how ZIKV proteins disrupt development can provide insights into the molecular mechanisms of symptoms caused by this virus including microcephaly. In this study, we generated a toolkit to ectopically express Zika viral proteins *in vivo* in *Drosophila melanogaster* in a tissue-specific manner using the GAL4/UAS system. We use this toolkit to identify phenotypes and host pathways targeted by the virus. Our work identified that expression of most ZIKV proteins cause scorable phenotypes, such as overall lethality, gross morphological defects, reduced brain size, and neuronal function defects. We further use this system to identify strain-dependent phenotypes that may contribute to the increased pathogenesis associated with the more recent outbreak of ZIKV in the Americas. Our work demonstrates *Drosophila*'s use as an efficient *in vivo* model to rapidly decipher how pathogens cause disease and lays the groundwork for further molecular study of ZIKV pathogenesis in flies.

Targeting Sex Determination to Suppress Mosquito Populations.

Akbari O, Li M, Kandul N, Sun R, Yang T, Benetta ED, Brogan D, Antoshechkin I, C HS, Zhan YP, DeBeaubien N, Loh Y, Su M, Montell C, Marshall J.

24-04-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37162925/>

Each year, hundreds of millions of people are infected with arboviruses such as dengue, yellow fever, chikungunya, and Zika, which are all primarily spread by the notorious mosquito *Aedes aegypti*. Traditional control measures have proven insufficient, necessitating innovations. In response, here we generate a next generation CRISPR-based precision-guided sterile insect technique (pgSIT) for *Aedes aegypti* that disrupts genes essential for sex determination and fertility, producing predominantly sterile males that can be deployed at any life stage. Using mathematical models and empirical testing, we demonstrate that released pgSIT males can effectively compete with, suppress, and eliminate caged mosquito populations. This versatile species-specific platform has the potential for field deployment to control wild populations, safely curtailing disease transmission.

Dracunculose

Protective effects of Typhonii Rhizoma in rheumatoid arthritis rats revealed by integrated metabolomics and network pharmacology.

Zhang X, Wang B, Chen S, Fu Y.

09-05-2023

Biomed Chromatogr.

<https://pubmed.ncbi.nlm.nih.gov/37161606/>

Loss of ancestral function in duckweed roots is accompanied by progressive anatomical reduction and a re-distribution of nutrient transporters.

Ware A, Jones DH, Flis P, Chrysanthou E, Smith KE, Kümpers BMC, Yant L, Atkinson JA, Wells DM, Bhosale R, Bishopp A.

08-05-2023

Curr Biol.

<https://pubmed.ncbi.nlm.nih.gov/36990089/>

Transport and removal mechanism of benzene by *Tradescantia zebrina* Bosse and *Epipremnum aureum* (Linden ex André) G.S. Bunting in air-plant-solution system.

Li X, Hu Y, Li D, Su Y.

Avr-2023

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/36977874/>

Phytoremediation is considered an effective method for indoor air pollution control. The removal rate and mechanism of benzene in air by two plants, *Tradescantia zebrina* Bosse and *Epipremnum aureum* (Linden ex André) G. S. Bunting, were investigated through fumigation experiments under the condition of plant hydroponics culturing. Results showed that the plant removal rates increased with increase in benzene concentration in air. When the benzene concentration in air was set at 432.25-1314.75 mg·m⁻³, the removal rates of *T. zebrina* and *E. aureum* ranged from 23.05 ± 3.07 to 57.42 ± 8.28 mg·kg⁻¹·h⁻¹ FW and from 18.82 ± 3.73 to 101.58 ± 21.20 mg·kg⁻¹·h⁻¹ FW, respectively. The removal capacity was positively related to the transpiration rate of plants, indicating that gas exchange rate could be a key factor for the evaluation of removal capacity. There existed fast reversible transport of benzene on air-shoot interface and root-solution interface. After shoot exposure to benzene for 1 h, downward transport was the dominant mechanism in the removal of benzene in air by *T. zebrina*, while in vivo fixation was the dominant mechanism at exposure time of 3 and 8 h. Within 1-8 h of shoot exposure time, in vivo fixation capacity was always the key factor affecting the removal rate of benzene in the air by *E. aureum*. Contribution ratio of in vivo fixation in the total benzene removal rate increased from 6.29 to 92.29% for *T. zebrina* and from 73.22 to 98.42% for *E. aureum* in the experimental conditions. Reactive oxygen species (ROS) burst induced by benzene exposure was responsible for the contribution ratio change of different mechanisms in the total removal rate, which also was verified by the change of activities of antioxidant enzymes (CAT, POD, and SOD). Transpiration rate and antioxidant enzyme activity could be considered parameters to evaluate the plant removal ability to benzene and to screen plants for establishment of plant-microbe combination technology.

Echinococcoses

Surgical Procedure and Perioperative Management of a Giant Orbital Echinococcus Cyst during and after Pregnancy.

Fränkl BCB, Chaloupka K.

Avr-2023

Klin Monbl Augenheilkd.

<https://pubmed.ncbi.nlm.nih.gov/37164424/>

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

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

10-05-2023

Infect Immun.

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

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

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

14-04-2023

Parasitology.

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

Molecular characterization and serodiagnostic evaluation of the *Echinococcus ortleppi* recombinant glutaredoxin 1 protein for cystic echinococcosis in buffalo (*Bubalus bubalis*).

Yashica KA, Samanta S, Balaji R, Jawalagatti V, Silamparasan M, Anandu S, Rialch A, Gupta SC, Tewari AK.

02-05-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37156090/>

Cystic echinococcosis (CE), caused by the metacestode of *Echinococcus granulosus sensu lato* (s.l.), adversely affects the physiology of the vital organs in which they grow. Condemnation of meat causes substantial economic loss to the livestock industry. Conventionally the infection is detected by necropsy as serological diagnosis of the infection in livestock is ambiguous. Identification of specific diagnostic antigens would be a substitute for the cyst fluid antigens which lack adequate diagnostic sensitivity and specificity. BLAST analysis supported by the negligible pairwise nucleotide distance of the 389 nt COX1, 489 nt NAD1, and 425 nt ITS1 with the related sequences of *E. ortleppi* ascertained the association of *E. ortleppi* with

CE in buffaloes. Given the extensive distribution of glutaredoxin 1 in every developmental stage of *Echinococcus granulosus* s.l that makes it an ideal serodiagnostic antigen for CE, we expressed the 14 kDa E. orteppi glutaredoxin 1 (rEoGrx1) protein in E. coli BL21 (DE3) and tested a total of 225 sera samples, including 126 sera samples from the necropsy-positive buffalo, by the rEoGrx1 IgG-ELISA. The ELISA could detect a total of 82/126 sera samples as positive. The diagnostic sensitivity and specificity of the rEoGrx1 IgG-ELISA were 65.1 % and 51.5 %, respectively. The protein showed serological cross-reaction against *Fasciola gigantica*, *Toxoplasma gondii*, and *Sarcocystis* sp. The in silico bioinformatics analysis of the E. orteppi, F. gigantica, and T. gondii glutaredoxin sequences revealed fully conserved amino acids at positions 11 and 21, the substitution of conserved amino acids at positions 14 and 6, and semi-conserved substitutions at positions 3 and 4, respectively. The findings partly explain the molecular basis of the serological cross-reactivity of the protein.

NIR-II fluorescence microscopic bioimaging for intrahepatic angiography and the early detection of *Echinococcus multilocularis* microlesions.

Alifu N, Yan T, Li J, Zhu L, Aini A, Amuti S, Wu J, Qi W, Guo G, Zhang W, Zhang X.

19-04-2023

Front Bioeng Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37152649/>

Hepatic alveolar echinococcosis (HAE) is caused by the metacestode of *Echinococcus multilocularis*, which shows characteristics of malignant tumors with high mortality. However, traditional diagnostic imaging methods are still not sufficient for the recognition of HAE microlesions in the early stages. Near-infrared-II (900-1700 nm, NIR-II) fluorescence microscopic imaging (NIR-II-FMI) has shown great potential for biomedical detection. A novel type of negative target imaging method based on NIR-II-FMI with the assistance of indocyanine green (ICG) was explored. Then, NIR-II-FMI was applied to the early detection of HAE for the first time. The negative targeting NIR-II fluorescence imaging of HAE-infected mice at different stages with the assistance of ICG under 808 nm of laser irradiation was obtained. Especially, HAE microlesions at the early stage were detected clearly. Moreover, clear intrahepatic angiography was achieved under the same NIR-II-FMI system.

Precordial pain induced by the isolated cardiac hydatid cyst in interventricular septum: a case report.

Li T, Ling Y, Qian Y.

06-05-2023

J Cardiothorac Surg.

<https://pubmed.ncbi.nlm.nih.gov/37149618/>

Background: Human hydatid disease occurs after infection with *Echinococcus granulosus*, mainly involves liver and lung, while hydatid involves heart is infrequent. A great majority of hydatid diseases could be asymptomatic, and incidentally found through examination. Here, we

reported a woman who suffered an isolated cardiac hydatid cyst located at the interventricular septum. **Case presentation:** A 48-year-old woman presented intermittent chest pain was admitted to the hospital. Imaging examination revealed a cyst located at the interventricular septum near the right ventricular apex. Considering medical history, radiological findings and serological results, cardiac hydatid disease was suspected. The cyst was successfully removed, while pathological biopsy confirmed the diagnosis of infection of *Echinococcus granulosus*. Postoperative course was uneventful, the patient was discharged from hospital without complications. **Conclusion:** For symptomatic cardiac hydatid cyst, surgical resection is necessary to avoid progression of disease. During surgical procedure, appropriate methods to reduce the potential risk of hydatid cyst metastasis are essential. Besides surgery, combined with regular drug therapy is an effective strategy to prevent reappearance.

Complete mitochondrial exploration of *Echinococcus multilocularis* from French alveolar echinococcosis patients.

Bohard L, Lallemand S, Borne R, Courquet S, Bresson-Hadni S, Richou C, Millon L, Bellanger AP, Knapp J.

04-05-2023

Int J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37148987/>

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

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

06-05-2023

Parasitol Res.

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

EgSeverin and Eg14-3-3zeta from *Echinococcus granulosus* are potential antigens for serological diagnosis of echinococcosis in dogs and sheep.

Zhang X, Wei C, Lv Y, Mi R, Guo B, Rahman SU, Zhang Y, Cheng L, Jia H, Huang Y, Han X, Gong H, Chen Z.

Juin-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37060967/>

Cystic echinococcosis (CE) is a zoonotic parasitic disease caused by the metacestode larva of *Echinococcus granulosus*. In this study, two-dimensional gel electrophoresis (2-DE) coupled with immunoblot analysis revealed that E. granulosus severin and 14-3-3zeta proteins (named EgSeverin and Eg14-3-3zeta, respectively) might be two potential biomarkers for serological diagnosis of echinococcosis. The recombinant EgSeverin (rEgSeverin, 45 kDa) and Eg14-3-3zeta (rEg14-3-3zeta, 35 kDa) were administered subcutaneously to BALB/c mice to obtain polyclonal antibodies for immunofluorescence analyses (IFAs). And IFAs showed that both proteins were located on the surface of

protoscoleces (PSCs). Western blotting showed that both proteins could react with sera from *E. granulosus*-infected sheep, dog, and mice. Indirect ELISAs (rEgSeverin- and rEg14-3-3zeta-iELISA) were developed, respectively, with sensitivities and specificities ranging from 83.33% to 100% and a coefficient of variation (CV %) of less than 10%. The rEgSeverin-iELISA showed cross-reaction with both *E. granulosus* and *E. multilocularis*, while the rEg14-3-3zeta-iELISA showed no cross-reaction with other sera except for the *E. granulosus*-infected ones. The field sheep sera from Xinjiang and Qinghai were analyzed using rEgSeverin-iELISA, rEg14-3-3zeta-iELISA, and a commercial kit respectively, and no significant differences were found among the three methods ($p > 0.05$). However, the CE positive rates in sheep sera from Qinghai were significantly higher than those from Xinjiang ($p < 0.01$). Overall, the results suggest that EgSeverin and Eg14-3-3zeta could be promising diagnostic antigens for *E. granulosus* infection.

Response of wild rodents to red fox feces: implication for the echinococcus infection.

Sasaki R, Okuma I, Asari Y.

03-05-2023

J Vet Med Sci.

<https://pubmed.ncbi.nlm.nih.gov/36990791/>

Inhibition of mouse colon cancer growth following immunotherapy with a fraction of hydatid cyst fluid.

Rostamirad S, Daneshpour S, Mofid MR, Andalib A, Eskandariyan A, Mousavi S, Yousofi Darani H.

Juin-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36931383/>

Background: Hydatid cyst is the larval stage of the tape worm *Echinococcus granulosus* which is located in human and livestock viscera. There are some scientific evidences indicating that parasitic infections induce antitumor activity against certain types of cancers. In this study, the effects of a fraction of hydatid cyst fluid on colon cancer tumor in BALB/c mice were investigated. **Materials and methods:** In this experimental work six groups of mice were challenged with mouse colon cancer cells. 5 days later when the sign of tumor growth in mice was seen, group 1-4 were injected with hydatid cyst fluid, the 78 kDa fraction, live protoscolices and BCG respectively. Group five was injected with alum alone and the sixth group left intact without any injection. The size of the tumor was measured and compared in all groups. Then blood samples of mice were evaluated for serum cytokine levels. **Result:** In mice injected with hydatid cyst antigens especially a fraction of hydatid cyst fluid, tumor size was smaller than the that of control groups and the difference of tumor size in cases and control groups was statistically significant. **Conclusion:** The results of this study showed that injection of mice with a fraction of hydatid cyst fluid significantly inhibits the growth of mouse colon cancer and this inhibition may be related to effect of immune response to these antigens.

Investigating intermediate hosts of Echinococcus multilocularis throughout Turkey: Focus on voles.

Gürler AT, Demirtaş S, Bölükbaş CS, Gençay EB, Barılı Ö, Karaca E, Akçay A, Açıcı M, Umur Ş, Deplazes P.

Juin-2023

Zoonoses Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36855863/>

Alveolar echinococcosis (AE), caused by *Echinococcus multilocularis*, is one of the most important zoonotic diseases. The parasite has a heterogeneous life cycle; more than 40 small mammal species have been determined to be potential intermediate hosts worldwide. Turkey is one of the highest endemic countries for AE, but only limited information is available concerning the transmission biology of *E. multilocularis*. The study aimed to provide data on potential intermediate host species (focus on genus *Microtus*) across Turkey involved in *E. multilocularis* transmission to foxes, which is a risk for public health. Trapping sites have been specially selected considering field voles' habitats and ecological requirements. In total, 843 rodents were collected from 141 locations. The metacestodes and lesions of AE were identified as macroscopy and microscopy and confirmed by PCR and DNA sequencing. Seventeen (2.0%) small mammals from 13 (9.2%) locations were found infected with *E. multilocularis*. Infected individuals were identified as *Microtus irani*, *Microtus mystacinus*, *Microtus hartingi*, *Microtus guentheri*, *Cricetulus migratorius* and *Mus macedonicus*. *M. hartingi* and *M. macedonicus* are documented for the first time as intermediate hosts of *E. multilocularis*. In conclusion, 15 of 17 infected small mammals were found in the *Microtus* genus. Therefore, the genus *Microtus*, which inhabits fields near villages and is potential prey for foxes, could be considered an important intermediate host for *E. multilocularis* across Turkey.

Echinococcus multilocularis protoscoleces enhance glycolysis to promote M2 Macrophages through PI3K/Akt/mTOR Signaling Pathway.

Zhang T, Zhang Y, Yang Z, Jiang Y, Sun L, Huang D, Tian M, Shen Y, Deng J, Hou J, Ma Y.

Juin-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/35876088/>

Filariose lymphatique

The development, implementation, and evaluation of an optimal model for the case detection, referral, and case management of Neglected Tropical Diseases.

Godwin-Akpan TG, Chowdhury S, Rogers EJ, Kollie KK, Zaizay FZ, Wickenden A, Zawolo GVK, Parker CBMC, Dean L.

10-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37163515/>

Background: People affected by Neglected Tropical Diseases (NTDs), specifically leprosy, Buruli ulcer (BU), yaws, and lymphatic filariasis, experience significant delays in accessing health services, often leading to catastrophic physical, psychosocial, and economic consequences. Global health actors have recognized that Sustainable Development Goal 3:3 is only achievable through an integrated inter and intra-sectoral response. This study evaluated existing case detection and referral approaches in Liberia, utilizing the findings to develop and test an Optimal Model for integrated community-based case detection, referral, and confirmation. We evaluate the efficacy of implementing the Optimal Model in improving the early diagnosis of NTDs, thus minimizing access delays and reducing disease burden. **Methods:** We used a participatory action research approach to develop, implement, and evaluate an Optimal Model for the case detection, referral, and management of case management NTDs in Liberia. We utilized qualitative and quantitative methods throughout the cycle and implemented the model for 12 months. **Results:** During the implementation of our optimal model, the annual number of cases detected increased compared to the previous year. Cases were detected at an earlier stage of disease progression, however; gendered dynamics in communities shape the case identification process for some individuals. Qualitative data showed increased knowledge of the transmission, signs, symptoms, and management options among community health workers (CHW). **Conclusion:** The results provide evidence of the benefits of an integrated approach and the programmatic challenges to improve access to health services for persons affected by NTDs. The effectiveness of an integrated approach depends on a high level of collaboration, joint planning, and implementation embedded within existing health systems infrastructure.

Safety of integrated mass drug administration of azithromycin, albendazole and ivermectin versus standard treatment regimens: a cluster-randomised trial in Ethiopia.

McPherson S, Tafese G, Tafese T, Behaksra SW, Solomon H, Oljira B, Miecha H, Debebe KA, Kebede B, Gebre T, Kebede F, Seife F, Tadesse F, Mammo B, Aseffa A, Solomon AW, Mabey DCW, Marks M, Gadisa E.

27-05-2023

EClinicalMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37152362/>

First genome-wide association study for lymphatic filariasis in a West African population points to an HLA-mediated disease pathophysiology.

Grover S, Opoku VS, Debrah LB, Maj C, Osei-Mensah J, Mensah DA, Hoerauf A, Debrah AY, Schumacher J, Pfarr K.

03-05-2023

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37146673/>

How well do coverage surveys and programmatically reported mass drug administration coverage match? Results from 214 mass drug administration campaigns in 15 countries, 2008-2017.

Zoerhoff KL, Mbabazi PS, Gass K, Kraemer J, Fuller BB, Blair L, Bougma R, Meite A, Negussu N, Gashaw B, Nash SD, Biritwum NK, Lemoine JF, Uliyartha Pangaribuan H, Wijayanti E, Kollie K, Rasoamananjana CF, Juziwele L, Mkwanda S, Rimal P, Gnanou I, Diop B, Dorkenoo AM, Bronzan R, Tukahebwa EM, Kabole F, Yevstigneyeva V, Bisanzio D, Courtney L, Koroma J, Endayishimye E, Reithinger R, Baker MC, Fleming FM.

Mai-2023

BMJ Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37142297/>

Introduction: Delivering preventive chemotherapy through mass drug administration (MDA) is a central approach in controlling or eliminating several neglected tropical diseases (NTDs). Treatment coverage, a primary indicator of MDA performance, can be measured through routinely reported programmatic data or population-based coverage evaluation surveys. Reported coverage is often the easiest and least expensive way to estimate coverage; however, it is prone to inaccuracies due to errors in data compilation and imprecise denominators, and in some cases measures treatments offered as opposed to treatments swallowed. **Objective:** Analyses presented here aimed to understand (1) how often coverage calculated using routinely reported data and survey data would lead programme managers to make the same programmatic decisions; (2) the magnitude and direction of the difference between these two estimates, and (3) whether there is meaningful variation by region, age group or country. **Methods:** We analysed and compared reported and surveyed treatment coverage data from 214 MDAs implemented between 2008 and 2017 in 15 countries in Africa, Asia and the Caribbean. Routinely reported treatment coverage was compiled using data reported by national NTD programmes to donors, either directly or via NTD implementing partners, following the implementation of a district-level MDA campaign; coverage was calculated by dividing the number of individuals treated by a population value, which is typically based on national census projections and occasionally community registers. Surveyed treatment coverage came from post-MDA community-based coverage evaluation surveys, which were conducted as per standardised WHO recommended methodology. **Results:** Coverage estimates using routine reporting and surveys gave the same result in terms of whether the minimum coverage threshold was reached in 72% of the MDAs surveyed in the Africa region and in 52% in the Asia region. The reported coverage value was within ± 10 percentage points of the surveyed coverage value in 58/124 of the surveyed MDAs in the Africa region and 19/77 in the Asia region. Concordance between routinely reported and surveyed coverage estimates was 64% for the total population and 72% for school-age children. The study data showed variation across countries in the number of surveys conducted as well as the frequency with which there was concordance between the two coverage

estimates. **Conclusions:** Programme managers must grapple with making decisions based on imperfect information, balancing needs for accuracy with cost and available capacity. The study shows that for many of the MDAs surveyed, based on the concordance with respect to reaching the minimum coverage thresholds, the routinely reported data were accurate enough to make programmatic decisions. Where coverage surveys do show a need to improve accuracy of routinely reported results, NTD programme managers should use various tools and approaches to strengthen data quality in order to use data for decision-making to achieve NTD control and elimination goals.

Gale

A new sign with UV dermoscope in the diagnosis of scabies: Ball sign.

Yürekli A.

Mai-2023

Skin Res Technol.

<https://pubmed.ncbi.nlm.nih.gov/37158220/>

Topical treatment failure in scabies: a survey in resistant patients.

Trave I, Cozzani E, Parodi A.

Avr-2023

Ital J Dermatol Venerol.

<https://pubmed.ncbi.nlm.nih.gov/37153954/>

Efficacy evaluation of scabies treatment through super high magnification dermoscopy.

DI Bartolomeo L, Argenziano G, Borgia F, Vaccaro F, Vaccaro M.

Avr-2023

Ital J Dermatol Venerol.

<https://pubmed.ncbi.nlm.nih.gov/37153952/>

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

Updates on parasite infection prevalence in the Joseon period based on parasitological studies of human coprolites isolated from archaeological sites in the cities of Euijeongbu, Gumi, and Wonju.

Oh CS, Chai JY, Min S, Oh KT, Seol J, Song MK, Shin DH, Seo M.

Fév-2023

Parasites Hosts Dis.

<https://pubmed.ncbi.nlm.nih.gov/37170469/>

Parasite infection rates estimated by examining ancient coprolites can provide insights into parasitism in Joseon

society. Using newly discovered Joseon period cases is essential to regularly update the parasite infection rates and reinforce the reliability of our previous estimations. In the present study, we investigated parasite infections in Joseon coprolites newly isolated from the cities of Euijeongbu, Gumi, and Wonju. We then updated the overall parasite infection rates of Joseon period samples (n= 30) as follows: 86.7% (26/30) for *Trichuris trichiura*, 56.7% (17/30) for *Ascaris lumbricoides*, 30.0% (9/30) for *Clonorchis sinensis*, and 30.0% (9/30) for *Paragonimus westermani*. The parasite infection rates in the Joseon society, estimated through coprolite examination, were very similar to those determined previously despite the addition of new cases to the existing data pool.

Development of a hookworm egg hatching assay to determine the ovicidal effects of anthelmintics.

Easland E, Biendl S, Keiser J.

Mai-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37143169/>

Background: Few anthelmintics are currently available, manifesting the urgent need for new treatment options. In vitro profiling of current anthelmintics against larval and adult stage helminths displayed varying effects on closely related worm species and between life stages of the same species. Conversely, limited research has been performed on the egg stage of human hookworms, and the effects of investigational compounds on the egg stage are not routinely assessed. **Methods:** We profiled the development and hatching of *Heligmosomoides polygyrus*, *Ancylostoma duodenale* and *Necator americanus* eggs isolated from rodent faeces in liquid media with various nutrient levels, osmolar concentrations, and acidities in dependence on incubation temperature and light exposure. Incubation conditions were optimised to allow the study of drug effect on immature and embryonated eggs. We analysed concentration-effect relationships of commercially available anthelmintics over 72 h. **Results:** Rapid embryonation and hatching were observed at room temperature with and without light exposure without nutrient supplementation in a wide range of acidities. Hookworms hatched optimally at room temperature in PBS achieving > 75% hatching over 34 h. Developmental delays were seen when eggs were stored at 4 °C with no effect on viability. Similar delays were also seen with increased osmolar concentrations resulting in decreased viability. Benzimidazole anthelmintics effectively reduced the viability and prevented hatching of hookworm eggs, with albendazole and thiabendazole eliciting particularly potent effects at EC₅₀ values below 1 µM. Macrolide anthelmintics as well as emodepside, oxantel pamoate, and pyrantel pamoate were inactive while monepantel, levamisole, and tribendimidine displayed varied potencies among the hookworm species. **Conclusion:** The presented egg-hatching assay will complement ongoing anthelmintic drug discovery and allow a full characterisation of drug activity against all life stages. In the development and application of the egg-hatching assay, good accordance was observed between

the three hookworm species evaluated. Marketed anthelmintics show differences of drug action compared to larval and adult stages highlighting the importance of profiling drug activity against all life stages.

Leishmaniose

Ecological interactions of sand flies, hosts, and *Leishmania panamensis* in an endemic area of cutaneous leishmaniasis in Colombia.

Posada-López L, Velez-Mira A, Cantillo O, Castillo-Castañeda A, Ramírez JD, Galati EAB, Galvis-Ovallos F.
11-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37167348/>

The Role of Asn11 in Catalysis by Triosephosphate Isomerase.

Hegazy R, Cordara G, Wierenga RK, Richard JP.
10-05-2023

Biochemistry.

<https://pubmed.ncbi.nlm.nih.gov/37162263/>

Formation and three-dimensional architecture of *Leishmania* adhesion in the sand fly vector.

Yanase R, Moreira-Leite F, Rea E, Wilburn L, Sádlová J, Vojtkova B, Pružinová K, Taniguchi A, Nonaka S, Volf P, Sunter JD.
10-05-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37162189/>

Attachment to a substrate to maintain position in a specific ecological niche is a common strategy across biology, especially for eukaryotic parasites. During development in the sand fly vector, the eukaryotic parasite *Leishmania* adheres to the stomodeal valve, as the specialised haptomonad form. Dissection of haptomonad adhesion is a critical step for understanding the complete life cycle of *Leishmania*. Nevertheless, haptomonad studies are limited, as this is a technically challenging life cycle form to investigate. Here, we have combined three-dimensional electron microscopy approaches, including serial block face scanning electron microscopy (SBFSEM) and serial tomography to dissect the organisation and architecture of haptomonads in the sand fly. We showed that the attachment plaque contains distinct structural elements. Using time-lapse light microscopy of in vitro haptomonad-like cells, we identified five stages of haptomonad-like cell differentiation, and showed that calcium is necessary for *Leishmania* adhesion to the surface in vitro. This study provides the structural and regulatory foundations of *Leishmania* adhesion, which are critical for a holistic understanding of the *Leishmania* life cycle.

First Report of Natural Infection of *Phlebotomus mongolensis* to *Leishmania major* and *Leishmania*

turanica in the Endemic Foci of Zoonotic Cutaneous Leishmaniasis in Iran.

Absavaran A, Mohebbali M, Moin-Vaziri V, Zahraei-Ramazani A, Akhavan AA, Rafizadeh S, Rassi A, Barmaki A, Rassi Y.
31-12-2023

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37159599/>

Accurate Identification of *Leishmania* Parasites in Sand Flies by Polymorphism Analysis of Cytochrome Oxidase Subunit 2 Gene Using Polymerase Chain Reaction and Quantitative PCR-High Resolution Melting Techniques in Iranian Border with Iraq.

Ghafari SM, Fotouhi-Ardakani R, Parvizi P.
31-12-2023

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37159596/>

Background: Firmly identification of *Leishmania* in *Phlebotomus papatasi* and understanding of natural transmission cycles of parasites in sand flies are important for treatment and local control. **Methods:** Modified and developed method of High Resolution Melting (HRM) as a preferable technique was employed to accurate identification of *Leishmania* in sand flies from Iranian border with Iraq, by targeting cytochrome oxidase II (COII) gene and designing suitable primers. PCR products cloned into pTG19-T vector, then purified plasmid concentration was measured at 260 and 280nm wavelength. The melting curve plots were generated and DNA sequences were analyzed using Sequencher 3.1.1, CLC Main Workbench 5.5, MEGA 6, DnaSP5.10.01 and MedCalc® version 13.3.3 soft wares. **Results:** Among about 3000 collected sand flies, 89 female *Ph. papatasi* were identified and two with *L. major*. In amplified fragment of COII gene among 611bp, 452bp had no genetic variations with low polymorphic sites ($P=0.001$) and high synonymous (79.8%) as compare to non-synonymous sites (20.2%). *Leishmania major* was discriminated in *Ph. papatasi* with 0.84 °C melting temperature (T_m) and unique curve based on thermodynamic differences was an important criterion using HRM technique. **Conclusion:** Subsequent war in Iraq made a high risk habitat for parasites transmission. It is important to discover accurate diagnostic procedures for leishmaniasis control.

Hit-to-lead optimization of a pyrazinylpiperazine series against *Leishmania infantum* and *Leishmania braziliensis*.

Jacques Dit Lapierre TJW, Cruz MGFML, Brito NPF, Resende DM, Souza FO, Pilau EJ, da Silva MFB, Neves BJ, Murta SMF, Rezende Júnior CO.
02-05-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37156183/>

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

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

08-05-2023

Parasitol Res.

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

Development of *Leishmania* Species Strains with Constitutive Expression of eGFP.

Carrasco J, Chang JH, Pineda L, Quintero I, Giovani R, Spadafora C, Leonart R, Restrepo CM.

21-04-2023

J Vis Exp.

<https://pubmed.ncbi.nlm.nih.gov/37154542/>

Protozoan parasites of the genus *Leishmania* cause leishmaniasis, a disease with variable clinical manifestations that affects millions of people worldwide. Infection with *L. donovani* can result in fatal visceral disease. In Panama, Colombia, and Costa Rica, *L. panamensis* is responsible for most of the reported cases of cutaneous and mucocutaneous leishmaniasis. Studying a large number of drug candidates with the methodologies available to date is quite difficult, given that they are very laborious for evaluating the activity of compounds against intracellular forms of the parasite or for performing in vivo assays. In this work, we describe the generation of *L. panamensis* and *L. donovani* strains with constitutive expression of the gene that encodes for an enhanced green fluorescent protein (eGFP) integrated into the locus that encodes for 18S rRNA (ssu). The gene encoding eGFP was obtained from a commercial vector and amplified by polymerase chain reaction (PCR) to enrich it and add restriction sites for the BglII and KpnI enzymes. The eGFP amplicon was isolated by agarose gel purification, digested with the enzymes BglII and KpnI, and ligated into the *Leishmania* expression vector pLEXY-sat2.1 previously digested with the same set of enzymes. The expression vector with the cloned gene was propagated in *E. coli*, purified, and the presence of the insert was verified by colony PCR. The purified plasmid was linearized and used to transfect *L. donovani* and *L. panamensis* parasites. The integration of the gene was verified by PCR. The expression of the eGFP gene was evaluated by flow cytometry. Fluorescent parasites were cloned by limiting dilution, and clones with the highest fluorescence intensity were selected using flow cytometry.

Genome diversity of *Leishmania aethiopica*.

Hadermann A, Heeren S, Maes I, Dujardin JC, Domagalska MA, Van den Broeck F.

20-04-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37153154/>

Systems biology of autophagy in leishmanial infection and its diverse role in precision medicine.

Guhe V, Ingale P, Tambekar A, Singh S.

21-04-2023

Front Mol Biosci.

<https://pubmed.ncbi.nlm.nih.gov/37152895/>

Autophagy is a contentious issue in leishmaniasis and is emerging as a promising therapeutic regimen. Published research on the impact of autophagic regulation on *Leishmania* survival is inconclusive, despite numerous pieces of evidence that *Leishmania* spp. triggers autophagy in a variety of cell types. The mechanistic approach is poorly understood in the *Leishmania* parasite as autophagy is significant in both *Leishmania* and the host. Herein, this review discusses the autophagy proteins that are being investigated as potential therapeutic targets, the connection between autophagy and lipid metabolism, and microRNAs that regulate autophagy and lipid metabolism. It also highlights the use of systems biology to develop novel autophagy-dependent therapeutics for leishmaniasis by utilizing artificial intelligence (AI), machine learning (ML), mathematical modeling, network analysis, and other computational methods. Additionally, we have shown many databases for autophagy and metabolism in *Leishmania* parasites that suggest potential therapeutic targets for intricate signaling in the autophagy system. In a nutshell, the detailed understanding of the dynamics of autophagy in conjunction with lipids and miRNAs unfolds larger dimensions for future research.

Visceral leishmaniasis complicated by hemophagocytic lymphohistiocytosis: A case report from a nonendemic area.

Joudeh AI, Elsiddig Awadelkarim HA, Gul MI, Elayana MS, Soliman DS, Amer A, Alsamawi M.

04-05-2023

Clin Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37151937/>

Key clinical message: Visceral leishmaniasis and hemophagocytic lymphohistiocytosis share many features in common and may coincide in the same patient. Timely diagnosis and management of visceral leishmaniasis could save patients from unnecessary toxic treatment. **Abstract:** Visceral leishmaniasis and hemophagocytic lymphohistiocytosis share many clinical features in common and may coexist in the same patient. Visceral leishmaniasis should be promptly ruled out in patients coming from endemic areas before starting immunosuppressive therapy for hemophagocytic lymphohistiocytosis. The mainstay treatment, in this case, is anti-leishmania medications preferably liposomal amphotericin-B.

A Case of *Leishmania Infantum* Mimicking Lymphoma.

Çulha G, Doğramacı AÇ, Kaya T, Seçinti İE.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151251/>

Transgenic overexpression of heat shock protein (HSP83) enhances protein kinase A activity, disrupts GP63 surface protease expression and alters promastigote morphology in *Leishmania amazonensis*.

Nation CS, Stephany-Brassesso I, Kelly BL, Pizarro JC.

05-05-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37150327/>

Temporal relationship between human and canine visceral leishmaniasis in an urban area in southeastern Brazil: An application of the ARIMAX model.

Braz MS, Sáfadi T, Ferreira RA, Morais MHF, Silva Z, Rocha CMBMD.

12-04-2023

Prev Vet Med.

<https://pubmed.ncbi.nlm.nih.gov/37149992/>

Visceral leishmaniasis (VL) is a neglected disease of public and animal health importance. With the urbanization of the disease, there is evidence of a temporal correlation between the occurrence of human (HVL) and canine (CVL) visceral leishmaniasis, usually with cases in dogs preceding those in humans. In this context, the objective of this study was to develop a time series model suitable for canine-human transmission of *Leishmania infantum*. Monthly cases of HVL and CVL from 2006 to 2018 in Belo Horizonte, Minas Gerais, Brazil, were evaluated, and monthly health indicators were calculated for HVL and CVL, i.e., incidence coefficient (HVL_IC) and proportion of seropositive dogs (PSD), respectively. The temporal relationship was evaluated using an autoregressive integrated moving average with exogenous variable (ARIMAX) model for two different periods (January 2006-August 2013 and September 2013-December 2018). During the 13 years studied, 1115 new cases of HVL and 103,358 dogs seropositive for CVL were recorded. HVL_IC and PSD exhibited decreasing trends throughout the first study period (January 2006-August 2013). According to the ARIMAX model adjusted for this period, there was a temporal relationship between HVL_IC and PSD, with HVL_IC being influenced by HVL_IC for the last two and five months and by PSD for the third previous month. For the second study period (September 2013-December 2018), it was not possible to fit an ARIMAX model. This study highlights the improvements made by VL surveillance since 2006 in Belo Horizonte and contributes to a better understanding of the epidemiology of the disease by public health policy-makers, doctors and veterinarians involved in the prevention and control of zoonoses.

Deletion of MIF gene from live attenuated LdCen^{-/-} parasites enhances protective CD4⁺ T cell immunity.

Fiuza JA, Gannavaram S, Gaze ST, de Ornellas LG, Alves ÉA, Ismail N, Nakhasi HL, Correa-Oliveira R.

05-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37147351/>

Translational reprogramming as a driver of antimony-drug resistance in *Leishmania*.

Gutierrez Guarnizo SA, Tikhonova EB, Karamyshev AL, Muskus CE, Karamysheva ZN.

05-05-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37147291/>

Leishmania is a unicellular protozoan that has a limited transcriptional control and mostly uses post-transcriptional regulation of gene expression, although the molecular mechanisms of the process are still poorly understood. Treatments of leishmaniasis, pathologies associated with *Leishmania* infections, are limited due to drug resistance. Here, we report dramatic differences in mRNA translation in antimony drug-resistant and sensitive strains at the full transcriptome level. The major differences (2431 differentially translated transcripts) were demonstrated in the absence of the drug pressure supporting that complex preemptive adaptations are needed to efficiently compensate for the loss of biological fitness once they are exposed to the antimony. In contrast, drug-resistant parasites exposed to antimony activated a highly selective translation of only 156 transcripts. This selective mRNA translation is associated with surface protein rearrangement, optimized energy metabolism, amastins upregulation, and improved antioxidant response. We propose a novel model that establishes translational control as a major driver of antimony-resistant phenotypes in *Leishmania*.

G-quadruplexes as key transcriptional regulators in neglected trypanosomatid parasites.

Monti L, Di Antonio M.

05-05-2023

Chembiochem.

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

Systematic study of 1,2,3-triazolyl sterols for the development of new drugs against parasitic Neglected Tropical Diseases.

Porta EOJ, Ballari MS, Carlucci R, Wilkinson S, Ma G, Tekwani BL, Labadie GR.

05-06-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37084599/>

The management of Babesia, amoeba and other zoonotic diseases provoked by protozoa.

Capasso C, Supuran CT.

Mars-2023

Expert Opin Ther Pat.

<https://pubmed.ncbi.nlm.nih.gov/37078205/>

Introduction: There are 12 protozoan genera that provoke zoonotic disease in humans and animals. We discuss the most common ones with a highlight on *Babesia* spp and *Entamoeba histolytica*, also mentioning *Toxoplasma gondii*, *Trypanosoma cruzi*, and *Leishmania* spp. **Areas covered:** The complex life cycle of pathogenic protozoans is deeply understood but this did not contribute to the discovery of new drugs. The clinical armamentarium is poor and includes anti-infectives originally proposed as antibacterial (azithromycin, clindamycin, paromomycin, sulfadiazole), antifungals (amphotericin B), or they are outdated compounds with poor efficacy and many side effects (nitroazoles, antimonials, etc.). Few patents and innovative ideas are available. **Expert opinion:** Protozoan diseases are not restricted to tropical countries and are difficult or impossible to treat with currently available drugs, which are limited and restricted to a low number of clinical classes. The antiprotozoal drug targets are also limited, and this had deleterious effects on translational studies for designing efficient antiprotozoal drugs. There is a stringent need for innovative approaches to tackle these problems.

Structural design, synthesis, and anti-Trypanosomatidae profile of new Pyridyl-thiazolidinones.

Conceição JMD, Santos ACDS, Brayner FA, Alves LC, Pinto AF, Brondani GL, Oliveira Filho GB, Bedor DCG, Silva JWVD, Sales Junior PA, Cavalcante MKA, Silva EDD, Pereira VRA, Leite ACL.

05-06-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37062170/>

The present work reports the synthesis of a novel series of pyridine-thiazolidinones with anti-*Trypanosoma cruzi* and leishmanicidal activities (compounds 10-27), derived from 2 or 4-pyridine thiosemicarbazones (1-9). The *in vitro* assays were performed with *Trypanosoma cruzi* trypomastigotes and amastigotes, as well as with *Leishmania amazonensis* promastigotes and amastigotes. The cytotoxicity profile was evaluated using the cell line RAW 264.7. From the 18 pyridine-thiazolidinones, 5 were able to inhibit trypomastigotes. Overall, all compounds inhibited amastigotes, highlighting compounds 15 (0.60 μ M), 18 (0.64 μ M), 17 (0.81 μ M), and 27 (0.89 μ M). Compounds 15 and 18 were able to induce parasite cell death through necrosis induction. Analysis by scanning electron microscopy showed that *T. cruzi* trypomastigotes treated with compounds 15 and 18 induced morphological changes such as shortening, retraction and curvature of the parasite body and leakage of internal content. Regarding the antiparasitic evaluation against *Leishmania amazonensis*, only compound 27 had a higher selectivity compared to Miltefosine against the amastigote form (IC_{50} = 5.70 μ M). Our results showed that compound 27 presented an antiparasitic activity for both *Trypanosoma cruzi* and *Leishmania amazonensis*. After *in silico* evaluation, it was suggested that the new pyridine-thiazolidinones had an appropriate drug-likeness profile. Our results pointed out a new chemical frame with an anti-Trypanosomatidae profile. The pyridine-thiazolidinones presented here for the first time could be used as a

starting point for the development of new antiparasitic agents.

Molecular detection of Wolbachia and Bartonella as part of the microbiome of phlebotomine sand flies from Chiapas, Mexico.

Lozano-Sardaneta YN, Marina CF, Torres-Monzón JA, Sánchez-Cordero V, Becker I.

June-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37055642/>

Cloning, expression and in vitro validation of chimeric multi epitope vaccine candidate against visceral leishmaniasis infection.

Ojha R, Chand K, Vellingiri B, Prajapati VK.

15-06-2023

Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/37044174/>

Visceral Leishmaniasis or Kala-Azar is one of the most severe and deadly neglected tropical disease caused by the *Leishmania* parasite. A few number of vaccines are going through different phases in clinical trial but failing of these vaccines in successive phase trial or less efficacy, urge to develop highly immunogenic and cost-effective treatment to get rid of deadly VL. This study focuses on the development of more potent vaccine candidate against VL. The recombinant vaccine candidate LeiSp was expressed in *Pichia pastoris*, followed by purification and characterization. The purified protein was also tested for any post-translation modification, which favors being a potent immunogenic candidate. Further, the expression modulation of different pro-inflammatory and anti-inflammatory cytokines was evaluated in THP1 cell lines. A significant upregulation in the expression of pro-inflammatory cytokines while no significant changes were observed in the expression of anti-inflammatory cytokines. The impact of recombinant vaccine protein candidates in infected conditions were determined. Here, upon treatment with chimeric vaccine protein candidate, we observed a considerable recovery in the expression level of pro-inflammatory cytokines, which were downregulated upon infection alone. In addition to this, we found a significant decrease in the expression of anti-inflammatory cytokines, which were upregulated during infection alone. We further validated our findings in infected hPBMCs and observed similar expression modulation of pro-inflammatory and anti-inflammatory cytokines with and without treatment. Thus, the present study indicates that the chimeric LeiSp protein which was designed using bioinformatics approaches shows a potential inductive efficacy for pro-inflammatory cytokines in *Leishmania*-infected cells.

Drugs and nanoformulations for the management of Leishmania infection: a patent and literature review (2015-2022).

Verdan M, Taveira I, Lima F, Abreu F, Nico D.

Mar-2023

Expert Opin Ther Pat.

<https://pubmed.ncbi.nlm.nih.gov/37038719/>

Genetic diversity and haplotype analysis of *Leishmania tropica* identified in sand fly vectors of the genera *Phlebotomus* and *Sergentomyia* using next-generation sequencing technology.

Al-Jawabreh A, Erekat S, Al-Jawabreh H, Dumaidi K, Nasereddin A.

Juin-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37036520/>

Urinary cystatin C and N-acetyl-beta-D-glucosaminidase (NAG) as early biomarkers for renal disease in dogs with leishmaniosis.

Ruiz P, Durán Á, Duque FJ, González MA, Cristóbal JJ, Nicolás P, Pérez-Merino EM, Macías-García B, Barrera R.

Juin-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37030024/>

Canine leishmaniasis (CanL) is a disease caused by *Leishmania infantum* that can vary from a subclinical infection to a severe disease. Dogs affected with CanL present varying degrees of renal dysfunction. Unfortunately, traditional biomarkers such as urea and creatinine detect renal damage in advanced stages of the disease, so more accurate biomarkers are needed. Hence, we aimed to study how urinary cystatin C (CysC) and N-acetyl-beta-D-glucosaminidase (NAG), behave in dogs with CanL at different stages of the disease. Eighty-six CanL infected dogs were classified according to LeishVet stages: LI (16 dogs), LIIa (12 dogs), LIIb (12 dogs), LIII (16 dogs) and LIV (30 dogs); as a control, 17 healthy dogs were studied. Blood samples were collected for complete haematological and biochemistry analysis including plasma cystatin C. Urine analysis included urine specific gravity (USG), urine protein to creatinine ratio (UPC), CysC and NAG expressed as a ratio with creatinine uCysCc ($\mu\text{g/g}$) and uNAGc (IU/g). The haematological, biochemical and urinary analysis coincided with the LeishVet guidelines. The statistical study of the uCysCc ratio and the uNAGc, showed significant increase when compared against control starting from group LI ($p < 0.05$). Interestingly, when the cut-off values were calculated using the ROC curve, uCysCc ($258.85 \mu\text{g/g}$) and uNAGc (2.25 IU/g) 75 % of the dogs included in LI groups surpassed the threshold. Hence our study indicates that uCysCc and uNAGc, could help to detect early renal damage in CanL affected dogs.

A short-term method to evaluate anti-leishmania drugs by inhibition of stage differentiation in *Leishmania mexicana* using flow cytometry.

Teh-Poot CF, Dzul-Huchim VM, Mercado JM, Villanueva-Lizama LE, Bottazzi ME, Jones KM, Tsai FTF, Cruz-Chan JV.

Juin-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37004860/>

Leukoreduction as a control measure in transfusion transmission of visceral leishmaniasis.

Pereira LQ, Tanaka SCSV, Ferreira-Silva MM, Gomes FVBAF, Santana MP, Aguiar PR, de Araújo Pereira G, Gómez-Hernández C, Junior VR, De Vito FB, Moraes-Souza H.

Mai-2023

Transfusion.

<https://pubmed.ncbi.nlm.nih.gov/36929836/>

Exploration of ethylene glycol linked nitrofurantoin derivatives against *Leishmania*: Synthesis and in vitro activity.

Ndlovu K, Kannigadu C, Aucamp J, van Rensburg HDJ, N'Da DD.

Mai-2023

Arch Pharm (Weinheim).

<https://pubmed.ncbi.nlm.nih.gov/36759973/>

Prevalence of cutaneous Leishmaniasis in the Middle East: a systematic review and meta-analysis.

Karami M, Gorgani-Firouzjaee T, Chehrazhi M.

Juin-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36222473/>

Cutaneous leishmaniasis (CL), caused by an obligate intracellular protozoan parasite from the genus *Leishmania*, imposing a significant burden on underdeveloped countries especially those located in the Middle East. Four electronic databases were searched to evaluate the prevalence of CL in the Middle East. The random effects model (95% confidence intervals (CI)) were applied to determine the overall and subgroup pooled prevalence. Heterogeneity was assessed by Cochran's Q test and I² statistics. Among 2424 peer-reviewed papers, 37 datasets from 34 studies were included in the current meta-analysis. 285560 individuals were assessed across 9 Middle Eastern countries. The pooled prevalence of CL was estimated at 12% (95% CI 9-15 %; 10718/285560). The highest prevalence rate was observed in Syria (39%, 37-42%), and the lowest one was found in Iraq and Lebanon (0%, 0-1%). The prevalence of CL in studies that applied LST assays had the highest rate (48%, 17-80%). The infection rate in males was similar to females (7%, 4-10%). The prevalence of infection in individuals living in urban areas was higher than in rural areas (14%, 10-19%). The prevalence of CL in the age group 0-15 years was higher than in individuals 16-40 and >40 years (9%, 6-13%). Most of the lesions were found on the face, and single lesions were more prevalent than two and three ones. In conclusion, the occurrence of CL was considerable in Middle Eastern countries. Therefore, more efforts should be made to precisely report the CL in this region for developing appropriate preventive and controlling strategies.

Evaluation of the antileishmanial effect of polyclonal antibodies and cationic antimicrobial peptides.

Esmaeilifallah M, Khanahmad H, Ghayour Z, Saberi S, Kalantari R, Hejazi SH.

Juin-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/35861705/>

Low genetic heterogeneity of *Leishmania* major in different geographical regions of Iran.

Spotin A, Rouhani S, Haghighi A, Parvizi P.

Mai-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37155684/>

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

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

09-05-2023

Toxicon.

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

This study reports the isolation of CollinLAO-I, a new L-amino acid oxidase from *Crotalus durissus collilineatus* snake venom, its biochemical characterization and leishmanicidal potential in *Leishmania* spp. CollinLAO-I (63.1 kDa) was successfully isolated with high purity using two chromatographic steps and represents 2.5% of total venom proteins. CollinLAO-I displayed high enzymatic activity (4262.83 U/mg/min), significantly reducing after 28 days. The enzymatic activity of CollinLAO-I revealed higher affinity for hydrophobic amino acids such as L-leucine, high enzymatic activity in a wide pH range (6.0-10.0), at temperatures from 0 to 25 °C, and showed complete inhibition in the presence of Na⁺ and K⁺. Cytotoxicity assays revealed IC₅₀ of 18.49 and 11.66 µg/mL for *Leishmania* (L.) *amazonensis* and *Leishmania* (L.) *infantum*, respectively, and the cytotoxicity was completely suppressed by catalase. CollinLAO-I significantly increased the intracellular concentration of reactive oxygen species (ROS) and reduced the mitochondrial potential of both *Leishmania* species. Furthermore, CollinLAO-I decreased the parasite capacity to infect macrophages by around 70%, indicating that even subtoxic concentrations of CollinLAO-I can interfere with *Leishmania* vital processes. Thus, the results obtained for CollinLAO-I provide important support for developing therapeutic strategies against leishmaniasis.

Antileishmanial effects and drugability characteristics of a heterocyclic copper

complex: An in silico, in vitro and molecular study.

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

05-05-2023

J Inorg Biochem.

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

Lèpre

Biallelic variants in COQ7 cause distal hereditary motor neuropathy with upper motor neuron signs.

Rebelo AP, Tomaselli PJ, Medina J, Wang Y, Dohrn M, Nyvltova E, Denzi M, Garrett M, Smith S, Pestronk A, Li C, Ruiz A, Jacobs E, Feely SME, França MC, Gomes MV, Santos D, Kumar S, Lombard DB, Saporta M, Hekimi S, Barrientos A, Wehl C, Shy M, Marques W, Zuchner S.

12-05-2023

Brain.

<https://pubmed.ncbi.nlm.nih.gov/37170631/>

COQ7 encodes a hydroxylase responsible for the penultimate step of coenzyme Q10 (CoQ10) biosynthesis in mitochondria. CoQ10 is essential for multiple cellular functions, including mitochondrial oxidative phosphorylation, lipid metabolism, and reactive oxygen species homeostasis. Mutations in COQ7 have been previously associated with primary coenzyme Q10 deficiency, a clinically heterogeneous multisystemic mitochondrial disorder. We identified COQ7 biallelic variants in nine families diagnosed with distal hereditary motor neuropathy (dHMN) with upper neuron involvement, expanding the clinical phenotype associated with defects in this gene. A recurrent p.Met1? change was identified in five families from Brazil with evidence of a founder effect. Fibroblasts isolated from patients revealed a substantial depletion of COQ7 protein levels, indicating protein instability leading to loss of enzyme function. HPLC assay showed that fibroblasts from patients had reduced levels of CoQ10, and abnormal accumulation of the biosynthetic precursor DMQ10. Accordingly, fibroblasts from patients displayed significantly decreased oxygen consumption rates in patients, suggesting mitochondrial respiration deficiency. iPSC-derived motor neurons from patient fibroblasts showed significantly increased levels of extracellular neurofilament light protein, indicating axonal degeneration. Our findings indicate a molecular pathway involving CoQ10 biosynthesis deficiency and mitochondrial dysfunction in patients with dHMN. Further studies will be important to evaluate the potential benefits of CoQ10 supplementation in the clinical outcome of the disease.

Phantom Hernia—Two Cases of Post Herpetic Abdominal Bulge.

Suvarna P, Pai SB, Prabhu SS.

09-05-2023

Actas Dermosifiliogr.

<https://pubmed.ncbi.nlm.nih.gov/37169333/>

Gait analysis of leprosy patients with foot drop using principal component analysis.

Cohen JC, de Souza Muniz AM, Carvalho Junior RB, de Oliveira HLC, Miranda ST, Gomes MK, da Cunha AJLA, Menegaldo LL.

04-05-2023

Clin Biomech (Bristol, Avon).

<https://pubmed.ncbi.nlm.nih.gov/37167843/>

K.V. Desikan. An extraordinary life in the service of leprosy patients.

Pandya S.

Nov-Dec 2023

Natl Med J India.

<https://pubmed.ncbi.nlm.nih.gov/37167519/>

The development, implementation, and evaluation of an optimal model for the case detection, referral, and case management of Neglected Tropical Diseases.

Godwin-Akpan TG, Chowdhury S, Rogers EJ, Kollie KK, Zaizay FZ, Wickenden A, Zawolo GVK, Parker CBMC, Dean L.

10-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37163515/>

Background: People affected by Neglected Tropical Diseases (NTDs), specifically leprosy, Buruli ulcer (BU), yaws, and lymphatic filariasis, experience significant delays in accessing health services, often leading to catastrophic physical, psychosocial, and economic consequences. Global health actors have recognized that Sustainable Development Goal 3:3 is only achievable through an integrated inter and intra-sectoral response. This study evaluated existing case detection and referral approaches in Liberia, utilizing the findings to develop and test an Optimal Model for integrated community-based case detection, referral, and confirmation. We evaluate the efficacy of implementing the Optimal Model in improving the early diagnosis of NTDs, thus minimizing access delays and reducing disease burden. **Methods:** We used a participatory action research approach to develop, implement, and evaluate an Optimal Model for the case detection, referral, and management of case management NTDs in Liberia. We utilized qualitative and quantitative methods throughout the cycle and implemented the model for 12 months. **Results:** During the implementation of our optimal model, the annual number of cases detected increased compared to the previous year. Cases were detected at an earlier stage of disease progression, however; gendered dynamics in communities shape the case identification process for some individuals. Qualitative data showed increased knowledge of the transmission, signs, symptoms, and management options among community health workers (CHW). **Conclusion:** The results provide evidence of the benefits of an integrated approach and the programmatic challenges to improve access to health services for persons affected by NTDs. The effectiveness of an integrated approach depends on a high

level of collaboration, joint planning, and implementation embedded within existing health systems infrastructure.

Evaluation of completeness, consistency and non-duplication of leprosy notification data on the Notifiable Health Conditions Information System, João Pessoa, Paraíba, Brazil: a descriptive study, 2001-2019.

Mendes MDS, Oliveira ALS, Schindler HC.

08-05-2023

Epidemiol Serv Saude.

<https://pubmed.ncbi.nlm.nih.gov/37162110/>

Objective: to analyze the completeness, consistency and non-duplication of leprosy notification data in João Pessoa, Paraíba, Brazil, 2001-2019. **Methods:** this was a descriptive study, conducted with data from the Notifiable Health Conditions Information System, which checked for "duplication" (acceptable: < 5%), "completeness" (excellent = incompleteness ≤ 5%) and "consistency" (excellent: ≥ 90.0%), based on the proportion of complete and consistent fields. **Results:** the sample consisted of 2,410 notifications. Duplication was acceptable (0.3%). The completeness of the "bacilloscopy", "affected nerves", "examined contacts" and "reactive episode" fields was very poor (more than 50% incomplete). Consistency between the "operational classification" and "initial treatment regimen" fields was excellent (99.6%), while consistency between "operational classification" and "clinical form" was low (50.7%). **Conclusion:** although duplication was acceptable, poor completeness of diagnosis and follow-up fields hinders epidemiological analysis, recognition of the status of the disease and adoption of measures to control it.

Protocol, rationale and design of BE-PEOPLE (Bedaquiline enhanced exposure prophylaxis for LEprosy in the Comoros): a cluster randomized trial on effectiveness of rifampicin and bedaquiline as post-exposure prophylaxis of leprosy contacts.

Younoussa A, Samidine SN, Bergeman AT, Piubello A, Attoumani N, Grillone SH, Braet SM, Tsoumanis A, Baco A, Mzembaba A, Salim Z, Amidy M, Grillone S, Snijders R, Corstjens P, Ortuno-Gutierrez N, Hoof C, Geluk A, de Jong BC, Hasker E.

09-05-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37161571/>

Ethnobotanical uses, phytochemistry and biological activity of the genus *Euclea*: A review.

Taye AD, Bizuneh GK, Kasahun AE.

19-04-2023

Front Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37153774/>

Euclea (Ebenaceae) is a genus of flowering shrubs and trees widely distributed in Africa, the Comoro Islands, and

Arabia. This review aimed to evaluate the ethnobotanical uses, phytochemistry, and biological activities of the genus *Euclea* on available research reports. This was achieved through PubMed, Medline, Google Scholar, Science Direct, Taylor and Francis Online, Wiley Online Library which provides access to scientific and medical research. The extensive literature survey revealed that plants that belong to this genus are used as folkloric medicine for the treatment of diabetes mellitus, toothache, diarrhea, cancer, malaria, leprosy, and genital and oral diseases in the case of HIV/AIDS-related diseases. To date, more than 40 secondary metabolites have been isolated and identified from these plants, especially from *E natalensis* and *E. divinorum*. Among these, naphthoquinones, terpenes, and flavonoids are potential secondary metabolites with profound biological activities. *Euclea* plant extracts and their bioactive compounds possess outstanding pharmacological properties, especially antimalarial, antidiabetic, anticancer, antimicrobial, and antioxidant properties.

Differential expression of programmed death 1 (PD-1) on various immune cells and its role in human leprosy.

Tarique M, Naz H, Suhail M, Turan A, Saini C, Muhammad N, Shankar H, Zughaibi TA, Khan TH, Khanna N, Sharma A.

21-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37153623/>

Mycobacterial development for drug target identification.

Bannerman BP, Oarga A, Júlvez J.

30-04-2023

GigaByte.

<https://pubmed.ncbi.nlm.nih.gov/37153490/>

Antibiotic resistance is increasing at an alarming rate, and three related mycobacteria are sources of widespread infections in humans. According to the World Health Organization, *Mycobacterium leprae*, which causes leprosy, is still endemic in tropical countries; *Mycobacterium tuberculosis* is the second leading infectious killer worldwide after COVID-19; and *Mycobacteroides abscessus*, a group of non-tuberculous mycobacteria, causes lung infections and other healthcare-associated infections in humans. Due to the rise in resistance to common antibacterial drugs, it is critical that we develop alternatives to traditional treatment procedures. Furthermore, an understanding of the biochemical mechanisms underlying pathogenic evolution is important for the treatment and management of these diseases. In this study, metabolic models have been developed for two bacterial pathogens, *M. leprae* and *My. abscessus*, and a new computational tool has been used to identify potential drug targets, which are referred to as bottleneck reactions. The genes, reactions, and pathways in each of these organisms have been highlighted; the potential drug targets can be further explored as broad-spectrum antibacterials and the unique

drug targets for each pathogen are significant for precision medicine initiatives. The models and associated datasets described in this paper are available in GigaDB, Biomodels, and PatMeDB repositories.

Integrating TB screening into house-to-house polio vaccination campaigns.

Ugwu C, Chukwulobelu U, Okeke E, Igboekwu C, Onyima A, Ibeziako V, Ebede C, Orjiagu U, Unamba V.

21-05-2023

Public Health Action.

<https://pubmed.ncbi.nlm.nih.gov/37152214/>

Evaluating TB diagnosis and care in the Union of the Comoros.

Noeske J, Mzembaba A, Assoumani Y, Maoulida S, Makpenon A.

21-05-2023

Public Health Action.

<https://pubmed.ncbi.nlm.nih.gov/37152213/>

Clinical and Metabolic Characteristics in Hidradenitis Suppurativa - An Indian Perspective.

Mendiratta V, Yadav V, Bhardwaj AV, Pangti R.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151284/>

Background: Hidradenitis suppurativa (HS) is a chronic, inflammatory, recurrent follicular disorder affecting apocrine gland bearing areas such as axillae, inframammary area and groin. Significant association of HS with metabolic derangements such as hypertension, obesity, hyperlipidemia and hyperinsulinemia has been found. There is dearth of literature on epidemiological and metabolic profile of HS in Indian subjects.

Aim: The aim of this study is to assess abnormalities in the levels of fasting blood glucose, serum insulin, and lipid profile in patients with HS. **Primary objective:** To assess the frequency of abnormal levels of fasting blood sugar, serum insulin and lipid profile in patients with HS. **Secondary objectives:** To assess the frequency of hypertension, raised basal metabolic index, polycystic ovarian syndrome, follicular disorder, erythrocyte sedimentation rate (ESR) and c-reactive protein (CRP) in patients with HS and to assess the severity of clinical presentation HS using Hurley staging system. **Methodology:** This is a retrospective record based study. Records of clinically diagnosed patients of HS, aged > 18 years fulfilling the inclusion and exclusion criteria were analysed. **Results:** Total 30 patients were recruited with 1:1 male to female ratio. Five (16.67%) cases fulfilled NCEP ATP III criteria for the diagnosis of metabolic syndrome. Statistically significant association was observed between severity of HS, in younger age group (<20 years), moderate to severe BMI, fasting serum insulin, fasting total cholesterol and raised ESR. **Limitations:** This is retrospective, hospital record based study with small sample size. **Conclusion:** Holistic management of HS should be individualized according to need of patient and it should be combined

approach including dermatologist, plastic surgeon, psychiatrist and dietician. We recommend an initial screening for derangements in metabolic profile in these patients for more effective management and preventing long term cardiovascular complications.

Klippel Trenaunay Syndrome-The Pulsating Calf; A Rare Case Presentation.

Kololgi SP, Hulmani M, Kololgi PD, Lahari CS.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151281/>

The Changing Trend of Syphilis: Is It a Sign of Impending Epidemic?

Gupta M, Verma GK, Sharma R, Sankhyan M, Rattan R, Negi AK.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151273/>

Isolated Pili Torti: A Rare Case Revisited.

Davis CT, Bhuiya S, Potom K, Das S.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151268/>

Clinicoetiological Study of Stevens-Johnson Syndrome and Toxic Epidermal Necrolysis Spectrum and the Correlation of SCORTEN with Prognosis.

Kanagarajan A, Murthy AB, Moni PK, Palanivel N.

Jan-Fév 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151260/>

Background: Stevens-Johnson syndrome (SJS) and Toxic Epidermal Necrolysis (TEN) are severe cutaneous adverse reactions of major concern because of its high mortality. The prognosis of SJS and TEN is widely assessed with SCORTEN (SCORE of TEN). Although, it is a largely useful scale, the predictive ability is still variable. **Aims and objectives:** This study was conducted to assess the clinicoetiological profile and outcome of SJS and TEN and to evaluate the validity of SCORTEN in assessing the prognosis in South Indian population. **Methods:** This prospective observational study was conducted in the Department of Dermatology, Venereology and Leprosy in a Tertiary care hospital from January 2016 to June 2017. Detailed history, examination findings, treatment and SCORTEN scores were recorded. SCORTEN's accuracy in predicting the mortality was assessed on day 1, 3 and 5 of admission. **Results:** The incidence of SJS/TEN among other drug reactions was 29.5%. The most common age group affected was 30-49years (41.1%), with male preponderance (76.5%). The age range of patients was 6 and 67 years. TEN (64.7%) was the predominant spectrum followed by SJS and SJS-TEN overlap in 17.6% each. Anticonvulsants (47%) were the commonest causative drug, followed by analgesics (35%) and antibiotics (11%). The validity of SCORTEN was the same on days 1, 3, and 5.

There was good agreement between the actual and predicted mortality on all three days. A mortality of 17.6% (3 cases) was recorded in this study. Three patients (17.6%) died in our study. All survivors had a score of 4 or less. The predicted mortalities were 0.417, 1.836, and 2.574 and the observed mortalities were 0, 2, and 1 in SJS, SJS-TEN overlap, and TEN respectively. Analysis of SCORTEN on a single day, either day 1, 3, or 5 was found to be as useful as the serial analysis. **Conclusion:** SCORTEN gave a significant estimation of mortality in SJS-TEN overlap patients, whereas it overestimated mortality in TEN patients. An increase in individual scores for the elevation of blood urea nitrogen (BUN) in existing SCORTEN and the inclusion of new parameters like raised liver enzymes, thrombocytopenia, and pulmonary infiltrates aided in proposing a modified SCORTEN for the South Indian population. Further studies on a larger scale, are needed to validate the modified SCORTEN proposed by us.

Pitted keratolysis.

Palaniappan V, Murthy AB, Karthikeyan K.

08-05-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37151115/>

Leprosy in French Guiana, 2015 to 2021: Dynamics of a Persistent Public Health Problem.

Petiot A, Drak Alsibai K, Dossou C, Couppie P, Blaizot R.

05-05-2023

Acta Derm Venereol.

<https://pubmed.ncbi.nlm.nih.gov/37144514/>

Use of local data to evaluate TB contact investigation in Malawi.

Kaswaswa K, Mlauzi L, Mpunga J, Mandambwe C, Kawatsu L, Uchimura K.

01-05-2023

Int J Tuberc Lung Dis.

<https://pubmed.ncbi.nlm.nih.gov/37143224/>

Genomic analysis unveils genome degradation events and gene flux in the emergence and persistence of *S. Paratyphi A* lineages.

Jacob JJ, Pragasam AK, Vasudevan K, Velmurugan A, Priya Teekaraman M, Priya Thirumoorthy T, Ray P, Gupta M, Kapil A, Bai SP, Nagaraj S, Saigal K, Chandola TR, Thomas M, Bavdekar A, Ebenezer SE, Shastri J, De A, Dutta S, Alexander AP, Koshy RM, Jinka DR, Singh A, Srivastava SK, Anandan S, Dougan G, John J, Kang G, Veeraraghavan B, Mutreja A.

28-04-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37115804/>

Phytochemical profiling of *Symplocos tanakana* Nakai and *S. sawafutagi*

Nagam. leaf and identification of their antioxidant and anti-diabetic potential.

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

02-05-2023

J Pharm Biomed Anal.

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

Symplocos sp. contains various phytochemicals and is used as a folk remedy for treatment of diseases such as enteritis, malaria, and leprosy. In this study, we discovered that 70% ethanol extracts of Symplocos sawafutagi Nagam. and S. tanakana Nakai leaves have antioxidant and anti-diabetic effects. The components in the extracts were profiled using high-performance liquid chromatography coupled to electrospray ionization and quadrupole time-of-flight mass spectrometry; quercetin-3-O-(6"-O-galloyl)- β -D-galactopyranoside (6) and tellimagrandin II (7) were the main phenolic compounds. They acted as strong antioxidants with excellent radical scavenging activity and as inhibitors of non-enzymatic advanced glycation end-products (AGEs) formation. Mass fragmentation analysis demonstrated that compounds 6 and 7 could form mono- or di-methylglyoxal adducts via reaction with methylglyoxal, which is a reactive carbonyl intermediate and an important precursor of AGEs. In addition, compound 7 effectively inhibited the binding between AGE2 and receptor for AGEs as well as the activity of α -glucosidase. Enzyme kinetic study revealed that compound 7 acts as a competitive inhibitor of α -glucosidase, through interaction with the active site of the enzyme. Therefore, compounds 6 and 7, the major constituents of S. sawafutagi and S. tanakana leaves, are promising for developing drugs for preventing or treating diseases caused by aging and excessive sugar consumption.

Critical observation of WHO recommended multidrug therapy on the disease leprosy through mathematical study.

Ghosh S, Saha S, Roy PK.

21-06-2023

J Theor Biol.

<https://pubmed.ncbi.nlm.nih.gov/37080386/>

A comparative study of modulatory interaction between cytokines and apoptotic proteins among Scleroderma patients with and without pulmonary involvement.

Khadilkar P, Chougule D, Tipnis T, Khopkar U, Nadkar M, Rajadhyaksha A, Kini S, Kharkar V, Athvale A, Athvale T, Madkaikar M, Pradhan V.

Juin-2023

Cytokine.

<https://pubmed.ncbi.nlm.nih.gov/37011542/>

Hand Foot Mouth Disease During the SARS-CoV-2 Pandemic: A Multicentric Study.

Mohta A, Pareek S, Sharma MK, Aggrwal A, Vyas K, Pandey H, Jain SK.

15-05-2023

Indian Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36814120/>

Objectives: This prospective observational study aimed to identify the current trend of the circulating viral strains responsible for HFMD outbreak in four tertiary care centers in Rajasthan, amidst the COVID-19 pandemic (April-October 2022). **Methods:** Cases with suspected HFMD, presenting to our skin outpatient department were assessed clinically and serologically (IgM antibodies against coxsackie virus (CV) A6, A16 and enterovirus 71) for evidence of the disease. **Results:** We identified 718 new HFMD patients (161 adults) with peaks in May and August, 2022. Male:female ratio decreased with increasing age. Most children were asymptomatic. A total of 385/409 patients assessed serologically, were found positive, most commonly against CV-A6. **Conclusion:** Though HFMD typically affects young children, an unusually higher proportion of adults were affected during the current pandemic. There were some subtle differences between pediatric and adult presentation of HFMD.

Ulcerated cutaneous lesions in type 1 lepra reaction healing with morpheaform scarring: an unusual presentation.

Mushtaq S.

Juin-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36683019/>

Impact of NB-UVB phototherapy on Caveolin-1 expression in chronic plaque psoriasis.

Elsherbeni MB, Neinaa YME, Fawzy MM, Elwan NM.

Mai-2023

Photodermatol Photoimmunol Photomed.

<https://pubmed.ncbi.nlm.nih.gov/35860958/>

Morsures de serpent

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

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

09-05-2023

Int J Biol Macromol.

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

Snake Envenomation Simulating ST Elevation Myocardial Infarction.

Ninad N, Andharia N, Schneibel E, Parel R.

10-05-2023

Am Surg.

<https://pubmed.ncbi.nlm.nih.gov/37165662/>

Envenomation syndromes following snakebites can include tissue reaction, coagulopathy, nephrotoxicity, and neurotoxicity. Cardiotoxicity is rare but usually presents with dysrhythmias. Myocardial infarction after envenomation has rarely been reported. We discuss a case of snake bite simulating ST-elevation myocardial infarction (STEMI). Our patient is a 49-year-old male who sustained a snake bite in his left hand. Patient had hemodynamic collapse requiring increasing pressor support; EKG and troponin results confirmed STEMI. Cardiac catheterization did not demonstrate any thrombosis, rather severe cardiomyopathy with left ventricular ejection fraction 20-25%. Even though our patient did not require any coronary intervention, an angiogram was warranted given the clinical presentation. Our case demonstrates severe cardiotoxicity following snake bite. Further research is warranted to study the mechanism behind such phenomena.

Guillain-Barré's Syndrome Post Snake Envenomation: Rare Case Report and Literature Review.

Aradhey P, Gade N, Panjwani D, Kathpal JS.

Mars-Avril 2023

Neurol India.

<https://pubmed.ncbi.nlm.nih.gov/37148060/>

Treatment of a Snakebite Injury With Secondary Bacterial Infection: A Case Study.

Sachett JAG, Vieira SSC, Soares FGS, Alcântara JA, Carvalho HBS, da Silva EMG, da Silva IM, Monteiro WM.

Mai-Juin 2023

J Wound Ostomy Continence Nurs.

<https://pubmed.ncbi.nlm.nih.gov/37146116/>

Effect of the time to antivenom administration on recovery from snakebite envenoming-related coagulopathy in French Guiana.

Houcke S, Pujo JM, Vauquelin S, Lontsi Ngoula GR, Matheus S, Nkontcho F, Pierre-Demar M, Gutiérrez JM, Resiere D, Hommel D, Kallel H.

24-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37093856/>

Background: Snakebite (SB) envenoming is an acute emergency requiring an early care delivery. We aimed to search for the time to reach healthcare facilities in various regions of French Guiana (FG) and to assess the impact of time to antivenom (AV) on the correction of coagulation parameters in these patients. **Methodology:** This is a prospective observational study conducted in Cayenne General Hospital between January 1st, 2016, and July 31st, 2022. We included all patients hospitalized for SB envenoming less than 48h after the bite, and receiving antivenom (AV). We assessed the time lapse between SB and medical attention and the time needed to return of the coagulation parameters to normal. **Principal findings:** Overall, 119 patients were investigated, and 48.7% were from remote areas. The median time from SB to AV

therapy was 09:15 h (05:32-17:47). The time was longer in patients from remote rural locations. AV was dispensed within the first six hours after the SB in 45 cases (37.8%). Time from SB to reaching normal plasma fibrinogen concentration was 23:27 h (20:00-27:10) in patients receiving AV \leq 6h vs. 31:23 h (24:00-45:05) in those receiving AV $>$ 6h ($p<0.001$). Whereas, the time from AV administration to reach normal fibrinogen dosage was similar in the two groups. **Conclusions:** Patients from rural settings in FG suffer from a delay in AV administration after SB envenoming leading to an extended time in which patients are coagulopathic. Once AV is administered, clotting parameters recover at a similar rate. Supplying remote healthcare facilities with AV and with medical teams trained on its use should be planned.

What drives the risk of being bitten by a viper? A fine spatial scale study in western France.

Le Roux G, Guillon M, Bernard L, de Haro L, Lourdaïs O, Descatha A.

Juin-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37080341/>

Previous studies on viper bites in France have focused on clinical consequences of envenomation, efficacy of antivenom and epidemiology of bites. Herein, we wanted to clarify temporal and spatial patterns in bite incidence using a fine spatial scale (municipality level). We focused on viper bites recorded over the last 10 years in 4 regions of western France. We addressed the determinants of bite occurrence and number of bites considering the following variables: predicted probability of viper presence, species (*V. aspis* or *V. berus*), climatic data, tourism function rate, soil transformation and landscape use. 703 bite cases were retained with significant disparities between areas. Bites occurred either during a garden-related activity (339 cases, 51.2%) or during an activity in the countryside (300 cases, 45.3%). The probability of presence of a viper at the municipality level positively influenced the risk of being bitten (multiplied by 3 for a variation in probability of 0.25 from 0.5) but varied between species (lower in *V. berus* than *V. aspis*). Artificial land development had a positive effect on bite risks. Finally, a tourism function rate above 50 beds/100 inhabitants was strongly associated with an increase in the risk of occurrence and frequency of bites. Overall, viper bites recorded in our study were concentrated on the south coastline of Pays de la Loire region. The coastal towns are significant areas of tourist attraction and are located close to preserved semi-natural landscapes that provide favorable habitats for vipers. This convergence may favor human/wildlife encounters.

Comparison of snakebite in children and adults in Nigeria.

Iliyasu G, Dajel TB, Abubakar SB, Azi NA, Danamaryia NM, Obateru OA, Dayyab AM, Hamza M, Alabi OA, Habib AG.

Juin-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37062344/>

Neutrophil-mediated erythrophagocytosis following Russell's viper (*Daboia russelii*) bite.

Senthilkumaran S, Arathisenthil SV, Williams J, Almeida JR, Williams HF, Rajan E, Thirumalaikolundusubramanian P, Patel K, Vaiyapuri S. 01-06-2023
Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37060927/>

Snakebite envenomation is regarded as a high-priority neglected tropical disease by the World Health Organisation, as it results in significant loss of lives and permanent disabilities. Russell's viper is one of the important venomous snakes that causes morbidities, mortalities and disabilities in India. The clinical presentation of Russell's viper envenomation is characterised by local envenoming effects including tissue damage, venom-induced coagulopathy, neurotoxicity, and kidney injury. However, venom composition and its mechanisms of toxicity are highly variable even within snakes of the same species including Russell's viper. This variation in venom composition results in a broad range of clinical complications. Here, we present a previously undocumented case of neutrophil-mediated erythrophagocytosis in a healthy 28-year-old female following Russell's viper bite. Systemic envenomation effects and bleeding abnormalities in this patient were corrected by the administration of polyvalent antivenom. Two days later, the patient developed progressive swelling and ecchymosis in the bitten limb. Observed abnormal limits within blood testing were followed up by a peripheral blood smear where it was found that 30% of neutrophils had phagocytosed erythrocytes as they were found within the cytoplasm. The patient underwent a fasciotomy for compartmental syndrome and received packed red cells and a course of corticosteroids. Following this treatment, the patient made a full recovery. This case report outlines a previously undocumented pathological event induced by Russell's viper envenomation, guiding diagnosis and treatment. Clinicians' knowledge of the mechanisms of toxicity of Russell's viper envenomation and its clinical manifestations are essential for improving the treatment of snakebites to achieve positive outcomes.

Musa spp. cultivars as a neutralising source against some toxic activities of Bothrops and Crotalus genus snake venoms.

Matos da Silva M, Pereira Alexandre G, Magalhães MR, Torres AM, Kato L, Costa da Silva V, Teixeira de Saboia Morais SM, Garcia Rodriguez A, Pacheco Fill T, Pereira AK, Roque J, Souza Simão JL, Pasqualotto Severino VG. 01-06-2023
Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37031872/>

Accidents involving snakes from *Bothrops* spp. and *Crotalus* spp. constitute the most important cause of envenomation in Brazil and Argentina. *Musa* spp. (banana) have been reported to be used in popular medicine against snakebite by the members of the Canudos Settlement, located in Goiás. In this way, the aim of this

work was to evaluate the antivenom effect of the Ouro (AA), Prata (AAB), Prata-anã (AAB) and Figo (ABB) cultivars against in vitro (phospholipase, coagulation and proteolytic) and in vivo (lethality and toxicity) activities caused by the venoms and toxicity (*Artemia salina* nauplii and *Danio rerio* embryos) of *Musa* spp. as well as the annotation of chemical compounds possibly related to these activities. From the in vitro antiophidic tests with the sap, we observed 100% inhibition of the phospholipase and coagulant activities with the cultivars Prata-anã and Figo against the venoms of *B. alternatus* and *C. d. collineatus*, *B. diporus* and *B. pauloensis*, respectively, and neutralisation of the lethality against the *B. diporus* venom. It was observed that the cultivars of *Musa* spp. did not show toxicity against *Artemia salina* nauplii and *Danio rerio* embryos. The sap analysis via HPLC-MS/MS allowed the annotation of the 13 compounds: abscisic acid, shikimic acid, citric acid, quinic acid, afzelechin, Glp-hexose, glucose, sucrose, isorhamnetin-3-O-galactoside-6-raminoside, kaempferol-3-glucoside-3-raminoside, myricetin-3-O-rutinoside, procyanidin B1 and rutin. Therefore, it can be seen that *Musa* spp. is a potential therapeutic agent that can act to neutralise the effects caused by snakebites.

Mycétome

Primary Cutaneous Actinomycosis: A Diagnostic Enigma.

Khan S, Khan B, Batool W, Khan M, Khan AH. 04-04-2023
Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37162764/>

Actinomyces are Gram-positive, filamentous rods found endogenously as a part of the normal flora and can be acquired exogenously as they are present in the soil. The most common species known to infect humans is *Actinomyces israelii*. Five forms of the disease have been identified so far, of which the primary infection of the skin is the most uncommon. It is also commonly considered one of the most misdiagnosed diseases. We present a case of a young male diagnosed with primary cutaneous actinomycosis based on a histopathology specimen after multiple failed diagnoses of Madura foot/mycetoma, cutaneous tuberculosis, and malignancy. The patient was successfully treated with antibiotics with the restoration of his functional disability caused by the lesion.

Burden of fungal infections in Kenya.

Ratemo SN, Denning DW. 27-04-2023
Mycology.

<https://pubmed.ncbi.nlm.nih.gov/37152847/>

The burden of fungal infections has been on the rise globally and remains a significant public health concern in Kenya. We estimated the incidence and prevalence of fungal infections using all mycology publications in Kenya up to January 2023, and from neighbouring countries where data lacked. We used deterministic modelling using populations at risk to calculate the disease burden. The

total burden of serious fungal infections is estimated to affect 6,328,294 persons which translates to 11.57% of the Kenyan population. Those suffering from chronic infections such as chronic pulmonary aspergillosis are estimated to be 100,570 people (0.2% of the population) and probably nearly 200,000 with fungal asthma, all treatable with oral antifungal therapy. Serious acute fungal infections secondary to HIV (cryptococcal meningitis, disseminated histoplasmosis, pneumocystis pneumonia, and mucosal candidiasis) affect 196,543 adults and children (0.4% of the total population), while cancer-related invasive fungal infection cases probably exceed 2,299 and those in intensive care about 1,230 incident cases, including *Candida auris* bloodstream infection. The burden of fungal infections in Kenya is high; however, limited diagnostic test availability, low clinician awareness and inadequate laboratory capacity constrain the country's health system in responding to the syndemic of fungal disease in Kenya.

Cutaneous tuberculosis of the foot clinically mimicking mycetoma: A case report.

Ahmed A, Hagelnur AA, Eltigani HF, Siddig EE.

04-05-2023

Clin Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37151934/>

Onchocercose

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

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

08-05-2023

Parasitol Res.

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

Onchocerciasis, the second leading infectious cause of blindness, afflicts approximately 21 million people globally. Its control is limited to the use of the microfilaricidal drugs, ivermectin and moxidectin. Both drugs are unable to kill the adult worms which can survive for up to 15 years in patients, justifying the urgent need for potent and novel macrofilaricides that kill adult worms. The development of such drugs has been hindered by the lack of an appropriate small laboratory animal model to evaluate potential drug candidates in vivo. This study assessed the survival of *O. ochengi* female worms and their embryos over time in two laboratory rodents: gerbils and hamsters and tested using "proof-of-concept" studies, whether known macrofilaricidal drugs can kill these worms. Animals were surgically implanted with mechanical or collagenase-liberated *O. ochengi* worm masses, and necropsied at various time points to test for survival. Recovered worm masses were assessed for viability by biochemical analysis (MTT/formazan assay) or fecundity (embryogram). Flubendazole (FBZ) administered at 20 mg/kg body weight was used to validate both rodent

models. By day 26 post-implantation of 15 worm masses, a median of 7.00 (4.00-10.00) was recovered from hamsters, and 2.50 (2.00-4.00) from gerbils. Worm masses recovered from gerbils were mostly disintegrated or fragmented, with significantly higher fragmentation observed with collagenase-liberated worm masses. FBZ had no significant effect on the number of worm masses recovered, but enhanced embryo degradation in gerbils and reduced worm mass viability in hamsters. This exploratory study has revealed the gerbil and hamster as permissible rodents to adult female worms of *O. ochengi*. The hamsters appeared to maintain the worms longer, compared to gerbils.

Case definitions for onchocerciasis-associated epilepsy and nodding syndrome: A focused review.

Van Cutsem G, Siewe Fodjo JN, Dekker MCJ, Amaral LJ, Njamnshi AK, Colebunders R.

Avr-2023

Seizure.

<https://pubmed.ncbi.nlm.nih.gov/37023626/>

"One-shot" combined therapy with oral ivermectin and local benzyl benzoate: is the current best therapeutic option in the era of permethrin resistant scabies?

Bassi A, Piccolo V, Mazzatenta C.

04-05-2023

Travel Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37149241/>

Prevalence of scabies worldwide - an updated systematic literature review in 2022.

Schneider S, Wu J, Tizek L, Ziehfrennd S, Zink A.

06-05-2023

J Eur Acad Dermatol Venereol.

<https://pubmed.ncbi.nlm.nih.gov/37147907/>

Scabies is a World Health Organization-defined neglected tropical disease, with continuously rising incidence worldwide in recent years. The aim of this study was to provide an update of the worldwide prevalence and new treatment approaches of scabies in population-based settings. MEDLINE (PubMed), Embase and LILACS databases were reviewed for English and German language population-based studies from October 2014 to March 2022. Two authors independently screened the records for eligibility, extracted all data and one critically appraised the quality of the studies and risk of bias. Systematic review registration: PROSPERO CRD42021247140. Overall, 1273 records were identified through database searching, of which 43 studies were included for the systematic review. Most of the studies (n = 31) examined the scabies prevalence in medium or low human development index countries. The highest prevalence of scabies reported in the general population (children and adults) was recorded in five randomly selected communities in Ghana (71.0%), whereas the highest scabies prevalence in studies, which only examined children (76.9%), was recorded in an Indonesian

boarding school. The lowest prevalence was recorded in Uganda (0.18%). The systematic review highlights the prevalence of scabies worldwide, showing that scabies is still a serious, increasing disease that occurs globally and is clustered in developing countries. More transparent data on scabies prevalence are needed to identify risk factors to find new prevention measures.

Correction: Beliefs, attitudes and practices towards scabies in central Ghana.

PLOS Neglected Tropical Diseases Staff.

05-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37146080/>

[Infectious diseases in migrants].

Stich A.

Mai-2023

Inn Med (Heidelb).

<https://pubmed.ncbi.nlm.nih.gov/37140630/>

Identification and genetic characterisation of cathepsin L in *Demodex*.

Li H, Chenglin G, Yae Z, Wanyu Z, Rong C.

Avr-2023

Exp Appl Acarol.

<https://pubmed.ncbi.nlm.nih.gov/37058174/>

Owing to difficulties in obtaining functional gene sequences, molecular pathogenic mechanisms in *Demodex* have been understudied. In this study, overlap extension PCR was used to obtain the sequences of cathepsin L (CatL), a pathogenicity-related gene, to provide a foundation for subsequent functional research. *Demodex folliculorum* and *Demodex brevis* mites were obtained from the face skin of Chinese individuals, and *Demodex canis* mites were isolated from the skin lesions of a dog. RNA was extracted and used to synthesise double-stranded cDNA. PCR amplification, cloning, sequencing, and bioinformatics analysis of CatL were performed. CatL gene sequences of 1005, 1008, and 1008 bp were successfully amplified for *D. brevis*, *D. folliculorum*, and *D. canis*, respectively. These sequences showed 99.9 or 100% identity with templates previously obtained by RNA-seq. The Maximum Likelihood (ML) phylogenetic tree showed that *D. folliculorum* clustered with *D. canis* first, then with *D. brevis*, and finally with other Acariformes mite species. The three *Demodex* species had nine similar motifs to those of *Sarcoptes scabiei*, *Dermatophagoides pteronyssinus*, and *Dermatophagoides farinae*, and motifs 10-13 were valuable for identification. CatL proteins of *Demodex* species were predicted to be approximately 38 kDa, be located in lysosomes, have a signal peptide but no transmembrane region, and have two functional domains, I29 and Pept_C1. However, interspecific differences were observed in secondary and tertiary protein structures. In conclusion, we successfully obtained CatL sequences of three *Demodex* species by overlap extension PCR, which

creates conditions for further pathogenic mechanism studies.

Pian

The development, implementation, and evaluation of an optimal model for the case detection, referral, and case management of Neglected Tropical Diseases.

Godwin-Akpan TG, Chowdhury S, Rogers EJ, Kollie KK, Zaizay FZ, Wickenden A, Zawolo GVK, Parker CBMC, Dean L.

10-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37163515/>

Rage

Immune response after rabies pre-exposure prophylaxis and a booster dose in Australian bat carers.

Guo Y, Mills DJ, Lau CL, Mills C, Furuya-Kanamori L.

11-05-2023

Zoonoses Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37170441/>

Periodic vaccination against rabies is essential for individuals at continuing risk of rabies exposure. There is limited evidence on long-term immunogenicity after a 3-dose intramuscular (3IM) pre-exposure prophylaxis (PrEP) and single IM booster dose, thus current guideline recommendations differ in the interval for serology tests following PrEP and boosters. This study investigated post-PrEP and post-booster persistence of antibodies in Australian bat carers. Bat carers who received 3IM PrEP/booster doses and had post-PrEP/booster serology test results were included. The proportion of antibody-negative (<0.5 EU/mL) individuals after PrEP/booster dose were examined. Three hundred and five participants (65.6% females, median age at PrEP 43.1 years) were included. The proportion who were antibody-negative varied depending on the time between 3IM PrEP and the serology test: 8.0% <1 year, 29.8% 1-2 years, 21.2% 2-3 years and 7.7% >3 years. Ninety-one participants receiving booster doses were further assessed. Only one participant was antibody-negative at >3 years after receiving one IM booster dose. Our findings support that a serology test should be performed 1 year after 3IM PrEP, followed by first booster if required. Rabies antibodies persist for many years after receiving the booster doses. The interval between subsequent serology tests and the first booster dose should be no longer than 3 years. Future studies are required to provide more insight into the most appropriate timing of subsequent boosters.

A novel epitope tag from rabies virus has versatile in vitro applications.

Zhang Y, Zhao L, Wang Q, Zhang Z, Ren X, Yang X, Zeng S, Lv L, Zhao L, Su S, Chen X, Fu B.

11-05-2023

Appl Microbiol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37166480/>

Rabies in Southeast Asia: a systematic review of its incidence, risk factors and mortality.

Jane Ling MY, Halim AFNA, Ahmad D, Ramly N, Hassan MR, Syed Abdul Rahim SS, Saffree Jeffree M, Omar A, Hidrus A.

10-05-2023

BMJ Open.

<https://pubmed.ncbi.nlm.nih.gov/37164462/>

Sf9 Cell Metabolism Throughout the Recombinant Baculovirus and Rabies Virus-Like Particles Production in Two Culture Systems.

Guardalini LGO, Leme J, da Silva Cavalcante PE, de Mello RG, Bernardino TC, Jared SGS, Antoniazzi MM, Astray RM, Tonso A, Núñez EGF, Jorge SAC.

10-05-2023

Mol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37162721/>

This work aimed to assess the Sf9 cell metabolism during growth, and infection steps with recombinant baculovirus bearing rabies virus proteins, to finally obtain rabies VLP in two culture systems: Schott flask (SF) and stirred tank reactor (STR). Eight assays were performed in SF and STR (four assays in each system) using serum-free SF900 III culture medium. Two non-infection growth kinetics assays and six recombinant baculovirus infection assays. The infection runs were carried out at 0.1 pfu/cell multiplicity of infection (MOI) for single baculovirus bearing rabies glycoprotein (BVG) and matrix protein (BVM) and a coinfection with both baculoviruses at MOI of 3 and 2 pfu/cell for BVG and BVM, respectively. The SF assays were done in triplicate. The glucose, glutamine, glutamate, lactate, and ammonium uptake or release specific rates were quantified over the exponential growth phase and infection stage. The highest uptake specific rate was observed for glucose (42.5×10^{-12} mmol cell/h) in SF and for glutamine (30.8×10^{-12} mmol/cell/h) in STR, in the exponential growth phases. A wave pattern was observed for assessed analytes throughout the infection phase and the glucose had the highest wave amplitude within the 10^{-10} mmol cell/h order. This alternative uptake and release behavior is in harmony with the lytic cycle of baculovirus in insect cells. The virus propagation and VLP generation were not limited by glucose, glutamine, and glutamate, neither by the toxicity of lactate nor ammonium under the conditions appraised in this work. The findings from this work can be useful to set baculovirus infection processes at high cell density to improve rabies VLP yield, purity, and productivity.

Bats (Mammalia: Chiroptera) in urban-rural interfaces: community structure associated with pathogen screening in São Paulo-the largest metropolitan region in Brazil.

Brito JEC, de Mello BGV, Gaeta NC, Batista JMN, Brito TR, Agostinho WC, Brandão PE, Heinemann MB, Dias RA.

08-05-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/37154860/>

Little is known about the influence of the urban environments on bat species 'ecology. The urbanization process potentially lead to critical ecological changes in bat communities' intra and interspecific pathogenic transmissions dynamics. To date, the monitoring of pathogens in bats in Brazil has only been done with bats found dead or alive in households, from rabies surveillance systems. The present work aimed to investigate how urbanization influenced bat richness, relative abundance and pathogen occurrence. Most captured bats were Phyllostomidae, especially *Sturnira lilium*, *Artibeus lituratus*, *A. fimbriatus*, *Glossophaga soricina*, and *Platyrrhinus lineatus*, among others. From preserved-rural towards urban areas the lesser the bat richness, the higher the relative abundance of the captured bats. Noise level, luminosity and relative humidity correlated with bat abundance. The proportion of genders, sexually active bats and their size (weight, right forearm length, and body condition index) were stable throughout the investigation. Still, the proportion of pregnant females was higher in Spring and the number of juveniles in Summer, evidencing the seasonality of reproduction. Several Enterobacteria were isolated, evidencing a significant role of bats in the circulation of pathogens of medical and veterinary interest. These results are crucial in the pursuit of a harmonious coexistence between humans, bats and domestic animals in areas with different levels of anthropization.

Immune interference in effectiveness of influenza and COVID-19 vaccination.

Xie Y, Tian X, Zhang X, Yao H, Wu N.

19-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37153582/>

Notifications of suspected rabies exposure increased in Finland: 26 years of one health surveillance, 1995-2020.

Rimhanen-Finne R, Ollgren J, Gadd T, Nokireki T.

07-05-2023

Infect Dis (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37151089/>

Background: Finland is a rabies virus-free country since 1991. Notification of suspected cases of rabies exposures, leading to post-exposure prophylaxis, is mandatory. We characterised suspected cases of rabies exposure, analysed animal surveillance data and calculated costs for vaccine and immunoglobulin and treatment to estimate the financial burden of rabies control in Finland. **Methods:** The incidence rate ratios of suspected cases of rabies exposure were calculated from Finnish Infectious Disease Registry and Statistics Finland data. Animal surveillance data were obtained from the Finnish Food Authority's registries. Calculation of costs were based on the medical and treatment costs of rabies control. **Results:** In 2007, one

human rabies infection linked to a dog bite in the Philippines and rabies infection in a dog imported from India were diagnosed in Finland. In 2009, 2016 and 2017, lyssaviruses were found in bats. Notifications of suspected rabies exposures increased during 2007-2019. Two-thirds of the exposures occurred abroad, mainly in Asian and African countries. Bats were the most frequent domestic exposing animal. The import of vaccine and immunoglobulin doses increased. The annual cost of Finnish rabies control is estimated to be over €1.65 million.

Conclusions: Increased awareness of rabies and bat lyssavirus infections probably increased post-exposure prophylaxis and reporting. Travellers need country-specific guidance on how to prevent exposures, and citizens need instructions on animal imports and how to handle bats.

Schistosomiasis

Rare presentation of gallbladder schistosomiasis: a case report.

Mahli Y, Aldamegh MS, Aljohani M.

Mai-2023

J Int Med Res.

<https://pubmed.ncbi.nlm.nih.gov/37170560/>

DNA barcoding as a valuable tool for delimiting mollusk species of the genus *Biomphalaria* Preston, 1910 (Gastropoda: Planorbidae).

de Araújo AD, Carvalho ODS, Gava SG, Caldeira RL.

24-04-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37168391/>

Test-Treat-Track-Test-Treat Strategy for Control of Schistosomiasis in Two Low-Prevalence Villages in Northwestern Tanzania.

Maganga JK, Campbell CH, Angelo T, Mosha J, Mwangi JR, Kinung'hi SM.

09-05-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37160273/>

Mass drug administration of praziquantel becomes a less attractive strategy for elimination of schistosomiasis in low-prevalence areas due to cost implications and low treatment compliance. We aimed to determine the feasibility of a Test-Treat-Track-Test-Treat (5T) strategy in two low-prevalence villages; the 5T strategy has been successfully implemented in diseases such as malaria. A total of 200 school children aged 6-12 years were randomly selected from two schools and tested for *Schistosoma mansoni* infection using the point-of-care circulating cathodic antigen test. *Schistosoma mansoni*-positive children, referred to as first-generation cases (FGCs), were tracked and treated including up to five members of their families. Second-generation cases, identified by the FGCs as their close, non-relative contacts, were also tracked, tested, and treated, including up to five

members of their families. The prevalence of schistosomiasis among screened FGCs was 16.5% (33/200) in both villages. Twenty-four FGCs were included in the study. Prevalence among 94 contacts of FGCs was 46.8% (44/94). The proportion was higher in Muda than Bulunga village (61.2% versus 31.1%, $\chi^2 = 10.6611$, $P = 0.005$). Prevalence among SGCs and their contacts was 37.5% (9/24) and 47.1% (49/104), respectively. Overall, the 5T strategy identified 102 additional cases out of 222 tracked from FGCs, 95% of whom were treated, at a total time of 52 hours. Our data demonstrate the potential of the 5T strategy in identifying and treating additional cases in the community and hence its practicality in schistosomiasis control in low-prevalence settings at relatively low time and resources investment.

Identification of *Bulinus forskalii* as a potential intermediate host of *Schistosoma haematobium* in Senegal.

Gaye PM, Doucouré S, Sow D, Sokhna C, Ranque S.

09-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37159452/>

Understanding the transmission of *Schistosoma haematobium* in the Senegal River Delta requires knowledge of the snails serving as intermediate hosts. Accurate identification of both the snails and the infecting *Schistosoma* species is therefore essential. Cercarial emission tests and multi-locus (COX1 and ITS) genetic analysis were performed on *Bulinus forskalii* snails to confirm their susceptibility to *S. haematobium* infection. A total of 55 *Bulinus forskalii*, adequately identified by MALDI-TOF mass spectrometry, were assessed. Cercarial shedding and RT-PCR assays detected 13 (23.6%) and 17 (31.0%), respectively, *Bulinus forskalii* snails parasitized by *S. haematobium* complex fluke. Nucleotide sequence analysis identified *S. haematobium* in 6 (11.0%) using COX1 and 3 (5.5%) using ITS2, and *S. bovis* in 3 (5.5%) using COX1 and 3 (5.5%) using ITS2. This result is the first report of infection of *Bulinus forskalii* by *S. haematobium* complex parasites in Senegal using innovative and more accurate identification methods to discriminate this snail and characterize its infection by *S. haematobium*.

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

Tang RY, Yin L, Yao L, Zhang QF, Chen XP.

08-05-2023

Microbiol Spectr.

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

Single-sex schistosomiasis: a mini review.

Zhong H, Jin Y.

19-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37153566/>

A case report of conus intramedullary mansonii neuroschistosomiasis.

Mohandas P, Sarkar H, Jain D, Sundaram VKG.

21-04-2023

Surg Neurol Int.

<https://pubmed.ncbi.nlm.nih.gov/37151453/>

Background: Conus schistosomiasis is an extremely rare entity in which patients present with a wide range of neurological symptoms such as low back pain, paresthesia, fever, myalgia, paraparesis, and paraplegia. This neglected tropical parasitic disease causes significant neurological morbidity. The migration of parasitic worms and their eggs into the central nervous system can lead to profound and life-altering disabilities. Early, accurate diagnosis, and treatment can lead to the complete resolution of symptoms. **Case description:** A 5-year-old boy from South Sudan presented with complaints of sudden onset, progressive bilateral lower limb weakness for the past month, inability to walk or stand without assistance, and urinary incontinence. Magnetic resonance imaging spine showed an irregular enhancing lesion within the conus. The various possibilities, such as Astrocytoma, and granulomatous disorders were considered. However, a biopsy revealed the lesion to be Conus schistosomiasis, a rare condition with only a few cases reported in children. Typical clinicoradiological presentation and the treatment paradigm have been discussed in this manuscript. Appropriate management of this lesion can avert surgical intervention needed for either a diagnosis or treatment. **Conclusion:** This case report aims to emphasize the importance of considering schistosomiasis as an important differential diagnosis of a conus intramedullary lesion, especially in patients from tropical endemic countries. The neurological recovery in this infestation is directly related to early diagnosis and treatment. Therefore, it is essential to recognize this entity, as early detection and management would result in significant neurological improvement without undergoing surgery.

Visual diagnosis of female genital schistosomiasis in Zambian women from hand-held colposcopy: agreement of expert image review and association with clinical symptoms.

Sturt A, Bristowe H, Webb E, Hansingo I, Phiri C, Mudenda M, Mapani J, Mweene T, Levecke B, Cools P, van Dam G, Corstjens P, Ayles H, Hayes R, Francis S, van Lieshout L, Vwalika B, Kjetland E, Bustinduy A.

04-05-2023

Wellcome Open Res.

<https://pubmed.ncbi.nlm.nih.gov/36864924/>

Antiparasitic properties of 4-nerolidylcatechol from *Pothomorphe umbellata* (L.) Miq. (Piperaceae) in vitro and in mice models with either prepatent or patent *Schistosoma mansonii* infections.

Costa DS, Leal CM, Cajas RA, Gazolla MC, Silva LM, Carvalho LSA, Lemes BL, Moura RO, Almeida J, de Moraes J, da Silva Filho AA.

05-05-2023

J Ethnopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37149066/>

Ethnopharmacological relevance: Roots of *Pothomorphe umbellata* (L.) Miq. are used in traditional medicine of Africa and South America for the treatment of malaria and helminthiasis. However, neither *P. umbellata* nor its isolated compounds have been evaluated against *Schistosoma* species. **Aims of this study:** To investigate the antischistosomal effects of *P. umbellata* root extracts and the isolated compound 4-nerolidylcatechol (4-NC) against *Schistosoma mansonii* ex vivo and in murine models of schistosomiasis. **Materials and methods:** The crude hydroalcoholic (PuE) and hexane (PuH) extracts of *P. umbellata* roots were prepared and initially submitted to an ex vivo phenotypic screening against adult *S. mansonii*. PuH was analyzed by HPLC-DAD, characterized by UHPLC-HRMS/MS, and submitted to chromatographic fractionation, leading to the isolation of 4-NC. The anthelmintic properties of 4-NC were assayed ex vivo against adult schistosomes and in murine models of schistosomiasis for both patent and prepatent *S. mansonii* infections. Praziquantel (PZQ) was used as a reference compound. **Results:** PuE (EC₅₀: 18.7 µg/mL) and PuH (EC₅₀: 9.2 µg/mL) kill adult schistosomes ex vivo. The UHPLC-HRMS/MS analysis of PuH, the most active extract, revealed the presence of 4-NC, peltatol A, and peltatol B or C. After isolation from PuH, 4-NC presented remarkable in vitro schistosomicidal activity with EC₅₀ of 2.9 µM (0.91 µg/mL) and a selectivity index higher than 68 against Vero mammalian cells, without affecting viability of nematode *Caenorhabditis elegans*. In patent *S. mansonii* infection, the oral treatment with 4-NC decreased worm burden and egg production in 52.1% and 52.3%, respectively, also reducing splenomegaly and hepatomegaly. 4-NC, unlike PZQ, showed in vivo efficacy against juvenile *S. mansonii*, decreasing worm burden in 52.4%. **Conclusions:** This study demonstrates that *P. umbellata* roots possess antischistosomal activity, giving support for the medicinal use of this plant against parasites. 4-NC was identified from *P. umbellata* roots as one of the effective in vitro and in vivo antischistosomal compound and as a potential lead for the development of novel anthelmintics.

Nematophagous fungus *Pochonia chlamydosporia* to control parasitic diseases in animals.

Dos Santos Fonseca J, Altoé LSC, de Carvalho LM, de Freitas Soares FE, Braga FR, de Araújo JV.

06-05-2023

Appl Microbiol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37148335/>

Long non-coding RNAs are essential for *Schistosoma mansonii* pairing-dependent adult worm homeostasis and fertility.

Silveira GO, Coelho HS, Pereira ASA, Miyasato PA, Santos DW, Maciel LF, Olberg GGG, Tahira AC, Nakano E, Oliveira MLS, Amaral MS, Verjovski-Almeida S.

05-05-2023

PLoS Pathog.
<https://pubmed.ncbi.nlm.nih.gov/37146077/>

The association of systemic inflammation and cognitive functions of pre-school aged children residing in a *Schistosoma haematobium* endemic area in Zimbabwe.

Kasambala M, Mukaratirwa S, Vengesai A, Mduluzza-Jokonya T, Jokonya L, Midzi H, Makota RB, Mutemeri A, Maziti E, Dube-Marimbe B, Chibanda D, Mutapi F, Mduluzza T.

18-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37143686/>

Background: Cognitive function is negatively impacted by schistosomiasis and might be caused by systemic inflammation which has been hypothesized to be one of the mechanisms driving cognitive decline. This study explored the association of systemic inflammatory biomarkers; interleukin (IL)-10, IL-6, IL-17, transforming growth factor (TGF- β), tumor necrosis factor (TNF- α), C-reactive protein (CRP) and hematological parameters with cognitive performance of preschool-aged children (PSAC) from an *Schistosoma haematobium* endemic area.

Methods: The Griffith III tool was used to measure the cognitive performance of 136 PSAC. Whole blood and sera were collected and used to quantify levels of IL-10, TNF- α , IL-6, TGF- β , IL-17 A and CRP using the enzyme-linked immunosorbent assay and hematological parameters using the hematology analyzer. Spearman correlation analysis was used to determine the relationship between each inflammatory biomarker and cognitive performance. Multivariate logistic regression analysis was used to determine whether systemic inflammation due to *S. haematobium* infection affected cognitive performance in PSAC. **Results:** Higher levels of TNF- α and IL-6, were correlated with lower performance in the Foundations of Learning domain ($r = -0.30$; $p < 0.001$ and $r = -0.26$; $p < 0.001$), respectively. Low cognitive performance in the Eye-Hand-Coordination Domain was observed in PSAC with high levels of the following inflammatory biomarkers that showed negative correlations to performance; TNF- α ($r = -0.26$; $p < 0.001$), IL-6 ($r = -0.29$; $p < 0.001$), IL-10 ($r = -0.18$; $p < 0.04$), WBC ($r = -0.29$; $p < 0.001$), neutrophils ($r = -0.21$; $p = 0.01$) and lymphocytes ($r = -0.25$; $p = 0.003$). The General Development Domain correlated with TNF- α ($r = -0.28$; $p < 0.001$) and IL-6 ($r = -0.30$; $p < 0.001$). TGF- β , IL-17A and MXD had no significant correlations to performance in any of the cognitive domains. The overall general development of PSAC was negatively impacted by *S. haematobium* infections (OR = 7.6; $p = 0.008$) and (OR = 5.6; $p = 0.03$) where the PSAC had higher levels of TNF- α and IL-6 respectively. **Conclusion:** Systemic inflammation and *S. haematobium* infections are negatively associated with cognitive function. We recommend the inclusion of PSAC into mass drug treatment programs.

Ethnobotanical knowledge on native Brazilian medicinal plants traditionally used as anthelmintic agents - A review.

Kuhn Agnes KN, Boeff DD, de Oliveira Carvalho L, Konrath EL.

Juin-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37044282/>

Intestinal helminthiasis is a neglected disease that affects a significant portion of the global population, specifically in developing countries, where medicinal plants are widely used for therapeutic purposes. With the purpose to identify the native species used in traditional Brazilian medicine for the management of helminthiasis, ethnopharmacological books edited in Brazil documenting the folk use of medicinal plants were analyzed. The native species cited in at least three studies were selected, and bibliographic research was performed using electronic databases to identify their scientifically validated anthelmintic properties. The search retrieved 133 native species belonging to 88 genera and 43 families from all six Brazilian biomes. Fabaceae (14 Genera and 25 Species) and Asteraceae (7 Genera and 8 Species) were the most frequently cited families. The most reported native species were *Baccharis crispa* Spreng., *Hymenaea courbaril* L., *Senna occidentalis* (L.) Link, *Carapa guianensis* Aubl., *Stachytarpheta cayennensis* (Rich.) Vahl, *Annona glabra* L., *Hymenaea stigonocarpa* Mart. ex Hayne, *Spigelia anthelmia* L., *Simarouba versicolor* A.St.-Hil. and *Anacardium occidentale* L. Bark (19%) and leaves (17%) were the most commonly used plant parts, and decoction (27%) was the most preferred method of preparation. Evidence of the anthelmintic properties of most species was confirmed using in vitro assays for key human and animal parasites, including *Haemonchus contortus*, *Hymenolepis diminuta*, *Schistosoma mansoni* and *Trichostrongylus* spp. The species *S. alata*, *S. occidentalis*, *A. occidentale*, and *S. anthelmia* have been the subject of many biological studies, supporting their use as vermicides. The overall results obtained in this review revealed that Brazil is rich in traditional herbal medicines used to manage helminthiasis; however pharmacological investigations are lacking to confirm their therapeutic properties. Thus, this study could serve as a baseline to validate their use and encourage further clinical investigation of their vermifuge potential.

Trachome

Safety of integrated mass drug administration of azithromycin, albendazole and ivermectin versus standard treatment regimens: a cluster-randomised trial in Ethiopia.

McPherson S, Tafese G, Tafese T, Behaksra SW, Solomon H, Oljira B, Miecha H, Debebe KA, Kebede B, Gebre T, Kebede F, Seife F, Tadesse F, Mammo B, Aseffa A, Solomon AW, Mabey DCW, Marks M, Gadisa E.

27-04-2023

EClinicalMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37152362/>

Validation of immunoassays for the *Chlamydia trachomatis* antigen Pgp3 using a chimeric monoclonal antibody.

Goodhew B, Tang X, Goldstein J, Lee J, Martin D, Gwyn S.

04-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37142607/>

Seroepidemiology, or measuring antibodies to pathogens to estimate population-level exposure, can provide useful public health data. The tests used, however, often lack sufficient validation data due to absence of a gold standard. For many pathogens, serum antibodies can be detected long after resolution of infection, but infection status is often used as a gold standard for antibody positivity. To ensure that recently developed antibody tests for seroepidemiology of *Chlamydia trachomatis* (Ct), the causative agent of urogenital chlamydia and the blinding eye disease trachoma, have high performance, we generated a chimeric antibody to the immunodominant Ct antigen Pgp3. Two clones were selected to evaluate the test performance of three assays to measure antibodies to Pgp3: multiplex bead assay (MBA), enzyme-linked immunosorbent assay (ELISA), and lateral flow assay (LFA). Overall, each assay demonstrated high accuracy and precision when tested using either clone, and the clones were stable when stored at - 20 °C and 4 °C for almost 2 years. The limit of detection was similar for MBA and LFA, but almost a log-fold higher (i.e. less sensitive) using ELISA. Overall, the chimeric antibodies represent stable control reagents for tests with robust performance and will facilitate deployment of these tests to other laboratories.

How well do coverage surveys and programmatically reported mass drug administration coverage match? Results from 214 mass drug administration campaigns in 15 countries, 2008-2017.

Zoerhoff KL, Mbabazi PS, Gass K, Kraemer J, Fuller BB, Blair L, Bougma R, Meite A, Negussu N, Gashaw B, Nash SD, Biritwum NK, Lemoine JF, Ulliyartha Pangaribuan H, Wijayanti E, Kollie K, Rasoamananjana CF, Juzziwelo L, Mkwanda S, Rimal P, Gnanou I, Diop B, Dorkenoo AM, Bronzan R, Tukahebwa EM, Kabole F, Yevstigneyeva V, Bisanzio D, Courtney L, Koroma J, Endayishimye E, Reithinger R, Baker MC, Fleming FM.

Mai-2023

BMJ Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37142297/>

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

Updates on parasite infection prevalence in the Joseon period based on parasitological studies of human coprolites isolated from archaeological sites in the cities of Euijeongbu, Gumi, and Wonju.

Oh CS, Chai JY, Min S, Oh KT, Seol J, Song MK, Shin DH, Seo M.

Fév-2023

Parasites Hosts Dis.

<https://pubmed.ncbi.nlm.nih.gov/37170469/>

Parasite infection rates estimated by examining ancient coprolites can provide insights into parasitism in Joseon society. Using newly discovered Joseon period cases is essential to regularly update the parasite infection rates and reinforce the reliability of our previous estimations. In the present study, we investigated parasite infections in Joseon coprolites newly isolated from the cities of Euijeongbu, Gumi, and Wonju. We then updated the overall parasite infection rates of Joseon period samples (n= 30) as follows: 86.7% (26/30) for *Trichuris trichiura*, 56.7% (17/30) for *Ascaris lumbricoides*, 30.0% (9/30) for *Clonorchis sinensis*, and 30.0% (9/30) for *Paragonimus westermani*. The parasite infection rates in the Joseon society, estimated through coprolite examination, were very similar to those determined previously despite the addition of new cases to the existing data pool.

TLR3 activation by *Clonorchis sinensis* infection alleviates the fluke-induced liver fibrosis.

Wang Y, Gong P, Zhang X, Wang X, Zhang X, Zhang N, Yu Y, Ma Y, Zhang H, Zhang X, Li X, Li J.

11-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37167198/>

A common presentation of uncommon disease - Biliary Fasciola Hepatica.

Yousaf MS, Kamani L, Fareed G, Khan AMK.

10-05-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37165596/>

Molecular characterization and serodiagnostic evaluation of the *Echinococcus ortleppi* recombinant glutaredoxin 1 protein for cystic

echinococcosis in buffalo (*Bubalus bubalis*).

Yashica KA, Samanta S, Balaji R, Jawalagatti V, Silamparasan M, Anandu S, Rialch A, Gupta SC, Tewari AK.

02-05-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37156090/>

Cystic echinococcosis (CE), caused by the metacestode of *Echinococcus granulosus sensu lato* (s.l.), adversely affects the physiology of the vital organs in which they grow. Condemnation of meat causes substantial economic loss to the livestock industry. Conventionally the infection is detected by necropsy as serological diagnosis of the infection in livestock is ambiguous. Identification of specific diagnostic antigens would be a substitute for the cyst fluid antigens which lack adequate diagnostic sensitivity and specificity. BLAST analysis supported by the negligible pairwise nucleotide distance of the 389 nt COX1, 489 nt NAD1, and 425 nt ITS1 with the related sequences of *E. ortleppi* ascertained the association of *E. ortleppi* with CE in buffaloes. Given the extensive distribution of glutaredoxin 1 in every developmental stage of *Echinococcus granulosus* s.l. that makes it an ideal serodiagnostic antigen for CE, we expressed the 14 kDa *E. ortleppi* glutaredoxin 1 (rEoGrx1) protein in *E. coli* BL21 (DE3) and tested a total of 225 sera samples, including 126 sera samples from the necropsy-positive buffalo, by the rEoGrx1 IgG-ELISA. The ELISA could detect a total of 82/126 sera samples as positive. The diagnostic sensitivity and specificity of the rEoGrx1 IgG-ELISA were 65.1 % and 51.5 %, respectively. The protein showed serological cross-reaction against *Fasciola gigantica*, *Toxoplasma gondii*, and *Sarcocystis* sp. The in silico bioinformatics analysis of the *E. ortleppi*, *F. gigantica*, and *T. gondii* glutaredoxin sequences revealed fully conserved amino acids at positions 11 and 21, the substitution of conserved amino acids at positions 14 and 6, and semi-conserved substitutions at positions 3 and 4, respectively. The findings partly explain the molecular basis of the serological cross-reactivity of the protein.

Diversity and prevalence of gastrointestinal parasites of Black Bengal goats in Natore, Bangladesh.

Chakraborty M, Shohana NN, Begum N, Dey AR, Rony SA, Akter S, Alam MZ.

31-03-2023

J Adv Vet Anim Res.

<https://pubmed.ncbi.nlm.nih.gov/37155548/>

Objectives: The objective of this work was to estimate the diversity of gastrointestinal (GI) parasite species, their prevalence, and risk factors in Black Bengal goats (BBGs) of Natore, Bangladesh. **Materials and methods:** Fecal samples from randomly selected 260 BBGs were processed through Stoll's ova counting method, floatation, and simple sedimentation method. Microscopy-based identification of parasitic eggs, cysts, or oocysts was made. A semi-structured questionnaire-based data on host and management practices were collected from the owner. Data analysis was done using Statistical Package for Social

Sciences. **Results:** The overall prevalence of GI parasites in BBGs was 65.4%, with an individual prevalence of 8.5% for *Fasciola gigantica*, 21.5% for *Paramphistomum* spp., 20% for *Haemonchus* spp., 34.2% for *Strongyloides* spp., 8.5% for *Trichuris* spp., and 9.2% for *Eimeria* spp. No significant effect of host age, gender, body condition, animal rearing system, or housing floor type was observed on parasitism. Animals of young age, female, poorly body-conditioned, living in a free-range system, and housed on a muddy floor had a relatively higher susceptibility to infection. Deworming had a significant impact on reducing the frequency of caprine GI parasitism. **Conclusions:** Despite the significant effect of anthelmintic, the elevated prevalence of GI parasites in BBGs suggests a critical need for developing effective strategies to prevent caprine parasitoses.

Secondary infection of *Fasciola gigantica* in buffaloes shows a similar pattern of serum cytokine secretion as in primary infection.

Meng Z, Zhai L, Guo Y, Zheng M, Li L, Wen C, Zhang W, Di W.

20-04-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37152685/>

Mediastinal Cysts Associated with *Paragonimus westermani*.

Chae KJ, Kim JH.

05-05-2023

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37150353/>

Incidence of fish-borne trematode infections and associated factors: results from a cohort study in highly endemic communities in northern Vietnam.

Nguyen TTB, Dermauw V, Bui DT, Dahma H, Le DT, Nguyen HTT, Do DT, Dorny P, Losson B, Vandenberg O.

Juin-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37072586/>

Fish-borne trematodes (FIBT) are an important group of zoonotic parasites negatively affecting human health, mainly in Asia. Most studies on FIBT have applied a cross-sectional design, which provides weaker evidence on potential risk factors for transmission than a cohort study. This cohort study aimed to estimate the incidence and identify associated risk factors for FIBT infection in Vietnam. Between April 2018 and May 2019, two communes in Yen Bai province, a highly endemic area for FIBT, were visited for sampling. Participants with a negative stool result for FIBT at baseline, were invited for follow-up and data collection, at months 4, 9, and 13. Stools were examined using Kato-Katz and formalin-ethyl acetate concentration techniques to detect FIBT eggs, whereas a questionnaire was used for interviewing participants to determine the risk factors for FIBT infection during each follow-up period. The incidence risk and the incidence rate were calculated, and univariate and

multivariable models were run to identify the risk factors for FiBT. A total of 194 people, negative for FiBT eggs at the baseline survey, were invited to participate in the study, and 111 people agreed to enroll in the follow-up. The incidence risk at months 4, 9, and 13 was 9.0%, 6.4%, and 5.1%, respectively. We finally used data from 95 participants for the risk factor analysis, excluding 16 people lost for the follow-up. Overall, 20 people became infected with FiBT (IR = 21.1%). The incidence rate of FiBT infection was 21.4/100 person-year. In the univariate analysis, consumption of raw fish was the main risk factor (RR = 4.59, 95%CI = 1.95-10.82), followed by being male (RR = 3.41, 95%CI = 1.56-7.45) and drinking alcohol (RR = 3.25, 95%CI = 1.49-7.11). In the multivariable analysis, only consumption of raw-fish dishes was significantly associated with FiBT infection. The people who consumed raw fish were 3.44 (95%CI = 1.11-10.70) times more at risk of infection with FiBT as compared to individuals who did not consume raw fish. It can be concluded that the FiBT incidence is high in the study area. More awareness campaigns are needed to stop eating raw fish in these areas to reduce FBT infection.

A case of a dog with paragonimiasis after consumption of raw deer meat.

Yoshimura A, Azakami D, Kishimoto M, Ohmori T, Hirao D, Morita S, Hasegawa S, Morita T, Fukushima R.

03-05-2023

J Vet Med Sci.

<https://pubmed.ncbi.nlm.nih.gov/36948633/>

Trypanosomes (trypanosomiasis et maladie de Chagas)

Profiling the bloodstream form and procyclic form *Trypanosoma brucei* cell cycle using single cell transcriptomics.

Briggs EM, Marques CA, Oldrieve GR, Hu J, Otto TD, Matthews KR.

11-05-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37166108/>

Extracellular vesicles of trypomastigotes of *Trypanosoma cruzi* induce changes in ubiquitin-related processes, cell-signaling pathways and apoptosis.

Cornet-Gomez A, Retana Moreira L, Kronenberger T, Osuna A.

10-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37165081/>

Influence of amino acid size at the P3 position of N-Cbz-tripeptide Michael acceptors targeting falcipain-2 and rhodesain for the treatment of malaria and human african trypanosomiasis.

Previti S, Ettari R, Di Chio C, Legac J, Bogacz M, Zimmer C, Schirmeister T, Rosenthal PJ, Zappalà M.

04-05-2023

Bioorg Chem.

<https://pubmed.ncbi.nlm.nih.gov/37163812/>

High growth hormone serum partially protects mice against *Trypanosoma cruzi* infection.

Mora-Criollo P, Basu R, Qian Y, Funk K, Bell S, Young JA, List EO, Costales JA, Guevara-Aguirre J, Grijalva MJ, Kopchick JJ.

10-05-2023

FEBS Open Bio.

<https://pubmed.ncbi.nlm.nih.gov/37163287/>

Chagas disease (CD) is one of the most devastating parasitic diseases in the Americas, affecting 7-8 million people worldwide. In vitro and in vivo experiments have demonstrated that growth hormone (GH) serum levels decrease as CD progresses. Interestingly, inactivating mutations in the GH receptor in humans result in Laron syndrome (LS), a clinical entity characterized by increased serum levels of GH and decreased insulin growth factor-1 (IGF-1). The largest cohort of LS subjects lives in the southern provinces of Ecuador. Remarkably, no clinical CD cases have been reported in these individuals despite living in highly endemic areas. In the current ex vivo study, we employed serum from GHR^{-/-} mice, also known as LS mice (a model of GH resistance with high GH and low IGF-1 levels), and serum from bovine GH (bGH) transgenic mice (high GH and IGF-1), to test the effect on *Trypanosoma cruzi* infection. We infected mouse fibroblast L-cells with *T. cruzi* (etiological CD infectious agent) and treated them with serum from each mouse type. Treatment with GHR^{-/-} serum (LS mice) significantly decreased L-cell infection by 28% compared with 48% from control wild-type mouse serum (WT). Treatment with bGH mouse serum significantly decreased infection of cells by 41% compared with 54% from WT controls. Our results suggest that high GH and low IGF-1 in blood circulation, as typically seen in LS individuals, confer partial protection against *T. cruzi* infection. This study is the first to report decreased *T. cruzi* infection using serum collected from two modified mouse lines with altered GH action (GHR^{-/-} and bGH).

The Role of Asn11 in Catalysis by Triosephosphate Isomerase.

Hegazy R, Cordara G, Wierenga RK, Richard JP.

10-05-2023

Biochemistry.

<https://pubmed.ncbi.nlm.nih.gov/37162263/>

Four catalytic amino acids at triosephosphate isomerase (TIM) are highly conserved: N11, K13, H95, and E167. Asparagine 11 is the last of these to be characterized in mutagenesis studies. The ND2 side chain atom of N11 is hydrogen bonded to the O-1 hydroxyl of enzyme-bound dihydroxyacetone phosphate (DHAP), and it sits in an extended chain of hydrogen-bonded side chains that includes T75' from the second subunit. The N11A variants of wild-type TIM from *Trypanosoma brucei brucei*

(*TbbTIM*) and *Leishmania mexicana* (*LmTIM*) undergo dissociation from the dimer to monomer under our assay conditions. Values of $K_{as} = 8 \times 10^3$ and $1 \times 10^6 \text{ M}^{-1}$, respectively, were determined for the conversion of monomeric N11A *TbbTIM* and *LmTIM* into their homodimers. The N11A substitution at the variant of *LmTIM* previously stabilized by the E65Q substitution gives the N11A/E65Q variant that is stable to dissociation under our assay conditions. The X-ray crystal structure of N11A/E65Q *LmTIM* shows an active site that is essentially superimposable on that for wild-type *TbbTIM*, which also has a glutamine at position 65. A comparison of the kinetic parameters for E65Q *LmTIM* and N11A/E65Q *LmTIM*-catalyzed reactions of (*R*)-glyceraldehyde 3-phosphate (GAP) and (DHAP) shows that the N11A substitution results in a (13-14)-fold decrease in k_{cat}/K_m for substrate isomerization and a similar decrease in k_{cat} for DHAP but only a 2-fold decrease in k_{cat} for GAP.

Cytogenetic Key to Identification of Triatominae Species Reported in an Outbreak Region of Oral Transmission of Chagas Disease in the Brazilian Northeast.

Nhapulo EF, de Mello DV, Cesaretto LP, Alevi JJ, Cristal DC, Montanari G, Azevedo LMS, Masarin IDS, Galvão C, Alevi KCC.

09-05-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37160280/>

Targeting the nucleotide metabolism of *Trypanosoma brucei* and other trypanosomatids.

Hofer A.

08-05-2023

FEMS Microbiol Rev.

<https://pubmed.ncbi.nlm.nih.gov/37156497/>

African sleeping sickness, Chagas disease, and leishmaniasis are life-threatening diseases that together affect millions of people around the world and are caused by different members of the protozoan family Trypanosomatidae. The most-studied member of the family is *Trypanosoma brucei*, which is spread by tsetse flies and causes African sleeping sickness. Nucleotide metabolism in *T. brucei* and other trypanosomatids is significantly different from that of mammals and was recognized as a target for chemotherapy already in the 1970s-1980 s. A more thorough investigation of the nucleotide metabolism in recent years has paved the way for identifying nucleoside analogues that can cure *T. brucei* brain infections in animal models. Specific features of *T. brucei* nucleotide metabolism include the lack of de novo purine biosynthesis, the presence of very efficient purine transporters, the lack of salvage pathways for CTP synthesis, unique enzyme localizations, and a recently discovered novel pathway for dTTP synthesis. This review describes the nucleotide metabolism of *T. brucei*, highlights differences and similarities to other trypanosomatids, and discusses how to exploit the parasite-specific features for drug development.

Spatial-Temporal Variations in Parasitological Prevalence and Host-Related Risk Factors of Camel Trypanosomiasis and Its Vectors in North Eastern Kenya: A Repeated Cross-Sectional Study.

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

28-04-2023

J Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37153519/>

First report of *Rhodnius amazonicus* Almeida, Santos & Sposina, 1973 (Hemiptera, Reduviidae, Triatominae) invading a dwelling in the state of Amapá, Brazil.

Galeno ÉO, Oliveira J, Santos WMD, Galardo AKR, Müller JN.

18-04-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37153416/>

Rhodnius amazonicus has been previously reported in the Brazilian states of Amazonas and Pará, as well as in French Guiana. However, this is the first recorded presence of this species in Amapá, which is situated in the northern region of Brazil. The specimen was collected from a house in the rural area of the municipality of Porto Grande. Other triatomines, such as *Panstrongylus geniculatus*, *Rhodnius pictipes*, and *Eratyrus mucronatus*, were also found in the same locality in different houses. These species are vectors of *Trypanosoma cruzi*, which causes Chagas disease. Therefore, this report may contribute to understanding transmission in the state of Amapá, where new infections and outbreaks of Chagas disease have been recorded.

Neuropsychiatric Aspects of Parasitic Infections-A Review.

Goyal G, Kaur U, Sharma M, Sehgal R.

Mar-Apr 2023

Neurol India.

<https://pubmed.ncbi.nlm.nih.gov/37148042/>

Prevalence of natural infection by *Trypanosoma evansi* in Crioula LAGEANA cattle.

Fiorin FE, Casa MDS, Griebeler LB, Goedel MF, Nascimento LFND, Neves GBD, Fontequê GV, Miletti LC, Saito ME, Fontequê JH.

03-05-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37146700/>

G-quadruplexes as key transcriptional regulators in neglected trypanosomatid parasites.

Monti L, Di Antonio M.

05-05-2023

Chembiochem.

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

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

A modelling assessment of short- and medium-term risks of programme interruptions for gambiense human African trypanosomiasis in the DRC.

Huang CI, Crump RE, Crowley EH, Hope A, Bessell PR, Shampa C, Mwamba Miaka E, Rock KS.

28-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37115809/>

Gambiense human African trypanosomiasis (gHAT) is a deadly vector-borne, neglected tropical disease found in West and Central Africa targeted for elimination of transmission (EoT) by 2030. The recent pandemic has illustrated how it can be important to quantify the impact that unplanned disruption to programme activities may have in achieving EoT. We used a previously developed model of gHAT fitted to data from the Democratic Republic of the Congo, the country with the highest global case burden, to explore how interruptions to intervention activities, due to e.g. COVID-19, Ebola or political instability, could impact progress towards EoT and gHAT burden. We simulated transmission and reporting dynamics in 38 regions within Kwilu, Mai Ndombe and Kwango provinces under six interruption scenarios lasting for nine or twenty-one months. Included in the interruption scenarios are the cessation of active screening in all scenarios and a reduction in passive detection rates and a delay or suspension of vector control deployments in some scenarios. Our results indicate that, even under the most extreme 21-month interruption scenario, EoT is not predicted to be delayed by more than one additional year compared to the length of the interruption. If existing vector control deployments continue, we predict no delay in achieving EoT even when both active and passive screening activities are interrupted. If passive screening remains as functional as in 2019, we expect a marginal negative impact on

transmission, however this depends on the strength of passive screening in each health zone. We predict a pronounced increase in additional gHAT disease burden (morbidity and mortality) in many health zones if both active and passive screening were interrupted compared to the interruption of active screening alone. The ability to continue existing vector control during medical activity interruption is also predicted to avert a moderate proportion of disease burden.

Modeling the impact of xenointoxication in dogs to halt *Trypanosoma cruzi* transmission.

Rokhsar JL, Raynor B, Sheen J, Goldstein ND, Levy MZ, Castillo-Neyra R.

08-05-2023

PLoS Comput Biol.

<https://pubmed.ncbi.nlm.nih.gov/37155680/>

Ulcère de Buruli

The development, implementation, and evaluation of an optimal model for the case detection, referral, and case management of Neglected Tropical Diseases.

Godwin-Akpan TG, Chowdhury S, Rogers EJ, Kollie KK, Zaizay FZ, Wickenden A, Zawolo GVK, Parker CBMC, Dean L.

10-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37163515/>

Background: People affected by Neglected Tropical Diseases (NTDs), specifically leprosy, Buruli ulcer (BU), yaws, and lymphatic filariasis, experience significant delays in accessing health services, often leading to catastrophic physical, psychosocial, and economic consequences. Global health actors have recognized that Sustainable Development Goal 3:3 is only achievable through an integrated inter and intra-sectoral response. This study evaluated existing case detection and referral approaches in Liberia, utilizing the findings to develop and test an Optimal Model for integrated community-based case detection, referral, and confirmation. We evaluate the efficacy of implementing the Optimal Model in improving the early diagnosis of NTDs, thus minimizing access delays and reducing disease burden. **Methods:** We used a participatory action research approach to develop, implement, and evaluate an Optimal Model for the case detection, referral, and management of case management NTDs in Liberia. We utilized qualitative and quantitative methods throughout the cycle and implemented the model for 12 months. **Results:** During the implementation of our optimal model, the annual number of cases detected increased compared to the previous year. Cases were detected at an earlier stage of disease progression, however; gendered dynamics in communities shape the case identification process for some individuals. Qualitative data showed increased knowledge of the transmission, signs, symptoms, and management options among community health workers (CHW). **Conclusion:** The

results provide evidence of the benefits of an integrated approach and the programmatic challenges to improve access to health services for persons affected by NTDs. The effectiveness of an integrated approach depends on a high level of collaboration, joint planning, and implementation embedded within existing health systems infrastructure.