



Veille scientifique

Maladies tropicales négligées

Semaine 21
22 au 28 mai 2023

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Cysticercose

Diagnostic Dilemma of Central Nervous System Tuberculosis with Neurocysticercosis and Neurosarcoidosis: A Case Report.

Bajracharya N, Lamichhane S, Lamichhane P, Bishowkarma D, Acharya A, Sharma S, Pandit P.

01-02-2023

JNMA J Nepal Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37203964/>

Neurocysticercosis and epilepsy: Imaging and clinical characteristics.

Rodríguez-Leyva I, Cantú-Flores K, Domínguez-Frausto A, Vaudano AE, Archer J, Bernhardt B, Caciagli L, Cendes F, Chinvarun Y, Federico P, Gaillard WD, Kobayashi E, Ogbole G, Rampp S, Wang I, Wang S, Concha L.

Fév-2023

Epileptic Disord.

<https://pubmed.ncbi.nlm.nih.gov/37039375/>

The ILAE Neuroimaging Task Force aimed to publish educational case reports highlighting basic aspects related to neuroimaging in epilepsy consistent with the educational mission of the ILAE. Neurocysticercosis (NCC) is highly endemic in resource-limited countries and increasingly more often seen in non-endemic regions due to migration. Cysts with larva of the tapeworm *Taenia solium* lodge in the brain and cause several neurological conditions, of which seizures are the most common. There is great heterogeneity in the clinical presentation of neurocysticercosis because cysts vary in number, larval stage, and location among patients. We here present two illustrative cases with different clinical features to highlight the varying severity of symptoms secondary to this parasitic infestation. We also present several examples of imaging characteristics of the disease at various stages, which emphasize the central role of neuroimaging in the diagnosis of neurocysticercosis.

Dengue, chikungunya et maladie à virus Zika

Genotyping of dengue virus from infected tissue samples embedded in paraffin.

Rivera JA, Rengifo AC, Rosales-Munar A, Díaz-Herrera TH, Ciro JU, Parra E, Alvarez-Díaz DA, Laiton-Donato K, Caldas ML.

25-03-2023

Viol J.

<https://pubmed.ncbi.nlm.nih.gov/37231481/>

Holobiont perspectives on tripartite interactions among microbiota, mosquitoes, and pathogens.

Zheng R, Wang Q, Wu R, Paradkar PN, Hoffmann AA, Wang GH.

25-03-2023

ISME J.

<https://pubmed.ncbi.nlm.nih.gov/37231184/>

Mosquito-borne diseases like dengue and malaria cause a significant global health burden. Unfortunately, current insecticides and environmental control strategies aimed at the vectors of these diseases are only moderately effective in decreasing disease burden. Understanding and manipulating the interaction between the mosquito holobiont (i.e., mosquitoes and their resident microbiota) and the pathogens transmitted by these mosquitoes to humans and animals could help in developing new disease control strategies. Different microorganisms found in the mosquito's microbiota affect traits related to mosquito survival, development, and reproduction. Here, we review the physiological effects of essential microbes on their mosquito hosts; the interactions between the mosquito holobiont and mosquito-borne pathogen (MBP) infections, including microbiota-induced host immune activation and Wolbachia-mediated pathogen blocking (PB); and the effects of environmental factors and host regulation on the composition of the microbiota. Finally, we briefly overview future directions in holobiont studies, and how these may lead to new effective control strategies against mosquitoes and their transmitted diseases.

Bridging the immunogenicity of a tetravalent dengue vaccine (TAK-003) from children and adolescents to adults.

LeFevre I, Bravo L, Folschweiller N, Medina EL, Moreira ED Jr, Nordio F, Sharma M, Tharenos LM, Tricou V, Watanaveeradej V, Winkle PJ, Biswal S.

25-03-2023

NPJ Vaccines.

<https://pubmed.ncbi.nlm.nih.gov/37230978/>

Immunobridging is an important methodology that can be used to extrapolate vaccine efficacy estimates to populations not evaluated in clinical studies, and that has been successfully used in developing many vaccines. Dengue, caused by a mosquito-transmitted flavivirus endemic to many tropical and subtropical regions, is traditionally thought of as a pediatric disease but is now a global threat to both children and adults. We bridged immunogenicity data from a phase 3 efficacy study of a tetravalent dengue vaccine (TAK-003), performed in children and adolescents living in endemic areas, with an immunogenicity study in adults in non-endemic areas. Neutralizing antibody responses were comparable in both studies following receipt of a two-dose TAK-003 schedule (months 0 and 3). Similar immune responses were observed across exploratory assessments of additional humoral responses. These data support the potential for clinical efficacy of TAK-003 in adults.

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

Rao S, Abeyratne E, Freitas JR, Yang C, Tharmarajah K, Mostafavi H, Liu X, Zaman M, Mahalingam S, Zaid A, Taylor A.
23-03-2023
Vaccine.
<https://pubmed.ncbi.nlm.nih.gov/37230889/>

Heart failure after dengue infection- a population-based self-controlled case-series study.

Wei KC, Wang WH, Wu CL, Chang SH, Huang YT.
23-03-2023
Travel Med Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37230157/>

Early Detection of Chikungunya Virus Utilizing the Surface Plasmon Resonance Comprising a Silver-Silicon-PtSe₂ Multilayer Structure.

Singh TI, Singh P, Karki B.
2023
Plasmonics.
<https://pubmed.ncbi.nlm.nih.gov/37229147/>

The sensing performance parameters of the SPR sensors are sensitivity, detection accuracy, the figure of merit (FOM), and full-width half maximum (FWHM), and it has been discussed with refractive indexes of analyte 1.33, 1.35, 1.38, and 1.39. In this, we proposed a multilayer structure comprising nanofilms of Ag, Silicon, and PtSe₂ for the early diagnosis of chikungunya virus. The suggested sensor structure consists of a BK7 (borosilicate crown) coupling prism over which the nanofilm of silver metal is present. The layer thicknesses and the number of silicon and PtSe₂ sheets are optimized for high performance. At the operating wavelength of 633 nm, a Kretschmann-based SPR sensor has been proposed, which gives the highest sensitivity of 287.3 Deg/RIU. The principle of attenuated total reflection has been employed for the performance analysis of the sensor.

Effect of voluntary human mobility restrictions on vector-borne diseases during the COVID-19 pandemic in Japan: A descriptive epidemiological study using a national database (2016 to 2021).

Hibiya K, Shinzato A, Iwata H, Kinjo T, Tateyama M, Yamamoto K, Fujita J.
25-03-2023
PLoS One.
<https://pubmed.ncbi.nlm.nih.gov/37228070/>

Mosquito gene targeted RNAi studies for vector control.

Yadav M, Dahiya N, Sehrawat N.
25-03-2023
Funct Integr Genomics.
<https://pubmed.ncbi.nlm.nih.gov/37227504/>

Vector-borne diseases are serious public health concern. Mosquito is one of the major vectors responsible for the

transmission of a number of diseases like malaria, Zika, chikungunya, dengue, West Nile fever, Japanese encephalitis, St. Louis encephalitis, and yellow fever. Various strategies have been used for mosquito control, but the breeding potential of mosquitoes is such tremendous that most of the strategies failed to control the mosquito population. In 2020, outbreaks of dengue, yellow fever, and Japanese encephalitis have occurred worldwide. Continuous insecticide use resulted in strong resistance and disturbed the ecosystem. RNA interference is one of the strategies opted for mosquito control. There are a number of mosquito genes whose inhibition affected mosquito survival and reproduction. Such kind of genes could be used as bioinsecticides for vector control without disturbing the natural ecosystem. Several studies have targeted mosquito genes at different developmental stages by the RNAi mechanism and result in vector control. In the present review, we included RNAi studies conducted for vector control by targeting mosquito genes at different developmental stages using different delivery methods. The review could help the researcher to find out novel genes of mosquitoes for vector control.

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

Viettri M, Caraballo G, Sanchez ME, Espejel-Núñez A, Betanzos A, Ortiz-Navarrete V, Estrada-Gutierrez G, Nava P, Ludert JE.
25-03-2023
Microbiol Spectr.
<https://pubmed.ncbi.nlm.nih.gov/37227282/>

Spatial and temporal distribution of reported dengue cases and hot spot identification in Quezon City, Philippines, 2010-2017.

Medina JRC, Takeuchi R, Mercado CEG, de Los Reyes CS, Cruz RV, Abrigo MDR, Hernandez PMR, Garcia FB Jr, Salangit M, Gregorio ER Jr, Kawamura S, Hung KE, Kaneko M, Nonaka D, Maude RJ, Kobayashi J.
25-03-2023
Trop Med Health.
<https://pubmed.ncbi.nlm.nih.gov/37226211/>

Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing.

Claro IM, Ramundo MS, Coletti TM, da Silva CAM, Valenca IN, Candido DS, Sales FCS, Manuli ER, de Jesus JG, de Paula A, Felix AC, Andrade PDS, Pinho MC, Souza WM, Amorim MR, Proenca-Modena JL, Kallas EG, Levi JE, Faria NR, Sabino EC, Loman NJ, Quick J.
24-04-2023
Wellcome Open Res.
<https://pubmed.ncbi.nlm.nih.gov/37224315/>

Emerging and re-emerging viruses are a global health concern. Genome sequencing as an approach for monitoring circulating viruses is currently hampered by

complex and expensive methods. Untargeted, metagenomic nanopore sequencing can provide genomic information to identify pathogens, prepare for or even prevent outbreaks. SMART (Switching Mechanism at the 5' end of RNA Template) is a popular approach for RNA-Seq but most current methods rely on oligo-dT priming to target polyadenylated mRNA molecules. We have developed two random primed SMART-Seq approaches, a sequencing agnostic approach 'SMART-9N' and a version compatible rapid adapters available from Oxford Nanopore Technologies 'Rapid SMART-9N'. The methods were developed using viral isolates, clinical samples, and compared to a gold-standard amplicon-based method. From a Zika virus isolate the SMART-9N approach recovered 10kb of the 10.8kb RNA genome in a single nanopore read. We also obtained full genome coverage at a high depth coverage using the Rapid SMART-9N, which takes only 10 minutes and costs up to 45% less than other methods. We found the limits of detection of these methods to be 6 focus forming units (FFU)/mL with 99.02% and 87.58% genome coverage for SMART-9N and Rapid SMART-9N respectively. Yellow fever virus plasma samples and SARS-CoV-2 nasopharyngeal samples previously confirmed by RT-qPCR with a broad range of Ct-values were selected for validation. Both methods produced greater genome coverage when compared to the multiplex PCR approach and we obtained the longest single read of this study (18.5 kb) with a SARS-CoV-2 clinical sample, 60% of the virus genome using the Rapid SMART-9N method. This work demonstrates that SMART-9N and Rapid SMART-9N are sensitive, low input, and long-read compatible alternatives for RNA virus detection and genome sequencing and Rapid SMART-9N improves the cost, time, and complexity of laboratory work.

Relationship between Climate Variables and Dengue Incidence in Argentina.

López MS, Gómez AA, Müller GV, Walker E, Robert MA, Estallo EL.

Mai-2023

Environ Health Perspect.

<https://pubmed.ncbi.nlm.nih.gov/37224070/>

Phase 1 trial to model primary, secondary, and tertiary dengue using a monovalent vaccine.

Odio CD, Lowman KE, Law M, Aogo RA, Hunsberger S, Wood BJ, Kassim M, Levy E, Callier V, Firdous S, Hasund CM, Voirin C, Kattappuram R, Yek C, Manning J, Durbin A, Whitehead SS, Katzelnick LC.

23-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37221466/>

Vaccine effectiveness against delta and omicron variants of SARS-CoV-2.

Kundi M.

23-05-2023

BMJ.

<https://pubmed.ncbi.nlm.nih.gov/37220942/>

Complement Activation by an Anti-Dengue/Zika Antibody with Impaired Fcγ Receptor Binding Provides Strong Efficacy and Abrogates Risk of Antibody-Dependent Enhancement.

Sampei Z, Koo CX, Teo FJ, Toh YX, Fukuzawa T, Gan SW, Nambu T, Ho A, Honda K, Igawa T, Ahmed F, Wang CI, Fink K, Nezu J.

15-05-2023

Antibodies (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37218902/>

To combat infectious diseases, vaccines are considered the best prophylactic strategy for a wide range of the population, but even when vaccines are effective, the administration of therapeutic antibodies against viruses could provide further treatment options, particularly for vulnerable groups whose immunity against the viruses is compromised. Therapeutic antibodies against dengue are ideally engineered to abrogate binding to Fcγ receptors (FcγRs), which can induce antibody-dependent enhancement (ADE). However, the Fc effector functions of neutralizing antibodies against SARS-CoV-2 have recently been reported to improve post-exposure therapy, while they are dispensable when administered as prophylaxis. Hence, in this report, we investigated the influence of Fc engineering on anti-virus efficacy using the anti-dengue/Zika human antibody SIgN-3C and found it affected the viremia clearance efficacy against dengue in a mouse model. Furthermore, we demonstrated that complement activation through antibody binding to C1q could play a role in anti-dengue efficacy. We also generated a novel Fc variant, which displayed the ability for complement activation but showed very low FcγR binding and an undetectable level of the risk of ADE in a cell-based assay. This Fc engineering approach could make effective and safe anti-virus antibodies against dengue, Zika and other viruses.

The Diabetic Platelets.

Verma SK, Kalra S.

Mai-2023

J Pak Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37218252/>

This communication describes the platelet morphology and physiology noted in persons with diabetes and its complications. It reviews the effects of glucose lowering drugs on platelet function, and summarizes the role of anti-platelet drugs in diabetes management.

Spontaneous splenic rupture during dengue fever.

Zafarullah S, Mujahid NU, Waheed R, Asghar MS, Afzal A, Anwar J.

Mai-2023

J Pak Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37218246/>

Association of climate factors with dengue incidence in Bangladesh, Dhaka City: A count regression approach.

Hossain S, Islam MM, Hasan MA, Chowdhury PB, Easty IA, Tusar MK, Rashid MB, Bashar K.

05-05-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37215791/>

Mosquito repellent fabric: Development and characterization of peppermint and garlic mixture finish on knitted fabric to examine mosquito repellency.

Parvez AA, Hossain MJ, Hossain MZ, Sohan MSH, Hoque F, Ahsan MH, Hoque MS.

03-05-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37215766/>

Mosquito-repellent textiles are a part of protective textiles which help in protection from the species that are prone to cause diseases like malaria and dengue fever. This study explored the possibility of natural extract (alcoholic) from peppermint leaves, stems, and garlic cloves to use as a mosquito-repellent finish material on knit fabric. Accordingly, different concentration (5%, 15%, 25%, and 35%) of PGE (Peppermint Garlic Extract) solution was prepared and applied to the developed fabric using an exhaust dyeing process to assess the mosquito (*Aedes Aegypti* L.) repellency performance. Following WHO (World Health Organization) standard (cone bioassay) and a self-modified cage technique from literature survey, mosquito protection and repellency tests have been performed for characterization. The findings revealed that the PGE-treated fabric samples C (25% PGE) and D (35% PGE) had the highest mosquito mortality (50.00% and 76.67%, respectively) and repellency (78.6% and 85.6%, respectively) rates. Moreover, this study evaluated the prepared PGE formulations' shelf-life performance and colorfastness properties of PGE-treated fabrics, including the impact of washing cycles on the treated fabrics. There was no fungal growth, and the fabric showed excellent colorfastness properties. However, the efficacy of treated fabrics decreased with an increasing number of washes.

The influence of the larval microbiome on susceptibility to Zika virus is mosquito genotype dependent.

Accoti A, Multini LC, Diouf B, Becker M, Vulcan J, Sylla M, Yap DAY, Khanipov K, Weaver SC, Diallo M, Gaye A, Dickson LB.

11-05-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37215022/>

Longitudinal Analysis of the Burden of Post-Acute Chikungunya-Associated Arthralgia in Children and Adults: A Prospective Cohort Study in Managua, Nicaragua (2014-2019).

Warnes CM, Bustos Carrillo FA, Zambrana JV, Mercado BL, Arguello S, Ampié O, Collado D, Sanchez N, Ojeda S, Kuan G, Gordon A, Balmaseda A, Harris E.

17-05-2023

medRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37214808/>

Multiple virus sorting based on aptamer-modified microspheres in a TSAW device.

Liu X, Chen X, Dong Y, Zhang C, Qu X, Lei Y, Jiang Z, Wei X.

17-05-2023

Microsyst Nanoeng.

<https://pubmed.ncbi.nlm.nih.gov/37213822/>

Due to the overlapping epidemiology and clinical manifestations of flaviviruses, differential diagnosis of these viral diseases is complicated, and the results are unreliable. There is perpetual demand for a simplified, sensitive, rapid and inexpensive assay with less cross-reactivity. The ability to sort distinct virus particles from a mixture of biological samples is crucial for improving the sensitivity of diagnoses. Therefore, we developed a sorting system for the subsequent differential diagnosis of dengue and tick-borne encephalitis in the early stage. We employed aptamer-modified polystyrene (PS) microspheres with different diameters to specifically capture dengue virus (DENV) and tick-borne encephalitis virus (TBEV), and utilized a traveling surface acoustic wave (TSAW) device to accomplish microsphere sorting according to particle size. The captured viruses were then characterized by laser scanning confocal microscopy (LSCM), field emission scanning electron microscopy (FE-SEM) and reverse transcription-polymerase chain reaction (RT-PCR). The characterization results indicated that the acoustic sorting process was effective and damage-free for subsequent analysis. Furthermore, the strategy can be utilized for sample pretreatment in the differential diagnosis of viral diseases.

Identifying and Managing Vector-Borne Diseases in Migrants and Recent Travelers in the Emergency Department.

Wiltz P.

2023

Curr Emerg Hosp Med Rep.

<https://pubmed.ncbi.nlm.nih.gov/37213267/>

Nanoparticles: A Potential and Effective Method to Control Insect-Borne Diseases.

Nie D, Li J, Xie Q, Ai L, Zhu C, Wu Y, Gui Q, Zhang L, Tan W.

11-05-2023

Bioinorg Chem Appl.

<https://pubmed.ncbi.nlm.nih.gov/37213220/>

Insects act as vectors to carry a wide range of bacteria and viruses that can cause multiple vector-borne diseases in humans. Diseases such as dengue fever, epidemic encephalitis B, and epidemic typhus, which pose serious risks to humans, can be transmitted by insects. Due to the absence of effective vaccines for most arbovirus, insect control was the main strategy for vector-borne diseases control. However, the rise of drug resistance in the vectors brings a great challenge to the prevention and control of

vector-borne diseases. Therefore, finding an eco-friendly method for vector control is essential to combat vector-borne diseases. Nanomaterials with the ability to resist insects and deliver drugs offer new opportunities to increase agent efficacy compared with traditional agents, and the application of nanoagents has expanded the field of vector-borne disease control. Up to now, the reviews of nanomaterials mainly focus on biomedicines, and the control of insect-borne diseases has always been a neglected field. In this study, we analyzed 425 works of the literature about different nanoparticles applied on vectors in PubMed around keywords, such as "nanoparticles against insect," "NPs against insect," and "metal nanoparticles against insect." Through these articles, we focus on the application and development of nanoparticles (NPs) for vector control, discussing the lethal mechanism of NPs to vectors, which can explore the prospect of applying nanotechnology in the prevention and control of vectors.

Monitoring Changes in Human Umbilical Vein Endothelial Cells upon Viral Infection Using Impedance-Based Real-Time Cell Analysis.

Wong JE, Zainal N, AbuBakar S, Tan KK.

05-05-2023

J Vis Exp.

<https://pubmed.ncbi.nlm.nih.gov/37212555/>

Endothelial cells line the inner surface of all blood and lymphatic vessels, creating a semi-permeable barrier regulating fluid and solute exchange between blood or lymph and their surrounding tissues. The ability of a virus to cross the endothelial barrier is an important mechanism that facilitates virus dissemination in the human body. Many viruses are reported to alter endothelial permeability and/or cause endothelial cell barrier disruption during infection, which is able to cause vascular leakage. The current study describes a real-time cell analysis (RTCA) protocol, using a commercial real-time cell analyzer to monitor endothelial integrity and permeability changes during Zika virus (ZIKV) infection of the human umbilical vein endothelial cells (HUVECs). The impedance signals recorded before and after ZIKV infection were translated to cell index (CI) values and analyzed. The RTCA protocol allows the detection of transient effects in the form of cell morphological changes during a viral infection. This assay could also be useful for studying changes in the vascular integrity of HUVECs in other experimental setups.

Comparison of the reactogenicity and immunogenicity between two-dose mRNA COVID-19 vaccine and inactivated COVID-19 vaccine followed by an mRNA vaccine in children aged 5-11 years.

Wanlapakorn N, Kanokudom S, Phowatthanasathian H, Chansaenroj J, Suntronwong N, Assawakosri S, Yorsaeng R, Nilyanimit P, Vichaiwattana P, Klinfueng S, Thongmee T, Aeemjinda R, Khanarat N, Srimuan D, Thatsanatorn T, Chantima W, Pakchotanon P, Duangchinda T, Sudhinaraset N, Poovorawan Y.

Mai-2023

J Med Virol.

<https://pubmed.ncbi.nlm.nih.gov/37212319/>

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

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

20-05-2023

Acta Trop.

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

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

transmission and the establishment of prevention and control measures for this neglected disease more effectively.

Investigating the folding dynamics of NS2B protein of Zika virus.

Kumar A, Kumar P, Mishra PM, Giri R.

06-05-2023

Virology.

<https://pubmed.ncbi.nlm.nih.gov/37210794/>

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

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

18-05-2023

Vaccine.

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

Zika virus triggers autophagy to exploit host lipid metabolism and drive viral replication.

Stoyanova G, Jabeen S, Landazuri Vinueza J, Ghosh Roy S, Lockshin RA, Zakeri Z.

19-05-2023

Cell Commun Signal.

<https://pubmed.ncbi.nlm.nih.gov/37208782/>

Background: Zika virus (ZIKV), an arbovirus of global concern, has been associated with neurological complications including microcephaly in newborns and Guillain-Barré syndrome in adults. Like other flaviviruses, ZIKV depends on cholesterol to facilitate its replication; thus, cholesterol has been proposed as a therapeutic target to treat the infection using FDA-approved statins. Cholesterol is stored in intracellular lipid droplets (LD) in the form of cholesterol esters and can be regulated by autophagy. We hypothesize that the virus hijacks autophagy machinery as an early step to increase the formation of LD and viral replication, and that interference with this pathway will limit reproduction of virus. **Methods:** We pretreated MDCK cells with atorvastatin or other inhibitors of autophagy prior to infection with ZIKV. We measured viral expression by qPCR for NS1 RNA and immunofluorescence for Zika E protein. **Results:** Autophagy increases in virus-infected cells as early as 6 h post infection (hpi). In the presence of atorvastatin, LD are decreased, and cholesterol is reduced, targeting key steps in viral replication, resulting in suppression of replication of ZIKV is suppressed. Other both early- and late-acting autophagy inhibitors decrease both the number of LD and viral replication. Bafilomycin renders cholesterol is inaccessible to ZIKV. We also confirm previous reports of a bystander effect, in which neighboring uninfected cells have higher LD counts compared to infected cells. **Conclusions:** We conclude that atorvastatin and inhibitors of autophagy lead to lower availability of LD, decreasing viral replication. We conclude that bafilomycin A1 inhibits

viral expression by blocking cholesterol esterification to form LD. Video Abstract.

Immune-related transcripts, microbiota and vector competence differ in dengue-2 virus-infected geographically distinct *Aedes aegypti* populations.

Chen TY, Bozic J, Mathias D, Smartt CT.

19-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37208697/>

Author Correction: Chikungunya fever.

Bartholomeeusen K, Daniel M, LaBeaud DA, Gasque P, Peeling RW, Stephenson KE, Ng LFP, Ariën KK.

19-05-2023

Nat Rev Dis Primers.

<https://pubmed.ncbi.nlm.nih.gov/37208376/>

Collecting, Storing, and Hatching *Aedes aegypti* Eggs.

Rose NH, Shepard JJ, Ayala D.

19-05-2023

Cold Spring Harb Protoc.

<https://pubmed.ncbi.nlm.nih.gov/37208147/>

Laboratory study of natural populations of mosquitoes can play a key role in determining the underlying causes of variation in burdens of mosquito-borne disease. *Aedes aegypti* is the main vector of the viruses that cause dengue, chikungunya, Zika, and yellow fever, making it a high priority for laboratory study. *Ae. aegypti* eggs provide an ideal starting point for new laboratory colonies. Eggs can be collected using ovicups, which are small plastic cups lined with seed-germination paper and partially filled with leaf-infused H₂O. Once collected, dry eggs will remain viable for months and can be safely transported long distances back to the laboratory as long as they are properly stored. This protocol provides step-by-step instructions for preparing for collecting, storing, and hatching *Ae. aegypti* eggs and has successfully yielded laboratory colonies from locations across both the native and invasive range of this species.

COVID-19 impact on EuroTravNet infectious diseases sentinel surveillance in Europe.

Grobusch MP, Weld L, Schnyder JL, Larsen CS, Lindner AK, Popescu CP, Huits R, Goorhuis A, Gautret P, Schlagenhauf P; for EuroTravNet.

18-05-2023

Travel Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37207977/>

Neutralizing antibodies against omicron BA.5 among children with infection alone, vaccination alone, and hybrid immunity.

Suntronwong N, Kanokudom S, Assawakosri S, Vichaiwattana P, Klinfueng S, Phowattanasathian H,

Chansaenroj J, Srimuan D, Thatsanathorn T, Duangchinda T, Chantima W, Pakchotanon P, Sudhinaset N, Wanlapakorn N, Poovorawan Y.
17-05-2023
Int J Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37207716/>

Design, synthesis and biological evaluation of novel lipophilic 2, 5-disubstituted tetrazole analogues of muramyl dipeptide as NOD2 agonists.

Mhamane TB, Sambyal S, Vemireddy S, Paturu RSR, Katragadda SB, Syed S, Khan A, Halmuthur M SK.
29-04-2023
Bioorg Med Chem.
<https://pubmed.ncbi.nlm.nih.gov/37207469/>

A focused library of six new 2, 5-disubstituted tetrazole (2, 5-DST) analogues of N-acetylmuramyl-L-alanyl-D-isoglutamine (MDP) as potential immunomodulators were synthesized by the bioisosteric replacement of α -amide of D-isoglutamine with 5-substituted tetrazole (5-ST). Another parameter 'lipophilicity' was also considered to improve the pharmacological properties of MDP through the alkylation of 5-substituted tetrazole during synthesis. In total, six 2, 5-DST analogues of MDP were synthesized and bio-evaluated for the study of human NOD2 stimulation activity in the innate immune response. Interestingly, among the varied lengths of the alkyl chain in 2, 5-disubstituted tetrazole derivatives, the tetrazole analogues 12b bearing the -Butyl (C4) and 12c having -Octyl (C8) chain showed the best NOD2 stimulation potency equivalent with reference compound MDP. These analogues were evaluated for their adjuvant activity against dengue antigen and analogues 12b and 12c have elicited a potent humoral and cell mediated response.

Flavivirus Antibodies Reactive to Zika Virus Detected in Multiple Species of Nonhuman Primates in Kenya, 2008-2017.

Makio A, Widdowson MA, Ambala P, Ozwara H, Munyua P, Hunsperger E.
19-05-2023
Vector Borne Zoonotic Dis.
<https://pubmed.ncbi.nlm.nih.gov/37205849/>

Background: Zika virus (ZIKV), first described in 1947, is an arthropod-borne virus associated with sporadic outbreaks and interepidemic transmission. Recent studies have implicated nonhuman primates (NHPs) as the probable reservoir hosts. We tested archived serum samples of NHPs collected in Kenya for evidence of neutralizing ZIKV antibodies. **Methods:** We randomly selected 212 archived serum samples from Institute of Primate Research in Kenya collected between 1992 and 2017. These specimens were tested by microneutralization test. **Results:** The 212 serum samples were collected in 7 counties from 87 (41.0%) Olive baboons, 69 (32.5%) Vervet monkeys, and 49 (23.1%) Sykes monkeys. Half (50.9%) were male and 56.4% were adult. We detected ZIKV antibodies in 38 (17.9%; 95% confidence interval: 13.3-23.6) samples. **Conclusions:** These results suggest

ZIKV transmission and potential maintenance in nature by NHPs in Kenya.

Optical Coherence Tomography and Optical Coherence Tomography Angiography in Neglected Diseases.

Mahendradas P, Acharya I, Rana V, Bansal R, Ben Amor H, Khairallah M.
19-05-2023
Ocul Immunol Inflamm.
<https://pubmed.ncbi.nlm.nih.gov/37205786/>

Correction: Long-term Chikungunya sequelae and quality of life 2.5 years post-acute disease in a prospective cohort in Curaçao.

PLOS Neglected Tropical Diseases Staff.
19-05-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37205717/>

Dengue among Suspected Patients Admitted to Department of Medicine of a Tertiary Care Centre: A Descriptive Cross-sectional Study.

Lamsal DK, Chaurasiya PS, Khatri A, Karki S, Singh S, Shilpakar G, Sangroula RK.
01-02-2023
JNMA J Nepal Med Assoc.
<https://pubmed.ncbi.nlm.nih.gov/37203973/>

Introduction: Dengue virus incidence has been increasing trends in every year due to the expansion of the vectors *Aedes aegypti* and *Aedes albopictus*. The objective of this study was to find out the prevalence of dengue among suspected patients admitted to the department of medicine of a tertiary care centre. **Methods:** A descriptive cross-sectional study was conducted among patients admitted to the medicine department from 30 September 2022 to 30 December 2022 after obtaining ethical approval from the Institutional Review Committee (Reference number: 019/2022). Demographic, clinical characteristics and laboratory profiles were collected from dengue patients by using a structured questionnaire. Convenience sampling method was used. Point estimate and 95% Confidence Interval were calculated. **Results:** Among 500 patients, 242 (48.40%) (40.66-56.14, 95% Confidence Interval) were found to be dengue positive. The average age of the enrolled patients was 39.13 \pm 20.64 years. Most dengue fever patients were diagnosed in the category of dengue with a warning sign of 234 (96.69%). The mean hospital stay of dengue patients was 4.05 \pm 2.03 days, 229 (94.62%) of patients stayed less than 7 days before discharge. **Conclusions:** The prevalence of dengue among suspected patients admitted to the department of medicine is found to be higher than in other similar studies done in similar settings. Patients with clinical symptoms and laboratory findings corroborating with dengue should undergo early diagnosis and facilitate prompt treatment in individual patients.

Dengue Fever in a Neonate: A Case Report.

Bhattarai CD, Yadav BK, Basnet R, Karki M, Chauhan S.
01-02-2023

JNMA J Nepal Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37203936/>

Dengue is one of the most common viral infections affecting the general population in endemic areas annually. However, it is barely reported in newborns owing to a widespread belief that they are protected from severe viral infections in the first six months of life by the presence of maternal antibodies. Here we present a case of a 23-day-old male infant born to primigravida with dengue fever with the post-natal transmission of infection. He presented with complaints of fever for three days. On general examination, red-coloured pinpoint macular rashes were observed bilaterally on lower limbs. No significant findings were present on systemic examination. On routine sepsis workup, thrombocytopenia was present. Acknowledging the endemicity and expanding dengue cases, NS1 antigen and antibody IgM and IgG of the baby were tested which came positive for antigen and IgM antibody. Even so, the mother was asymptomatic with NS1 antigen, IgG and IgM antibodies negative with a normal range of platelet count.

COVID-19 vaccination, dengue hepatitis, and recurrent unilateral anterior uveitis.

Sanjay S, Kawali A, Mahendradas P.

Mai-2023

Indian J Ophthalmol.

<https://pubmed.ncbi.nlm.nih.gov/37202968/>

Mechanism of glycoform specificity and in vivo protection by an anti-afucosylated IgG nanobody.

Gupta A, Kao KS, Yamin R, Oren DA, Goldgur Y, Du J, Lollar P, Sundberg EJ, Ravetch JV.

18-05-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37202422/>

A nonstructural protein 1 capture enzyme-linked immunosorbent assay specific for dengue viruses.

Lim PY, Ramaprabha A, Loy T, Rouers A, Thein TL, Leo YS, Burton DR, Fink K, Wang CI.

18-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37200264/>

Long lasting anti-IgG chikungunya seropositivity in the Mayotte population will not be enough to prevent future outbreaks: A seroprevalence study, 2019.

Ortu G, Grard G, Parenton F, Ruello M, Paty MC, Durand GA, Hassani Y, De Valk H, Noël H; Unono Wa Maore group.

18-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37200250/>

Chikungunya is an arboviral disease causing arthralgia which may develop into a debilitating chronic arthritis. In Mayotte, a French overseas department in the Indian Ocean, a chikungunya outbreak was reported in 2006, affecting a third of the population. We aimed at assessing the chikungunya seroprevalence in this population, after over a decade from that epidemic. A multi-stage cross sectional household-based study exploring socio-demographic factors, and knowledge and attitude towards mosquito-borne disease prevention was carried out in 2019. Blood samples from participants aged 15-69 years were taken for chikungunya IgG serological testing. We analyzed associations between chikungunya serological status and selected factors using Poisson regression models, and estimated weighted and adjusted prevalence ratios (w/a PR). The weighted seroprevalence of chikungunya was 34.75% (n = 2853). Seropositivity for IgG anti-chikungunya virus was found associated with living in Mamoudzou (w/a PR = 1.49, 95%CI: 1.21-1.83) and North (w/a PR = 1.41, 95%CI: 1.08-1.84) sectors, being born in the Comoros islands (w/a PR = 1.30, 95%CI: 1.03-1.61), being a student or unpaid trainee (w/a PR = 1.35, 95%CI: 1.01-1.81), living in precarious housing (w/a PR = 1.30, 95%CI: 1.02-1.67), accessing water streams for bathing (w/a PR = 1.72, 95%CI: 1.1-2.7) and knowing that malaria is a mosquito-borne disease (w/a PR = 1.42, 95%CI: 1.21-1.83). Seropositivity was found inversely associated with high education level (w/a PR = 0.50, 95%CI: 0.29-0.86) and living in households with access to running water and toilets (w/a PR = 0.64, 95%CI: 0.51-0.80) (n = 1438). Our results indicate a long-lasting immunity from chikungunya exposure. However, the current population seroprevalence is not enough to protect from future outbreaks. Individuals naïve to chikungunya and living in precarious socio-economic conditions are likely to be at high risk of infection in future outbreaks. To prevent and prepare for future chikungunya epidemics, it is essential to address socio-economic inequalities as a priority, and to strengthen chikungunya surveillance in Mayotte.

Electrostatic interaction between sulfated polysaccharides and oligopeptides from viral envelope glycoproteins using surface plasmon resonance.

Battulga T, Dagaerbieke A, Bai C, Asai D, Koshikawa T, Takemura H, Miyazaki K, Yoshida T.

Jun-2023

Carbohydr Res.

<https://pubmed.ncbi.nlm.nih.gov/37121180/>

Biotinylated oligopeptides from the envelope glycoproteins of dengue fever virus, influenza A and B viruses, and human immunodeficiency virus (HIV) were synthesized and their interaction with curdlan and dextran sulfates was investigated using surface plasmon resonance to evaluate the antiviral mechanisms of sulfated polysaccharides. More than two clusters consisting of basic amino acids in the oligopeptides from dengue fever virus, strongly interacted with the sulfated polysaccharides elucidated by the association- and

dissociation-rate constants. Interactions decreased with the decreasing molecular weights of the sulfated polysaccharides. Although oligopeptides from influenza A virus potentially interacted with the sulfated polysaccharides, no interaction was detected on a B/Hong Kong virus oligopeptide bearing few basic amino acids. For the C terminus and V3 region short and long oligopeptides from HIV gp120, the interaction was enhanced by the number of clustered basic amino acids and was inhibited by acidic and bulky amino acids.

CSNK2B modulates IRF1 binding to functional DNA elements and promotes basal and agonist-induced antiviral signaling.

Matsumoto M, Modliszewski JL, Shinozaki K, Maezawa R, Perez VM, Ishikawa Y, Suzuki R, McKnight KL, Masaki T, Hirai-Yuki A, Kohara M, Lemon SM, Selitsky SR, Yamane D.

22-05-2023

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/37094077/>

Continuous surveillance and viral discovery in animals and humans are a core component of a one-health approach to address recent viral reverse zoonoses.

Kibenge FSB.

18-04-2023

J Am Vet Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37072119/>

Human brain microphysiological systems in the study of neuroinfectious disorders.

Barreras P, Pamies D, Hartung T, Pardo CA.

Juill-2023

Exp Neurol.

<https://pubmed.ncbi.nlm.nih.gov/37061175/>

Contemporary human and animal viruses have a broad or narrow host range-those with a broad host range are potentially transmitted from animals to humans (ie, zoonosis) or humans to animals (ie, reverse zoonosis). This Currents in One Health article reviews the recent reverse zoonoses involving Coronaviridae, Poxviridae, arboviruses, and, for nonhuman primate species, the human respiratory viruses. The prevention and control of reverse zoonoses are also reviewed. Coronaviruses continue to emerge as new zoonotic agents, including a canine coronavirus, CCoV-HuPn-2018, circulating in people at low levels, and a pangolin coronavirus, MjHKU4r-CoV-1, circulating in Malayan pangolins. Moreover, the risk for SARS-CoV-2 variants to mutate in animal reservoirs and reinfect humans is ongoing. In the case of mpox, the risk of reverse zoonosis is low and there are vaccines for use in humans at risk. The situation with arboviruses is as varied as the number of human arboviruses, and only yellow fever virus and dengue virus have licensed vaccines in the Americas. As for reverse zoonoses in endangered species, solutions require changing human behavior and policies at

all levels impacting wildlife. Overall, continuous surveillance and viral discovery in humans and animals remain core components of a one-health approach to reduce and, where possible, eliminate zoonotic and reverse zoonotic diseases. Viral zoonosis and viral reverse zoonosis focusing on recent influenza A virus disease events in humans and other species are the subjects of the companion Currents in One Health by Kibenge, AJVR, June 2023.

Clinical evaluation of BioFire® multiplex-PCR panel for acute undifferentiated febrile illnesses in travellers: a prospective multicentre study.

Camprubí-Ferrer D, Cobuccio L, Van Den Broucke S, Balerdi-Sarasola L, Genton B, Bottieau E, Navero-Castillejos J, Martinez MJ, Jay C, Grange A, Borland S, Vaughn M, Rodriguez-Valero N, Almuedo-Riera A, D'Acremont V, Subirà C, de Alba T, Cruz A, Van Esbroeck M, Smith C, Hillman A, Hanberg B, Trauscht R, Spanpanato N, Muñoz J.

18-05-2023

J Travel Med.

<https://pubmed.ncbi.nlm.nih.gov/36988415/>

Identification and validation of ferroptosis-related genes in patients infected with dengue virus: implication in the pathogenesis of DENV.

Li J, Yan X, Li B, Huang L, Wang X, He B, Xie H, Wu Q, Chen L.

Juin 2023

Virus Genes.

<https://pubmed.ncbi.nlm.nih.gov/36973608/>

Ferroptosis, an iron-dependent form of regulated cell death, has been associated with many virus infections. However, the role of ferroptosis in dengue virus (DENV) infection remains to be clarified. In our study, a dengue fever microarray dataset (GSE51808) of whole blood samples was downloaded from the Gene Expression Omnibus (GEO), and a list of ferroptosis related genes (FRGs) was extracted from the FerrDb. We identified 37 ferroptosis-related differentially expressed genes (FR-DEGs) in DENV-infected patient blood samples compared to healthy individuals. Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses as well as protein-protein interaction (PPI) network of FR-DEGs revealed that these 37 FR-DEGs were mainly related to the C-type lectin receptor and p53 signaling pathway. Nine out of the 37 FR-DEGs (HSPA5, CAV1, HRAS, PTGS2, JUN, IL6, ATF3, XBP1, and CDKN2A) were hub genes, of which 5 were validated by qRT-PCR in DENV-infected HepG2 cells. Finally, using miRNA-mRNA regulatory network, we identified has-miR-124-3p and has-miR-16-5p as the most critical miRNAs in regulating the expression of these hub genes. In conclusion, our findings demonstrated that 5 FR-DEGs, JUN, IL6, ATF3, XBP1, and CDKN2A, and two miRNAs, has-miR-124-3p and has-miR-16-5p may implicate an essential role of

ferroptosis in DENV infection, and further studies are warranted to explore the underlying mechanisms.

Clinical and Laboratory Characteristics of Hemophagocytic Lymphohistiocytosis in Children With Severe Dengue During the 2019-2020 Outbreak in Southern Colombia.

Restrepo Arias VC, Salgado García DM, Merchán-Galvis AM, Narváez CF.

01-06-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/36916863/>

Healthcare seeking during travel: an analysis by the GeoSentinel surveillance network of travel medicine providers.

Piyaphanee W, Stoney RJ, Asgeirsson H, Appiah GD, Díaz-Menéndez M, Barnett ED, Gautret P, Libman M, Schlagenhauf P, Leder K, Plewes K, Grobusch MP, Huits R, Mavunda K, Hamer DH, Chen LH.

18-05-2023

J Travel Med.

<https://pubmed.ncbi.nlm.nih.gov/36637429/>

Background: International travellers may seek care abroad to address health problems that arise during their trip or plan healthcare outside their country of residence as medical tourists. **Methods:** Data were collected on travellers evaluated at GeoSentinel Network sites who reported healthcare during travel. Both unplanned and planned healthcare were analysed, including the reason and nature of healthcare sought, characteristics of the treatment provided and outcomes. Travellers that presented for rabies post-exposure prophylaxis were described elsewhere and were excluded from detailed analysis. **Results:** From May 2017 through June 2020, after excluding travellers obtaining rabies post-exposure prophylaxis (n = 415), 1093 travellers reported care for a medical or dental issue that was an unanticipated part of the travellers' planned itinerary (unplanned healthcare). Travellers who sought unplanned healthcare abroad had frequent diagnoses of acute diarrhoea, dengue, falciparum malaria and unspecified viral syndrome, and obtained care in 131 countries. Thirty-four (3%) reported subsequent deterioration and 230 (21%) reported no change in condition; a third (n = 405; 37%) had a pre-travel health encounter. Forty-one travellers had sufficient data on planned healthcare abroad for analysis. The most common destinations were the US, France, Dominican Republic, Belgium and Mexico. The top reasons for their planned healthcare abroad were unavailability of procedure at home (n = 9; 19%), expertise abroad (n = 9; 19%), lower cost (n = 8; 17%) and convenience (n = 7; 15%); a third (n = 13; 32%) reported cosmetic or surgical procedures. Early and late complications occurred in 14 (33%) and 4 (10%) travellers, respectively. Four travellers (10%) had a pre-travel health encounter. **Conclusions:** International travellers encounter health problems during travel that often could be prevented by pre-travel consultation. Travellers obtaining planned healthcare abroad can experience negative health consequences

associated with treatments abroad, for which pre-travel consultations could provide advice and potentially help to prevent complications.

Identification of Novel Zika Virus Inhibitors: A Screening using Thiosemicarbazones and Thiazoles Templates.

de Moraes Gomes PAT, Barros Freitas LA, Pessoa Siqueira LR, da Conceição JM, Dos Santos IR, Pinto AF, de Melo Silva VG, Nunes JS, de Oliveira Cardoso MV, Pena LJ, Lima Leite AC.

2023

Curr Top Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36567284/>

Background: Zika virus (ZIKV) remains an important cause of congenital infection, fetal microcephaly, and Guillain-Barré syndrome in the population. In 2016, WHO declared a cluster of microcephaly cases and other neurological disorders reported as a global public health emergency in Brazil. There is still no specific treatment for Zika virus fever, only palliative care. Therefore, there is a need for new therapies against this disease. According to the literature, thiosemicarbazone, phthalimide and thiazole are privileged structures with several biological activities, including antiviral activity against various viruses.

Objective: Based on this, this work presents an antiviral screening using previously synthesized compounds derived from thiosemicarbazone, phthalimide, and thiazole as new hits active against ZIKV. **Methods:** After synthesis and characterization, all compounds were submitted to Cytotoxicity by MTT and Antiviral activity against ZIKV assays. **Results:** Compounds 63, 64, 65, and 73 exhibited major reductions in the ZIKV titre from this evaluation. Compounds 63 (99.74%), 64 (99.77%), 65 (99.92%), and 73 (99.21%) showed a higher inhibition than the standard 6MMPr (98.74%) at the CC20 dose. These results revealed new chemical entities with anti-ZIKV activity. **Conclusion:** These derivatives are promising candidates for further assays. In addition, the current approach brings a new privileged scaffolding, which may drive future drug discovery for ZIKV.

CD8+ T Cells Trigger Auricular Dermatitis and Blepharitis in Mice after Zika Virus Infection in the Absence of CD4+ T Cells.

Lee CY, Carissimo G, Teo TH, Tong SJM, Chang ZW, Rajarethinam R, Chua TK, Chen Z, Chee RS, Tay A, Howland SW, Ang KS, Chen J, Renia L, Ng LFP.

Juin-2023

J Invest Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36566875/>

Zika virus (ZIKV) became a public health concern when it re-emerged in 2015 owing to its ability to cause congenital deformities in the fetus and neurological complications in adults. Despite extensive data on protection, the interplay of protective and pathogenic adaptive immune responses toward ZIKV infection remains poorly understood. In this study, using a T-cell-deficient mouse model that retains persistent ZIKV viral titers in the blood and organs, we

show that the adoptive transfer of CD8+ T cells led to a significant reduction in viral load. This mouse model reveals that ZIKV can induce grossly visible auricular dermatitis and blepharitis, mediated by ZIKV-specific CD8+ T cells. Single-cell RNA sequencing of these causative CD8+ T cells from the ears shows an overactivated and elevated cytotoxic signature in mice with severe symptoms. Our results strongly suggest a role for CD8+ T-cell-associated pathologies after ZIKV infection in CD4+ T-cell-immunodeficient patients.

Bortezomib inhibits ZIKV/DENV by interfering with viral polyprotein cleavage via the ERAD pathway.

Ci Y, Yao B, Yue K, Yang Y, Xu C, Li DF, Qin CF, Shi L.
18-05-2023
Cell Chem Biol.
<https://pubmed.ncbi.nlm.nih.gov/36351431/>

Visual findings in children exposed to Zika in utero in Nicaragua.

Martinez E, Max R, Bucardo F, Stringer EM, Becker-Dreps S, Toval-Ruiz C, Chavarria M, Meléndez-Balmaceda MJ, Nuñez C, Collins MH, Boivin M, Ortiz-Pujols S, Zepeda O, Cross K, Gower EW, Bowman NM, Grace SF.
19-05-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37205701/>

Development of inclusion complexes of 2-hydroxypropyl-β-cyclodextrin with Psidium guajava L. essential oil by freeze-drying and kneading methods for application as Aedes aegypti L. larvicide.

Mendes LA, Silva RRA, Soares NFF, Martins GF, Teixeira RR, da Silva Ferreira MF, Moreira RPL.
Juin-2023
Nat Prod Res.
<https://pubmed.ncbi.nlm.nih.gov/35979669/>

Inclusion complexes (ICs) of 2-hydroxypropyl-β-cyclodextrin with the essential oil (EO) from Seculo XXI cultivar of *Psidium guajava* were prepared using kneading (KN) and freeze-drying (FD) methods. The resulting ICs clusters have a nanometric size, with a diameter of approximately 80 and 40 nm for KN and FD, respectively. Complexation efficiency was 80.3% and 50.8% for KN and FD methods, respectively. The larvicidal activity of the EO in DMSO on *A. aegypti* had LC₅₀ and LC₉₀ values of 51.49 and 64.51 µg mL⁻¹, respectively. For the KN method, the toxicity corresponded to 77.54 and 107.29 µg mL⁻¹ for LC₅₀ and LC₉₀, respectively. FD method demonstrated toxicity at concentrations above 600 µg mL⁻¹. Thus, ICs enable the use of EO in breeding sites for *A. aegypti*, thus being potential products to be commercially exploited.

Immunomodulatory therapy in dengue: need for clinical trials and evidence base.

Bhat CS, Shetty R, Sundaram B, Ramanan AV.
Juin-2023
Arch Dis Child.

<https://pubmed.ncbi.nlm.nih.gov/35680407/>

Anti-Dengue Activity of ZnO Nanoparticles of Crude Fucoidan from Brown Seaweed *S.marginatum*.

Kothai R, Arul B, Anbazhagan V.
Juin-2023
Appl Biochem Biotechnol.
<https://pubmed.ncbi.nlm.nih.gov/35587327/>

Dracunculose

First report of Pseudocercaria paullula causing aroid leaf rust on Swiss cheese plant *Monstera deliciosa* in South Carolina, USA.

Yang X, Colburn C, Roach K, Zee T, Long S.
23-05-2023
Plant Dis.
<https://pubmed.ncbi.nlm.nih.gov/37221241/>

Evaluating the effect of gamma rays on Zamiifolia (*Zamioculcas zamiifolia*) plant in vitro and genetic diversity of the resulting genotypes using the ISSR marker.

Beyramizadeh E, Arminian A, Fazeli A.
23-05-2023
Sci Rep.
<https://pubmed.ncbi.nlm.nih.gov/37221200/>

Zamiifolia (*Zamioculcas* sp.) is a perennial plant in the Araceae family and one of the new apartment plants in the world. In this study, in order to increase the effectiveness of the breeding program, tissue culture technique and explants of leaf parts were used. The results indicated that 2,4-D (1 mg/l) and BA (2 mg/l) hormones affected positively and significantly callus formation and simultaneous application of NAA and BA (both in 0.5 mg/l) caused the best results regarding seedling production and number, leaves, complete tubers, and root in tissue culture of Zamiifolia. In the study, three cultivars of Zamiifolia (green, black and Dutch) and 12 genotypes resulted from callus formation stage, irradiated with different gamma rays (0 to 175 Gy, with LD₅₀ as 68 Gy) were selected and the presence of genetic diversity was investigated using 22 ISSR primers. Applying ISSR marker showed that the highest amount of PIC values related to the F19(0.47) and F20(0.38) primers, which persuasively isolated the studied genotypes. Moreover, the highest efficiency was detected for AK66 marker based on the MI parameter. The PCA and clustering categorization via UPGMA methodology based on molecular information and Dice index, differentiated the genotypes into 6 groups. Genotypes 1(callus), 2(100 Gy) and 3(cultivar from Holland) created separated groups. The 4th group included 6(callus), 8(0 Gy), 9(75 Gy), 11(90 Gy), 12(100 Gy) and 13(120 Gy) genotypes appearing as the largest group. The 5th group included 7(160 Gy), 10(80 Gy), 14(140 Gy) and 15(Zanzibar gem black) genotypes. The last group included 4(mather plant) and 5(callus) genotypes. In this context, genotypes 1, 5, and 6 had probably somaclonal

variation. Moreover, genotypes that received doses of 100 and 120 Gy, had a medium diversity. There is a high possibility of introducing a cultivar with a low dose and high genetic diversity in the whole group. Genotype 7 in this classification, received the highest dose of 160 Gy. In this population, the Dutch variety, was used as a new variety. As a result, the ISSR marker could correctly group the genotypes. This is an interesting finding, and it could be hypothesized that the ISSR marker could correctly differentiate *Zaamifolia* genotypes and probably other ornamental plants under the effect of gamma rays mutagenesis in order to achieve novel variants.

Pinellia ternata-containing traditional Chinese medicine combined with 5-HT₃RAs for chemotherapy-induced nausea and vomiting: A PRISMA-compliant systematic review and meta-analysis of 22 RCTs.

Zhai X, He Q, Chen M, Yu L, Tong C, Chen Y, Wang J, Fan X, Xie H, Liang Z, Sui X, Zeng L, Wu Q.

Jul. 2023

Phytomedicine.

<https://pubmed.ncbi.nlm.nih.gov/37099981/>

The phytoremediation capacity of *Lemna minor* prevents deleterious effects of anti-HIV drugs to nontarget organisms.

Kitamura RSA, Marques RZ, Kubis GC, Kochi LY, Barbato ML, Maranhão LT, Juneau P, Gomes MP.

15-07-2023

Environ Pollut.

<https://pubmed.ncbi.nlm.nih.gov/37080511/>

We investigated physiological responses of *Lemna minor* plants and their capacity to remove tenofovir (TNF; 412 ng l⁻¹), lamivudine (LMV; 5428 ng l⁻¹) and/or efavirenz (EFV; 4000 ng l⁻¹) from water through phytoremediation. In addition, the toxicological safety of water contaminated with these drugs after treatment with *L. minor* plants to photosynthetic microorganisms (*Synechococcus elongatus* and *Chlorococcum infusionum*) was evaluated. The tested environmental representative concentrations of drugs did not have a toxic effect on *L. minor*, and their tolerance mechanisms involved an increase in the activity of P450 and antioxidant enzymes (catalase and ascorbate peroxidase). *L. minor* accumulated significant quantities of TNF, LMV and EFV from the media (>70%), and the interactive effect of LMV and EFV increased EFV uptake by plants submitted to binary or tertiary mixture of drugs. Photosynthetic microorganisms exposed to TNF + LMV + EFV showed toxicological symptoms which were not observed when exposed to contaminated water previously treated with *L. minor*. An increased H₂O₂ concentrations but no oxidative damage in *S. elongatus* cells exposed to non-contaminated water treated with *L. minor* was observed. Due to its capacity to tolerate and reclaim anti-HIV drugs, *L. minor* plants must be considered in phytoremediation programs. They constitute a natural-based solution to decrease environmental contamination by anti-HIV drugs and toxicological effects of these pharmaceuticals to nontarget organisms.

Curcumin inhibits the pruritus in mice through mast cell MrgprB2 receptor.

Jiang Y, Zong Y, Du Y, Zhang M, Ye F, Zhang J, Yang Y, Zhu C, Tang Z.

Mai-2023

Inflamm Res.

<https://pubmed.ncbi.nlm.nih.gov/36997814/>

Background: Curcumin is a diketone compound extracted from the rhizomes of some plants in the Zingiberaceae and Araceae family. It possesses a variety of biological activities, including antioxidant, anti-inflammatory and anti-cancer properties. However, the cellular and molecular antipruritic mechanisms of curcumin remain to be explored. **Objective:** Our objective was to study the role of curcumin in pruritus and determine whether its antipruritic effect is related to MrgprB2 receptor. **Methods:** The effect of curcumin on pruritus in mice was examined by scratching behavior test. The antipruritic mechanism of curcumin was explored by using transgenic mice (MrgprB2^{-/-} mice, MrgprB2Cre^{Td/tomato} mice), histological analysis, western blot and immunofluorescence. In addition, the relationship between curcumin and MrgprB2/X2 receptor was studied in vitro by using calcium imaging, plasmid transfection and molecular docking. **RESULTS:** In the current study, we found that curcumin had obvious antipruritic effect. Its antipruritic effect was related to the regulation of MrgprB2 receptor activation and mast cells tryptase release. In vitro, mouse peritoneal mast cells activated by compound 48/80 could be inhibited by curcumin. In addition, curcumin was also found to suppress the calcium flux in MrgprX2 or MrgprB2-overexpression HEK cells induced by compound 48/80, substance P, and PAMP 9-20, displaying the specific relation with the MrgprB2/X2 receptor. Moreover, molecular docking results showed that curcumin had affinity to MrgprX2 protein. **Conclusions:** Overall, these results indicated that curcumin has the potential to treat pruritus induced by mast cell MrgprB2 receptor.

Echinococcose

In vitro and ex vivo protoscolicidal effects of hydroalcoholic extracts of *Eucalyptus microtheca* on protoscoleces of *Echinococcus granulosus sensu stricto*: A light and scanning electron microscopy (SEM) study.

Mahmoodpour H, Spotin A, Hatam GR, PourmahdiGhaemmaghami A, Sadjjadi SM.

23-05-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37230322/>

Novel molecular diagnostic (PCR) diagnosis and outcome of intestinal *Echinococcus multilocularis* in a dog from western Canada.

Evason MD, Jenkins EJ, Kolapo TU, Mitchell KD, Leutenegger CM, Peregrine AS.

23-05-2023

J Am Vet Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37225160/>

Objective: To describe the novel PCR diagnosis and outcome of intestinal *Echinococcus multilocularis* in a dog.

Animal: A 13-month-old female intact dog with naturally occurring intestinal *E. multilocularis*.

Clinical presentation, progression, and procedures: The 13-month-old dog initially presented with a reduced appetite and weight loss and then developed hematochezia. The clinical history included a lack of endoparasite preventive care (fecal testing, deworming), exposure to coyotes, fox, sheep, and rodents and the dog had intermittently been fed a raw food diet. Physical examination revealed a thin dog, with a 2/9 body condition score, that was otherwise clinically unremarkable. A fecal sample was submitted for screening for gastrointestinal parasites as part of an infectious disease assessment. The fecal PCR test reported detection of *E. multilocularis*. This result was sequenced as the European haplotype E3/E4. Centrifugal flotation (same sample) did not detect taeniid eggs.

Treatment and outcome: The dog was treated with metronidazole, maropitant, and milbemycin oxime/praziquantel. Clinical improvement was noted within 48 hours. No DNA of *E. multilocularis* was detected in a fecal sample collected approximately 10 days after treatment. The dog's owner was advised to provide monthly deworming (praziquantel) for all dogs on the property and to contact their human health-care provider due to potential zoonotic exposure risk. **Clinical relevance:** Increasing detection of *E. multilocularis* is occurring in dogs in Canada and the US. Alveolar echinococcosis can cause severe disease in dogs and humans. Fecal PCR detection and surveillance may alert practitioners to canine intestinal cases and allow dogs to serve as sentinels for human exposure risk.

Isolated greater omentum solid mass, a rare manifestation of hydatid disease; A Case Report and Review of Literature.

Jangjoo A, Norouzi Asl S, Azadmanesh Y, Zandbaf T.

Printemps 2023

Caspian J Intern Med.

<https://pubmed.ncbi.nlm.nih.gov/37223303/>

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

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

21-05-2023

Acta Trop.

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

Cystic echinococcosis (CE), caused by *Echinococcus granulosus sensu lato*, is a neglected tropical disease known mainly for its zoonotic nature. CE is endemic to Pakistan, however, the disease is not given due consideration and millions of people remain at health risk.

This study was undertaken to assess the species and genotypes of *E. granulosus sensu lato* in sheep, buffaloes and cattle, brought to slaughterhouses of two major cities (Multan and Bahawalpur) of south Punjab, Pakistan. A total of 26 hydatid cyst specimens were characterized through complete *cox1* mitochondrial gene (1609 bp) sequencing. Species and genotypes of *E. granulosus sensu lato* discovered in the southern Punjab consisted of *E. granulosus sensu stricto* (n =21), *E. orteppi* (n=4) and *E. canadensis* G6 genotype (n=1). Of *E. granulosus s.s.* isolates, the genotype G3 was predominantly involved in causing infections to the livestock of this region. Since all of these species are zoonotic, wide and effective surveillance studies are required to ascertain the risks to human population in Pakistan. Additionally, a global overview on *cox1* phylogenetic structure of *E. orteppi* was carried out. Despite the widespread occurrence, the species is mostly limited to the southern hemisphere. The highest burden has been reported in the South America (62.15%) and Africa (28.44%) and by far the most common host is cattle, accounting for >90% of cases.

Mixed epithelial and stromal tumour of the kidney masquerading as hydatid cyst: a rare case report from the developing world.

Mahar NA, Hussain M, Shehzad Shah SA, Qureshi HH, Kalwar SR, Sultan G.

Mai-2023

J Pak Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37218248/>

Mixed epithelial and stromal tumour (MEST) is a rare entity with an incidence of 0.2% among renal cancers. It has strong predilection towards females with a 1:6 male to female ratio, the tumour is cystic with some solid component with biphasic proliferation of stromal and epithelial cells. The case of a 37-years-old female is presented with right lumbar pain since 3 months. The family history was unremarkable. The routine workup revealed mild neutrophilia and borderline *Echinococcus* antibody titres. Ultrasound revealed a complex cystic lesion with a solid component in the right kidney. CT scan with contrast confirmed a multiloculated mixed density lesion with daughter cysts arising from the middle lobe of the right kidney. Initial diagnosis of renal hydatid cyst was established and she underwent partial nephrectomy with excision of the cystic mass. Surprisingly the histopathology revealed mixed epithelial and stromal tumour.

Attitude and awareness of Algerian university students about cystic echinococcosis: A cross-sectional study.

Lounis M, Bencherit D, Laoues K, Telha T, Chebbah O, Belabbas Z.

Juin-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37208085/>

High species diversity of *Echinococcus* spp. in wild mammals of Namibia.

Aschenborn O, Aschenborn J, Beytell P, Wachter B, Melzheimer J, Dumendiak S, R  ffler B, Mackenstedt U, Kern P, Romig T, Wassermann M.

24-04-2023

Int J Parasitol Parasites Wildl.

<https://pubmed.ncbi.nlm.nih.gov/37206437/>

An opportunistic survey for *Echinococcus* spp. in wild mammals was conducted in seven distinct study areas throughout Namibia, representing all major ecosystems, between 2012 and 2021. In total, 184 individually attributable faeces and 40 intestines were collected from eight species of carnivores, and 300 carcasses or organs of thirteen species of ungulates were examined for *Echinococcus* cysts. Nested PCR and sequencing of the mitochondrial *nad1* gene led to the identification of five species of the *Echinococcus granulosus sensu lato* complex. *Echinococcus canadensis* G6/7 was found throughout Namibia at low frequency in lions, cheetahs, African wild dogs, black-backed jackals and oryx antelopes. *Echinococcus equinus* was present only in northern Namibia, locally at high frequency in lions, black-backed jackals and plains zebras. *Echinococcus felidis* was found only in one small area in the north-east of Namibia, but with high frequency in lions and warthogs. *Echinococcus granulosus sensu stricto* was identified only in two African wild dogs in the north-east of Namibia, and *Echinococcus ortleppi* occurred in central and southern Namibia in black-backed jackals and oryx antelopes. The development of fertile cysts indicated active intermediate host roles of oryx antelopes for *E. canadensis* and *E. ortleppi*, of warthogs for *E. felidis*, and of plains zebras for *E. equinus*. Our data support earlier hypotheses of exclusive or predominant wildlife life-cycles for *E. felidis* involving lions and warthogs, and - in Namibia - for *E. equinus* involving lions and/or black-backed jackals and plains zebras. Our data further support an interlink of wild and domestic transmission for *E. ortleppi*. A possible involvement of livestock and domestic dogs in transmission of *E. canadensis* G6/7 and *E. granulosus* s.s., the two parasite species with highest zoonotic potential, is uncertain for Namibia and needs further investigation.

Cardiac Hydatid Disease with Palpitations as the Only Presenting Complaint: The Egg in the Nest.

Azari A, Bigdelu L, Maadarani O, Bitar Z.

27-04-2023

Eur J Case Rep Intern Med.

<https://pubmed.ncbi.nlm.nih.gov/37205207/>

Upregulation of LAG3 modulates the immune imbalance of CD4+ T-cell subsets and exacerbates disease progression in patients with alveolar echinococcosis and a mouse model.

Li D, Ainiwaer A, Zheng X, Wang M, Shi Y, Rousu Z, Hou X, Kang X, Maimaiti M, Wang H, Li J, Zhang C.

12-05-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37172058/>

Infection with the cestode *Echinococcus multilocularis* (*E. multilocularis*) causes alveolar echinococcosis (AE), a tumor-like disease predominantly affecting the liver but able to spread to any organ. T cells develop functional defects during chronic *E. multilocularis* infection, mostly due to upregulation of inhibitory receptors such as T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibitory motif domains (TIGIT) and programmed death-1 (PD-1). However, the role of lymphocyte activation gene-3 (LAG3), an inhibitory receptor, in AE infection remains to be determined. Here, we discovered that high expression of LAG3 was mainly found in CD4+ T cells and induced regulatory T cells (iTregs) in close liver tissue (CLT) from AE patients. In a mouse model of *E. multilocularis* infection, LAG3 expression was predominantly found in T helper 2 (Th2) and Treg subsets, which secreted significantly more IL-4 and IL-10, resulting in host immune tolerance and disease progression at a late stage. Furthermore, LAG3 deficiency was found to drive the development of effector memory CD4+ T cells and enhance the type 1 CD4+ T-cell immune response, thus inhibiting metacestode growth in vivo. In addition, CD4+ T cells from LAG3-deficient mice produced more IFN- γ and less IL-4 when stimulated by *E. multilocularis* protoscoleces (EmP) antigen in vitro. Finally, adoptive transfer experiments showed that LAG3-knockout (KO) CD4+ T cells were more likely to develop into Th1 cells and less likely to develop into Tregs in recipient mice. Our work reveals that high expression of LAG3 accelerates AE disease progression by modulating the immune imbalance of CD4+ T-cell subsets. These findings may provide a novel immunotherapeutic strategy against *E. multilocularis* infection.

Brief report prevalence of Echinococcus species in wild foxes in parts of Qinghai Province, China.

Zhang X, Fu Y, Ma Y, Guo Z, Shen X, Li Z, Jiunai G, Wang X, Maji W, Duo H.

Juin-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/36333528/>

Echinococcosis, caused by tapeworms of the genus *Echinococcus*, is a zoonotic parasitic disease. Various *Echinococcus* spp. are endemic and distributed in the Qinghai Province of China. Currently, few studies on the prevalence of *Echinococcus* spp. in the wild foxes are available. Hence, the aim of the study was to evaluate the prevalence of *Echinococcus* spp. in wild foxes in highly endemic areas of Qinghai Province, China. A total of 600 wild canid fecal samples were collected from Yushu, Qilian and Guinan in the study region, and 521 samples were successfully molecularly identified as wild foxes (Tibetan fox: 448, red foxes: 70, corsac fox: 3). Among the wild foxes, 5.57% (29/521) tested positive for *Echinococcus* spp. The prevalence rates of *Echinococcus* spp. in wild foxes in the Yushu, Qilian and Guinan areas were 2.51%, 15.22% and 0.96%, respectively. Furthermore, sequencing analysis indicated that *E. multilocularis* was the most prevalent species, occurring in 4.03% (21/521) of the wild foxes. Compared to *E. granulosus* occurring in 0.58% (3/521) of the foxes, *E. shiquicus* occurred in 1.54%

(8/521), and *E. shiquicus* was first reported with 2.17% (3/138) prevalence in the Qilian area, indicating its transmission range is expanding. The current results provide useful epidemiological data for understanding and monitoring the dissemination of *Echinococcus* spp. by wild foxes in Qinghai Province, China.

Bacterial and Fungal Occurrence in Hydatid Cysts from Livestock in Central Iran.

Zandi S, Mariconti M, Zandi H, Jafari A, Hajimohammadi B, Eslami G, Vakili M, Sheykhzadegan M, Askari V, Hosseini SS.

Juin-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/35732851/>

Filariose lymphatique

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.

26-05-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37232124/>

A randomized, open-label study of the tolerability and efficacy of one or three daily doses of ivermectin plus diethylcarbamazine and albendazole (IDA) versus one dose of ivermectin plus albendazole (IA) for treatment of onchocerciasis.

Opoku NO, Doe F, Dubben B, Fetcho N, Fischer K, Fischer PU, Gordor S, Goss CW, Gyasi ME, Hoerauf A, Hong AR, Kanza E, King CL, Laryea R, Lew D, Seidu MA, Weil GJ.

19-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37205721/>

Background: Onchocerciasis ("river blindness") has been targeted for elimination. New treatments that kill or permanently sterilize female worms could accelerate this process. Prior studies have shown that triple drug treatment with ivermectin plus diethylcarbamazine and albendazole (IDA) leads to prolonged clearance of microfilaremia in persons with lymphatic filariasis. We now report results from a randomized clinical trial that compared the tolerability and efficacy of IDA vs. a comparator treatment (ivermectin plus albendazole, IA) in persons with onchocerciasis. **Methods and findings:** The study was performed in the Volta region of Ghana. Persons with microfilaridermia and palpable subcutaneous nodules were pre-treated with two oral doses of ivermectin (150 µg/kg) separated by at least 6 months prior to treatment with either a single oral dose of ivermectin 150 µg/kg plus albendazole 400 mg (IA), a single oral dose of IDA (IDA1, IA plus diethylcarbamazine (DEC. 6 mg/kg) or three

consecutive daily doses of IDA (IDA3). These treatments were tolerated equally well. While adverse events were common (approximately 30% overall), no severe or serious treatment-emergent adverse events were observed. Skin microfilariae were absent or present with very low densities after all three treatments through 18 months, at which time nodules were excised for histological assessment. Nodule histology was evaluated by two independent assessors who were masked regarding participant infection status or treatment assignment. Significantly lower percentages of female worms were alive and fertile in nodules recovered from study participants after IDA1 (40/261, 15.3%) and IDA3 (34/281, 12.1%) than after IA (41/180, 22.8%). This corresponds to a 40% reduction in the percentage of female worms that were alive and fertile after IDA treatments relative to results observed after the IA comparator treatment ($P = 0.004$). Percentages of female worms that were alive (a secondary outcome of the study) were also lower after IDA treatments (301/574, 52.4%) than after IA (127/198, 64.1%) ($P = 0.004$). Importantly, some comparisons (including the reduced % of fertile female worms after IDA1 vs IA treatment, which was the primary endpoint for the study) were not statistically significant when results were adjusted for intraclass correlation of worm fertility and viability for worms recovered from individual study participants. **Conclusions:** Results from this pilot study suggest that IDA was well tolerated after ivermectin pretreatment. They also suggest that IDA was more effective than the comparator treatment IA for killing or sterilizing female *O. volvulus* worms. No other short-course oral treatment for onchocerciasis has been demonstrated to have macrofilaricidal activity. However, this first study was too small to provide conclusive results. Therefore, additional studies will be needed to confirm these promising findings.

The impact of ivermectin, diethylcarbamazine citrate, and albendazole mass drug administration on the prevalence of scabies and soil-transmitted helminths in school-aged children in three municipalities in Timor-Leste: a before-after assessment.

Le B, Monteiro MAA, Amaral S, Wand H, Matthews A, Hii SF, Clarke NE, Arkell P, Yan J, Engelman D, Fancourt N, Fernandes JL, Steer A, Kaldor J, Traub R, Francis JR, Nery SV.

Juin-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37202027/>

Background: Integrated programmes that use combination mass drug administration (MDA) might improve control of multiple neglected tropical diseases simultaneously. We investigated the impact of Timor-Leste's national ivermectin, diethylcarbamazine citrate, and albendazole MDA, for lymphatic filariasis elimination and soil-transmitted helminth (STH) control, on scabies, impetigo, and STH infections. **Methods:** We did a before-after study in six primary schools across three municipalities in Timor-Leste (urban [Dili], semi-urban [Ermera], and rural [Manufahi]) before (April 23 to May 11, 2019) and 18

months after (Nov 9 to Nov 27, 2020) MDA delivery between May 17 and June 1, 2019. Study participants included schoolchildren, as well as infants, children, and adolescents who were incidentally present at school on study days. All schoolchildren whose parents provided consent were eligible to participate in the study. Infants, children, and adolescents younger than 19 years who were not enrolled in the school but were incidentally present at schools on study days were also eligible to participate if their parents consented. Ivermectin, diethylcarbamazine citrate, and albendazole MDA was implemented nationally, with single doses of oral ivermectin (200 µg/kg), diethylcarbamazine citrate (6 mg/kg), and albendazole (400 mg) administered by the Ministry of Health. Scabies and impetigo were assessed by clinical skin examinations, and STHs using quantitative PCR. The primary (cluster-level) analysis adjusted for clustering while the secondary (individual-level) analysis adjusted for sex, age, and clustering. The primary outcomes of the study were prevalence ratios for scabies, impetigo, and STHs (*Trichuris trichiura*, *Ascaris lumbricoides*, *Necator americanus*, and moderate-to-heavy *A. lumbricoides* infections) between baseline and 18 months from the cluster-level analysis. **Findings:** At baseline, 1043 (87.7%) of 1190 children registered for the study underwent clinical assessment for scabies and impetigo. The mean age of those who completed skin examinations was 9.4 years (SD 2.4) and 514 (53.8%) of 956 were female (87 participants with missing sex data were excluded from this percentage calculation). Stool samples were received for 541 (45.5%) of 1190 children. The mean age of those for whom stool samples were received was 9.8 years (SD 2.2) and 300 (55.5%) were female. At baseline, 348 (33.4%) of 1043 participants had scabies, and 18 months after MDA, 133 (11.1%) of 1196 participants had scabies (prevalence ratio 0.38, 95% CI 0.18-0.88; $p=0.020$) in the cluster-level analysis. At baseline, 130 (12.5%) of 1043 participants had impetigo, compared with 27 (2.3%) of 1196 participants at follow-up (prevalence ratio 0.14, 95% CI 0.07-0.27; $p<0.0001$). There was a significant reduction in *T. trichiura* prevalence from baseline (26 [4.8%] of 541 participants) to 18-month follow-up (four [0.6%] of 623 participants; prevalence ratio 0.16, 95% CI 0.04-0.66; $p<0.0001$). In the individual-level analysis, moderate-to-heavy *A. lumbricoides* infections reduced from 54 (10.0%; 95% CI 0.7-19.6) of 541 participants to 28 (4.5%, 1.2-8.4) of 623 participants (relative reduction 53.6%; 95% CI 9.1-98.1; $p=0.018$). **Interpretation:** Ivermectin, diethylcarbamazine citrate, and albendazole MDA was associated with substantial reductions in prevalence of scabies, impetigo, and *T. trichiura*, and of moderate-to-heavy intensity *A. lumbricoides* infections. Combination MDA could be used to support integrated control programmes to target multiple NTDs.

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, HOUNGBO OA, ANAGONOU EG, BIAOU CAO, AYÉLO AG, HOUZO JG,

Boccarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

PBPK modeling of ivermectin- Considerations for the purpose of developing alternative routes to optimize its safety profile.

Rowland Yeo K, Wesche D.

Mai-2023

CPT Pharmacometrics Syst Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36840414/>

Although single-dose ivermectin has been widely used in mass-drug administration programs for onchocerciasis and lymphatic filariasis for many years, ivermectin may have utility as an endectocide with mosquito-lethal effects at dosages greater and longer than those used to treat helminths. The final physiologically-based pharmacokinetic (PBPK) model for ivermectin described here was able to capture, with reasonable accuracy, observed plasma drug concentration-time profiles and exposures of ivermectin after a single oral dose of the drug in healthy male (dose range 6-30 mg) and female subjects, in both fasted and fed states, in African patients with onchocerciasis (150 µg/kg) and in African children. The PBPK model can be used for further work on lactation, pediatric dosing (considering CYP3A4 and P-gp ontogenies), and pregnancy, especially if nonstandard doses will be used. The key findings of our study indicate that absorption of ivermectin may be highly dependent on bile micelle-mediated solubility. The drug is highly lipophilic and permeable, and its plasma exposure appears to be associated with the body mass index of an individual. These are all factors that need to be considered when extrapolating to more complex oral formulations or alternative routes of administration. Administering lower doses over a longer period may attenuate the dependence on bile micelle-mediated solubility. With relevant inputs, the verified PBPK model developed here could be used to simulate plasma exposures following administration of ivermectin by complex generics in development.

Gale

Analysis of Prescribing Practices in the Dermatology Outpatient Department of a Tertiary Care Teaching Hospital.

Patil B, Patil J, Hugar L, Moharir G.

20-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37220430/>

Evaluating the role of asymptomatic throat carriage of *Streptococcus pyogenes* in impetigo transmission in remote Aboriginal communities in Northern Territory, Australia: a retrospective genomic analysis.

Lacey JA, Marcato AJ, Chisholm RH, Campbell PT, Zachreson C, Price DJ, James TB, Morris JM, Gorrie CL, McDonald MI, Bowen AC, Giffard PM, Holt DC, Currie BJ, Carapetis JR, Andrews RM, Davies MR, Geard N, McVernon J, Tong SYC.

18-05-2023

Lancet Microbe.

<https://pubmed.ncbi.nlm.nih.gov/37211022/>

Background: Streptococcus pyogenes, or group A Streptococcus (GAS), infections contribute to a high burden of disease in Aboriginal Australians, causing skin infections and immune sequelae such as rheumatic heart disease. Controlling skin infections in these populations has proven difficult, with transmission dynamics being poorly understood. We aimed to identify the relative contributions of impetigo and asymptomatic throat carriage to GAS transmission. **Methods:** In this genomic analysis, we retrospectively applied whole genome sequencing to GAS isolates that were collected as part of an impetigo surveillance longitudinal household survey conducted in three remote Aboriginal communities in the Northern Territory of Australia between Aug 6, 2003, and June 22, 2005. We included GAS isolates from all throats and impetigo lesions of people living in two of the previously studied communities. We classified isolates into genomic lineages based on pairwise shared core genomes of more than 99% with five or fewer single nucleotide polymorphisms. We used a household network analysis of epidemiologically and genomically linked lineages to quantify the transmission of GAS within and between households. **Findings:** We included 320 GAS isolates in our analysis: 203 (63%) from asymptomatic throat swabs and 117 (37%) from impetigo lesions. Among 64 genomic lineages (encompassing 39 emm types) we identified 264 transmission links (involving 93% of isolates), for which the probable source was asymptomatic throat carriage in 166 (63%) and impetigo lesions in 98 (37%). Links originating from impetigo cases were more frequent between households than within households. Households were infected with GAS for a mean of 57 days (SD 39 days), and once cleared, reinfected 62 days (SD 40 days) later. Increased household size and community presence of GAS and scabies were associated with slower clearance of GAS. **Interpretation:** In communities with high prevalence of endemic GAS-associated skin infection, asymptomatic throat carriage is a GAS reservoir. Public health interventions such as vaccination or community infection control programmes aimed at interrupting transmission of GAS might need to include consideration of asymptomatic throat carriage.

Examining the cyclical nature of scabies using historical texts.

Walker MD.

19-05-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37203874/>

The impact of ivermectin, diethylcarbamazine citrate, and albendazole mass drug administration

on the prevalence of scabies and soil-transmitted helminths in school-aged children in three municipalities in Timor-Leste: a before-after assessment.

Le B, Monteiro MAA, Amaral S, Wand H, Matthews A, Hii SF, Clarke NE, Arkell P, Yan J, Engelman D, Fancourt N, Fernandes JL, Steer A, Kaldor J, Traub R, Francis JR, Nery SV.

Juin-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37202027/>

Background: Integrated programmes that use combination mass drug administration (MDA) might improve control of multiple neglected tropical diseases simultaneously. We investigated the impact of Timor-Leste's national ivermectin, diethylcarbamazine citrate, and albendazole MDA, for lymphatic filariasis elimination and soil-transmitted helminth (STH) control, on scabies, impetigo, and STH infections. **Methods:** We did a before-after study in six primary schools across three municipalities in Timor-Leste (urban [Dili], semi-urban [Ermera], and rural [Manufahi]) before (April 23 to May 11, 2019) and 18 months after (Nov 9 to Nov 27, 2020) MDA delivery between May 17 and June 1, 2019. Study participants included schoolchildren, as well as infants, children, and adolescents who were incidentally present at school on study days. All schoolchildren whose parents provided consent were eligible to participate in the study. Infants, children, and adolescents younger than 19 years who were not enrolled in the school but were incidentally present at schools on study days were also eligible to participate if their parents consented. Ivermectin, diethylcarbamazine citrate, and albendazole MDA was implemented nationally, with single doses of oral ivermectin (200 µg/kg), diethylcarbamazine citrate (6 mg/kg), and albendazole (400 mg) administered by the Ministry of Health. Scabies and impetigo were assessed by clinical skin examinations, and STHs using quantitative PCR. The primary (cluster-level) analysis adjusted for clustering while the secondary (individual-level) analysis adjusted for sex, age, and clustering. The primary outcomes of the study were prevalence ratios for scabies, impetigo, and STHs (*Trichuris trichiura*, *Ascaris lumbricoides*, *Necator americanus*, and moderate-to-heavy *A lumbricoides* infections) between baseline and 18 months from the cluster-level analysis. **Findings:** At baseline, 1043 (87.7%) of 1190 children registered for the study underwent clinical assessment for scabies and impetigo. The mean age of those who completed skin examinations was 9.4 years (SD 2.4) and 514 (53.8%) of 956 were female (87 participants with missing sex data were excluded from this percentage calculation). Stool samples were received for 541 (45.5%) of 1190 children. The mean age of those for whom stool samples were received was 9.8 years (SD 2.2) and 300 (55.5%) were female. At baseline, 348 (33.4%) of 1043 participants had scabies, and 18 months after MDA, 133 (11.1%) of 1196 participants had scabies (prevalence ratio 0.38, 95% CI 0.18-0.88; $p=0.020$) in the cluster-level analysis. At baseline, 130 (12.5%) of 1043 participants had impetigo, compared with 27 (2.3%) of 1196 participants at follow-up (prevalence ratio 0.14, 95% CI 0.07-0.27; $p<0.0001$). There was a significant reduction in *T trichiura*

prevalence from baseline (26 [4.8%] of 541 participants) to 18-month follow-up (four [0.6%] of 623 participants; prevalence ratio 0.16, 95% CI 0.04-0.66; $p < 0.0001$). In the individual-level analysis, moderate-to-heavy *A lumbricoides* infections reduced from 54 (10.0%; 95% CI 0.7-19.6) of 541 participants to 28 (4.5%, 1.2-8.4) of 623 participants (relative reduction 53.6%; 95% CI 9.1-98.1; $p = 0.018$). **Interpretation:** Ivermectin, diethylcarbamazine citrate, and albendazole MDA was associated with substantial reductions in prevalence of scabies, impetigo, and *T trichiura*, and of moderate-to-heavy intensity *A lumbricoides* infections. Combination MDA could be used to support integrated control programmes to target multiple NTDs.

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, Hounbo OA, Anagonou EG, Biaou CAO, Ayélo AG, Houezo JG, Boccarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

Context: Since 2013, the World Health Organization has recommended integrated control strategies for neglected tropical diseases (NTDs) with skin manifestations. We evaluated the implementation of an integrated approach to the early detection and rapid treatment of skin NTDs based on mobile clinics in the Ouémé and Plateau areas of Benin. **Methods:** This descriptive cross-sectional study was performed in Ouémé and Plateau in Benin from 2018 to 2020. Consultations using mobile teams were performed at various sites selected by reasoned choice based on the epidemiological data of the National Program for the Control of Leprosy and Buruli Ulcer. All individuals presenting with a dermatological lesion who voluntarily approached the multidisciplinary management team on the day of consultation were included. The information collected was kept strictly anonymous and was entered into an Excel 2013 spreadsheet and analyzed with Stata 11 software. **Results:** In total, 5,267 patients with various skin conditions consulted the medical team. The median age of these patients was 14 years (IQR: 7-34 years). We saw 646 (12.3%) patients presenting NTDs with skin manifestations, principally scabies, in 88.4% (571/646), followed by 37 cases of Buruli ulcer (5.8%), 22 cases of leprosy (3.4%), 15 cases of lymphatic filariasis (2.3%) and one case of mycetoma (0.2%). We detected no cases of yaws. **Conclusion:** This sustainable approach could help to decrease the burden of skin NTDs in resource-limited countries.

[Translated article] RF - Resistance to Permethrin in Scabies Treatment: Does It Really Exist?

Velasco-Amador JP, Prados-Carmona A, Ruiz-Villaverde R.

Mai-2023

Actas Dermosifiliogr.

<https://pubmed.ncbi.nlm.nih.gov/37068634/>

RF - Resistance to Permethrin in Scabies Treatment: Does It Really Exist?

Velasco-Amador JP, Prados-Carmona A, Ruiz-Villaverde R.

Mai-2023

Actas Dermosifiliogr.

<https://pubmed.ncbi.nlm.nih.gov/36567030/>

Delusions of parasitosis and delusions of parasitosis by proxy in a mother and her children.

Kalra K, Whittington CP, Sevey W, Hunt E, Metz JB.

Mai-Juin 2023

Pediatr Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36519423/>

Delusions of parasitosis by proxy is an uncommon entity wherein an individual projects a delusional belief onto another person who lacks capacity to hold the same belief. We report a case of delusions of parasitosis by proxy in a mother who believed that she was infested with scabies and projected her fixed, delusional belief of scabies infestation onto her children. She subjected her children to numerous home remedies and medical treatments as well as removing them from school in an effort to cure them of the supposed infestation. Child maltreatment can be a concern in such cases with a low threshold for involving child protective services if harm to the children is suspected.

A scabies outbreak in an inpatient rehabilitation setting.

Xu T, Durst M, Keck T, Dixon H, Yassin MH.

Juin-2023

Am J Infect Control.

<https://pubmed.ncbi.nlm.nih.gov/36244573/>

Background: Scabies is a skin infection transmitted by close person-to-person contact. Crusted scabies is a more severe type which is more contagious. Delayed diagnosis of scabies could lead to an outbreak. **Methods:** The outbreak occurred at a 435-bed academic medical center with 76 inpatient rehabilitation beds. The index patient was incarcerated and admitted to our hospital in February 2022. The patient developed crusted scabies after steroids treatment. **Results:** The patient was treated with oral ivermectin (200 mcg/kg, maximum dose 15 mg) and topical permethrin 5%. All units were followed for 6 weeks since diagnosis of the index patient. A total of 46 healthcare workers (20 nurses and 26 physical therapists) were exposed. Twenty-nine presented symptoms and were treated with ivermectin and permethrin or only ivermectin. No physicians, other patients, or prison guards were affected. There was no secondary household transmission of those exposed healthcare workers. **Conclusions:** Scabies is highly contagious in high-risk

patients. Early diagnosis and effective infection control are of vital importance.

The burden of skin diseases in India: Global Burden of Disease Study 2017.

Kavita A, Thakur JS, Narang T.

Mai-Juin 2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/34877854/>

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

Giardia duodenalis and dysentery in Iron Age Jerusalem (7th-6th century BCE).

Mitchell PD, Wang T, Billig Y, Gadot Y, Warnock P, Langgut D.

26-05-2023

Parasitology.

<https://pubmed.ncbi.nlm.nih.gov/37231841/>

The aim of this study was to determine if the protozoa that cause dysentery might have been present in Jerusalem, the capital of the Kingdom of Judah, during the Iron Age. Sediments from 2 latrines pertaining to this time period were obtained, 1 dating from the 7th century BCE and another from the 7th to early 6th century BCE. Microscopic investigations have previously shown that the users were infected by whipworm (*Trichuris trichiura*), roundworm (*Ascaris lumbricoides*), *Taenia* sp. tapeworm and pinworm (*Enterobius vermicularis*). However, the protozoa that cause dysentery are fragile and do not survive well in ancient samples in a form recognizable using light microscopy. Enzyme-linked immunosorbent assay kits designed to detect the antigens of *Entamoeba histolytica*, *Cryptosporidium* sp. and *Giardia duodenalis* were used. Results for *Entamoeba* and *Cryptosporidium* were negative, while *Giardia* was positive for both latrine sediments when the analysis was repeated three times. This provides our first microbiological evidence for infective diarrhoeal illnesses that would have affected the populations of the ancient near east. When we integrate descriptions from 2nd and 1st millennium BCE Mesopotamian medical texts, it seems likely that outbreaks of dysentery due to giardiasis may have caused ill health throughout early towns across the region.

Reflecting on the past and fast forwarding to present day anthelmintic resistant *Ancylostoma caninum*-A critical issue we neglected to forecast.

Marsh AE, Lakritz J.

10-05-2023

Int J Parasitol Drugs Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37229949/>

Reports of anthelmintic resistance in *Ancylostoma caninum* are increasing in frequency in the United States

of America (USA). In the last few years in vitro and in vivo studies characterized individual isolates, demonstrating multiple anthelmintic drug resistance (MADR). In 2021, the American Association of Veterinary Parasitologists initiated a hookworm task force to address this issue. The first report of drug resistant *A. caninum* occurred in 1987 in Australian racing Greyhounds. In the last five years multiple case reports and investigations show drug resistant *A. caninum* is becoming a much greater problem in the USA and now extends beyond racing Greyhounds into the general companion animal dog population. The literature, regarding drug resistance in livestock and equine nematodes, provides helpful guidance along with diagnostic methods to better understand the evolution and selection of canine MADR hookworms; however, there are limitations and caveats due to *A. caninum*'s unique biology and zoonotic potential. Mass drug administration (MDA) of anthelmintic drugs to humans to reduce morbidity associated with human hookworms (*Necator americanus*) should consider the factors that contributed to the development of MADR *A. caninum*. Finally, as Greyhound racing undergoes termination in some regions and the retired dogs undergo subsequent rehoming, drug resistant parasites, if present, are carried with them. Drug resistant *A. caninum* requires greater recognition by the veterinary community, and small animal practitioners need to be aware of the spread into current pet dog populations. The current understanding of anthelmintic resistance, available treatments, and environmental mitigation for these drug resistant *A. caninum* isolates must be monitored for horizontal spread. A major goal in this emerging problem is to prevent continued dissemination.

Malaria, gastrointestinal parasite infection and nutritional status among febrile children in Accra, Ghana.

Darko BA, Owusu-Asenso CM, Addo-Osafo K, Appiah-Lawson E, Afrane YA, Tette EMA.

08-05-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37214835/>

The impact of ivermectin, diethylcarbamazine citrate, and albendazole mass drug administration on the prevalence of scabies and soil-transmitted helminths in school-aged children in three municipalities in Timor-Leste: a before-after assessment.

Le B, Monteiro MAA, Amaral S, Wand H, Matthews A, Hii SF, Clarke NE, Arkell P, Yan J, Engelman D, Fancourt N, Fernandes JL, Steer A, Kaldor J, Traub R, Francis JR, Nery SV.

Juin-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37202027/>

Background: Integrated programmes that use combination mass drug administration (MDA) might improve control of multiple neglected tropical diseases simultaneously. We investigated the impact of Timor-Leste's national

ivermectin, diethylcarbamazine citrate, and albendazole MDA, for lymphatic filariasis elimination and soil-transmitted helminth (STH) control, on scabies, impetigo, and STH infections. **Methods:** We did a before-after study in six primary schools across three municipalities in Timor-Leste (urban [Dili], semi-urban [Ermera], and rural [Manufahi]) before (April 23 to May 11, 2019) and 18 months after (Nov 9 to Nov 27, 2020) MDA delivery between May 17 and June 1, 2019. Study participants included schoolchildren, as well as infants, children, and adolescents who were incidentally present at school on study days. All schoolchildren whose parents provided consent were eligible to participate in the study. Infants, children, and adolescents younger than 19 years who were not enrolled in the school but were incidentally present at schools on study days were also eligible to participate if their parents consented. Ivermectin, diethylcarbamazine citrate, and albendazole MDA was implemented nationally, with single doses of oral ivermectin (200 µg/kg), diethylcarbamazine citrate (6 mg/kg), and albendazole (400 mg) administered by the Ministry of Health. Scabies and impetigo were assessed by clinical skin examinations, and STHs using quantitative PCR. The primary (cluster-level) analysis adjusted for clustering while the secondary (individual-level) analysis adjusted for sex, age, and clustering. The primary outcomes of the study were prevalence ratios for scabies, impetigo, and STHs (*Trichuris trichiura*, *Ascaris lumbricoides*, *Necator americanus*, and moderate-to-heavy *A. lumbricoides* infections) between baseline and 18 months from the cluster-level analysis. **Findings:** At baseline, 1043 (87.7%) of 1190 children registered for the study underwent clinical assessment for scabies and impetigo. The mean age of those who completed skin examinations was 9.4 years (SD 2.4) and 514 (53.8%) of 956 were female (87 participants with missing sex data were excluded from this percentage calculation). Stool samples were received for 541 (45.5%) of 1190 children. The mean age of those for whom stool samples were received was 9.8 years (SD 2.2) and 300 (55.5%) were female. At baseline, 348 (33.4%) of 1043 participants had scabies, and 18 months after MDA, 133 (11.1%) of 1196 participants had scabies (prevalence ratio 0.38, 95% CI 0.18-0.88; $p=0.020$) in the cluster-level analysis. At baseline, 130 (12.5%) of 1043 participants had impetigo, compared with 27 (2.3%) of 1196 participants at follow-up (prevalence ratio 0.14, 95% CI 0.07-0.27; $p<0.0001$). There was a significant reduction in *T. trichiura* prevalence from baseline [26 (4.8%) of 541 participants] to 18-month follow-up (four [0.6%] of 623 participants; prevalence ratio 0.16, 95% CI 0.04-0.66; $p<0.0001$). In the individual-level analysis, moderate-to-heavy *A. lumbricoides* infections reduced from 54 (10.0%; 95% CI 0.7-19.6) of 541 participants to 28 (4.5%, 1.2-8.4) of 623 participants (relative reduction 53.6%; 95% CI 9.1-98.1; $p=0.018$). **Interpretation:** Ivermectin, diethylcarbamazine citrate, and albendazole MDA was associated with substantial reductions in prevalence of scabies, impetigo, and *T. trichiura*, and of moderate-to-heavy intensity *A. lumbricoides* infections. Combination MDA could be used to support integrated control programmes to target multiple NTDs.

Leishmaniose

Efficacy of oleylphosphocholine in experimental cutaneous leishmaniasis.

Van Bocxlaer K, Dixon J, Platteeuw JJ, Van Den Heuvel D, McArthur KN, Harris A, Alavijeh M, Croft SL, Yardley V.

25-05-2023

J Antimicrob Chemother.

<https://pubmed.ncbi.nlm.nih.gov/37229566/>

Metabolic profiling of *Chimonanthus grammatus* via UHPLC-HRMS-MS with computer-assisted structure elucidation and its antimicrobial activity.

Hu H, Tekin V, Hu B, Yaghoobi M, Khan A, Ghosh AK, Panda SK, Huang H, Luyten W.

09-05-2023

Front Plant Sci.

<https://pubmed.ncbi.nlm.nih.gov/37229132/>

Chimonanthus grammatus is used as Hakka traditional herb to treat cold, flu, etc. So far, the phytochemistry and antimicrobial compounds have not been well investigated. In this study, the orbitrap-ion trap MS was used to characterize its metabolites, combined with a computer-assisted structure elucidation method, and the antimicrobial activities were assessed by a broth dilution method against 21 human pathogens, as well as the bioassay-guided purification work to clarify its main antimicrobial compounds. A total of 83 compounds were identified with their fragmentation patterns, including terpenoids, coumarins, flavonoids, organic acids, alkaloids, and others. The plant extracts can strongly inhibit the growth of three Gram-positive and four Gram-negative bacteria, and nine active compounds were bioassay-guided isolated, including homalomenol C, jasmonic acid, isofraxidin, quercitrin, stigmasta-7,22-diene-3 β ,5 α ,6 α -triol, quercetin, 4-hydroxy-1,10-secocadin-5-ene-1,10-dione, kaempferol, and *E*-4-(4,8-dimethylnona-3,7-dienyl)furan-2(5H)-one. Among them, isofraxidin, kaempferol, and quercitrin showed significant activity against planktonic *Staphylococcus aureus* (IC₅₀ = 13.51, 18.08 and 15.86 µg/ml). Moreover, their antibiofilm activities of *S. aureus* (BIC₅₀ = 15.43, 17.31, 18.86 µg/ml; BEC₅₀ = 45.86, \geq 62.50, and 57.62 µg/ml) are higher than ciprofloxacin. The results demonstrated that the isolated antimicrobial compounds played the key role of this herb in combating microbes and provided benefits for its development and quality control, and the computer-assisted structure elucidation method was a powerful tool for chemical analysis, especially for distinguishing isomers with similar structures, which can be used for other complex samples.

First molecular detection of *Leishmania (Leishmania) infantum chagasi* in a domestic cat (*Felis catus*) from an urban area in eastern Amazon.

Aguiar DCF, Nascimento DNDS, Penner DF, de Castro BDSL, Virgolino RR, Neves AMP, Siqueira ADS, Gonçalves EC.

22-05-2023

J Venom Anim Toxins Incl Trop Dis.

Background: Domestic cats have been implicated as accidental hosts of *Leishmania* sp. However, in recent years, the recurrent description of new cases in endemic and nonendemic areas draw attention to the potential epidemiological role of cats as reservoir hosts. Although dogs are considered urban reservoirs, cats could act as a secondary natural reservoirs in these areas. Thus, feline leishmaniasis has become an emerging disease in several countries worldwide. **Case presentation:** This study aimed to describe the first case of feline leishmaniasis in a stray animal that presented lesions compatible with the disease in Belém, Pará, Brazil, an important urban area in eastern Amazon. Serological tests for *Leishmania infantum* (ELISA and IFA) were nonreactive, whereas histopathological examination indicated infectious dermatitis caused by *Leishmania* spp. or *Toxoplasma gondii*. Cytopathological study of lesion aspirate confirmed the presence of *Leishmania* sp. amastigotes within macrophages. Finally, molecular analyses revealed that the feline infection was caused by *Leishmania (Leishmania) infantum chagasi*. **Conclusion:** To the best of the authors' knowledge, this study reports the first case of natural infection by *Leishmania (Leishmania) infantum chagasi* in a feline from eastern Amazon. These findings suggest domestic cats as potential secondary reservoir hosts of *Leishmania* spp. in Belém, which reinforces the importance of further epidemiological investigation of feline leishmaniasis, especially in urban areas with human cases.

Gene editing and scalable functional genomic screening in *Leishmania* species using the CRISPR/Cas9 cytosine base editor toolbox LeishBASEdit.

Engstler M, Beneke T.

24-05-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37222701/>

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

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

24-05-2023

Microbiol Spectr.

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

Wastewater treatment plants (WWTPs) receive and treat large volumes of domestic, industrial, and urban wastewater containing pathogenic and nonpathogenic microorganisms, chemical compounds, heavy metals, and other potentially hazardous substances. WWTPs play an essential role in preserving human, animal, and environmental health by removing many of these toxic and infectious agents, particularly biological hazards. Wastewater contains complex consortiums of bacterial, viral, archaeal, and eukaryotic species, and while bacteria in WWTP have been extensively studied, the temporal and spatial distribution of nonbacterial microflora (viruses, archaea, and eukaryotes) is less understood. In this study,

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

Molecular phylogeny of Psychodopygina (Diptera, Psychodidae) supporting morphological systematics of this group of vectors of New World tegumentary leishmaniasis.

Zapata S, Galati EAB, Chaves JA, Artigas P, Gantier JC, Barges MD, Mas-Coma S, Depaquit J.

2023

Parasite.

<https://pubmed.ncbi.nlm.nih.gov/37222517/>

Canine visceral leishmaniasis: risk factors and spatial analysis in an endemic area of Northeastern Brazil.

Silva SS, Macedo LO, Oliveira JCP, Alves LC, Carvalho GA, Ramos RAN.

22-05-2023

Rev Bras Parasitol Vet.

<https://pubmed.ncbi.nlm.nih.gov/37222306/>

High throughput biochemical profiling, and functional potential analysis for valorization of grape peduncles.

Akbar A, Gul Z, Hussain N, Al Haddad AH, Khan NA, Sadiq MB, Sher H.

23-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37221193/>

Vitis vinifera L., commonly known as grape is a major fruit crop in the world. Grapes seem to confer health benefits due to their chemical components, biological and antioxidant activities. The present study is conducted to evaluate the biochemical constituents, antioxidant, and antimicrobial potential of ethanolic grape peduncles (EGP) extract. The result of phytochemical analysis revealed the presence of various phytochemicals such as flavonoid, tannin, carbohydrates, alkaloids, cardiac glycoside, phenol, steroid, terpenoids, quinones and anthraquinones. Furthermore, total phenolic content (TPC) and total flavonoid contents (TFC) were 7.35 ± 0.25 mg GAE/g (Gallic Acid Equivalent per gram) and 29.67 ± 0.13 mg QE/g (Quercetin Equivalent per gram) respectively. DPPH (2, 2-diphenyl-1-picrylhydrazyl) free radical scavenging assay revealed $IC_{50} = 159.3 \mu\text{g/mL}$. The antibacterial and antifungal study disclosed that the extract was highly potent against *Salmonella typhi* with maximum zone of inhibition of 27.2 ± 1.60 mm and *Epidermophyton floccosum* with $74 \pm 1.81\%$ inhibition. The extract was analyzed for its cytotoxicity and antileishmanial activity and showed no activity against HeLa cell line and promastigotes of *Leishmania major*. Elements Fe, Mn, Ni, Pb and Cd were determined by atomic absorption spectroscopy and approximately 50 compounds were identified by Gas Chromatography-Mass Spectrometry (GC-MS). Current work suggest that grape peduncles can be a promising source of bioactive medicinal component.

Nodular lymphangitis related to methicillin-resistant staphylococcus aureus infection.

Trepanowski N, Alomran A, Mahalingam M, Yasuda MR, Hartman RI.

15-04-2023

Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37220287/>

Nodular lymphangitis, also known as lymphocutaneous syndrome or sporotrichoid lymphangitis, presents with inflammatory nodules along the lymphatic vessels, typically involving the upper or lower extremities. Although the most common cause of nodular lymphangitis is infection due to *Sporothrix schenckii*, *Nocardia brasiliensis*, *Mycobacterium marinum*, or *Leishmania braziliensis*, it is important for clinicians to be aware of methicillin-resistant *Staphylococcus aureus* as a rare cause of nodular lymphangitis and perform gram stain, bacterial culture, and antibiotic sensitivity profiles when appropriate. History of recent travel or exposures, incubation time, presence of systemic symptoms, and

presence of ulceration, suppuration, or drainage can serve as diagnostic clues, but microbiological tissue cultures and histopathologic studies confirm the diagnosis. Herein, we present a case of nodular lymphangitis caused by methicillin-resistant *Staphylococcus aureus* (MRSA); tissue culture and antibiotic sensitivities were used to guide treatment.

Treatment of canine cutaneous leishmaniasis by *Leishmania (Viannia) braziliensis* in dogs with furazolidone and β -cyclodextrin: case report.

Santos Zanini M, Ataíde Siqueira L, Vieira Almeida Y, Savergnini Poleze L, Gnecco Zanini D, Ramos Sobreira R, Madureira AP.

31-12-2022

Vet Ital.

<https://pubmed.ncbi.nlm.nih.gov/37219838/>

Optimization of Orally Bioavailable Antileishmanial 2,4,5-Trisubstituted Benzamides.

Kim HS, Ortiz D, Kadayat TM, Fargo CM, Hammill JT, Chen Y, Rice AL, Begley KL, Shoeran G, Pistel W, Yates PA, Sanchez MA, Landfear SM, Guy RK.

22-05-2023

J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37216489/>

Quinolone-3-amidoalkanol: A New Class of Potent and Broad-Spectrum Antimicrobial Agent.

Dube PS, Angula KT, Legoabe LJ, Jordaan A, Boitz Zarella JM, Warner DF, Doggett JS, Beteck RM.

04-05-2023

ACS Omega.

<https://pubmed.ncbi.nlm.nih.gov/37214682/>

Herein, we describe 39 novel quinolone compounds bearing a hydrophilic amine chain and varied substituted benzyloxy units. These compounds demonstrate broad-spectrum activities against acid-fast bacterium, Gram-positive and -negative bacteria, fungi, and leishmania parasite. Compound **30** maintained antitubercular activity against moxifloxacin-, isoniazid-, and rifampicin-resistant *Mycobacterium tuberculosis*, while **37** exhibited low micromolar activities ($<1 \mu\text{g/mL}$) against World Health Organization (WHO) critical pathogens: *Cryptococcus neoformans*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*. Compounds in this study are metabolically robust, demonstrating % remnant of $>98\%$ after 30 min in the presence of human, rat, and mouse liver microsomes. Several compounds thus reported here are promising leads for the treatment of diseases caused by infectious agents.

Species diversity of phlebotomine sand flies and sympatric occurrence of *Leishmania (Mundinia) martiniquensis*, *Leishmania (Leishmania) donovani* complex, and *Trypanosoma* spp. in the

visceral leishmaniasis focus of southern Thailand.

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

20-05-2023

Acta Trop.

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

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

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

19-05-2023

Biomed Pharmacother.

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

Leishmaniasis and Chagas disease, two of the most prevalent neglected tropical diseases, are a world health problem. The harsh reality of these infective diseases is the absence of effective and safe therapies. In this framework, natural products play an important role in overcoming the current need to development new antiparasitic agents. The present study reports the synthesis, antikinetoplastid screening, mechanism study of fourteen withaferin A derivatives (2-15). Nine of them (2-6, 8-10 and 12) showed a potent dose-dependent inhibitory effect on the proliferation of *Leishmania amazonensis* and *L. donovani* promastigotes and *Trypanosoma cruzi* epimastigotes with IC₅₀ values ranging from 0.19 to 24.01 µM. Outstandingly, the fully acetylated derivative 10 (4,27-diacetylwithaferin A) was the most potent compound showing IC₅₀ values of 0.36, 2.82 and 0.19 µM against *L. amazonensis*, *L. donovani* and *T. cruzi*, respectively. Furthermore, analogue 10 exhibited approximately 18 and 36-fold greater antikinetoplastid activity, on *L. amazonensis* and *T. cruzi*, than the reference drugs. The activity was accompanied by significantly lower cytotoxicity on the murine macrophage cell line. Moreover, compounds 2, 3, 5-7, 9 and 10 showed more potent activity than the reference drug against the intracellular amastigotes forms of *L. amazonensis* and *T. cruzi*, with a good selectivity index on a mammalian cell line. In addition, withaferin A analogues 3, 5-7, 9 and 10 induce programmed cell death through a process of apoptosis-like and autophagy. These results strengthen the anti-parasitic potential of withaferin A-related steroids against neglected tropical diseases caused by *Leishmania* spp. and *T. cruzi* parasites.

Limited Cutaneous Leishmaniasis as Ulcerated Verrucous Plaque on Leg, Tucson, Arizona, USA¹.

Dagenet CB, Davis MS, Murphy S, Thiede R, Culpepper KS, Fazel M.

Juin-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37209715/>

Detection of Leishmania RNA Virus 1 in Leishmania (Viannia) panamensis Isolates, Panama.

Gonzalez K, De León SS, Pineda V, Samudio F, Capitan-Barrios Z, Suarez JA, Weeden A, Ortiz B, Rios M, Moreno B, Gundacker ND, Pascale JM, López-Vergès S, Sosa N, Saldaña A, Ábrego LE.

Juin-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37209675/>

We detected *Leishmania* RNA virus 1 (LRV1) in 11 isolates of *Leishmania* (*Viannia*) *panamensis* collected during 2014-2019 from patients from different geographic areas in Panama. The distribution suggested a spread of LRV1 in *L. (V.) panamensis* parasites. We found no association between LRV1 and an increase in clinical pathology.

Clinical evolution of equine leishmaniasis with self-limiting cutaneous disease caused by Leishmania infantum in northeastern Brazil: A case report.

de Pinho FA, Mendes MO, de Magalhães VLP, Tinôco AAC, Seoane JHL, Rêgo FD, Soares RP, Barrouin-Melo SM.

Juin-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37208087/>

Combined immunohistochemical protocols to differentiate macrophages within the mononuclear-phagocyte system.

Lazzarini G, Abramo F, Albanese F, Pirone A, Miragliotta V.

17-05-2023

Ann Anat.

<https://pubmed.ncbi.nlm.nih.gov/37207851/>

Cysteine synthase: multiple structures of a key enzyme in cysteine synthesis and a potential drug target for Chagas disease and leishmaniasis.

Sowerby K, Freitag-Pohl S, Murillo AM, Silber AM, Pohl E.

01-06-2023

Acta Crystallogr D Struct Biol.

<https://pubmed.ncbi.nlm.nih.gov/37204818/>

Chagas disease is a neglected tropical disease (NTD) caused by *Trypanosoma cruzi*, whilst leishmaniasis, which is caused by over 20 species of *Leishmania*, represents a group of NTDs endemic to most countries in the tropical and subtropical belt of the planet. These diseases remain a significant health problem both in endemic countries and globally. These parasites and other trypanosomatids, including *T. theileri*, a bovine pathogen, rely on cysteine biosynthesis for the production of trypanothione, which is essential for parasite survival in hosts. The de novo pathway of cysteine biosynthesis requires the conversion

of O-acetyl-L-serine into L-cysteine, which is catalysed by cysteine synthase (CS). These enzymes present potential for drug development against *T. cruzi*, *Leishmania* spp. and *T. theileri*. To enable these possibilities, biochemical and crystallographic studies of CS from *T. cruzi* (TcCS), *L. infantum* (LiCS) and *T. theileri* (TthCS) were conducted. Crystal structures of the three enzymes were determined at resolutions of 1.80 Å for TcCS, 1.75 Å for LiCS and 2.75 Å for TthCS. These three homodimeric structures show the same overall fold and demonstrate that the active-site geometry is conserved, supporting a common reaction mechanism. Detailed structural analysis revealed reaction intermediates of the de novo pathway ranging from an apo structure of LiCS and holo structures of both TcCS and TthCS to the substrate-bound structure of TcCS. These structures will allow exploration of the active site for the design of novel inhibitors. Additionally, unexpected binding sites discovered at the dimer interface represent new potential for the development of protein-protein inhibitors.

TIM-3 increases the abundance of type-2 dendritic cells during *Leishmania donovani* infection by enhancing IL-10 production via STAT3.

Mishra M, Yadav M, Kumar S, Kumar R, Sen P.

18-05-2023

Cell Death Dis.

<https://pubmed.ncbi.nlm.nih.gov/37202419/>

The outcome of the disease visceral leishmaniasis (VL), caused by *Leishmania donovani* (LD), largely relies on the relative dominance of host-protective type-1 T helper (Th1) cell response versus disease-promoting type-2 T helper (Th2) cell response. The Th1 and Th2 responses, in turn, are believed to be elicited by type-1 conventional dendritic cells (cDC1) and type-2 conventional DCs (cDC2), respectively. However, it is still unknown which DC subtype (cDC1 or cDC2) predominates during chronic LD infection and the molecular mechanism governing such occurrence. Here we report that in chronically infected mice, the splenic cDC1-cDC2 balance shifted toward the cDC2 subtype and that the receptor T cell immunoglobulin and mucin protein-3 (TIM-3) expressed by DCs played a key role in mediating this effect. Transfer of TIM-3-silenced DCs in fact prevented the predominance of the cDC2 subtype in mice with chronic LD infection. We also found that LD actually upregulated TIM-3 expression on DCs by triggering a TIM-3-mediated signaling pathway STAT3 (signal transducer and activator of transcription 3)→interleukin (IL)-10→c-Src→transcription factors Ets1, Ets2, USF1, and USF2. Notably, TIM-3 promoted STAT3 activation via a non-receptor tyrosine kinase Btk. Adoptive transfer experiments further demonstrated a critical role for STAT3-driven TIM-3 upregulation on DCs in increasing cDC2 abundance in chronically infected mice, which ultimately aided disease pathogenesis by augmenting Th2 responses. These findings document a new immunoregulatory mechanism contributing to disease pathology during LD infection and define TIM-3 as a key mediator of this process.

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/>

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.

Juin-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.

Structural basis for guide RNA selection by the RESC1-RESC2 complex.

Dolce LG, Nesterenko Y, Walther L, Weis F, Kowalinski E.

22-05-2023

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/36999600/>

ULK4 and Fused/STK36 interact to mediate assembly of a motile flagellum.

McCoy CJ, Paupelin-Vaucelle H, Gorilak P, Beneke T, Varga V, Gluenz E.

01-06-2023

Mol Biol Cell.

<https://pubmed.ncbi.nlm.nih.gov/36989043/>

Unc-51-like kinase (ULK) family serine-threonine protein kinase homologues have been linked to the function of motile cilia in diverse species. Mutations in *Fused/STK36* and *ULK4* in mice resulted in hydrocephalus and other phenotypes consistent with ciliary defects. How either protein contributes to the assembly and function of motile cilia is not well understood. Here we studied the phenotypes of *ULK4* and *Fused* gene knockout (KO) mutants in the flagellated protist *Leishmania mexicana*. Both KO mutants exhibited a variety of structural defects of the flagellum cytoskeleton. Biochemical approaches indicate spatial proximity of these proteins and indicate a direct interaction between the N-terminus of LmxULK4 and LmxFused. Both proteins display a dispersed localization throughout the cell body and flagellum, with enrichment near the flagellar base and tip. The stable expression of LmxULK4 was dependent on the presence of LmxFused. *Fused/STK36* was previously shown to localize to mammalian motile cilia, and we demonstrate here that *ULK4* also localizes to the motile cilia in mouse ependymal cells. Taken together these data suggest a model where the pseudokinase *ULK4* is a positive regulator of the kinase *Fused/STK36* in a pathway required for stable assembly of motile cilia.

Assessing the effect of antimony pressure on trypanothione reductase activity in *Leishmania (Viannia) braziliensis*.

Zabala-Peñañiel A, Dias-Lopes G, Souza-Silva F, Miranda LFC, Conceição-Silva F, Alves CR.

Mai-2023

Biochimie.

<https://pubmed.ncbi.nlm.nih.gov/36586564/>

Lethal action of Licarin A derivatives in *Leishmania (L.) infantum*: Imbalance of calcium and bioenergetic metabolism.

de Castro Levatti EV, Costa-Silva TA, Morais TR, Fernandes JPS, Lago JHG, Tempone AG.

Mai-2023

Biochimie.

<https://pubmed.ncbi.nlm.nih.gov/36586562/>

Assessment of circulating immune complexes in canine leishmaniosis and dirofilariosis.

Iatta R, Paltrinieri S, Cavalera MA, Scavone D, Otranto D, Zatelli A.

Juin-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/36331788/>

Canine leishmaniosis (CanL) by *Leishmania infantum* (L.i.) and heartworm disease by *Dirofilaria immitis* (D.i.) are common zoonotic vector-borne diseases (VBDs) characterized by a variety of pathological and clinical signs. The immunopathology in both VBDs is extremely complex, and their clinical manifestations are strongly dependent on the type of immune response elicited by the parasites. In particular, the formation of circulating immune complexes (CICs) plays an important role in the pathogenesis of these VBDs. Based on the international guidelines, dogs with high anti-L. infantum antibody titres and one or more clinical and/or laboratory signs related to CanL require anti-Leishmania treatment. Consequently, the CICs measurement could be used for improving the clinical staging process of CanL. The aim of the study was to assess the CICs level by a competitive inhibition enzyme immunoassay, in healthy or sick dogs seropositive to L.i. and in healthy dogs positive to D.i.. Out of 51 enrolled dogs, 11 were included in Group A (seronegative to L.i., D.i. negative and healthy), 15 in Group B (exposed to L.i., D.i. negative and healthy), 12 in Group C (seropositive to L.i., D.i. negative and sick) and 13 in Group D (seronegative to L.i., D.i. positive and healthy). The comparison of CIC level in canine sera revealed a significant difference among groups ($P < 0.001$), with the highest concentration (i.e., median = 104.6 $\mu\text{g/mL}$) in dogs with CanL. The findings of the study highlight the CICs measurement as a useful tool in the clinical staging of CanL for avoiding misclassification of dogs as leishmaniotic, thus not requiring anti-Leishmania therapy, as well as the possibility of results misuse in geographical areas where both leishmaniosis and heart-worm disease are endemic.

Co-infection patterns of vector-borne zoonotic pathogens in owned free-ranging dogs in central Chile.

Cevitanes A, Di Cataldo S, Muñoz-San Martín C, Latrofa MS, Hernández C, Cattán PE, Otranto D, Millán J.

Juin-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/36323837/>

We investigated the co-occurrence of the nine of the most relevant canine vector-borne pathogens (CVBP) using conventional and real-time PCR and evaluated risk factors and potential non-apparent haematological alterations associated with co-infection in 111 rural, owned, free-ranging dogs in the Metropolitan Region of Chile. At least one pathogen was detected in 75% of the dogs. DNA of *Anaplasma platys* (Ap; 36%), *Candidatus Mycoplasma haematoparvum* (CMhp; 31%), *Mycoplasma haemocanis* (Mhc; 28%), *Trypanosoma cruzi* (17%), *Leishmania* spp. (4.5%), and *Acanthocheilonomes reconditum* (1%) was detected. All dogs were negative for *Ehrlichia* spp., *Rickettsia* spp., *Bartonella* spp., *Piroplasma* spp., and *Hepatozoon* spp. Thirty-eight dogs (34%) were coinfecting. CMhp was involved in 71%, Mhc in 58%, and Ap in 50% of the co-infections. The most common co-infection pattern was CMhp-Mhc (37% of the cases). The prevalence of Ap was higher in juvenile than in adult dogs, whereas the opposite was found for CMhp and Mhc. Adult dogs were four times more likely of being co-infected than juveniles. Co-infected animals showed higher white blood cell count,

segmented neutrophil count, and GGT levels than non-co-infected dogs. Clinically healthy but infected dogs may act as reservoirs of CVBP, and their free-ranging behavior would facilitate the spread of these pathogens to other dogs as well as human beings or wild carnivores.

A cross-sectional serosurvey of SARS-CoV-2 and co-infections in stray cats from the second wave to the sixth wave of COVID-19 outbreaks in Spain.

Villanueva-Saz S, Martínez M, Giner J, González A, Tobajas AP, Pérez MD, Lira-Navarrete E, González-Ramírez AM, Macías-León J, Verde M, Yzuel A, Hurtado-Guerrero R, Arias M, Santiago L, Aguiló-Gisbert J, Ruíz H, Lacasta D, Marteles D, Fernández A.

Juin-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/36229725/>

Lèpre

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.

26-05-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37232124/>

Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.

High seropositivity against NDO-LID in a group of household contacts of leprosy patients. Are we close to leprosy elimination in Colombia?

Serrano-Coll H, Muñoz M, Beltrán JC, Cardona-Castro N.

25-05-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37231779/>

COVID-19 increases a person's risk of cardiovascular problems: how common

is chronic heart failure in SARS-CoV-2 patients? a case report.

Bereda G.

18-04-2023

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37228985/>

The coronavirus disease of 2019 (COVID-19) infection typically affects the lungs but can also cause life-threatening heart issues. Heart failure is a common condition that can occur either with an existing heart condition or de novo as part of the clinical course of COVID-19. **Case presentation:** On 11 October 2022, a 60-year-old middle-aged black African woman widow was admitted with a history of muscular weakness for 2 days, a lack of appetite, and occasional vomiting for 1 day. She arrived at the emergency room after complaining for 2 days of peeing less than usual, a fast heartbeat, swelling in the feet, pink blood-tinged mucus, fever, headache, dehydration, a nonproductive cough, and shortness of breath. The left ventricular ejection fraction was 43% on the echocardiogram. Routine reverse transcription polymerase chain reaction testing was performed in the emergency room; she tested COVID-19 positive. To treat her proven COVID-19 infection, she received subcutaneous enoxaparin 80 mg every 12 h as prophylaxis for deep venous thromboembolism. **Clinical discussion:** A COVID-19 infection can induce cardiac failure and arrhythmias, as well as cause direct harm to the heart. This study explains how enoxaparin has dual benefits in this case report: it reduces the risk of venous thromboembolism in the COVID-19 hospitalized case and prevents death and cardiac ischemia in myocardial infarction. **Conclusion:** Higher mortality and more frequent acute decompensation may be caused by the capacity of severe acute respiratory syndrome associated coronavirus 2 to cause myocardial injury, as well as by patients with chronic heart failure's lower baseline features, decreased cardiopulmonary reserve, and susceptibility for myocardial injury.

How is Guillain-Barre syndrome associated with COVID-19 infection differentiated from hypokalemic periodic paralysis? a case report.

Bereda G.

18-04-2023

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37228914/>

Patients with coronavirus disease 2019 (COVID-19)-associated Guillain-Barre syndrome (GBS) exhibit a range of clinical symptoms, such as cranial nerve paralysis and axonal or motor-sensory electrophysiological signals. **Case presentation:** A 61-year-old retired black African female was brought into the emergency room on 13 May 2022, with a 4-day history of shortness of breath and high-grade fever and a 1-day history of global body weakness (bilateral paralysis of the upper and lower extremities). Motor examination indicated reduced muscular strength in all limbs, with a Medical Research Council score of 2/5 in the right arm of the upper extremities, 1/5 in the right leg of the lower extremities, 1/5 in the left leg of the lower

extremities, and 2/5 in the left arm of the upper extremities. Her electrocardiogram revealed ST depression in the anterior-lateral leads and sinus tachycardia. For the COVID-related infection, azithromycin 500 mg per day for 5 days was begun. After cerebrospinal fluid findings supported the diagnosis of GBS, she underwent intravenous immunoglobulin 400 mg/kg every day for 5 days. **Clinical discussion:** In the majority of COVID-19-related GBS cases, areflexic quadriparesis developed suddenly. A COVID-19 infection related to a GBS case was the only one that had preceding signs, including ageusia and hyposmia. By testing serum potassium levels, this study determined that there is no connection between GBS and hypokalemia, which can lead to diagnostic and therapeutic conundrums by evaluating serum potassium levels, which showed a normal value. **Conclusion:** One of the neurological symptoms of the COVID-19 infection is GBS. Several weeks after a COVID-19 acute infection, GBS is frequently observed.

Psoriasis: A Primer for General Physicians.

Dasari S, Choudhary A, Madke B.

24-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37228538/>

Contact sensitizers in commercial hair dye products in the Indian market: A consumer exposure study.

Palaniappan V, Murthy AB, Sadhasivamohan A, Karthikeyan K.

25-05-2023

Contact Dermatitis.

<https://pubmed.ncbi.nlm.nih.gov/37227133/>

Background: Hair dye is a concoction of various ingredients that can result in allergic contact dermatitis (ACD) which is a common problem encountered by dermatologists. **Objectives:** To find out the presence of potent contact sensitizers in commercially available hair dyes in Puducherry, a union territory in South India, and to compare the findings with similar studies conducted in different countries. **Methods:** Ingredients labels of 159 hair dye products from 30 brands that were manufactured and marketed in India screened for the presence of contact sensitizers. **Results:** A total of 25 potent contact sensitizers were found in 159 hair dye products. p-Phenylenediamine and resorcinol were the most frequent contact sensitizer found in the study. The mean contact sensitizer concentration in a single hair dye product is 3.72 ± 1.81 . The number of potent contact sensitizers in individual hair dye products ranged from 1 to 10. **Conclusion:** We observed that most of the consumer-available hair dyes contain multiple contact sensitizers. Also, an inadequacy in mentioning the p-Phenylenediamine content, and appropriate warning contents regarding hair dye use were not mentioned in the cartons.

Dermoscopic Features of Psoriatic Nails and Their Correlation to Disease Severity.

Mashal ZR, Elgamal EEA, Zaky MS, Elsaie ML.

15-05-2023

Dermatol Res Pract.

<https://pubmed.ncbi.nlm.nih.gov/37223320/>

Efficacy and safety of "Jollab Monzej" as a traditional persian compound medicine for the treatment of multiple sclerosis-related fatigue: A randomized placebo-controlled trial.

Yousefnia Babaki F, Khodadoost M, Rezaeizadeh H, Naser Moghadasi A, Fahimi S, Hosseini H, Movahhed M, Gharagozli K.

Printemps 2023

Caspian J Intern Med.

<https://pubmed.ncbi.nlm.nih.gov/37223302/>

Dendritic Cell Activation in Leprosy Using CD1a and Factor XIIIa Markers.

K K, S S, K S.

22-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37223172/>

Background: Leprosy is manifested in varied forms based on the immune status of the patient giving rise to the polar and borderline spectrum of tuberculoid (TT) and lepromatous leprosy (LL). The present study was conducted to assess the macrophage activation in the spectrum of leprosy using CD1a and Factor XIIIa immunohistochemical markers and to correlate the macrophage expression with the morphological spectrum and bacillary index. **Methodology:** The present study was an observational study. **Results:** The present study consisted of 40 biopsy-proven leprosy cases, in which a majority were males, and the most common age group was 20-40 years. The most common type encountered was borderline tuberculoid (BT) leprosy. Expression of epidermal dendritic cells and intensity of staining by CD1a was higher in TT (seven of 10 cases (70%)) when compared to LL (one of three cases (33%)). Similarly, Factor XIIIa showed higher expression of dermal dendritic cells in 90% of TT when compared to LL which was seen in 66%. **Conclusion:** The increased number and strong intensity of dendritic cells in the tuberculoid spectrum may indirectly indicate macrophage activation and possibly account for the low bacillary index.

Changes in inflammatory markers in patients treated for Buruli ulcer and their ability to predict paradoxical reactions.

Phelippeau M, Marion E, Robbe-Saule M, Ganlanon L, Chauty A, Adeye A, Blanchard S, Johnson C, Marsollier L, Dubee V.

23-05-2023

J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37221015/>

High-resolution ultrasonography for early diagnosis of neural impairment in seropositive leprosy household contacts.

Luppi AM, Ferreira GE, Prudêncio DL, Antunes DE, Araújo L, Dos Santos DF, Nogueira-Barbosa MH, Goulart IMB.
23-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37220153/>

Bacterial, fungal and parasitic co-infections in leprosy: A scoping review.

Fróes LAR Jr, Toma TS, Jachiet M, Rousset L, Poderoso RE, Trindade MAB.
22-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37216331/>

Background: In leprosy patients, the most commonly reported non-viral co-infections are Tuberculosis, Leishmaniasis, Chromoblastomycosis and Helminths. The presence of a secondary infection is believed to increase the likelihood of leprosy reactions. The purpose of this review was to describe the clinical and epidemiological characteristics of the most reported bacterial, fungal, and parasitic co-infections in leprosy. **Methodology/principal findings:** Following the PRISMA Extension for Scoping Reviews guidelines, a systematic literature search was conducted by two independent reviewers, resulting in the inclusion of 89 studies. For tuberculosis, a total of 211 cases were identified, with a median age of 36 years and male predominance (82%). Leprosy was the initial infection in 89% of cases, 82% of individuals had multibacillary disease, and 17% developed leprosy reactions. For leishmaniasis, 464 cases were identified, with a median age of 44 years and male predominance (83%). Leprosy was the initial infection in 44% of cases, 76% of individuals presented with multibacillary disease, and 18% developed leprosy reactions. Regarding chromoblastomycosis, we identified 19 cases with a median age of 54 years and male predominance (88%). Leprosy was the primary infection in 66% of cases, 70% of individuals had multibacillary disease, and 35% developed leprosy reactions. Additionally, we found 151 cases of co-infection with leprosy and helminths, with a median age of 43 years and male predominance (68%). Leprosy was the primary infection in 66% of cases, and 76% of individuals presented with multibacillary disease, while the occurrence of leprosy reactions varied from 37% to 81% across studies. **Conclusion:** We observed a male-dominated pattern of co-infections among working-age individuals with multibacillary leprosy. Unlike prior studies reporting increased leprosy reactions in chronic viral co-infections, our findings did not indicate any increase among bacterial, fungal, or parasitic co-infections. Rather, co-infections with tuberculosis and leishmaniasis appeared to reduce leprosy reactions.

Fabrication, characterization and evaluation of a new designed botulinum toxin-cell penetrating peptide nanoparticulate complex.

Ravari NS, Sheikhlou MG, Goodarzi N, Kharazian B, Amini M, Atyabi F, Nasrollahi SA, Dinarvand R.

20-05-2023

Daru.

<https://pubmed.ncbi.nlm.nih.gov/37209247/>

Background: To have a better and longer effect, botulinum neurotoxin (BoNT) is injected several times in a treatment course, which could increase side effects and cost. Some of the most cutting-edge strategies being investigated for proteins to their physiologic targets involve the reformulation of BoNT based on peptide-based delivery systems. For this purpose, cell-penetrating peptides (CPPs) are of particular interest because of their capacity to cross the biological membranes. **Objectives:** A short and simple CPP sequence was used as a carrier to create nanocomplex particles from BoNT/A, with the purpose of increasing toxin entrapment by target cells, reducing diffusion, and increasing the duration of the effect. **Method:** CPP-BoNT/A nanocomplexes were formed by polyelectrolyte complex (PEC) method, considering the anionic structure of botulinum toxin and the cationic CPP sequence. The cellular toxicity, and absorption profile of the complex nanoparticles were evaluated, and the digit abduction score (DAS) was used to assess the local muscle weakening efficacy of BoNT/A and CPP-BoNT/A. **Results:** The provided optimized polyelectrolyte complex nanoparticles had a 244 ± 20 nm particle size and 0.28 ± 0.04 Pdl. In cellular toxicity, CPP-BoNT/A nanocomplexes as extended-release formulations of BoNT/A showed that nanocomplexes had a more toxic effect than BoNT/A. Furthermore, the comparison of weakening effectiveness on muscle was done among nanoparticles and free toxin on mice based on the digit abduction score (DAS) method, and nanocomplexes had a slower onset effect and a longer duration of action than toxin. **Conclusion:** Using PEC method allowed us to form nanocomplex from proteins, and peptides without a covalent bond and harsh conditions. The muscle-weakening effect of toxin in CPP-BoNT/A nanocomplexes showed acceptable efficacy and extended-release pattern.

Authors' reply.

Ravindran S, Nazeer M, Criton S.

Mai-Juin 2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37204771/>

A comparison of the quality of images of chest X-ray between handheld portable digital X-ray & routinely used digital X-ray machine.

Kamal R, Singh M, Roy S, Adhikari T, Gupta AK, Singh H, Rao VV, Panda S, Khan AM, Bhargava B.

Fév-Mars 2023

Indian J Med Res.

<https://pubmed.ncbi.nlm.nih.gov/37202939/>

Mass drug administration in neglected tropical diseases: beyond elimination.

Karthikeyan K.

Juin-2023

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, Houngbo OA, Anagonou EG, Biaou CAO, Ayélo AG, Houezo JG, Bocarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

Context: Since 2013, the World Health Organization has recommended integrated control strategies for neglected tropical diseases (NTDs) with skin manifestations. We evaluated the implementation of an integrated approach to the early detection and rapid treatment of skin NTDs based on mobile clinics in the Ouémé and Plateau areas of Benin. **Methods:** This descriptive cross-sectional study was performed in Ouémé and Plateau in Benin from 2018 to 2020. Consultations using mobile teams were performed at various sites selected by reasoned choice based on the epidemiological data of the National Program for the Control of Leprosy and Buruli Ulcer. All individuals presenting with a dermatological lesion who voluntarily approached the multidisciplinary management team on the day of consultation were included. The information collected was kept strictly anonymous and was entered into an Excel 2013 spreadsheet and analyzed with Stata 11 software. **Results:** In total, 5,267 patients with various skin conditions consulted the medical team. The median age of these patients was 14 years (IQR: 7-34 years). We saw 646 (12.3%) patients presenting NTDs with skin manifestations, principally scabies, in 88.4% (571/646), followed by 37 cases of Buruli ulcer (5.8%), 22 cases of leprosy (3.4%), 15 cases of lymphatic filariasis (2.3%) and one case of mycetoma (0.2%). We detected no cases of yaws. **Conclusion:** This sustainable approach could help to decrease the burden of skin NTDs in resource-limited countries.

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.

Mai-2023

Clin Biomech (Bristol, Avon).

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

Lessons From the Wrong Isolation Policy Violating Human Rights for Leprosy in Japan.

Horikoshi Y, Toizumi M.

01-06-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/36916867/>

The unbreakable journey: using photovoice to raise awareness and fight leprosy stigma in Papua, Indonesia.

Dien R, Krismawati H, Ayomi I, Timoria D, Chambers M, Soebono H, Grijsen ML.

24-05-2023

Br J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36866652/>

In preparation of an ongoing trial to improve the treatment of leprosy (MetLep, clinicaltrials.gov: NCT05243654), we conducted a photovoice project among persons affected by leprosy in eastern Indonesia. Photovoice is a participatory visual method in which photographic images are used to explore community health and social issues among disadvantaged populations. This project generated opportunities to visualize stigma and misunderstandings people with leprosy face, and the social and mental burden that this puts on them and those around them.

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

Manjula B, Gopinath H, Karthikeyan K.

Mai-Juin 2023

Indian J Dermatol Venereol Leprol.

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

Implementation of National Leprosy Eradication Programme during COVID-19 era: A qualitative research.

Bhattacharya T, Das S, Sarkar AP, Patra AC, Sarkar D, Das NK.

Mai-Juin 2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/36331853/>

The burden of skin diseases in India: Global Burden of Disease Study 2017.

Kavita A, Thakur JS, Narang T.

Mai-Juin 2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/34877854/>

Morsures de serpent

Identifying high snakebite risk area under climate change for community education and antivenom distribution.

Yousefi M, Yousefkhani SH, Grünig M, Kafash A, Rajabizadeh M, Pouyani ER.

20-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37210435/>

A review of 95 pit viper envenomations in Northcentral Florida (2018-2020).

Bassett TE, Schaer M.

15-06-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37160192/>

The medical records of 95 pit viper envenomations in client-owned dogs presented to an academic emergency hospital in the Southeastern United States during the period spanning 2018 and 2020 were retrospectively examined. This study's primary objectives were to record the clinical abnormalities and treatment responses associated with envenomation and their relation to outcome. Approximately 80% of the bites involved the head region associated with varying degrees of hemorrhagic lymphedema. Some of the most common additional symptoms observed were; hypotension (10%), cardiac dysrhythmias (17%), and coagulopathy (21%). Treatment in most cases consisted of intravenous fluids, antivenom, and analgesic drugs. Blood products were used as indicated for anemia and persistent bleeding. The average dose of the F('ab')₂ was 1-2 vials. Additional vials (3-22) were administered as needed to counteract persistent or recurrent coagulopathy and hemolysis. Only 3% of the dogs had mild clinical signs of Type 1 hypersensitivity during their treatment period. Antihistamine use at the tertiary hospital was restricted to the three dogs showing signs of a suspected allergic reaction in response to antivenom administration; these patients received diphenhydramine intramuscularly. A glucocorticoid drug was used in only one dog prior to referral but not subsequently. Ninety dogs had a good outcome, while five died. Historically, pit viper envenomation in dogs in the southeastern United States has been a potentially life-threatening problem. Most dogs will survive if treated promptly and appropriately with adequate amounts of intravenous fluids, and antivenom titrated on severity of clinical presentation.

Effects of *Mauritia flexuosa* L. f. buriti oil on symptoms induced by *Bothrops moojeni* snake envenomation.

Rodrigues PSM, Cirqueira Martins H, Falcão MS, Trevisan M, Portaro FCV, da Silva LG, Sano-Martins IS, Gonçalves LRC, Seibert CS.

15-09-2023

J Ethnopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37156448/>

Ethnopharmacological relevance: In Brazil, there are species of snakes that become involved in accidents and cause serious health problems to the inhabitants, highlighting the genus *Bothrops* for being responsible for approximately 90% of accidents reported annually. In the northern region of the country, this genus is responsible for the largest number of accidents, especially among rural dwellers. These populations invest in alternative treatments for with the purpose of improving the symptoms caused by snakebites. The species *Mauritia flexuosa* L. f., known as buriti, is traditionally used for the treatment of envenomation by snakes. **Aim of the study:** This study aimed to evaluate the antiophidic potential of the oil of *Mauritia flexuosa* L. f. for *Bothrops moojeni* H. venom, confronting cultural and scientific knowledge. **Materials and methods:** The physicochemical properties were determined, and the components present in the oil,

extracted from fruit pulp, were analyzed by Gas Chromatography Coupled with Mass Spectrometry. The in vitro inhibitory capacity of the oil for phospholipase, metalloprotease and serine protease activities was investigated. In the in vivo studies, male Swiss mice were used to evaluate the effect of oil on lethality and toxicity, and hemorrhagic, myotoxic and edematogenic activities were assessed. **Results:** GC-MS analysis identification of 90.95% of the constituents of the oil, with the main components being 9-eicosenoic acid, (Z)- (34.54%), n-hexadecanoic acid (25.55%) and (E)-9-octadecenoic acid ethyl ester (12.43%). For the substrates, the outcomes indicate that the oil inhibited the activity of the main classes of toxins present in *Bothrops moojeni* H. venom (VBm) at the highest dose tested (0.5 µL), with inhibition of 84% for the hydrolysis of the selective substrate for serine protease and inhibition of 60% for the hydrolysis of substrates for PLA₂ and metalloproteases. The antiophidic activity in vivo was evaluated with two concentrations of the oil: 1.5 mg, the dosage the population, diluted in mineral oil to a volume of 1 tablespoon and 15 mg, administered by gavage 30 min before poisoning and at time zero (concomitant to poisoning), and both concentrations administered by gavage in combination with topical use at time zero. The bleeding time in the group treated with oil at a concentration of 15 mg administered at time zero was significantly lower than that in the control group (p < 0.05). However, a greater inhibition of bleeding time was observed when local application was combined with the gavage treatment at both concentrations tested at time zero (p < 0.05). In the myotoxicity test, oil was efficient in reducing the myotoxic effects induced by the venom at the two concentrations tested, with gavage administration at time zero and gavage plus topical administration at time zero (p < 0.05). **Conclusions:** The data obtained show that the oil is safe to use at the concentrations studied and contains fatty acids that may collaborate for cellular-level repair of the injuries caused by Bm poisoning. The in vitro and in vivo experiments showed that oil inhibits the main proteolytic enzymes present in the venom and that it has important activities to control the local effects caused by bothropic venom.

A case report of *Ovophis monitcola* (Mountain pit-viper) envenoming in northeastern India resulting in prolonged coagulopathy.

Ralph R, Garg D, Balachandran A, Ganesh SR, Lamb T.
15-06-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37127123/>

Recent advancements in snake antivenom production.

Rathore AS, Kumar R, Tiwari OS.
15-06-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37072061/>

Snakebite envenoming (SBE), a neglected tropical disease, claims lives of about 138,000 people globally, and

antivenom is the only approved treatment worldwide. However, this century-old therapy has serious limitations, including limited efficacy and some side effects. Although alternative and adjunct therapies are being developed, their commercialization will take time. Hence, improving existing antivenom therapy is crucial for immediate reduction in the global SBE burden. The neutralization potential and immunogenicity of antivenoms depend primarily on the venom pool used for animal immunization and the production host, along with antivenom purification procedure and quality control. Enhancing antivenom quality and production capacity are also critical actions of the World Health Organization (WHO) roadmap 2021 against SBE. The present review details the latest developments in antivenom production, such as immunogen preparation, production host, antibody purification methods, antivenom testing-including alternative animal models, in vitro assays, and proteomics and in silico methodologies, and storage, reported from 2018 to 2022. Based on these reports, we propose that production of broadly specific, affordable, safe, and effective (BASE) antivenoms is fundamental to realizing the WHO roadmap and reducing the global SBE burden. This concept can also be applied during the designing of alternative antivenoms.

Mycétome

Neurological manifestations of mycetoma: a cross-sectional community-based study.

Ali EA, Hussien Mohamed Ahmed KA, Alhusseini RT, Abdallah AM, Ibrahim MA, Siddig A, Bahi EO, Mahmoud Fadelallah Eljack M, Hussien A.

15-03-2023

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37228930/>

Mycetoma is a chronic specific granulomatous progressive and disfiguring subcutaneous inflammatory disease. It is caused by true fungi (Eumycetoma) or by higher bacteria (actinomycetoma). Mycetoma mainly affects the lower limbs, followed by the upper limbs, back, and rarely the head and neck. Mycetoma is mainly transmitted through trauma with infected sharp objects. Herein, we want to determine the neurological manifestations of mycetoma in Sudanese patients. **Methodology:** A descriptive cross-sectional community-based study included 160 patients with mycetoma seen in the White Nile state. A team of doctors collected data using standardized questionnaires that included clinical history, neurological examination, investigations including laboratory, neurophysiological studies, and imaging. **Results:** Almost 160 patients were included in the study; 90% of them were male. Two patients presented with entrapment neuropathy, one presented with proximal neuropathy, one had peripheral neuropathy, one had dorsal spine involvement and presented with spastic paraplegia with sensory level, one had cervical cord compression, and one patient had repeated attacks of convulsion. **Conclusion:** Although it is rare, clinicians should highly suspect neurological involvement in mycetoma patients.

Hyphae, pseudohyphae, yeasts, spherules, spores, and more: A review on the morphology and pathology of fungal and oomycete infections in the skin of domestic animals.

Rodrigues Hoffmann A, Ramos MG, Walker RT, Stranahan LW.

24-05-2023

Vet Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37222139/>

Sudden emergence and spread of cutaneous larva migrans in Sudan: A case series calls for urgent actions.

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

05-05-2023

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/37207175/>

Cutaneous larva migrans (CLM) is a self-limiting dermatosis parasitic disease that is caused by zoonotic hookworm mainly infects cats, dogs, and accidentally humans. The disease affects hosts through the invasion and the migration of the hookworm larva into top layers of the skin. The disease occurs in tropical and subtropical regions; where people commonly are infected when sitting or barefoot walking on places contaminated with feces of infected cats or dogs. Due to self-limiting nature of the disease, the exact burden and prevalence are commonly underestimated. In this communication, we investigated all cases presented to the skin-diseases outpatient clinic' at the reference hospital of Tropical Diseases Medicine in Khartoum state between January 2019 and January 2021. This is the first-ever a case series report of cutaneous larva migrans in Sudan. We identified 15 cases of CLM presented with rash (100 %), redness of skin (67 %), and only adults were presented with larva crawling under their skins (27 %). Infection sites were (53 %) leg, (40 %) foot, only 7 % showed abdominal infection. The majority of patients were children or young adults, 47 % of them are ≤5 year-old, male to female ratio is 2.75:1. Duration of infection was one to three weeks and all patients fully recovered after treatment with albendazole. This urges for One Health interventions including deworming cats and dogs, improving water, sanitation, and hygiene, community-engagement and raising awareness in area with risk of infection.

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, Hounbo OA, Anagonou EG, Biaou CAO, Ayélo AG, Houezo JG, Boccarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

Antifungal Activity of Natural Naphthoquinones and Anthraquinones against *Madurella mycetomatis*.

Ma J, Todd M, van de Sande WWJ, Biersack B.

Mai-2023

Chem Biodivers.

<https://pubmed.ncbi.nlm.nih.gov/37067830/>

Onchocercose

Wolbachia Ferrochelatase as a potential drug target against filarial infections.

Biney C, Graham GE, Asiedu E, Sakyi SA, Kwarteng A.

Jul-2023

J Mol Graph Model.

<https://pubmed.ncbi.nlm.nih.gov/37121168/>

Filarial infections are among the world's most disturbing diseases caused by 3 major parasitic worms; *Onchocerca volvulus*, *Wuchereria bancrofti*, and *Brugia malayi*, affecting more than 500 million people worldwide. Currently used drugs for mass drug administration (MDA) have been met with several challenges including the development of complications in individuals with filaria co-infections and parasitic drug resistance. The filarial endosymbiont, *Wolbachia*, has emerged as an attractive therapeutic target for filariasis elimination, due to the dependence of the filaria on this endosymbiont for survival. Here, we target an important enzyme in the *Wolbachia* heme biosynthetic pathway (ferrochelatase), using high-throughput virtual screening and molecular dynamics with MM-PBSA calculations. We identified four drug candidates; Nilotinib, Ledipasvir, 3-benzhydryloxy-8-methyl-8-azabicyclo[3.2.1]octane, and 2-(4-Aminopiperidin-1-yl)-ethanol as potential small molecules inhibitors as they could compete with the enzyme's natural substrate (Protoporphyrin IX) for active pocket binding. This prevents the worm from receiving the heme molecule from *Wolbachia* for their growth and survival, resulting in their death. This study which involved targeting enzymes in biosynthetic pathways of the parasitic worms' endosymbiont (*Wolbachia*), has proven to be an alternative therapeutic option leading to the discovery of new drugs, which will help facilitate the elimination of parasitic infections.

Pian

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, Houngbo OA, Anagonou EG, Biaou CAO, Ayélo AG, Houezo JG, Boccarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

Context: Since 2013, the World Health Organization has recommended integrated control strategies for neglected tropical diseases (NTDs) with skin manifestations. We evaluated the implementation of an integrated approach to the early detection and rapid treatment of skin NTDs based on mobile clinics in the Ouémé and Plateau areas of Benin. **Methods:** This descriptive cross-sectional study was performed in Ouémé and Plateau in Benin from 2018 to 2020. Consultations using mobile teams were performed at various sites selected by reasoned choice based on the epidemiological data of the National Program for the Control of Leprosy and Buruli Ulcer. All individuals presenting with a dermatological lesion who voluntarily approached the multidisciplinary management team on the day of consultation were included. The information collected was kept strictly anonymous and was entered into an Excel 2013 spreadsheet and analyzed with Stata 11 software. **Results:** In total, 5,267 patients with various skin conditions consulted the medical team. The median age of these patients was 14 years (IQR: 7-34 years). We saw 646 (12.3%) patients presenting NTDs with skin manifestations, principally scabies, in 88.4% (571/646), followed by 37 cases of Buruli ulcer (5.8%), 22 cases of leprosy (3.4%), 15 cases of lymphatic filariasis (2.3%) and one case of mycetoma (0.2%). We detected no cases of yaws. **Conclusion:** This sustainable approach could help to decrease the burden of skin NTDs in resource-limited countries.

Rage

Canine rabies: An epidemiological significance, pathogenesis, diagnosis, prevention, and public health issues.

Kumar A, Bhatt S, Kumar A, Rana T.

09-05-2023

Comp Immunol Microbiol Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37229956/>

Rabies is a zoonotic disease caused by rabies virus of the genus *Lyssa* virus and family *Rhabdoviridae*. It affects all mammals and is prevalent throughout the world and endemic in many countries except in Islands like Australia and Antarctica. It is highly fatal, but preventable. Disease causes threat to public health because rabid dogs bite humans, resulting in thousands of deaths every year. Around 59,000 people die every year from rabies in the world. Dogs play a vital role in most of the human exposure in rabies endemic areas. Transmission of virus occurs through the bite of an infected dog. Disease is manifested by fatal nervous symptoms leading to paralysis and death. Direct fluorescent antibody technique is the gold standard for the diagnosis of the disease in animals and humans. Prevention of rabies involves the vaccination of dogs and humans before or after an exposure. This review describes the etiology, pathogenesis, diagnosis, its prevention and control strategies.

Corrigendum: Electronic application for rabies management improves surveillance, data quality, and investigator experience in Haiti.

Schrodt CA, Dilius P, Gibson AD, Crowdis K, Fénelon N, Ross Y, Bonaparte S, Gamble L, Lohr F, Joseph HC, Wallace RM.

09-05-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37228843/>

Rabies virus in white-nosed coatis (*Nasua narica*) in Mexico: what do we know so far?

Puebla-Rodríguez P, Almazán-Marín C, Garcés-Ayala F, Rendón-Franco E, Chávez-López S, Gómez-Sierra M, Sandoval-Borja A, Martínez-Solís D, Escamilla-Ríos B, Sauri-González I, Alonzo-Góngora A, López-Martínez I, Aréchiga-Ceballos N.

09-05-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37228842/>

Evaluation of country infrastructure as an indirect measure of dog-mediated human rabies deaths.

Bonaparte SC, Moodie J, Undurraga EA, Wallace RM.

09-05-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37228840/>

Background: Rabies is a neglected disease, primarily due to poor detection stemming from limited surveillance and diagnostic capabilities in most countries. As a result, there is limited ability to monitor and evaluate country, regional, and global progress towards the WHO goal of eliminating human rabies deaths by 2030. There is a need for a low-cost, readily reproducible method of estimating rabies burden and elimination capacity in endemic countries.

Methods: Publicly available economic, environmental, political, social, public health, and One Health indicators were evaluated to identify variables with strong correlation to country-level rabies burden estimates. A novel index was developed to estimate infrastructural rabies elimination capacity and annual case-burden for dog-mediated rabies virus variant (DMRVV) endemic countries. **Findings:** Five country-level indicators with superior explanatory value represent the novel "STOP-R index:" (1) literacy rate, (2) infant mortality rate, (3) electricity access, (4) political stability, and (5) presence/severity of natural hazards. Based on the STOP-R index, 40,111 (95% CI 25,854-74,344) global human rabies deaths are estimated to occur in 2022 among DMRVV-endemic countries and are projected to decrease to 32,349 (95% CI 21,110-57,019) in 2030. **Interpretation:** The STOP-R index offers a unique means of addressing the data gap and monitoring progress towards eliminating dog-mediated human rabies deaths. Results presented here suggest that factors external to rabies programs influence the successes of rabies elimination, and it is now possible to identify countries exceeding or lagging in expected rabies control and elimination progress based on country infrastructure.

Integrating contact tracing and whole-genome sequencing to track the

elimination of dog-mediated rabies: an observational and genomic study.

Lushasi K, Bruncker K, Rajeev M, Ferguson EA, Jaswant G, Baker LL, Biek R, Chagalucha J, Cleaveland S, Czupryna A, Fooks AR, Govella NJ, Haydon DT, Johnson PCD, Kazwala R, Lembo T, Marston D, Masoud M, Maziku M, Mbunda E, Mchau G, Mohamed AZ, Mpolya E, Ngeleja C, Ng'habi K, Nonga H, Omar K, Rysava K, Sambo M, Sikana L, Steenson R, Hampson K.

25-05-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37227428/>

In silico design and immunoinformatics analysis of a universal multi-epitope vaccine against monkeypox virus.

Sanami S, Nazarian S, Ahmad S, Raeisi E, Tahir UI Qamar M, Tahmasebian S, Pazoki-Toroudi H, Fazeli M, Ghatreh Samani M.

23-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37220125/>

Human iPSC-derived midbrain organoids functionally integrate into striatum circuits and restore motor function in a mouse model of Parkinson's disease.

Zheng X, Han D, Liu W, Wang X, Pan N, Wang Y, Chen Z.

29-04-2023

Theranostics.

<https://pubmed.ncbi.nlm.nih.gov/37215566/>

Rationale: Parkinson's disease (PD) is a prevalent neurodegenerative disorder that is characterized by degeneration of dopaminergic neurons (DA) at the substantia nigra pars compacta (SNpc). Cell therapy has been proposed as a potential treatment option for PD, with the aim of replenishing the lost DA neurons and restoring motor function. Fetal ventral mesencephalon tissues (fVM) and stem cell-derived DA precursors cultured in 2-dimensional (2-D) culture conditions have shown promising therapeutic outcomes in animal models and clinical trials. Recently, human induced pluripotent stem cells (hiPSC)-derived human midbrain organoids (hMOs) cultured in 3-dimensional (3-D) culture conditions have emerged as a novel source of graft that combines the strengths of fVM tissues and 2-D DA cells. **Methods:** 3-D hMOs were induced from three distinct hiPSC lines. hMOs at various stages of differentiation were transplanted as tissue pieces into the striatum of naïve immunodeficient mouse brains, with the aim of identifying the most suitable stage of hMOs for cellular therapy. The hMOs at Day 15 were determined to be the most appropriate stage and were transplanted into a PD mouse model to assess cell survival, differentiation, and axonal innervation *in vivo*. Behavioral tests were conducted to evaluate functional restoration following hMO treatment and to compare the therapeutic effects between 2-D and 3-D cultures. Rabies virus were introduced to identify the host presynaptic input onto the transplanted cells. **Results:** hMOs showed a relatively homogeneous cell composition, mostly

consisting of dopaminergic cells of midbrain lineage. Analysis conducted 12 weeks post-transplantation of day 15 hMOs revealed that 14.11% of the engrafted cells expressed TH+ and over 90% of these cells were co-labeled with GIRK2+, indicating the survival and maturation of A9 mDA neurons in the striatum of PD mice. Transplantation of hMOs led to a reversal of motor function and establishment of bidirectional connections with natural brain target regions, without any incidence of tumor formation or graft overgrowth. **Conclusion:** The findings of this study highlight the potential of hMOs as safe and efficacious donor graft sources for cell therapy to treat PD.

A disynaptic basal ganglia connection to the inferior olive: potential for basal ganglia influence on cerebellar learning.

Ruigrok TJH, Wang X, Sabel-Goedknecht E, Coulon P, Gao Z.

05-05-2023

Front Syst Neurosci.

<https://pubmed.ncbi.nlm.nih.gov/37215357/>

Detection of immunity in sheep following anti-rabies vaccination.

Rathnadiwakara H, Gunatilake M, Cliquet F, Wasniewski M, Thammitiyagodage M, Karunakaran R, Thibault JC, Ijas M.

Avr-2023

Clin Exp Vaccine Res.

<https://pubmed.ncbi.nlm.nih.gov/37214148/>

Purpose: Rabies is a fatal but preventable disease with proper pre-exposure anti-rabies vaccination (ARV). Dogs, as household pets and strays, are the reservoir and vector of the disease, and dog bites have been associated with human rabies cases in Sri Lanka over the past few years. However, other susceptible species having frequent contact with humans may be a source of infection. One such species is sheep and immunity following ARV has never been tested in sheep reared in Sri Lanka. **Materials and methods:** We have tested serum samples from sheep reared in the Animal Centre, Medical Research Institute of Sri Lanka for the presence of anti-rabies antibodies following ARV. Sheep serum samples were tested with Bio-Pro Rabies enzyme-linked immunosorbent assay (ELISA) antibody kits used for the first time in Sri Lanka and our results were verified by a seroneutralization method on cells (fluorescent antibody virus neutralization, FAVN test) currently recommended by World Organization for Animal Health and World Health Organization. **Results:** Sheep received annual ARV and maintained high neutralizing antibody titers in their serum. No maternal antibodies were detected in lamb around 6 months of age. Agreement between the ELISA and FAVN test, i.e., coefficient concordance was 83.87%. **Conclusion:** Annual vaccination in sheep has an effect on maintaining adequate protection against rabies by measurements of anti-rabies antibody response. Lambs need to be vaccinated earlier than 6 months of age to achieve protective levels of neutralizing antibodies in their serum. Introducing this ELISA in Sri Lanka will be a good

opportunity to determine the level of anti-rabies antibodies in animal serum samples.

Comparing Recombinant Human Rabies Monoclonal Antibody (Ormutivimab) with Human Rabies Immunoglobulin (HRIG) for Postexposure Prophylaxis: A Phase 3, Randomized, Double-Blind, Non-inferiority Trial.

Liu X, Li Y, Li J, Zhou J, Guo J, Pu Y, Jiang Y, Zhou Y, Jiang Z, Shu Q, Wang C, Wang J, Zhao Y, Zhao W, Wang H, Wei J, Yu H, Gao J, Li X.

19-05-2023

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37211270/>

Objectives: To evaluate the immunogenicity and safety of an anti-rabies monoclonal antibody (mAb), Ormutivimab, compared with human rabies immunoglobulin (HRIG). **Methods:** This phase 3 trial was designed as a randomized, double-blind, non-inferiority clinical trial in patients aged ≥ 18 years with suspected WHO category III rabies exposures. The participants were randomized 1:1 to Ormutivimab and HRIG group. After thorough wound washing and injection of Ormutivimab/HRIG on Day 0, the vaccination was administered on Days 0, 3, 7, 14, and 28. The primary endpoint was the adjusted geometric mean concentration (GMC) of rabies virus neutralizing activity (RVNA) on Day 7. The endpoint of safety included the occurrence of adverse reactions (ARs) and serious adverse events (SAEs). **Results:** A total of 720 participants were recruited. The adjusted-GMC of RVNA (0.41 IU/mL) on Day 7 in Ormutivimab group was not inferior to that in HRIG group (0.41 IU/mL), with ratio of adjusted-GMC of 1.01 (95%CI: 0.91, 1.14). The seroconversion rate of the Ormutivimab-group was higher than that of the HRIG-group on Days 7, 14, and 42. The majority of local injection site and systemic ARs reported from both groups were mild to moderate in severity. **Conclusions:** Ormutivimab + vaccine can protect aged ≥ 18 years victims with category III suspected rabies exposure as a component of post-exposure prophylaxis. Ormutivimab has a weaker influence on immunity response of rabies vaccines.

A custom-made time-resolved fluoroimmunoassay for the quantitation of the host cell protein of Vero in rabies vaccine.

Yang Y, Li Z, Zhang Z, Zhai X, Li X, Cao Y, Fang H, He C, Wu Y, Lin G.

18-05-2023

J Virol Methods.

<https://pubmed.ncbi.nlm.nih.gov/37209780/>

COVID-19 impact on EuroTravNet infectious diseases sentinel surveillance in Europe.

Grobusch MP, Weld L, Schnyder JL, Larsen CS, Lindner AK, Popescu CP, Huits R, Goorhuis A, Gautret P, Schlagenhauf P; for EuroTravNet.

18-05-2023

Travel Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37207977/>

Background: The COVID-19 pandemic resulted in a sharp decline of post-travel patient encounters at the European sentinel surveillance network (EuroTravNet) of travellers' health. We report on the impact of COVID-19 on travel-related infectious diseases as recorded by EuroTravNet clinics. **Methods:** Travelers who presented between January 1, 2019 and September 30, 2021 were included. Comparisons were made between the pre-pandemic period (14 months from January 1, 2019 to February 29, 2020); and the pandemic period (19 months from March 1, 2020 to September 30, 2021). **Results:** Of the 15,124 visits to the network during the 33-month observation period, 10,941 (72%) were during the pre-pandemic period, and 4183 (28%) during the pandemic period. Average monthly visits declined from 782/month (pre-COVID-19 era) to 220/month (COVID-19 pandemic era). Among non-migrants, the top-10 countries of exposure changed after onset of the COVID-19 pandemic; destinations such as Italy and Austria, where COVID-19 exposure peaked in the first months, replaced typical travel destinations in Asia (Thailand, Indonesia, India). There was a small decline in migrant patients reported, with little change in the top countries of exposure (Bolivia, Mali). The three top diagnoses with the largest overall decreases in relative frequency were acute gastroenteritis (-5.3%), rabies post-exposure prophylaxis (-2.8%), and dengue (-2.6%). Apart from COVID-19 (which rose from 0.1% to 12.7%), the three top diagnoses with the largest overall relative frequency increase were schistosomiasis (+4.9%), strongyloidiasis (+2.7%), and latent tuberculosis (+2.4%). **Conclusions:** A marked COVID-19 pandemic-induced decline in global travel activities is reflected in reduced travel-related infectious diseases sentinel surveillance reporting.

Schistosomiasis

Executive summary consensus statement of imported diseases group (GEPI) of the Spanish Society of Infectious Diseases and Clinical Microbiology (SEIMC) and the Spanish Society of Tropical Medicine and International Health (SETMSI), on the diagnostic and treatment of imported schistosomiasis.

Bocanegra C, Álvarez-Martínez MJ, Arsuaga Vicente M, Belhassen-García M, Chamorro Tojeiro S, Camprubí-Ferrer D, Fernández Soto P, García Vázquez E, Herrador Ortiz Z, Martín O, Muro A, Pérez Arellano JL, Reguera Gómez M, Salas-Coronas J, Salvador F, Sotillo Gallego J, Sulleiro E, Torrés Tendero D, Velasco Arribas M, Rodríguez Guardado A.

23-05-2023

Enferm Infect Microbiol Clin (Engl Ed).

<https://pubmed.ncbi.nlm.nih.gov/37230838/>

Protective human IgE responses are promoted by comparable life-cycle dependent Tegument Allergen-Like expression in *Schistosoma haematobium* and *Schistosoma mansoni* infection.

Oettle RC, Dickinson HA, Fitzsimmons CM, Sacko M, Tukahebwa EM, Chalmers IW, Wilson S.

25-05-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37228019/>

Schistosoma haematobium is the most prevalent of the human-infecting schistosome species, causing significant morbidity in endemically exposed populations. Despite this, it has been relatively understudied compared to its fellow species, *S. mansoni*. Here we provide the first comprehensive characterization of the *S. haematobium* Tegument Allergen-Like protein family, a key protein family directly linked to protective immunity in *S. mansoni* infection. Comparable with observations for *S. mansoni*, parasite phylogenetic analysis and relative gene expression combined with host serological analysis support a cross-reactive relationship between *S. haematobium* TAL proteins, exposed to the host immune system as adult worms die, and closely related proteins, exposed during penetration by the infecting cercarial and early schistosomulae stages. Specifically, our results strengthen the evidence for host immunity driven by cross-reactivity between family members TAL3 and TAL5, establishing it for the first time for *S. haematobium* infection. Furthermore, we build upon this relationship to include the involvement of an additional member of the TAL protein family, TAL11 for both schistosome species. Finally, we show a close association between experience of infection and intensity of transmission and the development of protective IgE responses to these antigens, thus improving our knowledge of the mechanisms by which protective host immune responses develop. This knowledge will be critical in understanding how control efforts such as mass drug administration campaigns influence the development of host immunity and subsequent patterns of infection and disease within endemic populations.

Performance characteristics of diagnostic assays for schistosomiasis in Ontario, Canada.

Lau R, Makhani L, Omoruna O, Lecce C, Shao E, Cunanan M, Ralevski F, Cheema K, Boggild AK.

19-05-2023

Ther Adv Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37223452/>

Current Status of Urinary Schistosomiasis Among Communities in Kurmuk District, Western Ethiopia: Prevalence and Intensity of Infection.

Mohammed T, Hu W, Aemero M, Gebrehiwot Y, Erko B.

17-05-2023

Environ Health Insights.

<https://pubmed.ncbi.nlm.nih.gov/37223332/>

Background: Schistosomiasis is a highly prevalent but neglected tropical disease, particularly in sub-Saharan Africa. In Ethiopia, urogenital schistosomiasis due to *Schistosoma haematobium* has been known to be endemic in several lowland areas. This study was designed to determine the current prevalence and intensity of the urogenital schistosomiasis among communities in Kurmuk District, western Ethiopia. **Methods:** Urine filtration technique and urine dipstick test were used to screen for *S. haematobium* eggs and hematuria, respectively. The data were analyzed with SPSS version 23. Logistic regression and odds ratio were used to measure associations and strength between prevalence, intensity, and independent variables. *P*-values <.05 at 95% CI were considered statistically significant. **Results:** The overall prevalence of *S. haematobium* infection as determined by urine filtration was 34.2% (138/403). In bivariate analysis, the most infected (45.4%) age groups were 5 to 12 years (odds ratio [OR] = 4.16, 95% CI: 1.36-12.67), followed by 13 to 20 years (OR = 3.23, 95% CI: 1.01-10.35) with higher significant mean egg count (MEC). The mean egg intensity ranged from 2.39 in Ogendu (CI: 1.05-3.72) to 14.1 in Dulshatalo (CI: 4.98-23.12) villages. The main predictor of infection was swimming habits (adjusted odds ratio [AOR] = 2.43 [CI: 1.19-4.94]). The prevalence of hematuria was 39.2% (158/403), the odds being 2.64 times higher among participants who resided in Dulshatalo than those who resided in Kurmuk (AOR 2.64 [95% CI: 1.43-4.87], *P* = .004). **Conclusion:** To reduce the infection and interrupt transmission, the PC in place in the area using PZQ should be strengthened and continued, alongside with provision of sanitary facilities, safe alternative water supplies and health education. The Federal Ministry of Health of Ethiopia should also collaborate with the health authorities of the Sudan government for the control of trans-boundary transmission of the disease as the transmission foci are shared between the 2 countries.

Anaphylactic reaction to praziquantel following schistosomiasis treatment.

Vasconcelos GA, Costa BGG, Dos Santos RA, de Faria CD, Schramm Neto FAR, Machado YJ, Casaes AC, de Oliveira MVL, Fialho TRS, Dos Santos KR, Oliveira BSS, Oliveira RR, de Siqueira IC.

15-04-2023

IJID Reg.

<https://pubmed.ncbi.nlm.nih.gov/37223089/>

Praziquantel (PZQ) is a medication used to treat several parasitic infections, including human schistosomiasis. Although this drug commonly causes transient adverse effects, severe hypersensitivity is rare, and only eight cases have been reported worldwide. Herein we report a case of a 13-year-old Brazilian female who developed anaphylaxis, a severe hypersensitive reaction, after taking praziquantel to treat *Schistosoma mansoni* infection. During a mass drug administration event in a socially vulnerable endemic area of Bahia (Brazil), after taking 60 mg/kg of praziquantel the patient developed rash and generalized edema an hour later, evolving to somnolence and hypotension. Following the anaphylactic episode, she received adequate treatment and recovered approximately 1 day later. Although praziquantel is considered safe,

Sensitivity and specificity of human point-of-care circulating cathodic antigen (POC-CCA) test in African livestock for rapid diagnosis of schistosomiasis: A Bayesian latent class analysis.

Calvo-Urbano B, Léger E, Gabain I, De Dood CJ, Diouf ND, Borlase A, Rudge JW, Corstjens PLAM, Sène M, Van Dam GJ, Walker M, Webster JP.

22-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37216407/>

Exorchis sp. in the catfish *Silurus asotus* and *Oncomelania hupensis* in marshlands of Poyang Lake, China: A potential biological control tool for *Schistosoma japonicum*.

Yan W, Dibo N, Cao Y, Peng W, Tang C, Huang S.

29-04-2023

Int J Parasitol Parasites Wildl.

<https://pubmed.ncbi.nlm.nih.gov/37215532/>

Oncomelania hupensis is the obligate intermediate host of *Schistosoma japonicum*, highlighting the medical importance of interrupting this unique and long-standing parasite-host interaction in controlling schistosomiasis transmission. It has been reported that a catfish trematode *Exorchis* sp. could have the potential to function as an effective anti-schistosomal agent in the snail host. However, the feasibility of this eco-friendly biological control strategy should be comprehensively investigated and evaluated in endemic areas for schistosomiasis. In this study, a field survey was conducted from 2012 to 2016 in the marshlands of Poyang Lake, which is one of the highly endemic regions for schistosomiasis in China. Results showed that more than half of *Silurus asotus* (65.79%) were infected with *Exorchis* sp., and the average intensity of infection was 14.21 per fish. And the average infection rate of *Exorchis* sp. in *O. hupensis* is 1.11%. These findings indicated that there are abundant biological resources for the implementation of this biology control strategy in the marshlands of Poyang Lake. The data presented here provide solid evidences for the practical application of this biological control strategy, thereby contributing to achieving the goals of the elimination of schistosomiasis.

A Rare Case of Huge Schistosomiasis-Associated Cecal Polyp Mimicking Colon Carcinoma.

Abdelfattah AH, Ali M, Abd El Fattah AA, Ghazy M, Eladl AE, Elkot AN.

17-04-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37206495/>

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*.

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

15-09-2023

J Ethnopharmacol.

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

Molecular dynamics-derived pharmacophores of *Schistosoma glutathione transferase* in complex with bromosulphophthalein: Screening and analysis of potential inhibitors.

Valli A, Achilonu I.

Juil. 2023

J Mol Graph Model.

<https://pubmed.ncbi.nlm.nih.gov/37004419/>

Trachome

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.

26-05-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37232124/>

Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.

Behavioral Responses for Face Cleanliness Message to Prevent Trachoma Among Mothers Having Children Age 1-9 Years Old, in Fogera District, Northwest Ethiopia: An Application of Extended Parallel Process Model.

Muche N, Wasihun Y, Wondiyeh H, Bogale EK, Anagaw TF.

19-05-2023

Int J Gen Med.

<https://pubmed.ncbi.nlm.nih.gov/37228742/>

Background: Trachoma is an eye disease caused by bacteria called *Chlamydia trachomatis*. This infection causes papillary and/or follicular inflammation of the tarsal conjunctiva referred to as active trachoma. Active trachoma prevalence among 1 to 9 years old children is 27.2% in Fogera district (study area). Many people still require the implementation of the face cleanliness components of the SAFE strategy. Even if face cleanliness is an important component to prevent trachoma, there is limited research done on this area. Therefore, the purpose of this study is to assess behavioral responses to face cleanliness messages to prevent trachoma among mothers having children aged 1 to 9 years old. **Methods:** A community-based cross-sectional study was conducted with the guidance of an extended parallel process model in Fogera District from December 01 to December 30, 2022. A multi-stage sampling technique was used to select 611 study participants. Interviewer administered questionnaire was used to collect the data. Bivariable and multivariable logistic regression analysis was done to identify predictors of behavioral responses using SPSS V.23 significant variables were declared by AOR at a 95% confidence interval and a p-value <0.05. **Result:** Among the total participants, 292 (47.8%) were in danger control. Residence [AOR = 2.91; 95% CI: (1.44-3.86)], marital status [AOR = 0.79; 95% CI: (0.667-0.939)], level of education [AOR = 2.74; 95% CI: (1.546-3.65)], family size [AOR = 0.57; 95% CI: (0.453-0.867)], round trip to collect water [AOR = 0.79; 95% CI: (0.423-0.878)], having information about face washing [AOR = 3.79; 95% CI: (2.661-5.952)], Source of an information health facility [AOR = 2.76; 95% CI: (1.645-4.965)], school [AOR = 3.68; 95% CI: (1.648-7.530)], health extension workers [AOR = 3.96; 95% CI: (2.928-6.752)], Women development army [AOR = 2.809; 95% CI: (1.681-4.962)], knowledge [AOR = 2.065; 95% CI: (1.325-

4.427)) self-esteem [AOR = 1.013; 95% CI: (1.001-1.025)], self-control [AOR = 1.132; 95%CI: (1.04-1.24)], and future orientation [AOR = 2.16; 95% CI: (1.345-4.524)] were found to be statistically significant predictors of behavioral response. **Conclusion:** Less than half of the participants were in the danger control response. Residence, marital status, level of education, family size, face-washing information, source of information, knowledge, self-esteem, self-control, and future orientation were independent predictors of face cleanliness. Strategies of face cleanliness messages should give high attention to perceived efficacy with consideration of perceived threat.

An ophthalmologist fought against trachoma in Turkey and his books from an archive: Dr Nuri Fehmi Ayberk and The Development of Ophthalmology in Turkey.

Üstün Ç, Özçiftçi S.

23-05-2023

J Med Biogr.

<https://pubmed.ncbi.nlm.nih.gov/37221868/>

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

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

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

22-05-2023

J Proteomics.

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

Comparison of a Urine Antigen Assay and Multiple Examinations with the Formalin-Ethyl Acetate Concentration Technique for Diagnosis of Opisthorchiasis.

Worasith C, Techasen A, Duengngai K, Intuyod K, Kopolrat KY, Sithithaworn J, Loilome W, Cullen T, Haswell MR, Sithithaworn P.

22-05-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37217166/>

Detection of worm antigen in urine is a sensitive diagnostic method for opisthorchiasis, particularly for light-intensity infections; however, the presence of eggs in feces is essential for validating results from the antigen assay. To

address the issue of low sensitivity of fecal examination, we modified the protocol for the formalin-ethyl acetate concentration technique (FECT) and compared it against urine antigen measurements for detection of the parasite *Opisthorchis viverrini*. First, we optimized the FECT protocol by increasing the number of drops for examinations from the standard two drops to a maximum of eight. We were able to detect additional cases after examination of ≥ 3 drops, and the prevalence of *O. viverrini* saturated after examination of ≥ 5 drops. We then compared the optimized FECT protocol (examining five drops of suspension) against urine antigen detection for the diagnosis of opisthorchiasis in field-collected samples. The optimized FECT protocol detected *O. viverrini* eggs in 25 of 82 individuals (30.5%) who had positive urine antigen tests but were fecal egg negative by the standard FECT protocol. The optimized protocol also retrieved *O. viverrini* eggs in 2 of 80 antigen-negative cases (2.5%). In comparison with the composite reference standard (combined FECT and urine antigen detection), the diagnostic sensitivity of examining two and five drops of FECT and the urine assay was 58.2, 67, and 98.8%, respectively. Our results show that multiple examinations of fecal sediment increase the diagnostic sensitivity of FECT and thus provide further support for the reliability and utility of the antigen assay for diagnosis and screening of opisthorchiasis.

A rapid and visual detection assay for *Clonorchis sinensis* based on recombinase polymerase amplification and lateral flow dipstick.

Ma X, Bai X, Li H, Ding J, Zhang H, Qiu Y, Wang J, Liu X, Liu M, Tang B, Xu N.

19-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37208693/>

Background: Fish-borne zoonotic clonorchiasis, caused by *Clonorchis sinensis*, is an emerging public health problem in several countries with more than 15 million people infected globally. However, a lack of accurate point-of-care (POC) diagnostic tests in resource-limited areas is still a critical barrier to effective treatment and control of clonorchiasis. The development of the recombinase polymerase amplification (RPA) assay, a POC diagnostic test based on the amplification of pathogen DNA, has provided a new, simple and inexpensive tool for disease detection with high sensitivity and specificity. **Methods:** A novel RPA method was developed based on specific primers and probes, and combined with the dipstick, to allow for the rapid and intuitive detection of *C. sinensis* through the amplification of the mitochondrial cytochrome c oxidase subunit 1 (COX1) gene. The lower limit of detection for the combined RPA/lateral flow dipstick (RPA-LFD) assay was evaluated using dilutions of the target DNA sequence. Cross-reactivity was evaluated using genomic DNA from 10 additional control parasites. Forty human clinical stool samples were tested to verify its performance. **Results:** The evaluated primers designed from the *C. sinensis* COX1 region can be used to detect adult worms, metacercariae, and eggs at 39 °C within 20 min, and the results can be visually observed using the

LFD. The detection limit of pathogen genomic DNA was as low as 10 fg, and the number of metacercaria(e) in fish and egg(s) in faeces were both as low as one. This improved the sensitivity of low-infection detection tremendously. The test is species-specific, and no other related control parasites were detected. In human stool samples with eggs per gram (EPG) > 50, the RPA-LFD assay was performed consistent with conventional Kato-Katz (KK) and PCR methods. **Conclusion:** The established RPA-LFD assay provides a powerful tool for the diagnosis and epidemiological survey of *C. sinensis* from human and animal samples, and has important implications for the effective control of clonorchiasis.

Fascioliasis associated with chronic cholecystitis in a woman from Sistan and Baluchestan province, a non-endemic region in Southeastern Iran.

Shafiee M, Nasibi S, Lashkarizadeh MR, Fasihi Harandi M.

19-05-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37208607/>

Massive hepatic trematodosis in 5 juvenile bald eagles.

McDermott KA, Greenwood SJ, Conboy GA, Franzen-Klein DM, Wünschmann A.

19-05-2023

J Vet Diagn Invest.

<https://pubmed.ncbi.nlm.nih.gov/37204007/>

Pulmonary Paragonimiasis: A Case Series.

Shah P, Sah R, Pradhan S, Bhandari P, Baral R, Khanal B, Maskey R, Bhattarai NR.

01-02-2023

JNMA J Nepal Med Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37203942/>

Paragonimiasis contributes to significant foodborne zoonosis worldwide. The major mode of transmission in humans is by consumption of uncooked or undercooked crabs and crayfish harbouring *Paragonimus* metacercariae. It begins with symptoms like fever and lower respiratory involvement from a few months to a year, mimicking those of tuberculosis and leading to diagnostic delay. Here, we report two cases of paragonimiasis during a period of nine months. Both cases presented with symptoms of productive cough with rusty sputum, chest pain, along with eosinophilia, and pleural effusion and had a history of consumption of smoked crab from the local river. The diagnosis was established by microscopic demonstration of *Paragonimus* ova in the sputum. They were treated with praziquantel and recovered. Indeed, it is challenging to diagnose paragonimiasis due to the lack of its specific symptoms but should be considered in the differential diagnosis of eosinophilia and pleural effusion in such lung diseases.

Trypanosomes (trypanosomiasis et maladie de Chagas)

Serologic Profile of Donors In Argentina.

Cobos M, Hidalgo G, Soratti C.

23-05-2023

Transplant Proc.

<https://pubmed.ncbi.nlm.nih.gov/37230902/>

Identification of inhibitors for the trans-membrane *Trypanosoma cruzi* eIF2 α kinase relevant for parasite proliferation.

Marcelino TP, Fala AM, da Silva MM, Souza-Melo N, Malvezzi AM, Klippel AH, Zoltner M, Padilla-Mejia N, Kosto S, Field MC, Burle Caldas GA, Teixeira SMR, Couñago RM, Massier KB, Schenkman S.

23-05-2023

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/37230387/>

The Tck2 protein kinase of *Trypanosoma cruzi*, the causative agent of Chagas disease, is structurally similar to the human kinase PERK, which phosphorylates the initiation factor eIF2 α , and in turn, inhibits translation initiation. We have previously shown that absence of Tck2 kinase impairs parasite proliferation within mammalian cells, positioning it as a potential target for treatment of Chagas disease. To better understand its role in the parasite, here we initially confirmed the importance of Tck2 in parasite proliferation by generating CRISPR/Cas9 Tck2-null cells, albeit more efficiently differentiate into infective forms. Proteomics indicates that the Tck2 knockout of proliferative forms express proteins including trans-sialidases, normally restricted to infective and non-proliferative trypomastigotes explaining decreased proliferation and better differentiation. Tck2 knockout cells lost phosphorylation of eukaryotic initiation factor 3 and cyclic AMP responsive-like element, recognized to promote growth, likely explaining both decreased proliferation and augmented differentiation. To identify specific inhibitors, a library of 379 kinase inhibitors was screened by differential scanning fluorimetry using a recombinant Tck2 encompassing the kinase domain and selected molecules were tested for kinase inhibition. Only Dasatinib and PF-477736, inhibitors of Src/Abl and Chk1 kinases, showed inhibitory activity with IC₅₀ of 0.2 \pm 0.02 mM and 0.8 \pm 0.1, respectively. In infected cells Dasatinib inhibited growth of parental amastigotes (IC₅₀ = 0.6 \pm 0.2 mM) but not Tck2 of depleted parasites (IC₅₀ > 34 mM) identifying Dasatinib as a potential lead for development of therapeutics for Chagas disease targeting Tck2.

Simplifying screening for *Trypanosoma cruzi* in pregnant persons and their infants.

Buekens P, Alger J, Cafferata ML, Dumonteil E, Herrera C, Tulio Luque M, Carlier Y.

25-05-2023

Exploring the performance of *Escherichia coli* outer membrane vesicles as a tool for vaccine development against Chagas disease.

Vázquez ME, Mesías AC, Acuña L, Spangler J, Zabala B, Parodi C, Thakur M, Oh E, Walper SA, Brandán CP.

22-05-2023

Mem Inst Oswaldo Cruz.

<https://pubmed.ncbi.nlm.nih.gov/37222309/> ;

Background: Vaccine development is a laborious craftwork in which at least two main components must be defined: a highly immunogenic antigen and a suitable delivery method. Hence, the interplay of these elements could elicit the required immune response to cope with the targeted pathogen with a long-lasting protective capacity. **Objectives:** Here we evaluate the properties of *Escherichia coli* spherical proteoliposomes - known as outer membrane vesicles (OMVs) - as particles with natural adjuvant capacities and as antigen-carrier structures to assemble an innovative prophylactic vaccine for Chagas disease. **Methods:** To achieve this, genetic manipulation was carried out on *E. coli* using an engineered plasmid containing the Tc24 *Trypanosoma cruzi* antigen. The goal was to induce the release of OMVs displaying the parasite protein on their surface. **Findings:** As a proof of principle, we observed that native OMVs - as well as those carrying the *T. cruzi* antigen - were able to trigger a slight, but functional humoral response at low immunization doses. Of note, compared to the non-immunized group, native OMVs-vaccinated animals survived the lethal challenge and showed minor parasitemia values, suggesting a possible involvement of innate trained immunity mechanism. **Main conclusion:** These results open the range for further research on the design of new carrier strategies focused on innate immunity activation as an additional immunization target and venture to seek for alternative forms in which OMVs could be used for optimizing vaccine development.

ChagasDB: 80 years of publicly available data on the molecular host response to *Trypanosoma cruzi* infection in a single database.

Brochet P, Mouren JC, Hannouche L, Lopez F, Ballester B, Cunha-Neto E, Spinelli L, Chevillard C.

23-05-2023

Database (Oxford).

<https://pubmed.ncbi.nlm.nih.gov/37221041/>

Chagas disease is a parasitological disease caused by *Trypanosoma cruzi* which affects ~7 million people worldwide. Per year, ~10 000 people die from this pathology. Indeed, ~30% of humans develop severe chronic forms, including cardiac, digestive or neurological disorders, for which there is still no treatment. In order to facilitate research on Chagas disease, a manual curation of all papers corresponding to 'Chagas disease' referenced on PubMed has been performed. All deregulated molecules in hosts (all mammals, humans, mice or others) following

T. cruzi infection were retrieved and included in a database, named ChagasDB. A website has been developed to make this database accessible to all. In this article, we detail the construction of this database, its contents and how to use it. Database URL <https://chagasdb.tagc.univ-amu.fr>.

Transcriptomic analysis of benznidazole-resistant and susceptible *Trypanosoma cruzi* populations.

Lima DA, Gonçalves LO, Reis-Cunha JL, Guimarães PAS, Ruiz JC, Liarte DB, Murta SMF.

22-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37217925/> ;

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

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

20-05-2023

Acta Trop.

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

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

TCS network analysis of these anuran *Trypanosoma* sequences also revealed high haplotype diversity ($H_d = 0.925 \pm 0.050$), but low nucleotide diversity ($\pi = 0.019 \pm 0.009$). Furthermore, the living anuran trypanosomes were microscopically demonstrated in a single specimen of *Gr. indica*, supporting the vectorial capacity. Importantly, our data confirmed the scarcity of *Se. gemmea* and also uncovered, for the first time, the co-circulation of *L. martiniquensis*, *L. donovani* complex, and suspected novel anuran *Trypanosoma* spp. in phlebotomine sand flies, implicating their potential role as vectors of trypanosomatid parasites. Therefore, the novel data from this study would greatly facilitate the comprehension of the complexity of trypanosomatid transmission and the establishment of prevention and control measures for this neglected disease more effectively.

Oxidative stress, cardiomyocytes senescence and contractile dysfunction in vitro and in vivo experimental models of Chagas disease.

Nogueira SS, Souza MA, Santos EC, Caldas IS, Gonçalves RV, Novaes RD.

19-05-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37211152/>

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

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

19-05-2023

Biomed Pharmacother.

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

Trypanosome infections in animals from tsetse infested areas of Cameroon and their sensitivity and resistance molecular profiles for diminazene aceturate and isometamidium chloride.

Mewamba EM, Magang EMK, Tiofack AAZ, Woguia GF, Bouaka CUT, Kamga RMN, Farikou O, Fogue PS, Tume C, Ravel S, Simo G.

Juin-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37208078/>

Monitoring and assessment of control strategies for African trypanosomoses' elimination require not only updating data on trypanosome infections, but also to have an overview on the molecular profiles of trypanocides resistance in different epidemiological settings. This study was designed to determine, in animals from six tsetse-infested areas of Cameroon, the prevalence of trypanosome infections as well as the diminazene aceturate (DA) and isometamidium chloride (ISM) sensitivity/resistance molecular profiles of these trypanosomes. From 2016 to 2019, blood was collected in pigs, dogs, sheep, goats and cattle from six tsetse infested

areas of Cameroon. DNA was extracted from blood and trypanosome species were identified by PCR. The sensitivity/resistance molecular profiles of trypanosomes to DA and ISM were investigated using PCR-RFLP. From 1343 blood samples collected, *Trypanosoma vivax*, *Trypanosoma congolense* forest and savannah, *Trypanosoma theileri* and trypanosomes of the sub-genus *Trypanozoon* were identified. The overall prevalence of trypanosome infections was 18.7%. These prevalence vary between trypanosome species, animal taxa, within and between sampling sites. *Trypanosoma theileri* was the predominant species with an infection rate of 12.1%. Trypanosomes showing resistant molecular profiles for ISM and DA were identified in animals from Tibati (2.7% for ISM and 65.6% for DA) and Kontcha (0.3% for ISM and 6.2% for DA). No trypanosome carrying resistant molecular profile for any of the two trypanocides was detected in animals from Fontem, Campo, Bipindi and Touboro. Mixed molecular profiles of sensitive/resistant trypanosomes were detected in animals from Tibati and Kontcha. Results of this study highlighted the presence of various trypanosome species as well as parasites carrying sensitive/resistant molecular profiles for DA and ISM in animals of tsetse infested areas of Cameroon. They indicate that the control strategies must be adapted according to epidemiological settings. The diversity of trypanosomes indicates that AAT remains a serious threat for animal breeding and animal health in these tsetse infested areas.

UMSBP2 is chromatin remodeler that functions in regulation of gene expression and suppression of antigenic variation in trypanosomes.

Soni A, Klebanov-Akopyan O, Erben E, Plaschkes I, Benyamini H, Mitesser V, Harel A, Yamin K, Onn I, Shlomai J.

19-05-2023

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/37207337/>

Universal Minicircle Sequence binding proteins (UMSBPs) are CCHC-type zinc-finger proteins that bind the single-stranded G-rich UMS sequence, conserved at the replication origins of minicircles in the kinetoplast DNA, the mitochondrial genome of kinetoplastids. *Trypanosoma brucei* USBP2 has been recently shown to colocalize with telomeres and to play an essential role in chromosome end protection. Here we report that TbUMSBP2 decondenses in vitro DNA molecules, which were condensed by core histones H2B, H4 or linker histone H1. DNA decondensation is mediated via protein-protein interactions between TbUMSBP2 and these histones, independently of its previously described DNA binding activity. Silencing of the TbUMSBP2 gene resulted in a significant decrease in the disassembly of nucleosomes in *T. brucei* chromatin, a phenotype that could be reverted, by supplementing the knockdown cells with TbUMSBP2. Transcriptome analysis revealed that silencing of TbUMSBP2 affects the expression of multiple genes in *T. brucei*, with a most significant effect on the upregulation of the subtelomeric variant surface glycoproteins (VSG) genes, which mediate the antigenic variation in African

trypanosomes. These observations suggest that UMSBP2 is a chromatin remodeling protein that functions in the regulation of gene expression and plays a role in the control of antigenic variation in *T. brucei*.

Cysteine synthase: multiple structures of a key enzyme in cysteine synthesis and a potential drug target for Chagas disease and leishmaniasis.

Sowerby K, Freitag-Pohl S, Murillo AM, Silber AM, Pohl E.

01-06-2023

Acta Crystallogr D Struct Biol.

<https://pubmed.ncbi.nlm.nih.gov/37204818/>

Chagas disease is a neglected tropical disease (NTD) caused by *Trypanosoma cruzi*, whilst leishmaniasis, which is caused by over 20 species of *Leishmania*, represents a group of NTDs endemic to most countries in the tropical and subtropical belt of the planet. These diseases remain a significant health problem both in endemic countries and globally. These parasites and other trypanosomatids, including *T. theileri*, a bovine pathogen, rely on cysteine biosynthesis for the production of trypanothione, which is essential for parasite survival in hosts. The de novo pathway of cysteine biosynthesis requires the conversion of O-acetyl-L-serine into L-cysteine, which is catalysed by cysteine synthase (CS). These enzymes present potential for drug development against *T. cruzi*, *Leishmania* spp. and *T. theileri*. To enable these possibilities, biochemical and crystallographic studies of CS from *T. cruzi* (TcCS), *L. infantum* (LiCS) and *T. theileri* (TthCS) were conducted. Crystal structures of the three enzymes were determined at resolutions of 1.80 Å for TcCS, 1.75 Å for LiCS and 2.75 Å for TthCS. These three homodimeric structures show the same overall fold and demonstrate that the active-site geometry is conserved, supporting a common reaction mechanism. Detailed structural analysis revealed reaction intermediates of the de novo pathway ranging from an apo structure of LiCS and holo structures of both TcCS and TthCS to the substrate-bound structure of TcCS. These structures will allow exploration of the active site for the design of novel inhibitors. Additionally, unexpected binding sites discovered at the dimer interface represent new potential for the development of protein-protein inhibitors.

Parasitological investigation of bovine Trypanosomosis, vector distribution and tsetse flies infection rate study, Dabo Hana District, Buno Bedelle Zone, Southwest Ethiopia.

Gebeyehu S, Degneh E.

Juin-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37208073/>

Ulcère de Buruli

Neglected tropical diseases in Republic of Guinea: disease endemicity, case

burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.

26-05-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37232124/>

Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.

Multi-centric evaluation of Biomeme Franklin Mobile qPCR for rapid detection of Mycobacterium ulcerans in clinical specimens.

Frimpong M, Frimpong VNB, Numfor H, Donkeng Donfack V, Amedior JS, Deegbe DE, Dadson B, Ablordey A, Eyangoh S, Phillips RO, Vedithi SC.

25-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37228126/>

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

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

24-05-2023

Microbiol Spectr.

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

Mycobacterium ulcerans, an environmental opportunistic pathogen, causes necrotic cutaneous and subcutaneous lesions, named Buruli ulcers, in tropical countries. PCR-derived tests used to detect *M. ulcerans* in environmental and clinical samples do not allow one-shot detection, identification, and typing of *M. ulcerans* among closely related *Mycobacterium marinum* complex mycobacteria. We established a 385-member *M. marinum*/*M. ulcerans* complex whole-genome sequence database by assembling and annotating 341 *M. marinum*/*M. ulcerans* complex genomes and added 44 *M. marinum*/*M. ulcerans* complex whole-genome sequences already deposited in the NCBI database. Pangenome, core genome, and single-nucleotide polymorphism (SNP) distance-based comparisons sorted the 385 strains into 10 *M. ulcerans* taxa and 13 *M. marinum* taxa, correlating with the geographic origin of strains. Aligning conserved genes identified one *PPE* (proline-proline-glutamate) gene

sequence to be species and intraspecies specific, thereby genotyping the 23 *M. marinum*/*M. ulcerans* complex taxa. PCR sequencing of the *PPE* gene correctly genotyped nine *M. marinum*/*M. ulcerans* complex isolates among one *M. marinum* taxon and three *M. ulcerans* taxa in the African taxon (T2.4). Further, successful *PPE* gene PCR sequencing in 15/21 (71.4%) swabs collected from suspected Buruli ulcer lesions in Côte d'Ivoire exhibited positive *M. ulcerans* IS2404 real-time PCR and identified the *M. ulcerans* T2.4.1 genotype in eight swabs and *M. ulcerans* T2.4.1/T2.4.2 mixed genotypes in seven swabs. *PPE* gene sequencing could be used as a proxy for whole-genome sequencing for the one-shot detection, identification, and typing of clinical *M. ulcerans* strains, offering an unprecedented tool for identifying *M. ulcerans* mixed infections. **IMPORTANCE** We describe a new targeted sequencing approach that characterizes the *PPE* gene to disclose the simultaneous presence of different variants of a single pathogenic microorganism. This approach has direct implications on the understanding of pathogen diversity and natural history and potential therapeutic implications when dealing with obligate and opportunistic pathogens, such as *Mycobacterium ulcerans* presented here as a prototype.

Changes in inflammatory markers in patients treated for Buruli ulcer and their ability to predict paradoxical reactions.

Phelippeau M, Marion E, Robbe-Saule M, Ganlonon L, Chauty A, Adeye A, Blanchard S, Johnson C, Marsollier L, Dubee V.

23-05-2023

J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37221015/>

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

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

22-05-2023

J Clin Microbiol.

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

Buruli ulcer (BU) is a neglected tropical disease caused by *Mycobacterium ulcerans*. Early diagnosis is crucial to prevent morbidity. In November 2012, a field laboratory fully equipped for the rapid on-site quantitative PCR (qPCR) diagnosis of *M. ulcerans* was established at the Buruli ulcer treatment center (CDTLUB) center in Pobè Benin, a region where BU is endemic. We describe its first 10 years of activity and its gradual evolution into an expert laboratory for BU diagnosis. From 2012 to 2022, the laboratory analyzed 3,018 samples from patients attending consultations for suspected BU at the CDTLUB in Pobè. Ziehl-Neelsen staining and qPCR targeting the IS2404 sequence were performed. Since 2019, the laboratory has also received and analyzed 570 samples

from other centers. The laboratory confirmed the diagnosis of BU by qPCR for 39.7% samples: *M. ulcerans* DNA was detected in 34.7% of swabs, 47.2% of all fine needle aspiration samples (FNA) and 44.6% of all skin biopsy specimens. Positive Ziehl-Neelsen staining results were obtained for 19.0% samples. Bacterial load, estimated by qPCR, was significantly greater for the Ziehl-Neelsen-positive samples than for Ziehl-Neelsen-negative samples, and detection rates were highest for FNA samples. Overall, 26.3% of the samples received from other centers were positive for BU. Most of these samples were sent by the CDTLUBs of Lalo, Allada, and Zagnanado, Benin. The establishment of the laboratory in the CDTLUB of Pobè has been a huge success. Optimal patient care depends on the close proximity of a molecular biology structure to BU treatment centers. Finally, FNA should be promoted among caregivers. **IMPORTANCE** Here, we describe the first 10 years of activity at a field laboratory established at the Buruli ulcer treatment center (CDTLUB) in Pobè, Benin, a country in which *Mycobacterium ulcerans* is endemic. Between 2012 and 2022, the laboratory analyzed 3,018 samples from patients consulting the CDTLUB of Pobè with a suspected clinical BU. Ziehl-Neelsen staining and qPCR targeting the IS2404 sequence were performed. In total, 39.7% of samples tested positive by qPCR and 19.0% tested positive by Ziehl-Neelsen staining. Detection rates were highest for FNA samples, and the bacterial loads estimated by qPCR were significantly higher for Ziehl-Neelsen-positive samples than for Ziehl-Neelsen-negative samples. Since 2019, the laboratory has also analyzed 570 samples received from outside the CDTLUB of Pobè, 26.3% of which were positive for BU. Most of these samples were sent by the CDTLUBs of Lalo, Allada, and Zagnanado in Benin. The establishment of the laboratory in the CDTLUB of Pobè has been a huge success, with major benefits for both the medical staff and patients. Our findings illustrate that the usefulness and feasibility of having a diagnostic center in rural Africa, where the disease is endemic, is a key part of optimal patient care, and that FNA should be promoted to increase detection rates.

Importance of consultations using mobile teams in the screening and treatment of neglected tropical skin diseases in Benin.

Gnimavo RS, Fajloun F, Al-Bayssari C, Sodjinou E, Habib A, Ganlonon L, Claco E, Agoundoté I, Houngho OA, Anagonou EG, Biaoou CAO, Ayélo AG, Houezo JG, Boccarossa A, Moussa EH, Gomez B, Gine A, Sopoh GE, Marion E, Johnson RC, Kempf M.

12-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37172044/>

Context: Since 2013, the World Health Organization has recommended integrated control strategies for neglected tropical diseases (NTDs) with skin manifestations. We evaluated the implementation of an integrated approach to the early detection and rapid treatment of skin NTDs based on mobile clinics in the Ouémé and Plateau areas of Benin. **Methods:** This descriptive cross-sectional study was performed in Ouémé and Plateau in Benin from 2018 to

2020. Consultations using mobile teams were performed at various sites selected by reasoned choice based on the epidemiological data of the National Program for the Control of Leprosy and Buruli Ulcer. All individuals presenting with a dermatological lesion who voluntarily approached the multidisciplinary management team on the day of consultation were included. The information collected was kept strictly anonymous and was entered into an Excel 2013 spreadsheet and analyzed with Stata 11 software. **Results:** In total, 5,267 patients with various skin conditions consulted the medical team. The median age of these patients was 14 years (IQR: 7-34 years). We saw 646 (12.3%) patients presenting NTDs with skin manifestations, principally scabies, in 88.4% (571/646), followed by 37 cases of Buruli ulcer (5.8%), 22 cases of leprosy (3.4%), 15 cases of lymphatic filariasis (2.3%) and one case of mycetoma (0.2%). We detected no cases of yaws. **Conclusion:** This sustainable approach could help to decrease the burden of skin NTDs in resource-limited countries.