



Veille scientifique Maladies tropicales négligées

Semaine 48
20 au 26 février 2023

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Dengue, chikungunya et maladie à virus Zika

Expanded profiling of Remdesivir as a broad-spectrum antiviral and low potential for interaction with other medications in vitro.

Radoshitzky SR, Iversen P, Lu X, Zou J, Kaptein SJF, Stuthman KS, Van Tongeren SA, Steffens J, Gong R, Truong H, Sapre AA, Yang H, Xie X, Chia JJ, Song ZJ, Leventhal SM, Chan J, Shornikov A, Zhang X, Cowfer D, Yu H, Warren T, Cihlar T, Porter DP, Neyts J, Shi PY, Wells J, Bilello JP, Feng JY.

23-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/36823196/>

Venezuelan equine encephalitis virus E1 protein interacts with PDIA6 and PDI inhibition reduces alphavirus production.

Panny L, Akrhymuk I, Bracci N, Woodson C, Flor R, Zhou W, Narayanan A, Campbell C, Kehn-Hall K.

21-02-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/36822370/>

Venezuelan equine encephalitis virus (VEEV) is an alphavirus transmitted by mosquitos that can cause a febrile illness and induce severe neurological complications in humans and equine populations. Currently there are no FDA approved vaccines or antiviral treatments to combat VEEV. Proteomic techniques were utilized to create an interactome of the E1 fusion glycoprotein of VEEV. VEEV E1 interacted with a number of cellular chaperone proteins including protein disulfide isomerase family A member 6 (PDIA6). PDI inhibition through LOC14 and/or nitazoxanide treatment effectively decreased production of VEEV and other alphaviruses in vitro, including eastern equine encephalitis virus, Sindbis virus, and chikungunya virus. Decreased oxidoreductive capabilities of PDIs through LOC14 or nitazoxanide treatment impacted both early and late events in viral replication, including the production of non-infectious virions and decreased VEEV E1 disulfide bond formation. Results from this study identified PDIs as critical regulators of alphavirus replication and potential therapeutic targets.

Some features on methodology of dengue modelling linked to data: Comment on "Mathematical modelling for dengue fever epidemiology: a 10-year systematic review" by M. Aguiar et al.

Pinho STR.

10-02-2023

Phys Life Rev.

<https://pubmed.ncbi.nlm.nih.gov/36821892/>

Spatial analysis of Chikungunya fever incidence and the associated socioeconomic, demographic, and vector infestation factors in municipalities of Pernambuco, Brazil, 2015-2021.

Aguiar-Santos M, Mendes LGDC, Passos DFD, Santos TGDS, Lins RHFB, Monte ACPD.

20-02-2023

Rev Bras Epidemiol.

<https://pubmed.ncbi.nlm.nih.gov/36820755/>

Dengue Burden and Circulation of Dengue-2 Serotype Among Children Along With Clinical Profiling in Uttarakhand, India: A Cross-Sectional Study From 2018 to 2020.

Badoni G, Gupta P, Pai MO, Kaistha N, Ratho R, Sokeechand N.

18-01-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/36819345/>

Background: The multiple serotypes of the dengue virus (DENV) are always a major public concern for dengue haemorrhagic fever (DHF) and dengue shock syndrome (DSS). **Objective:** This study aimed to analyse the demographic characteristics and circulating serotypes of dengue among the paediatric age group. **Methodology:** One hundred forty-one clinically suspected children were enrolled in the study from 2018 to 2020 in a tertiary care hospital in Uttarakhand, India. Central tendency, frequency, and One-Way ANOVA were measured for continuous and categorical data. The Shapiro-Wilks test was used to calculate the normality assumption. Dengue NS1 Ag, IgM, and IgG antibodies ELISA were performed, and NS1-positive samples were further tested for molecular studies. **Result:** From one hundred forty-one suspected cases, 100 (70.92%) came positive for dengue NS1 antigen, 18 (12.76%), and three (2.12%) came positive for IgM and IgG antibodies respectively. Rest 20 (14.18%) samples came negative for dengue. Fever with chills (97.5%), headache (89%), and arthralgia (82%) were the most common clinical features. Molecular studies showed the dengue serotype-2 (DEN-2) was found in most cases, followed by the dengue-3 serotype (DEN-3). **Conclusion:** This is the preliminary study as the authors' best knowledge which demonstrate the burden of dengue in children with prevalent serotypes for consecutive three years in Uttarakhand. This study identifies that the serotype-2 (DEN-2) of the dengue virus was the primary cause of infection in children at the tertiary care hospital in northern India. These results will help further to understand the nature of the disease so that improved patient care management will imply. Further molecular studies on large sample sizes during the endemic would be helpful to gain knowledge of the actual load of the disease and the genetic characteristics of the virus.

The Current Landscape of Bioactive Molecules against DENV: A Systematic Review.

Babbar R, Kaur R, Rana P, Arora S, Behl T, Albratty M, Najmi A, Meraya AM, Alhazmi HA, Singla RK.

10-02-2023

Evid Based Complement Alternat Med.

<https://pubmed.ncbi.nlm.nih.gov/36818227/>

With a 30-fold increase in incidence over the previous 50 years, dengue fever is now the most widespread viral disease transmitted by mosquitoes in the world. The intricate interaction of the human defense system, hereditary predisposition, and specific bitterness elements is more likely to be the pathogenesis of dengue. There are presently no viable treatments for dengue. Synthetic drugs which are used against this ailment also show major side effects. There must be a deeper understanding of the underlying mechanism generating severe symptoms to develop auguring markers, cutting-edge diagnostics, and treatments and finally a well-rounded and secure antiserum. Hence, the aim is to search for safer and more potent drugs derived from plants. Plants or herbs are mainly targeting replication or its enzyme or specific stereotypes, though an exact mechanism of phytoconstituents interfering with the viral replication is still undiscovered. The present attempt provided the update with the objective to bringing up forward pathophysiological eventualities involved in dengue virus along with the naturally derived treatment relevant to provide the impregnable therapy by evading the noxious symptoms for dengue fever. *Governor's plum, Cryptocarya chartacea*, magnolia berry, and Chinese ginger are such plants exhibiting many effective phytoconstituents against DENV and can be further explored for novel drug discovery by medicinal scientists.

Epidemiological profile of dengue in Champasak and Savannakhet provinces, Lao People's Democratic Republic, 2003-2020.

Zafar S, Overgaard HJ, Pongvongsa T, Vannavong N, Phommachanh S, Shipin O, Rocklöv J, Paul RE, Rahman MS, Mayxay M.

23-11-2023

Western Pac Surveill Response J.

<https://pubmed.ncbi.nlm.nih.gov/36817500/>

Epidemiological and clinical characteristics of children with confirmed COVID-19 infection in a tertiary referral hospital in Manila, Philippines.

Lota-Salvado R, Padua JR, Agrupis KA, Malijan GM, Sayo AR, Suzuki S, Go GD, Smith C.

22-02-2023

Trop Med Health.

<https://pubmed.ncbi.nlm.nih.gov/36814333/>

Background: COVID-19 has challenged the under-resourced health systems of low- and middle-income countries, significantly affecting child health. Available published data on Filipino children with COVID-19 infection are limited. This study aims to describe the epidemiological and clinical characteristics of pediatric patients with confirmed COVID-19 in an infectious disease

hospital in Manila, Philippines. **Main text:** This cross-sectional study reviewed data on patients ages 0 to 18 years with confirmed COVID-19 infection, admitted to San Lazaro Hospital from January 25, 2020 to January 25, 2022. Demographic data and clinical characteristics obtained from COVID-19 case investigation forms were summarized and compared between severe and non-severe cases. Risk factors for disease severity and mortality were analyzed. Of 115 patients, 64% were males. There were 87 patients (75.7%) with asymptomatic, mild, or moderate disease, and 28 cases (24.3%) with severe or critical illness. The median age of all patients was 10 years (interquartile range: 4-15 years). The majority of patients (40.9%) were adolescents ages 13 to 18 years. Predominant symptoms were fever (73.9%) and cough (55.7%). Patients with severe or critical illness were more likely to experience difficulty of breathing (55.2% vs 44.8%, $p < 0.001$), and have a longer hospital stay (11 days vs 8 days, $p = 0.043$). Among all patients, 48.7% had at least one underlying disease; and common infectious co-morbidities were tuberculosis (17.4%), dengue (12.2%), and HIV (4.3%). Having tuberculosis ($p = 0.008$) or at least one co-morbidity ($p < 0.001$) was associated with disease severity. Ten patients (8.7%) died; and mortality was higher among those with severe or critical illness (80% vs 20%, $p < 0.001$). Sepsis ($p = 0.020$) or having at least one co-morbidity ($p = 0.007$) was associated with death. **Conclusion:** Children of all ages remain susceptible to COVID-19 infection, and usually present with mild or moderate symptoms. In this study, many adolescents are affected, highlighting the value of COVID-19 vaccination in this age group. Understanding the clinical features of COVID-19 in Filipino children is essential to identifying and optimally managing those at highest risk of severe disease.

An innovative insecticidal approach based on plant protease inhibitor and Bt protoxins inhibits trypsin-like activity in zebrafish.

Gonçalves ÍFS, de Sousa Gomes C, Filho LCPA, da Costa Ribeiro Souza JA, Rocha BAM, de Souza PFN, de Freitas Júnior ACV, Carvalho AFU, Farias D.

20-02-2023

Comp Biochem Physiol C Toxicol Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36813018/>

Applied machine learning for the risk-stratification and clinical decision support of hospitalised patients with dengue in Vietnam.

Ming DK, Hernandez B, Sangkaew S, Vuong NL, Lam PK, Nguyet NM, Tam DTH, Trung DT, Tien NTH, Tuan NM, Chau NVV, Tam CT, Chanh HQ, Trieu HT, Simmons CP, Wills B, Georgiou P, Holmes AH, Yacoub S; Vietnam ICU Translational Applications Laboratory (VITAL) investigators.

18-01-2023

PLOS Digit Health.

<https://pubmed.ncbi.nlm.nih.gov/36812518/>

Dengue Virus Increases the Expression of TREM-1 and CD10 on Human Neutrophils.

Ruiz-Pacheco JA, Muñoz-Medina EJ, Castillo-Díaz LA, Chacón-Salinas R, Escobar-Gutiérrez A.

22-02-2023

Viral Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36811498/>

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

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

22-02-2023

Mol Omics.

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

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

Epidemiology of dengue, chikungunya and Zika virus infections in travellers: A 16-year retrospective descriptive study at a tertiary care centre in Prague, Czech Republic.

Trojánek M, Grebenyuk V, Mandáková Z, Sojková N, Zelená H, Roháčová H, Stejskal F.

21-02-2023

PLoS One. 2023 Feb 21

<https://pubmed.ncbi.nlm.nih.gov/36809441/>

Correction to: Higher Plasma Viremia in the Febrile Phase Is Associated With Adverse Dengue Outcomes Irrespective of Infecting Serotype or Host Immune Status: An Analysis of 5642 Vietnamese Cases.

[No authors listed]

20-02-2023

Clin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36808221/>

Pathogen inactivation methods to prevent transfusion-transmissible arboviruses.

Giménez-Richarte Á, Ortiz de Salazar MI, Giménez-Richarte MP, Larrea L, Arbona C, Marco P, Ramos-Rincón JM.

19-02-2023

Trop Med Int Health.

<https://pubmed.ncbi.nlm.nih.gov/36806816/>

Objective: Arboviruses are emerging as a relevant threat to transfusion safety. Pathogen inactivation methods may reduce the risk of transmission through transfusion, as long as they meet minimum standards for effectiveness. This study aims to assess the log reduction of viral load achieved with different pathogen inactivation methods, according to the blood product they are used on and the arbovirus targeted. **Methods:** Systematic literature review and meta-analysis. Searches were conducted in MEDLINE and Embase. The study protocol was registered in PROSPERO CRD42022312061. We selected records reporting the log reduction of viral load achieved with the main pathogen inactivation methods (amotosalen + UVA light [INTERCEPT], riboflavin + UV light [Mirasol], methylene blue + visible light/UVC light [THERAFLEX], solvent detergent, amustaline [INTERCEPT] and PEN110 [Inactine]), applied to any blood product (plasma, platelets, red blood cells or whole blood) and for any arbovirus. The log reduction of viral loads was assessed by obtaining the mean log reduction factor (LRF). We compared and classified the LRF of different techniques using statistical methods. **Results:** We included 59 publications reporting LRF results in 17 arboviruses. For 13 arboviruses, including Chikungunya virus, Dengue virus, West Nile virus, and Zika virus, at least one of the methods achieves adequate or optimal log reduction of viral load - mean LRF ≥ 4 . The LRF achieved with riboflavin + UV light is inferior to the rest of the techniques, both overall and specifically for plasma, platelets preserved in platelet additive solution (PAS)/plasma, and red blood cells/whole blood. The LRF achieved using Mirasol is also lower for inactivating chikungunya virus, dengue virus, and Zika virus. For West Nile virus, we found no significant differences. In plasma, the method that achieves the highest LRF is solvent/detergent; in platelets, THERAFLEX and INTERCEPT; and in red blood cells/whole blood, PEN110 (Inactine). **Conclusion:** Not all pathogen inactivation methods achieve the same LRF, nor is this equivalent between the different arboviruses or blood products. Overall, the LRFs achieved using riboflavin + UV light (Mirasol) are inferior to those achieved with the rest of the pathogen inactivation methods. Regarding the others, LRFs vary by arbovirus and blood product. In light of the threat of different arboviruses, blood establishments should have already validated pathogen inactivation methods and be logistically prepared to implement these techniques quickly.

Design, synthesis and anti-Chikungunya virus activity of lomerizine derivatives.

Chen CR, Ma Y, Wang HX, Liu XY, Liu Y, Meng QG, Jin YS.
15-02-2023

Bioorg Med Chem Lett.

<https://pubmed.ncbi.nlm.nih.gov/36804408/>

CLEC5A mediates Zika virus-induced testicular damage.

Wang HW, Li HH, Wu SC, Tang CK, Yu HY, Chang YC, Sung PS, Liu WL, Su MP, Yu GY, Huang LR, Chen CH, Hsieh SL.
17-02-2023

J Biomed Sci.

<https://pubmed.ncbi.nlm.nih.gov/36803804/>

Imported diseases in travellers presenting to the emergency department after a stay in a malaria-endemic country: a retrospective observational study.

Desmet S, Henckaerts L, Ombelet S, Damanet B, Vanbrabant P.

20-02-2023

Trop Dis Travel Med Vaccines.

<https://pubmed.ncbi.nlm.nih.gov/36803441/>

Dengue, chikungunya and zika arbovirus infections in Caribbean children.

Christie CDC, Lue AM, Melbourne-Chambers RH.

22-02-2023

Curr Opin Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36801979/>

Purpose of review: Dengue, chikungunya and zika have caused significant epidemics in the Caribbean in recent years. This review highlights their impact in Caribbean children. **Recent findings:** Dengue has been increasingly intense and severe, seroprevalence is 80-100% in the Caribbean, children have increased attributable morbidity and mortality. Severe dengue, especially dengue with haemorrhage was significantly associated with haemoglobin SC disease and multiple organ-systems involved. These included the gastrointestinal and haematologic systems with extremely high lactate dehydrogenases and creatinine phosphokinases and severely abnormal bleeding indices. Despite appropriate interventions, mortality was highest within the first 48 h of admission. Chikungunya, a togavirus, affected 80% of some Caribbean populations. Paediatric presentations included high fever, skin, joint and neurological manifestations. Children less than 5 years of age had the highest morbidity and mortality. This maiden chikungunya epidemic was explosive and overwhelmed public health systems. Zika, another flavivirus, has a seroprevalence of 15% in pregnancy, so the Caribbean remains susceptible. Paediatric complications include pregnancy losses, stillbirths, Congenital Zika syndrome, Guillain-Barre syndrome, acute disseminated encephalomyelitis and transverse myelitis. Neurodevelopment stimulation programs for zika-exposed infants have been effective in improving language and positive behaviour scores.

Piperazine-derived small molecules as potential Flaviviridae NS3 protease inhibitors. In vitro antiviral activity evaluation against Zika and Dengue viruses.

Del Rosario García-Lozano M, Dragoni F, Gallego P, Mazzotta S, López-Gómez A, Boccuto A, Martínez-Cortés C, Rodríguez-Martínez A, Pérez-Sánchez H, Manuel Vega-Pérez J, Antonio Del Campo J, Vicenti I, Vega-Holm M, Iglesias-Guerra F.

04-02-2023

Bioorg Chem.

<https://pubmed.ncbi.nlm.nih.gov/36801791/>

A quick prediction tool for Dengue fever: A timely response is essential!

Qureshi H, Khan MI, Bae SJ, Shah A.

13-02-2023

J Infect Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36801635/>

Improving the reliability of smartphone-based urine colorimetry using a colour card calibration method.

Noor Azhar M, Bustam A, Naseem FS, Shuin SS, Md Yusuf MH, Hishamudin NU, Poh K.

10-02-2023

Digit Health.

<https://pubmed.ncbi.nlm.nih.gov/36798885/>

Objective: Urine colorimetry using a digital image-based colorimetry is potentially an accessible hydration assessment method. This study evaluated the agreement between urine colorimetry values measured with different smartphone brands under various lighting conditions in patients with dengue fever. **Methods:** The urine samples were photographed in a customized photo box, under five simulated lighting conditions, using five smartphones. These images were analyzed using Adobe Photoshop to obtain urine Red, Green and Blue (RGB) values with and without colour correction. A commercially available colour calibration card was used for colour correction. Using intraclass correlation coefficient (ICC), inter-phone and intra-phone agreements of urine RGB values were analyzed. **Results:** Without colour correction, the various smartphones produced the highest agreement for Blue and Green values under the 'daylight' lighting condition. With colour correction, ICC values showed 'exceptional' inter-phone and intra-phone agreement for the Blue and Green values (ICC > 0.9). Red values showed 'poor' (ICC < 0.5) agreement with and without colour correction in all lighting conditions. Out of the five phones compared in this study, Phone 4 produced the lowest intra-phone agreement. **Conclusions:** Colour calibration using photo colour cards improved the reliability of smartphone-based urine colorimetry, making this a promising point-of-care hydration assessment tool using the ubiquitous smartphone.

Estimating the impact of the COVID-19 pandemic on dengue in Brazil.

Roster KO, Martinelli T, Connaughton C, Santillana M, Rodrigues F.

09-02-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/36798282/>

Early diagnostic indicators of dengue versus other febrile illnesses in Asia and Latin America (IDAMS study): a multicentre, prospective, observational study.

Rosenberger KD, Phung Khanh L, Tobian F, Chanpheaktra N, Kumar V, Lum LCS, Sathar J, Pleiteés Sandoval E, Maroén GM, Laksono IS, Mahendradhata Y, Sarker M, Rahman R, Caprara A, Souza Benevides B, Marques ETA, Magalhaes T, Brasil P, Amaral Calvet G, Tami A, Bethencourt SE, Dong Thi Hoai T, Nguyen Tan Thanh K, Tran Van N, Nguyen Tran N, Do Chau V, Yacoub S, Nguyen Van K, Guzmán MG, Martinez PA, Nguyen Than Ha Q, Simmons CP, Wills BA, Geskus RB, Jaenisch T; International Research Consortium on Dengue Risk Assessment, Management, and Surveillance Investigators.

Mar-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36796983/>

Background: Improvements in the early diagnosis of dengue are urgently needed, especially in resource-limited settings where the distinction between dengue and other febrile illnesses is crucial for patient management.

Methods: In this prospective, observational study (IDAMS), we included patients aged 5 years and older with undifferentiated fever at presentation from 26 outpatient facilities in eight countries (Bangladesh, Brazil, Cambodia, El Salvador, Indonesia, Malaysia, Venezuela, and Viet Nam). We used multivariable logistic regression to investigate the association between clinical symptoms and laboratory tests with dengue versus other febrile illnesses between day 2 and day 5 after onset of fever (ie, illness days). We built a set of candidate regression models including clinical and laboratory variables to reflect the need of a comprehensive versus parsimonious approach. We assessed performance of these models via standard measures of diagnostic values. **Findings:** Between Oct 18, 2011, and Aug 4, 2016, we recruited 7428 patients, of whom 2694 (36%) were diagnosed with laboratory-confirmed dengue and 2495 (34%) with (non-dengue) other febrile illnesses and met inclusion criteria, and were included in the analysis. 2703 (52%) of 5189 included patients were younger than 15 years, 2486 (48%) were aged 15 years or older, 2179 (42%) were female and 3010 (58%) were male. Platelet count, white blood cell count, and the change in these variables from the previous day of illness had a strong association with dengue. Cough and rhinitis had strong associations with other febrile illnesses, whereas bleeding, anorexia, and skin flush were generally associated with dengue. Model performance increased between day 2 and 5 of illness. The comprehensive model (18 clinical and laboratory predictors) had sensitivities of 0·80 to 0·87 and specificities of 0·80 to 0·91, whereas the parsimonious model (eight clinical and laboratory predictors) had sensitivities of 0·80 to 0·88 and

specificities of 0·81 to 0·89. A model that includes laboratory markers that are easy to measure (eg, platelet count or white blood cell count) outperformed the models based on clinical variables only. **Interpretation:** Our results confirm the important role of platelet and white blood cell counts in diagnosing dengue, and the importance of serial measurements over subsequent days. We successfully quantified the performance of clinical and laboratory markers covering the early period of dengue. Resulting algorithms performed better than published schemes for distinction of dengue from other febrile illnesses, and take into account the dynamic changes over time. Our results provide crucial information needed for the update of guidelines, including the Integrated Management of Childhood Illness handbook.

Differentiating dengue from other febrile illnesses: a dilemma faced by clinicians in dengue endemic countries.

Malavige GN, Wijewickrama A, Ogg GS.

Mar-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36796966/>

Epidemiological serosurvey of chikungunya fever post outbreak at Tanjung Sepat, Malaysia.

Khor CS, Teoh BT, Sam SS, Khoo HY, Azizan NS, CheMatSeri A, Chin KL, Hamim ZR, Mohamed-Romai-Noor NA, Yaacob CN, Abd-Jamil J, Lee HY, Soh YH, AbuBakar S.

31-01-2023

J Infect Dev Ctries.

<https://pubmed.ncbi.nlm.nih.gov/36795935/>

Octopamine and tyramine signalling in *Aedes aegypti*: Molecular characterization and insight into potential physiological roles.

Finetti L, Paluzzi JP, Orchard I, Lange AB.

16-02-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36795713/>

Arthropod-borne diseases among travellers arriving in Europe from Africa, 2015 to 2019.

Gossner CM, Hallmaier-Wacker L, Briet O, Haussig JM, de Valk H, Wijermans A, Bakonyi T, Madubuko T, Frank C, Noel H, Abdulaziz M.

Feb-2023

Euro Surveill.

<https://pubmed.ncbi.nlm.nih.gov/36795503/>

Background Travellers are generally considered good sentinels for infectious disease surveillance. **Aim** To investigate whether health data from travellers arriving from Africa to Europe could provide evidence to support surveillance systems in Africa. **Methods** We examined disease occurrence and estimated risk of infection among travellers arriving from Africa to Europe from 2015 to 2019

using surveillance data of arthropod-borne disease cases collected through The European Surveillance System (TESSy) and flight passenger volumes from the International Air Transport Association. Results Malaria was the most common arthropod-borne disease reported among travellers from Africa, with 34,235 cases. The malaria travellers' infection rate (TIR) was 28.8 cases per 100,000 travellers, which is 36 and 144 times higher than the TIR for dengue and chikungunya, respectively. The malaria TIR was highest among travellers arriving from Central and Western Africa. There were 956 and 161 diagnosed imported cases of dengue and chikungunya, respectively. The highest TIR was among travellers arriving from Central, Eastern and Western Africa for dengue and from Central Africa for chikungunya in this period. Limited numbers of cases of Zika virus disease, West Nile virus infection, Rift Valley fever and yellow fever were reported. Conclusions Despite some limitations, travellers' health data can efficiently complement local surveillance data in Africa, particularly when the country or region has a sub-optimal surveillance system. The sharing of anonymised traveller health data between regions/continents should be encouraged.

Electrochemical magneto-immunoassay for detection of zika virus antibody in human serum.

Castro KR, Setti GO, de Oliveira TR, Rodrigues-Jesus MJ, Botosso VF, Perini de Araujo AP, Durigon EL, Ferreira LCS, Faria RC.
01-05-2023
Talanta.
<https://pubmed.ncbi.nlm.nih.gov/36738622/>

N-Phenylpyridine-3-Carboxamide and 6-Acetyl-1H-Indazole Inhibit the RNA Replication Step of the Dengue Virus Life Cycle.

Sow AA, Pahmeier F, Ayotte Y, Anton A, Mazeaud C, Charpentier T, Angelo L, Woo S, Cerikan B, Falzarano D, Abrahamyan L, Lamarre A, Labonté P, Cortese M, Bartenschlager R, LaPlante SR, Chatel-Chaix L.
16-02-2023
Antimicrob Agents Chemother.
<https://pubmed.ncbi.nlm.nih.gov/36700643/>

Insights into the role of the cobalt(III)-thiosemicarbazone complex as a potential inhibitor of the Chikungunya virus nsP4.

Martins DOS, Souza RAC, Freire MCLC, de Moraes Roso Mesquita NC, Santos IA, de Oliveira DM, Junior NN, de Paiva REF, Harris M, Oliveira CG, Oliva G, Jardim ACG.
Feb-2023
J Biol Inorg Chem.
<https://pubmed.ncbi.nlm.nih.gov/36484824/>

Chikungunya virus (CHIKV) is the causative agent of chikungunya fever, a disease that can result in disability. Until now, there is no antiviral treatment against CHIKV, demonstrating that there is a need for development of new drugs. Studies have shown that thiosemicarbazones

and their metal complexes possess biological activities, and their synthesis is simple, clean, versatile, and results in high yields. Here, we evaluated the mechanism of action (MOA) of a cobalt(III) thiosemicarbazone complex named $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ based on its in vitro potent antiviral activity against CHIKV previously evaluated (80% of inhibition on replication). Furthermore, the complex has no toxicity in healthy cells, as confirmed by infecting BHK-21 cells with CHIKV-nanoluciferase in the presence of the compound, showing that $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ inhibited CHIKV infection with the selective index of 3.26. $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ presented a post-entry effect on viral replication, emphasized by the strong interaction of $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ with CHIKV non-structural protein 4 (nsP4) in the microscale thermophoresis assay, suggesting a potential mode of action of this compound against CHIKV. Moreover, in silico analyses by molecular docking demonstrated potential interaction of $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ with nsP4 through hydrogen bonds, hydrophobic and electrostatic interactions. The evaluation of ADME-Tox properties showed that $[\text{Co}^{\text{III}}(\text{L}^1)_2]\text{Cl}$ presents appropriate lipophilicity, good human intestinal absorption, and has no toxicological effect as irritant, mutagenic, reproductive, and tumorigenic side effects.

Fluid management in children with severe dengue: a narrative review.

Loi MV, Wang QY, Lee JH.
Feb-2023
Minerva Pediatr (Torino).
<https://pubmed.ncbi.nlm.nih.gov/36282485/>

Rage

DEVELOPMENT OF A VALIDATED MOLECULAR ANALYTICAL METHOD TO DETERMINE THE VIRAL SAFETY OF $\text{F}(\text{AB}')_2$ PRODUCTS: A NOVEL APPLICATION FOR A WELL-KNOWN TECHNIQUE.

Sánchez-Pacheco UA, Bahena-Mondragón BM, Hernández-Piedras FR, Soria-Osorio R, Meneses-Acosta A.
21-02-2023
J Virol Methods.
<https://pubmed.ncbi.nlm.nih.gov/36822561/>

Rabies in an imported dog, Ontario, Canada, 2022.

Di Salvo P, Anderson M, Fehlner-Gardiner C, Di Mauro F, Shapiro H, Miranda A, McClinchey H.
05-01-2023
Can Commun Dis Rep.
<https://pubmed.ncbi.nlm.nih.gov/36815867/>

Importation of rabies-infected dogs results in significant and costly public and animal health risks. In January 2022, a dog in Ontario, Canada, which was imported from Iran in June 2021, developed rabies, leading to an extensive public health investigation and administration of rabies post-exposure prophylaxis to 37 individuals. The dog was infected with a rabies virus variant known to circulate in

Iran. This is the second reported case of a rabies-infected dog imported into Canada in 2021 from a high-risk country for canine mediated rabies. This case emphasizes the need for public education regarding the risks associated with importing dogs from high-risk countries for canine-mediated rabies and the benefits of establishing a public health team specializing in rabies exposure investigations.

Modelling modifiable factors associated with the probability of human rabies deaths among self-reported victims of dog bites in Abuja, Nigeria.

Mshelbwala PP, J Soares Magalhães R, Weese JS, Ahmed NO, Rupprecht CE, Clark NJ.
21-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36809362/>

Canine-mediated rabies kills tens of thousands of people annually in lesser-developed communities of Asia, Africa, and the Americas, primarily through bites from infected dogs. Multiple rabies outbreaks have been associated with human deaths in Nigeria. However, the lack of quality data on human rabies hinders advocacy and resource allocation for effective prevention and control. We obtained 20 years of dog bite surveillance data across 19 major hospitals in Abuja, incorporating modifiable and environmental covariates. To overcome the challenge of missing information, we used a Bayesian approach with expert-solicited prior information to jointly model missing covariate data and the additive effects of the covariates on the predicted probability of human death after rabies virus exposure. Only 1155 cases of dog bites were recorded throughout the study period, out of which 4.2% (N = 49) died of rabies. The odds for risk of human death were predicted to decrease among individuals who were bitten by owned dogs compared to those bitten by free-roaming dogs. Similarly, there was a predicted decrease in the probability of human death among victims bitten by vaccinated dogs compared to those bitten by unvaccinated dogs. The odds for the risk of human death after bitten individuals received rabies prophylaxis were predicted to decrease compared to no prophylaxis. We demonstrate the practical application of a regularised Bayesian approach to model sparse dog bite surveillance data to uncover risk factors for human rabies, with broader applications in other endemic rabies settings with similar profiles. The low reporting observed in this study underscores the need for community engagement and investment in surveillance to increase data availability. Better data on bite cases will help to estimate the burden of rabies in Nigeria and would be important to plan effective prevention and control of this disease.

[Bitten or struck by dog - an increasingly common diagnosis].

Sarenbo S, Striwing H.

20-02-2023

Lakartidningen.

<https://pubmed.ncbi.nlm.nih.gov/36808574/>

Role of Brazilian bats in the epidemiological cycle of potentially zoonotic pathogens.

Castelo-Branco DSCM, Nobre JA, Souza PRH, Diógenes EM, Guedes GMM, Mesquita FP, Souza PFN, Rocha MFG, Sidrim JJC, Cordeiro RA, Montenegro RC.

17-02-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/36804526/>

Rabies virus uniquely reprograms the transcriptome of human monocyte-derived macrophages.

Embregts CWE, Wentzel AS, den Dekker AT, van Ijcken WFJ, Stadhouders R, GeurtsvanKessel CH.

31-01-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36798087/>

Macrophages are amongst the first immune cells that encounter rabies virus (RABV) at virus entry sites. Activation of macrophages is essential for the onset of a potent immune response, but insights into the effects of RABV on macrophage activation are scarce. In this study we performed high-throughput sequencing on RNA extracted from macrophages that were exposed to RABV for 48 hours, and compared their transcriptional profiles to that of non-polarized macrophages (M0), and macrophages polarized towards the canonical M1, M2a and M2c phenotypes. Our analysis revealed that RABV-stimulated macrophages show high expression of several M1, M2a and M2c signature genes. Apart from their partial resemblance to these phenotypes, unbiased clustering analysis revealed that RABV induces a unique and distinct polarization program. Closer examination revealed that RABV induced multiple pathways related to the interferon- and antiviral response, which were not induced under other classical polarization strategies. Surprisingly, our data show that RABV induces an activated rather than a fully suppressed macrophage phenotype, triggering virus-induced activation and polarization. This includes multiple genes with known antiviral (e.g. APOBEC3A, IFIT/OAS/TRIM genes), which may play a role in anti-RABV immunity.

Trachome

Seroreversion to *Chlamydia trachomatis* Pgp3 antigen among young children in a hyperendemic region of Amhara, Ethiopia.

Tedijanto C, Aragie S, Gwyn S, Wittberg DM, Zeru T, Tadesse Z, Chernet A, Thompson I, Nash SD, Lietman TM, Martin DL, Keenan JD, Arnold BF.

07-02-2023

medRxiv.

<https://pubmed.ncbi.nlm.nih.gov/36798251/>

Monitoring trachoma transmission with antibody data requires characterization of decay in IgG to *Chlamydia trachomatis* antigens. In a three-year longitudinal cohort

in a high transmission setting, we estimated a median IgG half-life of 3 years and a seroreversion rate of 2.5 (95% CI: 1.6, 3.8) per 100 person-years.

Ulcère de Buruli

Buruli ulcer caused by *Mycobacterium ulcerans* subsp. *shinshuense*: A case report.

Fujimori T, Hagiya H, Iio K, Yamasaki O, Miyamoto Y, Hoshino Y, Kakehi A, Okura M, Minabe H, Yokoyama Y, Otsuka F, Higashikage A.

21-02-2023

J Infect Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36813163/>

Lèpre

Increased uptake of tuberculosis preventive therapy (TPT) among people living with HIV following the 100-days accelerated campaign: A retrospective review of routinely collected data at six urban public health facilities in Uganda.

Musaazi J, Sekaggya-Wiltshire C, Okoboi S, Zawedde-Muyanja S, Senkoro M, Kalema N, Kavuma P, Namuwenge PM, Manabe YC, Castelnuovo B, Kiragga A.

23-02-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36821550/>

Tuberculosis preventive therapy (TPT) effectively decreases rates of developing active tuberculosis disease in people living with HIV (PLHIV) who are at increased risk. The Uganda Ministry of Health launched a 100-day campaign to scale-up TPT in PLHIV in July 2019. We sought to examine the effect of the campaign on trends of TPT uptake and characteristics associated with TPT uptake and completion among persons in HIV care. We retrospectively reviewed routinely collected data from 2016 to 2019 at six urban public health facilities in Uganda. HIV care database and paper-based TPT registers at six public health facilities in Kampala, Uganda were retrospectively reviewed. Estimated trends of TPT (given as Isoniazid monotherapy) uptake and completion across the 4 years, among PLHIV aged 15 years and above, and factors associated, were examined using Poisson regression model with robust standard errors using generalized estimating equation (GEE) models. On average, a total of 39,774 PLHIV aged 15 years and above were eligible for TPT each calendar year at the six health facilities. Across all 4 years, more than 70% were females (range: 73.5% -74.6%) and the median age ranged from 33 to 34 years. From 2016 quarter one to 2019 quarter two, TPT uptake was consistently below 25%, but, as expected, the uptake significantly increased by about 3-folds from 22.1% to 61.2%, in 2019 quarter two (i.e. before the roll-out of the 100-day accelerated TPT intervention) and quarter three (i.e. after the roll-out of the 100-day accelerated TPT intervention) respectively. This increase remained highly significant even after

adjusting for patients' baseline characteristics (adjusted prevalence ratio [aPR] = 2.58 [95%CI 2.45, 2.72], P-value<0.001). TPT completion was consistently high at above 70% at most of the time, but, it increased significantly among those initiated during 2018 quarter four and in the subsequent two quarters after the roll-out of the 100-day accelerated TPT intervention (i.e. TPT completion was: 83.2%, 95.3%, and 97.1% among individuals initiated during 2018 quarter4, and 2019 quarters 1 and 2, respectively). The increase in TPT completion during this period remained significant even after adjusting for patients' baseline characteristics (aPR [95%CI] = 1.09 [1.04, 1.14], P value<0.001, and 1.10 [1.05,1.15], P value<0.001, for individuals initiated during 2019 quarter 1, and 2, respectively compared to those initiated during 2018 quarter 4). Not on ART or newly started on ART compared to ART experienced, and pregnant at TPT initiation compared to not pregnant were associated with poor TPT completion, whereas older age (≥ 25 years versus 15-24 years) was associated with higher TPT completion. The targeted 100-day campaign dramatically increased TPT uptake and completion among PLHIV suggesting a viable catch up strategy to meet WHO guidelines. Future analysis with additional years of data post 100-days TPT intervention is required to evaluate the sustainability of the observed gains.

Spatial patterns of new leprosy cases in a northeastern state of Brazil, 2011-2021.

Silva MLFID, Farias SJM, Silva APSC, Rodrigues MOS, Oliveira ECA.

20-02-2023

Rev Bras Epidemiol.

<https://pubmed.ncbi.nlm.nih.gov/36820751/>

Profile of the leprosy endemic in the district of Murrupula, Nampula, Mozambique: A population-based study.

Ribeiro GC, Lages DDS, Lages ATC, Souza VB, Marega A, Lana FCF, Rocha MODC.

20-02-2023

Rev Bras Epidemiol.

<https://pubmed.ncbi.nlm.nih.gov/36820655/>

Background: Leprosy is a neglected chronic infection caused by *Mycobacterium leprae*, that is curable. The magnitude of the disease and severity of the debilitation it causes renders leprosy a public health problem. This study aimed to analyze the endemic profile of leprosy in the Murrupula district and evaluate the socioeconomic, clinical, and serological profiles of leprosy contacts.

Methods: A cross-sectional study of patients with leprosy diagnosed between 2013 and 2017 and their household and community contacts was conducted in Murrupula District, Nampula Province, Mozambique. Interviews, simplified dermatoneurological examinations, *Mycobacterium leprae* flow (ML Flow) tests, and Mitsuda tests were performed. **Results:** Most of the leprosy cases were multibacillary. The patients had some degree of physical disability. ML Flow positivity was more common in household contacts of the patients diagnosed with leprosy and in community individuals who spontaneously

presented for testing. In total, 17 patients were diagnosed with leprosy. **Conclusions:** This study revealed an active chain of transmission, hidden prevalence, and operational deficiencies in leprosy surveillance and care. The results suggest that the implementation of a public health policy for leprosy prevention and control in Nampula Province is necessary. In future, the possibility of expanding the policy to the entire country should be considered.

A Case of Lepromatous Leprosy With Erythema Nodosum Leprosum.

Park L, Wallace CE, Vasile G, Buckley C.

16-01-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/36819324/>

Progress on diagnosis and treatment of drug-resistant tuberculosis in line with World Health Organization recommendations in six priority countries in the Western Pacific Region.

Oh KH, Quelapio MI, Morishita F, Rahevar K, Yanagawa M, Islam T.

19-12-2022

Western Pac Surveill Response J.

<https://pubmed.ncbi.nlm.nih.gov/36817504/>

Clofazimine for the treatment of tuberculosis.

Stadler JAM, Maartens G, Meintjes G, Wasserman S.

02-02-2023

Front Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36817137/>

Shorter (6-9 months), fully oral regimens containing new and repurposed drugs are now the first-choice option for the treatment of drug-resistant tuberculosis (DR-TB). Clofazimine, long used in the treatment of leprosy, is one such repurposed drug that has become a cornerstone of DR-TB treatment and ongoing trials are exploring novel, shorter clofazimine-containing regimens for drug-resistant as well as drug-susceptible tuberculosis. Clofazimine's repurposing was informed by evidence of potent activity against DR-TB strains *in vitro* and in mice and a treatment-shortening effect in DR-TB patients as part of a multidrug regimen. Clofazimine entered clinical use in the 1950s without the rigorous safety and pharmacokinetic evaluation which is part of modern drug development and current dosing is not evidence-based. Recent studies have begun to characterize clofazimine's exposure-response relationship for safety and efficacy in populations with TB. Despite being better tolerated than some other second-line TB drugs, the extent and impact of adverse effects including skin discolouration and cardiotoxicity are not well understood and together with emergent resistance, may undermine clofazimine use in DR-TB programmes. Furthermore, clofazimine's precise mechanism of action is not well established, as is the genetic basis of clofazimine resistance. In this narrative review, we present an overview of the evidence base underpinning the use and limitations of clofazimine as an antituberculosis drug and discuss advances in the

understanding of clofazimine pharmacokinetics, toxicity, and resistance. The unusual pharmacokinetic properties of clofazimine and how these relate to its putative mechanism of action, antituberculosis activity, dosing considerations and adverse effects are highlighted. Finally, we discuss the development of novel riminophenazine analogues as antituberculosis drugs.

Epidemiological characteristics of nontuberculous mycobacteriosis and bronchiectasis: comparative study using national mortality statistics from 1970 to 2015 in Japan.

Morimoto K, Iwai K, Yoshiyama T, Ito M, Uesugi F, Asakura T, Osawa T, Furuuchi K, Kurashima A, Fujiwara K, Hasegawa N, Tanaka Y, Shoji K, Shiraishi Y, Mitarai S, Ato M, Ohta K.

20-02-2023

ERJ Open Res.

<https://pubmed.ncbi.nlm.nih.gov/36814552/>

Background: This study assessed longitudinal national data on mortality due to nontuberculous mycobacteriosis (NTMosis) and bronchiectasis and the association between the two diseases. **Methods:** We analysed the national death statistics of Japan from 1970 to 2015. The International Classification of Disease (ICD) codes were used to extract the relevant data. Crude mortality, age-adjusted mortality and standardised mortality rates were calculated using vital statistics and the population in 2000. We also identified domestic publications related to NTMosis and bronchiectasis with an internet-based search system. **Results:** The total number of bronchiectasis-related deaths remained at the same level, which was approximately 1000, for 45 years, although the number of deaths has consistently decreased in males but increased in females since the mid-1990s. A substantial increasing trend in females was also observed for NTMosis in the same period. The age-adjusted mortality data showed an increase in mortality in women due to NTMosis and confirmed the trend in bronchiectasis in women. The patterns in the number of domestic reports showed a recent slight increase in bronchiectasis and a marked increase in NTMosis. **Conclusions:** The trends in bronchiectasis-related mortality differed by sex. The epidemiological trends in the two diseases were associated, especially in elderly females since the mid-1990s. It is suggested that pulmonary NTMosis without pre-existing bronchiectasis might be a leading cause of postinfectious bronchiectasis in Japan.

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

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

21-02-2023

Indian Pediatr.

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

Buruli ulcer caused by *Mycobacterium ulcerans* subsp. *shinshuense*: A case report.

Fujimori T, Hagiya H, Iio K, Yamasaki O, Miyamoto Y, Hoshino Y, Kakehi A, Okura M, Minabe H, Yokoyama Y, Otsuka F, Higashikage A.

21-02-2023

J Infect Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36813163/>

Dermatological adverse drug reactions to tyrosine kinase inhibitors: a narrative review.

Das A, Sil A, Khan IA, Bandyopadhyay D.

20-02-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36806485/>

Tyrosine kinase inhibitors (TKIs) target the signal transduction pathways of protein kinases by several modes of inhibition. Adverse effects are generally dose-dependent, with certain side effects unique to each drug. However, due to similarities in target sites, different classes of TKIs may have identical or overlapping side effect profiles. This narrative review is an attempt to summarize the common and uncommon adverse effects of different classes of tyrosine kinase inhibitors.

A perspective into "TEL" - Tenofovir, Emtricitabine, and Lamivudine antileprotic activities by drug repurposing and exploring the possibility of combination chemotherapy with drug rescued molecules for a leprosy free mankind.

Thangaraju P, T Y SS, Vijayakumar AR, Navabshan I, Ansari T.

20-02-2023

Recent Adv Antiinfect Drug Discov.

<https://pubmed.ncbi.nlm.nih.gov/36803758/>

Relapsing donovanosis rhyming with unexplained decline in CD4 count in a person living with HIV/AIDS: Long-term follow up and therapeutic outcome.

Sinha S, Sardana K, Agarwal A, Ahuja A.

20-02-2023

Int J STD AIDS.

Donovanosis is a chronic genital ulcerative disease caused by the intracellular Gram-negative bacterium *Klebsiella granulomatis*, reported more frequently in people living with HIV/AIDS (PLHA). Here we present a case of relapsing donovanosis in a PLHA on second line antiretroviral therapy who had episodes of transient unexplained decrease in CD4 counts associated with rapid growth of the lesion and non-responsiveness to treatment followed by clinical resolution coinciding with recovery of the CD4 count.

<https://pubmed.ncbi.nlm.nih.gov/36802827/>

The "Hand as Foot" teaching method in the leprosy.

Bai S, Lv X, Wang R, Liu H.

18-02-2023

Asian J Surg.

<https://pubmed.ncbi.nlm.nih.gov/36801188/>

Establishing a standard method for analysing case detection delay in leprosy using a Bayesian modelling approach.

Hambridge T, Coffeng LE, de Vlas SJ, Richardus JH.

20-02-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/36800979/>

Leprosy among new child cases in China: Epidemiological and clinical analysis from 2011 to 2020.

Peng J, Sun P, Wang L, Wang H, Long S, Yu MW.

17-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36800375/>

Background: Leprosy, caused by *Mycobacterium leprae* infection, mainly affects skin and peripheral nerves and may further lead to disability and deformity if not treated timely. The new case detection rate of leprosy in children reflects the active transmission of leprosy infection. This study aims to present the epidemiology and clinical characteristics of new leprosy cases in children in China from 2011 to 2020. **Methodology/principal findings:** All data from leprosy patients younger than 15 years old were extracted from the Leprosy Management Information System in China (LEPMIS). Statistical Package for the Social Sciences (SPSS) version 12.0 was used for descriptive and analytical statistics of the epidemiological and clinical indicators by the Mann-Whitney test, Kruskal-Wallis test, and Fisher's exact test. And geographical distribution was analyzed by ArcGIS 10.5. A total of 152 pediatric new cases of leprosy were found over the last decade. The new case detection rate of pediatric leprosy cases decreased from 0.13 to 0.02 per 1,000,000 population over the last ten years. New pediatric cases had a higher new case detection rate in Guizhou, Sichuan, and Yunnan Provinces. All but 7 provinces in China achieved zero new child case for consecutive five years. The onset of leprosy peaked between 10 and 14 years of age, and the male to female ratio was 1.71:1. Pediatric patients were predominantly infected from symptomatic household adult contacts HHs. Multibacillary leprosy (MB) was the most common. However, a low proportion of patients developed leprosy reaction and grade 2 disability. **Conclusions/significance:** The new case detection rate of pediatric leprosy cases has decreased over the past ten years in China. Spatial analysis indicated clusters in high-endemic areas. Leprosy transmission has stopped in the majority of provinces in China. However, sporadic cases may continue to exist for a long time. Active surveillance especially contact tracing should be focused on in future plan for management of leprosy, and interventions in leprosy clusters should be prioritized.

Efficacy of autologous Platelet-rich plasma therapy versus topical Minoxidil

in men with moderate androgenetic alopecia: A randomized open-label trial.

Balasundaram M, Kumari R, Ramassamy S.

17-02-2023

J Dermatolog Treat.

<https://pubmed.ncbi.nlm.nih.gov/36800229/>

Erythema annulare centrifugum trailing behind dermatophytosis - Causation or association.

Verma SB, Gopinath N, Vasani R, Muddebihal A, Sardana K.

17-02-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36799107/>

The therapeutic effect of larval saliva and hemolymph of *Lucilia sericata* on the treatment of *Leishmania major* lesion in BALB/c mice946.

Rahimi S, Rafinejad J, Akhavan AA, Ahmadkhaniha R, Bakhtiyari M, Khamesipour A, Akbarzadeh K.

16-02-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36797798/>

Background: Treatment of cutaneous leishmaniasis (CL) remains a major challenge for the public health and medical community. It has been claimed that natural compounds derived from fly larvae have anti-leishmania properties against some species of *Leishmania*. The present study aimed at assessing the in vitro effects of larval products of *Lucilia sericata* against the promastigote and intracellular amastigote forms of *Leishmania major*. Also, the therapeutic effect of larval products on lesions induced by *L. major* infection was evaluated in BALB/c mice models. **Methods:** Parasite specimens and macrophage cells were exposed to varying concentrations of larval products for 24-120 h. Lesion progression and parasite load were investigated in the models to assess the therapeutic effects of the products. **Results:** The larval products displayed more potent cytotoxicity against *L. major* promastigotes. The IC_{50} values for larval saliva and hemolymph were 100.6 and 37.96 μ g/ml, respectively. The IC_{50} of glucantime was 9.480 μ g/ml. Also, the saliva and hemolymph of *L. sericata* exhibited higher cytotoxicity against the promastigotes of *L. major* but were less toxic to the macrophage cells. Treatment with leishmanicidal agents derived from larvae of *L. sericata* decreased the infection rate and the number of amastigotes per infected host cell at all concentrations. Lesion size was significantly ($F_{(7, 38)} = 8.54$, $P < 0.0001$) smaller in the treated mice compared with the untreated control group. The average parasite burden in the treated mice groups (1.81 ± 0.74 , 1.03 ± 0.45 and 3.37 ± 0.41) was similar to the group treated with a daily injection of glucantime (1.77 ± 0.99) and significantly lower ($F_{(7, 16)} = 66.39$, $P < 0.0001$) than in the untreated control group (6.72 ± 2.37). **Conclusions:** The results suggest that the larval products of *L. sericata* were effective against *L. major* parasites both in vivo and in vitro. However, more clinical trial studies are

recommended to evaluate the effects of these larval products on human subjects.

Trypanosomes (trypanosomiasis et maladie de Chagas)

Epidemiological indicators of Chagas disease in the metropolitan region of Salvador, Bahia, Brazil.

Lanza FC, Ribeiro-Jr G, Miranda DLP, Santos FLN, Carvalho CMM, Cunha GM, Carneiro IO, Reis RB, Cunha JMA, Cardoso CW, Soares JFS, Araújo FLV, Reis MG.

20-02-2023

Rev Soc Bras Med Trop.

<https://pubmed.ncbi.nlm.nih.gov/36820652/>

Background: Chagas disease (CD) is caused by *Trypanosoma cruzi* and transmitted by triatomines. Historical information from the 20th century demonstrates *T. cruzi* records in the metropolitan region of Salvador (MRS), the third largest urban agglomeration in the Brazilian Northeast and the eighth largest in Brazil, an area with intense migratory activity from CD-endemic regions. Therefore, this study aimed to evaluate CD indicators (prevalence and mortality) in the MRS. **Methods:** A mixed ecological and descriptive study was conducted using secondary data. We analyzed data from 2008 to 2015: deaths due to CD, self-reported cases of CD, and blood donors that were non-negative for *T. cruzi* infection. **Results:** São Francisco do Conde was one of the municipalities with the highest mortality rates due to CD. The seroprevalence rates varied by year and municipality; those with the highest values were 2008: Vera Cruz, 2009: Mata de São João, 2010: Dias D'Ávila, 2011 and 2015: São Francisco do Conde, 2012: São Sebastião do Passé, and 2013 and 2014: Pojuca. Spatial correlations between the municipalities were not detected. **Conclusions:** We conclude that CD is present in the MRS. The indicators analyzed in the MRS are below-state-level data. Given the importance of indicator analysis for the surveillance and control of CD at the state and national levels, it is important to strengthen the surveillance program at the municipal level, including the regions classified as low risk for *T. cruzi* vector transmission.

piRNA pathway evolution beyond gonad context: Perspectives from apicomplexa and trypanosomatids.

Horjales S, Li Calzi M, Francia ME, Cayota A, Garcia-Silva MR.

03-02-2023

Front Genet.

<https://pubmed.ncbi.nlm.nih.gov/36816026/>

Cardiomyocyte infection by *Trypanosoma cruzi* promotes innate immune response and glycolysis activation.

Venturini G, Alvim JM, Padilha K, Toepfer CN, Gorham JM, Wasson LK, Biagi D, Schenkman S, Carvalho VM, Salgueiro JS, Cardozo KHM, Krieger JE, Pereira AC, Seidman JG, Seidman CE.

06-02-2023

Front Cell Infect Microbiol.

Introduction: Chagas cardiomyopathy, a disease caused by *Trypanosoma cruzi* (*T. cruzi*) infection, is a major contributor to heart failure in Latin America. There are significant gaps in our understanding of the mechanism for infection of human cardiomyocytes, the pathways activated during the acute phase of the disease, and the molecular changes that lead to the progression of cardiomyopathy. **Methods:** To investigate the effects of *T. cruzi* on human cardiomyocytes during infection, we infected induced pluripotent stem cell-derived cardiomyocytes (iPSC-CM) with the parasite and analyzed cellular, molecular, and metabolic responses at 3 hours, 24 hours, and 48 hours post infection (hpi) using transcriptomics (RNAseq), proteomics (LC-MS), and metabolomics (GC-MS and Seahorse) analyses. **Results:** Analyses of multiomic data revealed that cardiomyocyte infection caused a rapid increase in genes and proteins related to activation innate and adaptive immune systems and pathways, including alpha and gamma interferons, HIF-1 α signaling, and glycolysis. These responses resemble prototypic responses observed in pathogen-activated immune cells. Infection also caused an activation of glycolysis that was dependent on HIF-1 α signaling. Using gene editing and pharmacological inhibitors, we found that *T. cruzi* uptake was mediated in part by the glucose-facilitated transporter GLUT4 and that the attenuation of glycolysis, HIF-1 α activation, or GLUT4 expression decreased *T. cruzi* infection. In contrast, pre-activation of pro-inflammatory immune responses with LPS resulted in increased infection rates. **Conclusion:** These findings suggest that *T. cruzi* exploits a HIF-1 α -dependent, cardiomyocyte-intrinsic stress-response activation of glycolysis to promote intracellular infection and replication. These chronic immuno-metabolic responses by cardiomyocytes promote dysfunction, cell death, and the emergence of cardiomyopathy.

A functional assay using human whole blood and flow cytometry analysis to evaluate cytotoxicity and immunomodulatory effect of anti-*Trypanosoma cruzi* drugs.

Lopes MEASA, Ribeiro JM, Teixeira-Carvalho A, Murta SMF, Souza-Fagundes EM.

19-02-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36809831/>

The discovery and development of new drugs for the treatment of Chagas disease is urgent due to the high toxicity and low cure efficacy, mainly during the chronic phase of this disease. Other chemotherapeutic approaches for Chagas disease treatment are being researched and require screening assays suitable for evaluating the effectivity of new biologically active compounds. This study aims to evaluate a functional assay using the internalization of epimastigotes forms of

Trypanosoma cruzi by human peripheral blood leukocytes from healthy volunteers and analyses by flow cytometry of cytotoxicity, anti-*T. cruzi* activity, and immunomodulatory effect of benznidazole, ravuconazole, and posaconazole. The culture supernatant was used to measure cytokines (IL-1 β , IL-6, INF- γ , TNF and IL-10) and chemokines (MCP-1/CCL2, CCL5/RANTES and CXCL8/IL-8). The data showed a reduction in the internalization of *T. cruzi* epimastigote forms treated with ravuconazole, demonstrating its potential anti-*T. cruzi* activity. In addition, an increased amount of IL-10 and TNF cytokines was observed in the supernatant of cultures upon the addition of the drug, mainly IL-10 in the presence of benznidazole, ravuconazole and posaconazole, and TNF in the presence of ravuconazole and posaconazole. Moreover, the results revealed a decrease in the MCP-1/CCL2 index in cultures in the presence of benznidazole, ravuconazole, and posaconazole. A decrease in the CCL5/RANTES and CXCL8/IL-8 index in cultures with BZ, when compared to the culture without drugs, was also observed. In conclusion, the innovative functional test proposed in this study may be a valuable tool as a confirmatory test for selecting promising compounds identified in prospecting programs for new drugs for Chagas disease treatment.

Design, synthesis and biological evaluations of quinolone amides against African trypanosomiasis with improved solubility.

Weinmann J, Kirchner L, Engstler M, Meinel L, Holzgrabe U.

06-02-2023

Eur J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/36805945/>

Structure-activity relationship study of antitrypanosomal analogues of gibbilibol B using multivariate analysis and computation-aided drug design.

Leão LPMO, de B Vieira N, Oliveira PPS, Chagas-Paula DA, Soares MG, Souza TB, Baldim JL, Costa-Silva TA, Tempone AG, Dias DF, Lago JHG.

19-02-2023

Bioorg Med Chem Lett.

<https://pubmed.ncbi.nlm.nih.gov/36805048/>

Genome-wide subcellular protein map for the flagellate parasite *Trypanosoma brucei*.

Billington K, Halliday C, Madden R, Dyer P, Barker AR, Moreira-Leite FF, Carrington M, Vaughan S, Hertz-Fowler C, Dean S, Sunter JD, Wheeler RJ, Gull K.

20-02-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36804636/>

Structural screens identify candidate human homologs of insect chemoreceptors and cryptic *Drosophila* gustatory receptor-like proteins.

Benton R, Himmel NJ.

20-02-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/36803935/>

Insect Odorant receptors and Gustatory receptors define a superfamily of seven-transmembrane domain ligand-gated ion channels (referred to here as 7TMICs), with homologs identified across Animalia except Chordata. Previously, we used sequence-based screening methods to reveal conservation of this family in unicellular eukaryotes and plants (DUF3537 proteins) (Benton *et al.*, 2020). Here we combine three-dimensional structure-based screening, *ab initio* protein folding predictions, phylogenetics and expression analyses to characterize additional candidate homologs with tertiary but little or no primary structural similarity to known 7TMICs, including proteins in disease-causing Trypanosoma. Unexpectedly, we identify structural similarity between 7TMICs and PHTF proteins, a deeply-conserved family of unknown function, whose human orthologs display enriched expression in testis, cerebellum and muscle. We also discover divergent groups of 7TMICs in insects, which we term the Gustatory receptor-like (Grl) proteins. Several *Drosophila melanogaster* Grls display selective expression in subsets of taste neurons, suggesting that they are previously-unrecognized insect chemoreceptors. Although we cannot exclude the possibility of remarkable structural convergence, our findings support the origin of 7TMICs in a eukaryotic common ancestor, counter previous assumptions of complete loss of 7TMICs in Chordata, and highlight the extreme evolvability of this protein fold, which likely underlies its functional diversification in different cellular contexts.

Experimental and Computational Study of Aryl-thiosemicarbazones Inhibiting Cruzain Reveals Reversible Inhibition and a Stepwise Mechanism.

Martins LC, de Oliveira RB, Lameira J, Ferreira RS.

20-02-2023

J Chem Inf Model.

<https://pubmed.ncbi.nlm.nih.gov/36802548/>

Circular mitochondrial-encoded mRNAs are a distinct subpopulation of mitochondrial mRNA in Trypanosoma brucei.

Smoniewski CM, Borujeni PM, Petersen A, Hampton M, Salavati R, Zimmer SL.

10-02-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/36798374/>

Translational control by Trypanosoma brucei DRBD18 contributes to the maintenance of the procyclic state.

Ciganda M, Sotelo-Silveira J, Smith JT, Shen S, Qu J, Smircich P, Read LK.

10-02-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/36798237/>

A volatile sex attractant of tsetse flies.

Ebrahim SAM, Dweck HKM, Weiss BL, Carlson JR.

17-02-2023

Science.

<https://pubmed.ncbi.nlm.nih.gov/36795837/>

Tsetse flies transmit trypanosomes-parasites that cause devastating diseases in humans and livestock-across much of sub-Saharan Africa. Chemical communication through volatile pheromones is common among insects; however, it remains unknown if and how such chemical communication occurs in tsetse flies. We identified methyl palmitoleate (MPO), methyl oleate, and methyl palmitate as compounds that are produced by the tsetse fly *Glossina morsitans* and elicit strong behavioral responses. MPO evoked a behavioral response in male-but not virgin female-*G. morsitans*. *G. morsitans* males mounted females of another species, *Glossina fuscipes*, when they were treated with MPO. We further identified a subpopulation of olfactory neurons in *G. morsitans* that increase their firing rate in response to MPO and showed that infecting flies with African trypanosomes alters the flies' chemical profile and mating behavior. The identification of volatile attractants in tsetse flies may be useful for reducing disease spread.

Textile wastewater phytoremediation using Spirodela polyrhiza (L.) Schleid. assisted by novel bacterial consortium in a two-step remediation system.

Parihar A, Malaviya P.

15-03-2023

Environ Res.

<https://pubmed.ncbi.nlm.nih.gov/36657596/>

Leishmaniose

The enemy within: lipid asymmetry in intracellular parasite-host interactions.

Fraser M, Matuschewski K, Maier AG.

23-02-2023

Emerg Top Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/36820809/>

Eukaryotic pathogens with an intracellular parasitic lifestyle are shielded from extracellular threats during replication and growth. In addition to many nutrients, parasites scavenge host cell lipids to establish complex membrane structures inside their host cells. To counteract the disturbance of the host cell plasma membrane they have evolved strategies to regulate phospholipid asymmetry. In this review, the function and importance of lipid asymmetry in the interactions of intracellular protozoan parasites with the target and immune cells of the host are highlighted. The malaria parasite Plasmodium infects red blood cells and extensively refurbishes these terminally differentiated cells. Cholesterol depletion and an altered intracellular calcium ion homeostasis can lead to disruption in erythrocyte membrane asymmetry and increased exposure of phosphatidylserine (PS). Binding to the PS receptor on monocytes and macrophages results in phagocytosis and destruction of infected erythrocytes.

Leishmania parasites display apoptotic mimicry by actively enhancing PS exposure on their surface to trigger increased infection of macrophages. In extracellular *Toxoplasma gondii* a P4-type ATPase/CDC50 co-chaperone pair functions as a flippase important for exocytosis of specialised secretory organelles. Identification and functional analysis of parasite lipid-translocating proteins, i.e. flippases, floppases, and scramblases, will be central for the recognition of the molecular mechanisms of parasite/host interactions. Ultimately, a better understanding of parasitic diseases, host immunity, and immune escape by parasites require more research on the dynamics of phospholipid bilayers of parasites and the infected host cell.

Discovery of pyrazolopyrrolidinones as potent, broad-spectrum inhibitors of Leishmania infection.

Kavouris JA, McCall LI, Giardini MA, De Muylder G, Thomas D, Garcia-Pérez A, Cantizani J, Cotillo I, Fiandor JM, McKerrow JH, De Oliveira CI, Siqueira-Neto JL, González S, Brown LE, Schaus SE.

2023

Front Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36818551/>

Discovery of pyrazolopyrrolidinones as potent, broad-spectrum inhibitors of Leishmania infection.

Kavouris JA, McCall LI, Giardini MA, De Muylder G, Thomas D, Garcia-Pérez A, Cantizani J, Cotillo I, Fiandor JM, McKerrow JH, De Oliveira CI, Siqueira-Neto JL, González S, Brown LE, Schaus SE.

2023

Front Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36818551/>

Introduction: Leishmaniasis is a parasitic disease that affects more than 1 million people worldwide annually, predominantly in resource-limited settings. The challenge in compound development is to exhibit potent activity against the intracellular stage of the parasite (the stage present in the mammalian host) without harming the infected host cells. We have identified a compound series (pyrazolopyrrolidinones) active against the intracellular parasites of *Leishmania donovani* and *L. major*; the causative agents of visceral and cutaneous leishmaniasis in the Old World, respectively. **Methods:** In this study, we performed medicinal chemistry on a newly discovered antileishmanial chemotype, with over 100 analogs tested. Studies included assessments of antileishmanial potency, toxicity towards host cells, and in vitro ADME screening of key drug properties. **Results and discussion:** Members of the series showed high potency against the deadliest form, visceral leishmaniasis (approximate $EC_{50} \geq 0.01 \mu M$ without harming the host macrophage up to $10.0 \mu M$). In comparison, the most efficient monotherapy treatment for visceral leishmaniasis is amphotericin B, which presents similar activity in the same assay ($EC_{50} = 0.2 \mu M$) while being cytotoxic to the host cell at $5.0 \mu M$. Continued development of this compound series with the Discovery Partnership with Academia (DPAC) program at the

GlaxoSmithKline Diseases of the Developing World (GSK DDW) laboratories found that the compounds passed all of GSK's criteria to be defined as a potential lead drug series for leishmaniasis. **Conclusion:** Here, we describe preliminary structure-activity relationships for antileishmanial pyrazolopyrrolidinones, and our progress towards the identification of candidates for future in vivo assays in models of visceral and cutaneous leishmaniasis.

Calomyscid Rodents (Rodentia: Calomyscidae) as a Potential Reservoir of Zoonotic Cutaneous Leishmaniasis in a Mountainous Residential Area in the Plateau of Iran: Inferring from Molecular Data of kDNA and ITS2 Genes of Leishmania Major.

Shahabi S, Azizi K, Asgari Q, Sarkari B.

10-02-2023

J Trop Med.

<https://pubmed.ncbi.nlm.nih.gov/36817555/>

Cutaneous leishmaniasis (CL), a neglected tropical disease, is an important health problem in Fars Province, southern Iran. Fars, the fourth most populous Province in Iran, is the center of both anthroponotic and zoonotic cutaneous leishmaniasis (ZCL). Rodents, the reservoir of *Leishmania major*, play an important role in transmitting ZCL. In the present study, we report *Leishmania* infection in calomyscid rodents for the first time in mountainous residential areas of Shiraz, the capital of Fars Province, in southern Iran. Rodents were trapped in urban mountainous areas. The skin, liver, and spleen of rodents were examined microscopically for *Leishmania* infection. In addition, DNA was extracted from the tissues and they were evaluated for *Leishmania* infection by targeting the kDNA and subsequent sequencing of the nuclear rDNA internal transcribed spacer two (ITS2) region. DNA of *L. major* was detected in the spleen and liver of calomyscid rodents. Molecular evolution based on DNA-sequencing of the ITS2 gene confirmed the taxonomic situation of the parasite as *L. major*. Our findings suggest the eco-epidemiological importance of calomyscid rodents in the foci of leishmaniasis in the mountainous residential area on the plateau of Iran. These rodents may play a role in the transmission of leishmaniasis in a residential area and could be considered a potential reservoir for CL.

Leishmaniasis: Recent epidemiological studies in the Middle East.

Knight CA, Harris DR, Alshammari SO, Gugssa A, Young T, Lee CM.

02-02-2032

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36817103/>

Sergentomyia species identification and their screening for possible infection to Leishmania spp. in Kaleybar, East-Azerbaijan province, Iran.

Firouzjaie F, Moin Vaziri V, Zahraei-Ramazani A, Behniafar H, Badakhshan M, Spotin A, Zarei Z.

2023

The paradigm of intracellular parasite survival and drug resistance in leishmanial parasite through genome plasticity and epigenetics: Perception and future perspective.

Kamran M, Bhattacharjee R, Das S, Mukherjee S, Ali N.
06-02-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36814446/>

Leishmania is an intracellular, zoonotic, kinetoplastid eukaryote with more than 1.2 million cases all over the world. The leishmanial chromosomes are divided into polymorphic chromosomal ends, conserved central domains, and antigen-encoding genes found in telomere-proximal regions. The genome flexibility of chromosomal ends of the leishmanial parasite is known to cause drug resistance and intracellular survival through the evasion of host defense mechanisms. Therefore, in this review, we discuss the plasticity of *Leishmania* genome organization which is the primary cause of drug resistance and parasite survival. Moreover, we have not only elucidated the causes of such genome plasticity which includes aneuploidy, epigenetic factors, copy number variation (CNV), and post-translation modification (PTM) but also highlighted their impact on drug resistance and parasite survival.

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

Rguez S, Essid R, Bettaieb I, Bourgou S, Hammami M, Hamrouni Sellami I.

22-02-2023

Acta Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36810938/>

Leishmaniasis: Omics approaches to understand its biology from molecule to cell level.

Kumari I, Lakhanpal D, Swargam S, Nath Jha A.
10-02-2023

Curr Protein Pept Sci.

<https://pubmed.ncbi.nlm.nih.gov/36809951/>

Leishmaniasis is the second deadliest vector-borne, neglected tropical zoonotic disease and is found in a variety of clinical forms based on genetic background. Its endemic type is present in tropical, sub-tropical and Mediterranean areas around the world which accounts for a lot of deaths every year. Currently, a variety of techniques are present to detect leishmaniasis with advantages and disadvantages. The advancing next-generation sequencing (NGS) techniques are employed to find out novel diagnostic markers based on single nucleotide variants. Total 274 NGS studies are available in European Nucleotide Archive (ENA) portal (<https://www.ebi.ac.uk/ena/browser/home>) that focused

on wild-type and mutated *Leishmania*, differential gene expression, miRNA expression, and detection of aneuploidy mosaicism by omics approaches. These studies have provided insights into the population structure, virulence, and extensive structural variation, including known and suspected drug resistance loci, mosaic aneuploidy and hybrid formation under stressed conditions and inside the midgut of the sandfly. The complex interactions occurring within the parasite-host-vector triangle can be better understood by omics approaches. Further, advanced CRISPR technology allows researchers to delete and modify each gene individually to know the importance of genes in the virulence and survival of the disease-causing protozoa. In vitro Generation of *Leishmania*, hybrids are helping to understand the mechanism of disease progression in its different stages of infection. This review will give a comprehensive picture of the available omics data of various *Leishmania* spp. which helped to reveal the effect of climate change on the spread of its vector, the pathogen survival strategies, emerging antimicrobial resistance and its clinical importance.

Data-driven predictions of potential Leishmania vectors in the Americas.

Vadmal GM, Glidden CK, Han BA, Carvalho BM, Castellanos AA, Mordecai EA.

21-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36809249/>

The incidence of vector-borne diseases is rising as deforestation, climate change, and globalization bring humans in contact with arthropods that can transmit pathogens. In particular, incidence of American Cutaneous Leishmaniasis (ACL), a disease caused by parasites transmitted by sandflies, is increasing as previously intact habitats are cleared for agriculture and urban areas, potentially bringing people into contact with vectors and reservoir hosts. Previous evidence has identified dozens of sandfly species that have been infected with and/or transmit *Leishmania* parasites. However, there is an incomplete understanding of which sandfly species transmit the parasite, complicating efforts to limit disease spread. Here, we apply machine learning models (boosted regression trees) to leverage biological and geographical traits of known sandfly vectors to predict potential vectors. Additionally, we generate trait profiles of confirmed vectors and identify important factors in transmission. Our model performed well with an average out of sample accuracy of 86%. The models predict that synanthropic sandflies living in areas with greater canopy height, less human modification, and within an optimal range of rainfall are more likely to be *Leishmania* vectors. We also observed that generalist sandflies that are able to inhabit many different ecoregions are more likely to transmit the parasites. Our results suggest that *Psychodopygus amazonensis* and *Nyssomia antunesi* are unidentified potential vectors, and should be the focus of sampling and research efforts. Overall, we found that our machine learning approach provides valuable information for *Leishmania* surveillance and management in an otherwise complex and data sparse system.

The new way to identify Leishmania amastigotes in peripheral blood smear using digital cell morphology instrument.

Zhang W, Lei N, Xu Y, Wang Y, Chen S, Wang T, Zhang L.
18-02-2023

Int J Lab Hematol.

<https://pubmed.ncbi.nlm.nih.gov/36808880/>

Role of Brazilian bats in the epidemiological cycle of potentially zoonotic pathogens.

Castelo-Branco DSCM, Nobre JA, Souza PRH, Diógenes EM, Guedes GMM, Mesquita FP, Souza PFN, Rocha MFG, Sidrim JJC, Cordeiro RA, Montenegro RC.

17-02-2023

Microb Pathog.

<https://pubmed.ncbi.nlm.nih.gov/36804526/>

Drug resistance in Leishmania: does it really matter?

Domagalska MA, Barrett MP, Dujardin JC.

16-02-2023

Trends Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36803859/>

Treatment failure (TF) jeopardizes the management of parasitic diseases, including leishmaniasis. From the parasite's point of view, drug resistance (DR) is generally considered as central to TF. However, the link between TF and DR, as measured by in vitro drug susceptibility assays, is unclear, some studies revealing an association between treatment outcome and drug susceptibility, others not. Here we address three fundamental questions aiming to shed light on these ambiguities. First, are the right assays being used to measure DR? Second, are the parasites studied, which are generally those that adapt to in vitro culture, actually appropriate? Finally, are other parasite factors - such as the development of quiescent forms that are recalcitrant to drugs - responsible for TF without DR?

Canine leishmaniosis in a non-travelled dog.

McGrotty Y, Kilpatrick S, Magowan D, Colville R.

FEB-2023

Vet Rec.

<https://pubmed.ncbi.nlm.nih.gov/36799573/>

The skin microbiome enhances disease through IL-1b and delays healing in cutaneous leishmaniasis patients.

Farias Amorim C, Lovins VM, Singh TP, Novais FO, Harris JC, Lago AS, Carvalho LP, Carvalho EM, Beiting DP, Scott P, Grice EA.

06-02-2023

medRxiv.

<https://pubmed.ncbi.nlm.nih.gov/36798406/>

Leishmania braziliensis infection results in inflammation and skin injury, with highly variable and unpredictable clinical outcomes. Here, we investigated the potential

impact of microbiota on infection-induced inflammatory responses and disease resolution by conducting an integrated analysis of the skin microbiome and host transcriptome on a cohort of 62 *L. braziliensis* -infected patients. We found that overall bacterial burden and microbiome configurations dominated with *Staphylococcus* spp. were associated with delayed healing and enhanced inflammatory responses, especially by IL-1 family members. Dual RNA-seq of human lesions revealed that high lesional *S. aureus* transcript abundance was associated with delayed healing and increased expression of IL-1 β . This cytokine was critical for modulating disease outcome in *L. braziliensis* -infected mice colonized with *S. aureus*, as its neutralization reduced pathology and inflammation. These results implicate the microbiome in cutaneous leishmaniasis disease outcomes in humans and suggest host-directed therapies to mitigate the inflammatory consequences.

The therapeutic effect of larval saliva and hemolymph of *Lucilia sericata* on the treatment of *Leishmania major* lesion in BALB/c mice⁹⁴⁶.

Rahimi S, Rafinejad J, Akhavan AA, Ahmadkhaniha R, Bakhtiyari M, Khamesipour A, Akbarzadeh K.

16-02-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36797798/>

Variants of NOD2 in *Leishmania guyanensis*-infected patients with cutaneous leishmaniasis and correlations with plasma circulating pro-inflammatory cytokines.

Mesquita TGR, Junior JDES, Souza JL, Silva LSD, Nascimento TAD, Souza MLG, Guerra MVF, Ramasawmy R.

16-02-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36795715/>

Efficacy of intralesional meglumine antimoniate in the treatment of canine tegumentary leishmaniasis: A Randomized controlled trial.

Lago J, Fraga D, Guimarães LH, Lago T, Santos Y, Lago E, Werneck GL, Bacellar O, Carvalho EM.

15-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36791065/>

Dogs living in areas of *Leishmania (Viannia) braziliensis* transmission may present canine tegumentary leishmaniasis (CTL) characterized by cutaneous or muzzle ulcers as well as asymptomatic *L. braziliensis* infection. It is not clear if dogs participate in the transmission chain of *L. braziliensis* to humans. However, dogs may remain with chronic ulcers for a long time, and as there are no public policies about CTL, these animals die or are sacrificed. Here we compare the efficacy of intralesional meglumine antimoniate with intralesional 0.9% NaCl solution in CTL treatment. This randomized control study included 32

dogs with cutaneous or muzzle lesions who had *L. braziliensis* DNA detected by PCR in tissue biopsied. Group one received 5ml of intralesional Glucantime, and group two received 5ml 0.9% NaCl solution, both applied in the four cardinal points on days 0, 15, and 30. Cure was defined as complete healing of the ulcers in the absence of raised borders on day 90. There was no difference in animals' demographic and clinical features in the two groups ($p > .05$). While at the endpoint, the cure rate was 87.5% in the group test, and in those who received 0.9 NaCl the cure rate was only 12.5%. As important as the high cure rate, the healing time was faster in dogs treated with antimony than in those treated with saline ($p < .001$). Intralesional meglumine antimoniate is effective in the treatment of dogs with *L. braziliensis* infection and accelerates the healing time of CTL.

Role of antigen-presenting cells in non-ulcerated skin lesions caused by *Leishmania (Leishmania) infantum chagasi*.

Sandoval Pacheco CM, Araujo Flores GV, Ferreira AF, da Matta VLR, de Castro Gomes CM, Sosa-Ochoa WH, Zúniga C, Silveira FT, Corbett CEP, Laurenti MD.

Mar-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36695719/>

In Central America, infection by *Leishmania (Leishmania) infantum chagasi* causes visceral leishmaniasis and non-ulcerated cutaneous leishmaniasis (NUCL). This work aimed to evaluate the participation of subpopulations of antigen-presenting cells in skin lesions of patients affected by NUCL through double-staining immunohistochemistry using cellular and intracellular markers. Twenty-three skin biopsies from patients affected by NUCL were used. Histological sections stained by HE were used for histopathological study. Immunohistochemical studies were performed using primary antibodies against Langerhans cells, dermal dendritic cells, T lymphocytes, and the cytokines IL-12, IFN- γ , TNF- α , iNOS, and IL-10. The histopathological lesions were characterized by an inflammatory infiltrate, predominantly lymphohistiocytic, of variable intensity, with a diffuse arrangement associated with epithelioid granulomas and discreet parasitism. Double-staining immunohistochemistry showed higher participation of dendritic cells producing the proinflammatory cytokine IL-12 in relation to the other evaluated cytokines. Activation of the cellular immune response was marked by a higher density of CD8 Tc1-lymphocytes followed by CD4 Th1-lymphocytes producing mainly IFN- γ . The data obtained in the present study suggest that antigen-presenting cells play an important role in the in situ immune response through the production of proinflammatory cytokines, directing the cellular immune response preferentially to the Th1 and Tc1 types in NUCL caused by *L. (L.) infantum chagasi*.

Chemokine receptors on human regulatory T cells during cutaneous leishmaniasis.

Brelaz de Castro MCA, de Freitas E Silva R, de Andrade Cavalcante MK, Silva LLSB, Santos Dos Gomes FO, de Brito MEF, Pereira VRA.

Mar-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36601688/>

Organ-specific immune profiling of *Leishmania donovani*-infected hamsters.

Saini S, Singh B, Dube A, Sahasrabudhe AA, Rai AK.

Mar-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36571298/>

Visceral leishmaniasis (VL) is a neglected disease with a broad spectrum of clinical manifestations and involvement of visceral organs. Organ-specific immune response against the *Leishmania donovani* (Ld) complex is not yet understood due to the unavailability of an appropriate experimental model. In reference to our recent work on comparing the hamster model with VL patients, it is now possible to understand immune profiling in different visceral organs. This may offer an answer to varying parasite loads in different visceral organs in the same host. Herein, we analysed a panel of immune markers (Th-2/Th-1) in visceral organs of Ld-infected hamsters and quantified parasitic load in the same tissues using qPCR assay. In spleen, liver, bone marrow and lymph node (mesenteric) from Ld-infected hamsters, the parasite burden was quantified along with mRNA expression of a panel of Th-2 and Th-1 type immune markers, namely IL-10, IL-4, Arginase-I, GATA-3, SOCS-3, IL-12, IFN- γ , iNOS, T-bet and SOCS-5. A clear dichotomy was absent between Th-2 and Th-1 type immune markers and the major players of this immune response were IFN- γ , IL-10, T-bet, GATA-3, SOCS-5 and SOCS-3.

Serological studies on rK39 negative Visceral Leishmaniasis in an endemic focus of *Leishmania donovani* induced Cutaneous Leishmaniasis.

Deepachandi B, Weerasinghe S, Soysa P, Chatterjee M, Siriwardana Y.

Mar-2023

Diagn Microbiol Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36543026/>

Cysticercose

Spatial and Temporal Distribution of *Taenia solium* and its Risk Factors in Uganda.

Ngwili N, Sentamu DN, Korir M, Adriko M, Beinamaryo P, Dione MM, Moriku Kaducu J, Mubangizi A, Mwinzi PN, Thomas LF, Dixon MA.

15-02-2023

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36805327/>

Background: The lack of sub-national mapping of the zoonotic cestode *Taenia solium* in endemic countries presents a major challenge to achieving intensified *T. solium* control milestones, as outlined in the "World Health Organization neglected tropical disease roadmap by 2030". We conducted a mapping study in Uganda, considered to be endemic, to identify sub-national high-risk areas. **Methods:** *T. solium* prevalence data, adjusted for diagnostic sensitivity and specificity in a Bayesian Framework, were identified through a systematic review. Spatial autocorrelation and interpolation techniques were used to transform Demographic and Health Survey cluster-level sanitation and poverty indicators, overlaid onto a pig density map for Uganda into modelled porcine cysticercosis (PCC) risk maps. **Findings:** Sixteen articles ($n = 11$ PCC and $n = 5$ human cysticercosis (HCC) and/or human taeniasis) were included in the final analysis. HCC observed prevalence ranged from 0.01% - 6.0 % (Confidence Interval (CI) range: 0.004 - 11.4%), while adjusted PCC ranged from 0.3 - 93.9% (uncertainty interval range: 0 - 99.8%). There was substantial variation in the modelled PCC risk factors and prevalence across Uganda and over time. **Interpretation:** High PCC prevalence and moderate HCC exposure estimates indicate the need for urgent implementation of *T. solium* control efforts in Uganda.

Spinal nerve root sleeve cysticercosis: a case report and review of the literature.

Tao B, Li T, Ji K, Shang A.

22-02-2023

J Med Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/36814326/>

Background: Neurocysticercosis is a parasitic infection of the central nervous system by tapeworm larvae. Spinal cysticercosis is thought to be relatively rare, and spinal nerve root sleeve cysticercosis have not been reported previously. **Case presentation:** A 46-year-old Chinese Han female patient presented with low back pain and radicular pain of the right lower limb. The visual analog scale was 6. Magnetic resonance imaging showed a subarachnoid cyst at the S1 level, with a slight enhanced rim. The patient underwent surgical treatment. During surgery, we found the cyst located mainly in the subarachnoid space and partly in a sacral nerve root sleeve. Cysticercosis was also confirmed by postoperative pathological examination. Postoperative drug therapy was performed after cysticercosis was confirmed. Postoperatively, the patient was treated with oral albendazole (15 mg/kg) for 1 month. Only mild sensory impairment was left when she was discharged. After 3 years of follow-up, the visual analog scale reduced from 6 to 2, and the patient's sensory function completely recovered. Magnetic resonance imaging showed no recurrence of cysticercosis. **Conclusion:** Subarachnoid cysticercosis may extend to nerve root sleeve causing back pain and radiculopathy, which may present with similar magnetic resonance imaging manifestations to Tarlov cysts. Hence, spinal subarachnoid cysticercosis should be considered as an important differential diagnosis of arachnoid cyst and sacral Tarlov cyst. Combined treatment with surgical removal and drug therapy is effective to manage spinal subarachnoid cysticercosis.

Echinococcoses

Differential Gene Expression Profiling in Alveolar Echinococcosis Identifies Potential Biomarkers Associated With Angiogenesis.

Yimingjiang M, Aini A, Tuergan T, Zhang W.

31-01-2023

Open Forum Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36817746/>

Current and future distribution of a parasite with complex life cycle under global change scenarios: *Echinococcus multilocularis* in Europe.

Cenni L, Simoncini A, Massetti L, Rizzoli A, Hauffe HC, Massolo A.

23-02-2023

Glob Chang Biol.

<https://pubmed.ncbi.nlm.nih.gov/36815401/>

Global change is expected to have complex effects on the distribution and transmission patterns of zoonotic parasites. Modelling habitat suitability for parasites with complex life cycles is essential to further our understanding of how disease systems respond to environmental changes, and to make spatial predictions of their future distributions. However, the limited availability of high quality occurrence data with high spatial resolution often constrains these investigations. Using 449 reliable occurrence records for *Echinococcus multilocularis* from across Europe published over the last 35 years, we modelled habitat suitability for this parasite, the aetiological agent of alveolar echinococcosis, in order to describe its environmental niche, predict its current and future distribution under three global change scenarios, and quantify the probability of occurrence for each European country. Using a machine learning approach, we developed large-scale (25 × 25 km) species distribution models based on seven sets of predictors, each set representing a distinct biological hypothesis supported by current knowledge of the autecology of the parasite. The best-supported hypothesis included climatic, orographic and land-use/land-cover variables such as the temperature of the coldest quarter, forest cover, urban cover and the precipitation seasonality. Future projections suggested the appearance of highly suitable areas for *E. multilocularis* towards northern latitudes and in the whole Alpine region under all scenarios, while decreases in habitat suitability were predicted for central Europe. Our spatially explicit predictions of habitat suitability shed light on the complex responses of parasites to ongoing global changes.

Central nervous system hydatidosis around the world: a systematic review.

Pour-Rashidi A, Turgut M, Fallahpour M, Mohammadi E, Hanaei S, Rezaei N.

20-02-2023

J Neurosurg Sci.

<https://pubmed.ncbi.nlm.nih.gov/36800683/>

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

Williams LBA, Walzthoni N.

17-02-2023

J Am Vet Med Assoc.

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

Objective: To describe the clinical disease, diagnostic findings, medical management, and outcome in dogs with alveolar echinococcosis (AE). **Animals:** 4 dogs with naturally occurring AE. **Procedures:** Medical records were retrospectively reviewed from 2020 to 2022 to identify dogs diagnosed with AE. Signalment, case history, clinical signs, imaging and pathological laboratory findings, treatment, and clinical outcome were reported. **Results:** All dogs developed systemic clinical illness and weight loss. Abdominal ultrasonography revealed multifocal to coalescent cystic masses of variable size distributed throughout the liver in all cases. Evaluation of aspirated hepatic cyst contents included membranous parasite structures and calcareous corpuscles. Echinococcus multilocularis was confirmed via PCR from hepatic cyst fluid in 3 of 4 cases. Treatment included systemic benzimidazole and praziquantel administration, 1 or more instances of ultrasound-guided cyst drainage in all cases, with ethanol ablation (percutaneous aspiration-injection-reaspiration) in 2 cases, and surgical resection in 1 case. Two of 4 dogs were euthanized within 5 months of diagnosis. One of these dogs was necropsied and had nearly complete obliteration of the hepatic parenchyma by multilocal cystic masses. One dog is still alive, and 1 dog has been lost to follow-up. **Clinical relevance:** This series of cases highlighted the diagnostic findings and therapeutic intervention in 4 dogs with AE. This was the first report of medical management incorporating the percutaneous aspiration-injection-reaspiration method used in humans. Reports of canine AE are rare in the US, so this series serves to help raise awareness of hepatic AE in the northwestern US.

Prediction of the potential suitable habitat of Echinococcus granulosus, the pathogen of echinococcosis, in the Tibetan Plateau under future climate scenarios.

Xu J, Song G, Xiong M, Zhang Y, Sanlang B, Long G, Wang R.

Feb-202

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/36269480/>

Echinococcosis is a zoonotic parasitic infectious disease caused by human or domestic animals infected with Echinococcus granulosus. China is the country with the heaviest disease burden caused by Echinococcosis in the world. Therefore, it is feasible to evaluate the prevalence and distribution of echinococcosis using relevant ecological methods, combined with environmental factors and human activities. In this study, MaxEnt was used to predict the distribution range of E. granulosus in China

under current and future climate scenarios and explain the impact of environmental variables on its distribution. The results showed that elevation (El), annual mean temperature (bio1), human footprint (Hf), annual precipitation (bio12), mean temperature of warmest quarter (bio10), and mean temperature of wettest quarter (bio8) were identified as the dominant environmental variables. In Tibet, the most suitable habitats (25.9×10^4 km²) of E. granulosus were distributed in Nyingchi and Qamdo in the east, Shigatse and Shannan in the south, and Ali in the west. In Sichuan, the most suitable habitat (18.83×10^4 km²) was located in Aba, Ganzi, and Liangshan. In Qinghai, the most suitable habitat (13.05×10^4 km²) mainly included Yushu in the southwest; Guoluo in the southeast; Haidong, Huangnan, Xining, and Hainan in the east; and Haixi in the west. In Gansu, the most suitable habitat (7.36×10^4 km²) was located in Gannan and Linxia in the southwest and Wuwei and Dingxi in the middle. In Yunnan, the most suitable habitat (1.53×10^4 km²) was distributed in Diqing in the northwest. Under future climate scenarios, the area of the most suitable habitat of E. granulosus showed an obvious expansion trend, with an increase of 44.64-70.76%. Trajectory trend of centroids showed that the most suitable habitat would move to the west in the future, and the increased areas were mainly located in the west of the current most suitable habitat. AUC values of the training data and test data were $0.936 \pm 0.001 \sim 0.97 \pm 0.006$ and $0.912 \pm 0.006 \sim 0.956 \pm 0.015$, respectively. The result can provide a theoretical basis for the prevention, monitoring, and early warning of echinococcosis in China.

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

The spatial-temporal risk profiling of Clonorchis sinensis infection over 50 years implies the effectiveness of control programs in South Korea: a geostatistical modeling study.

Xiao HY, Chai JY, Fang YY, Lai YS.

03-02-2023

Lancet Reg Health West Pac. 2023 Feb 3

<https://pubmed.ncbi.nlm.nih.gov/36817868/>

A Case of Concurrence of Clonorchis Sinensis and Pancreatic Adenocarcinoma-A Diagnostic Dilemma.

Mazhar Uddin SM, Khan OA, Tan WM, Kaur A, Alhanshali L, Farooqui AA, Maheshwari S, Mehta A, Yunina D, Astashkevich M.

10-01-2023

J Community Hosp Intern Med Perspect.

<https://pubmed.ncbi.nlm.nih.gov/36817293/>

Clonorchis Sinensis, a common liver fluke, is known to cause biliary disease and can present with a wide array of symptoms. It's mostly found in Asian countries due to consumption of undercooked or raw fish. Although Cholangiocarcinoma is a known serious complication of this disease, Pancreatic neoplasms are rare and have seldom been reported. Here, we report a case of an 80-year-old man who presents with pancreatic adenocarcinoma associated with Clonorchis Sinensis infection.

Clonorchis sinensis legumain promotes migration and invasion of cholangiocarcinoma cells via regulating tumor-related molecules.

Chu Y, Shi D, Wang N, Ren L, Liu N, Hu F, Meng W, Hong SJ, Bai X.

16-02-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36797792/>

Filariose lymphatique

[Evaluation of therapeutic coverage of mass treatment campaign against lymphatic filariasis in two health districts in Burkina Faso].

Serme M, Zida A, Bougma R, Kima A, Nassa C, Ouedraogo M, Kabre C, Zoromé H, Guire I, Nare D, Bougouma C.

13-12-2022

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/36815181/>

Background & rationale: Burkina Faso has been implementing preventive chemotherapy against lymphatic filariasis since 2001. While 61 health districts (HDs) have stopped mass drug administration (MDA), transmission persists in 9 HDs despite good reported MDA coverage. To validate the reported coverage, an independent post-MDA survey was conducted in Tenkodogo and Fada N'Gourma HDs in September 2018.

Materials & methods: The study population consisted of all persons in the visited communities. The Coverage survey sample builder (CSSB) tool was used to calculate the sample size and to conduct the random selection of households. A total of 30 villages per HD were selected. The investigators were Ministry of Education agents and health workers not involved in MDA. Data were collected on smartphones through the KoBoCollect application regarding age, sex, drug ingestion (ivermectin + albendazole), adverse events, and whether respondents understood MDA guidelines. Stata Version 14 software was used for data analysis. **Results:** A total of 3,741 individuals were surveyed, 53.3% were female and the median age was 14 years. Surveyed epidemiological coverage was 74% [95% CI: 72-76.1] in Fada N'Gourma and 79.1% [95% CI: 77.2-80.9] in Tenkodogo, compared to reported coverages of 82.6% and 83% respectively. Village-level coverage ranged from 32.9% to 100% in Fada N'Gourma and from 56.7% to 93.3% in Tenkodogo. In total, 99% of those treated said they had swallowed the

drugs in front of the community drug distributor (CDD) and confirmed the use of dose poles. The main reasons for non-treatment were non-visitation of the compound by CDD (54%) and absences during MDA (43%). Results showed that surveyed coverage was lower than reported coverage in both HDs, yet both were above the 65% threshold recommended by WHO. However, major variations of coverage have been noted among villages. Directly observed treatment appeared to have been well respected. **Discussion & conclusion:** The main challenges to increase coverage will be the systematic revisiting of households with absentees and the targeting of all households in each village.

Points to Consider When Establishing and Rearing Culex Mosquitoes in the Laboratory.

Meuti ME, Siperstein A, Wolkoff M.

22-02-2023

Cold Spring Harb Protoc.

<https://pubmed.ncbi.nlm.nih.gov/36813485/>

Culex mosquitoes transmit several pathogens to humans and animals, including viruses that cause West Nile fever and St. Louis encephalitis and filarial nematodes that cause canine heartworm and elephantiasis. Additionally, these mosquitoes have a cosmopolitan distribution and provide interesting models for understanding population genetics, overwintering dormancy, disease transmission, and other important and ecological questions. However, unlike *Aedes* mosquitoes that produce eggs that can be stored for weeks at a time, no obvious "stopping" point exists in the development of *Culex* mosquitoes. Therefore, these mosquitoes require nearly continuous care and attention. Here, we describe some general considerations when rearing laboratory colonies of *Culex* mosquitoes. We highlight different methods so that readers may choose what works best for their experimental needs and laboratory infrastructure. We hope that this information will enable additional scientists to conduct laboratory research on these important disease vectors.

Ivermectin systemic availability in adult volunteers treated with different oral pharmaceutical formulations.

Ceballos L, Alvarez L, Lifschitz A, Lanusse C.

15-02-2023

Biomed Pharmacother.

<https://pubmed.ncbi.nlm.nih.gov/36804122/>

Mycetome

Mycetoma (Madura foot): A Case Report of a Rare Tropical Disease in Turkey.

Kuzucular E, Eren A, Isik E, Ozden F.

22-02-2023

Int J Low Extrem Wounds.

<https://pubmed.ncbi.nlm.nih.gov/36814397/>

Mycetoma is a chronic discharging infection involving the skin, subcutaneous tissue, fascia, and bone, which is endemic in tropical and subtropical countries. We report a

rare case of mycetoma localized on the foot of a patient living in a country with a temperate climate. A 32-year-old male patient presented with painless swelling in the right foot. He had undergone surgery 3 years ago with the same complaints. Magnetic resonance imaging revealed a 90 × 65 × 37 mm cystic soft tissue lesion in the posterior of the right ankle. Histological analysis identified the fungus. Extensive resection was performed. Mycetoma is characterized by chronic granulomatous inflammatory response, often associated with sinus tract formations due to fungal (eumycetoma) or bacterial (actinomycetoma) organisms. Here we provide a literature review and highlight the importance of increasing awareness toward mycetoma, particularly in non-endemic regions.

Onchocercose

Onchocerca sp. in an imported Zangersheide gelding causing suspensory ligament desmitis.

Brown KA, Johnson AL, Bender SJ, Nolan TJ, Pfisterer B, Slack J, Willis E, Rule EK.

23-02-2023

J Vet Intern Med.

<https://pubmed.ncbi.nlm.nih.gov/36821075/>

A 5-year-old imported Zangersheide gelding was evaluated for SC swellings over both forelimbs and lameness localized to the distal metacarpus. Ultrasound examination of the SC masses was compatible with verminous granulomas. Linear hyperechoic foci were present within the suspensory ligament branches of both forelimbs, suggestive of ligamentous parasitic infiltrates. A diagnosis of onchocerciasis was confirmed on biopsy of a SC mass. The gelding was treated with ivermectin and a tapering course of PO dexamethasone but was eventually euthanized. Necropsy confirmed the presence of SC eosinophilic granulomas and degenerative suspensory ligament desmitis, both with intralesional nematodes. Given the location and appearance of the nematode, a diagnosis of *Onchocerca* sp., most likely *O. reticulata*, was made. Onchocerciasis should be included as a differential diagnosis for multifocal suspensory ligament desmitis with these sonographic characteristics when paired with SC masses in imported European Warmbloods.

Histopathological evaluation of Onchocerca volvulus nodules by microscopy and by digital image analysis for the study of macrofilaricidal drug efficacy.

Fischer K, Dubben B, Debrah LB, Kuehlwein JM, Ricchiuto A, Debrah AY, Hoerauf A, Weil GJ, Fischer PU, Klarmann-Schulz U.

02-02-2023

Front Med (Lausanne).

<https://pubmed.ncbi.nlm.nih.gov/36817770/>

Schistosomiasis

Association of Tumor Necrosis Factor-α (-G308A) Polymorphism with risk of Upper Gastrointestinal Bleeding from Schistosomiasis in Pernambuco.

Lima BL, Lima ELS, Muniz MTC, Domingues ALC, Silva PCV.

20-02-2023

Rev Soc Bras Med Trop.

<https://pubmed.ncbi.nlm.nih.gov/36820674/>

Background: We evaluated the association between polymorphisms in the tumor necrosis factor alpha (TNF-α) (-G308A) gene and upper gastrointestinal bleeding (UGIB) in schistosomiasis. **Methods:** This was a transverse study involving 294 Brazilian patients infected with *Schistosoma mansoni*. **Results:** The homozygous A/A genotype in TNF-α (-G308A) showed a risk association (prevalence ratio = 1.90, p = 0.008) with UGIB. There was no statistically significant difference in serum TNF-α levels between the clinical groups. **Conclusions:** The polymorphic TNF-α (-G308A) can be a risk factor for UGIB, in addition to being a potentially predictive factor for the severity of UGIB in schistosomiasis.

Subclinical signs of podocyte injury associated with Circulating Anodic Antigen (CAA) in Schistosoma mansoni-infected patients in Brazil.

Sousa MS, Meneses GC, Dam GJV, Corstjens PLAM, Galvão RLF, Pinheiro MCC, Martins AMC, Daher EF, Bezerra FSM.

20-02-2023

Rev Soc Bras Med Trop.

<https://pubmed.ncbi.nlm.nih.gov/36820657/>

Prevalence of Schistosoma mansoni, soil-transmitted helminths and intestinal protozoa in orphans and street children in Mwanza city, Northern Tanzania.

Franz A, Fuss A, Mazigo HD, Ruganuzi D, Müller A.

20-02-2023

Infection.

<https://pubmed.ncbi.nlm.nih.gov/36805439/>

Inhibition of alternative oxidase disrupts the development and oviposition of Biomphalaria glabrata snails.

Xu S, Zhang YW, Habib MR, Li SZ, Yuan Y, Ke WH, Jiang N, Dong H, Zhao QP.

17-02-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/36804043/>

Background: *Biomphalaria glabrata* is one of the main intermediate hosts of *Schistosoma mansoni*, the most widespread species of *Schistosoma*. Our previous studies proved that alternative oxidase (AOX), the terminal oxidase in the mitochondrial respiratory chain, widely

exists in several species of intermediate host snails of *Schistosoma*. Meanwhile, inhibition of AOX activity in *Oncomelania hupensis* snails could dramatically enhance the molluscicidal effect of niclosamide. As a hermaphroditic aquatic mollusc, the high fecundity and population density of *B. glabrata* increase the difficulty of snail control, which is one of the critical strategies for schistosomiasis elimination. The present study aimed to investigate the possible role of AOX in the development and fecundity of *B. glabrata* snail, which could be manipulated more manageable than other species of intermediate host snails of *Schistosoma*. **Methods:** The dynamic expression of the AOX gene was investigated in different developmental stages and tissues of *B. glabrata*, with morphological change and oviposition behaviour observed from juvenile to adult snails. Further, dsRNA-mediated knockdown of BgAOX mRNA and the AOX protein activity inhibiting was performed to investigate the effect of AOX on the development and oviposition of snails. **Results:** The BgAOX gene expression profile is highly related to the development from late juveniles to adults, especially to the reproductive system of snails, with a positive correlation of 0.975 between egg production and BgAOX relative expression in ovotestis of snails. The inhibition of BgAOX at the transcriptional level and AOX activity could efficiently inhibit snail growth. However, the interference at the BgAOX protein activity level led to more severe tissue damage and more significant inhibition of oviposition than at the transcriptional level. This inhibition of growth and oviposition decreased gradually with the increase in the snail size. **Conclusions:** The inhibition of AOX could efficiently disrupt the development and oviposition of *B. glabrata* snails, and the intervention targeting AOX at the juvenile stage is more effective for snails. This investigation explored the role of AOX in the growth and development of snails. It would benefit snail control in the future by providing a potential target while using molluscicides more efficiently.

MicroRNA dysregulation in schistosomiasis-induced hepatic fibrosis: a systematic review.

Nóbrega DND, Carvalho TL, do Ó KP, Emídio de Lima R, Farias ICC, Dos Santos Souza R, Pereira JB, Maranhão ACN, da Silva Lima VF, Trajano Manguiera de Melo AL, Silva TCG, de Mendonça Belmont TF, Christine de Souza Gomes E, Vasconcelos LRS.

20-02-2023

Expert Rev Mol Diagn.

<https://pubmed.ncbi.nlm.nih.gov/36803616/>

First report of *Biomphalaria tenagophila* (d'Orbigny, 1835) (Gastropoda/Planorbidae) in Pará State, Amazon region of Brazil.

Goveia CO, Caldeira RL, Barata RR, Lemos PDS, Teixeira Nunes MR, Dias IHL, Enk MJ.

17-02-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36801395/>

Introduction: Mollusks belonging to *Biomphalaria* genus are intermediate hosts of *Schistosoma mansoni*. In the Pará State, Northern Region of Brazil, there are reports of *B. glabrata*, *B. straminea*, *B. schrammi*, *B. occidentalis*, and *B. kuhniana* occurrence. Here, we report for the first time the presence of *B. tenagophila* in Belém, capital of Pará state. **Methods:** A total of 79 mollusks were collected and examined to search for possible *S. mansoni* infection. The specific identification was made by morphological and molecular assays. **Results:** No specimens parasitized by trematode larvae were detected. For the first time the presence of *B. tenagophila* in Belém, capital of Pará state, was reported. **Conclusion:** The result increases the knowledge about *Biomphalaria* mollusks occurrence in the Amazon Region and specifically alerts on the possible role of *B. tenagophila* in schistosomiasis transmission in Belém.

The trend of schistosomiasis related bladder cancer in the lake zone, Tanzania: a retrospective review over 10 years period.

Yohana C, Bakuza JS, Kinung'hi SM, Nyundo BA, Rambau PF.

19-02-2023

Infect Agent Cancer.

<https://pubmed.ncbi.nlm.nih.gov/36800971/>

Helminth infection impacts hematopoiesis.

Wijshake T, Wang J, Rose J, Marlar-Pavey M, Collins JJ, Agathocleous M.

10-02-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/36798229/>

A novel, non-neuronal acetylcholinesterase of schistosome parasites is essential for definitive host infection.

Skelly PJ, Da'dara AA.

31-01-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36798133/>

Schistosomes are long-lived parasitic worms that infect >200 million people globally. The intravascular life stages are known to display acetylcholinesterase (AChE) activity internally as well as, somewhat surprisingly, on external tegumental membranes. Originally it was hypothesized that a single gene (SmAChE1 in *Schistosoma mansoni*) encoded both forms of the enzyme. Here, we demonstrate that a second gene, designated "S. mansoni tegumental acetylcholinesterase, SmTACHe", is responsible for surface, non-neuronal AChE activity. The SmTACHe protein is GPI-anchored and contains all essential amino acids necessary for function. AChE surface activity is significantly diminished following SmTACHe gene suppression using RNAi, but not following SmAChE1 gene suppression. Suppressing SmTACHe significantly impairs the ability of parasites to establish infection in mice, showing that SmTACHe performs an essential function for the worms *in vivo*. Living *S. haematobium* and *S. japonicum* parasites

also display strong surface AChE activity, and we have cloned SmTAcHE homologs from these two species. This work helps to clarify longstanding confusion regarding schistosome AChEs and paves the way for novel therapeutics for schistosomiasis.

Phenotypic Profiling of Macrocyclic Lactones on Parasitic Schistosoma Flatworms.

Ryan KT, Wheeler NJ, Kamara IK, Johnson H, Humphries JE, Zamanian M, Chan JD.

16-02-2023

Antimicrob Agents Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36695583/>

Macrocyclic lactones are front-line therapies for parasitic roundworm infections; however, there are no comprehensive studies on the activity of this drug class against parasitic flatworms. Ivermectin is well known to be inactive against flatworms. However, the structure-activity relationship of macrocyclic lactones may vary across phyla, and it is entirely possible other members of this drug class do in fact show antiparasitic activity on flatworms. For example, there are several reports hinting at the anti-schistosomal activity of doramectin and moxidectin. To explore this class further, we developed an automated imaging assay combined with measurement of lactate levels from worm media. This assay was applied to the screening of 21 macrocyclic lactones (avermectins, milbemycins, and others such as spinosyns) against adult schistosomes. These *in vitro* assays identified several macrocyclic lactones (emamectin, milbemycin oxime, and the moxidectin metabolite 23-ketonemadectin) that caused contractile paralysis and lack of lactate production. Several of these were also active against miracidia, which infect the snail intermediate host. Hits prioritized from these *in vitro* assays were administered to mice harboring patent schistosome infections. However, no reduction in worm burden was observed. Nevertheless, these data show the utility of a multiplexed *in vitro* screening platform to quantitatively assess drug action and exclude inactive compounds from a chemical series before proceeding to *in vivo* studies. While the prototypical macrocyclic lactone ivermectin displays minimal activity against adult *Schistosoma mansoni*, this family of compounds does contain schistocidal compounds which may serve as a starting point for development of new anti-flatworm chemotherapies.

Schistosome proteomics: updates and clinical implications.

Castro-Borges W, Wilson RA.

Apr-Jun 2023

Expert Rev Proteomics.

<https://pubmed.ncbi.nlm.nih.gov/36331139/>

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

Intestinal Intussusception Due to Entrapped *Ascaris lumbricoides* in a 13-Year-Old Male Patient.

Khan MN, Khan I, Alvi E, Ahmad I.

18-01-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/36819331/>

Ascaris lumbricoides is a fairly common intestinal nematode affecting children worldwide, leading to major medical and surgical complications. Although most of the cases are asymptomatic, heavy infestation causes various acute abdominal complications. *Ascaris*-induced intestinal intussusception is one of the rare presentations. We report a case of a 13-year-old boy with *Ascaris lumbricoides* infestation presenting with ileocolic intussusception. The patient presented to the emergency unit with colicky abdominal pain, vomiting, and constipation for two days. He was sick-looking and dehydrated. Further examination revealed diffuse abdominal distension with tenderness, guarding, and palpable mass in the right lower quadrant. Ultrasonography showed long-segment ileocolic intussusception with several worms in the intestinal lumen and adjacent mesenteric lymphadenopathy. An exploratory laparotomy was performed, which revealed ileocolic intussusception. The telescopic loop of the ileum was found to be gangrenous and was resected, and a loop ileostomy was performed. The patient was discharged on the seventh day postoperatively without any complications. Physicians in tropical and subtropical countries should consider this condition in the differential diagnosis when they encounter similar presentations in their clinical practice. Sonography is a non-invasive, easy-to-use, and widely available imaging modality that can be employed to diagnose entrapped *Ascaris* in cases presenting with acute gastrointestinal complications. Early diagnosis and prompt surgical intervention can prevent bowel ischemia/gangrene and significantly reduce morbidity and mortality associated with such cases.

Gale

SCABIES CASES MISDIAGNOSED AND TREATED AS ALLERGIC DISEASES: ITCH AS ALARM.

Lugović-Mihić L, Delaš Aždajić M, Bešlić I.

Aug-2022

Acta Clin Croat.

<https://pubmed.ncbi.nlm.nih.gov/36818938/>

Beliefs, attitudes and practices towards scabies in central Ghana.

Amoako YA, van Rietschoten LS, Oppong MN, Amoako KO, Abass KM, Anim BA, Laryea DO, Phillips RO, Stienstra Y.

22-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36812249/>

Ivermectin systemic availability in adult volunteers treated with different oral pharmaceutical formulations.

Ceballos L, Alvarez L, Lifschitz A, Lanusse C.

15-02-2023

Biomed Pharmacother.

<https://pubmed.ncbi.nlm.nih.gov/36804122/>

Ivermectin (IVM) is currently approved as an antiparasitic agent for human use in the treatment of onchocerciasis, lymphatic filariasis, strongyloidiasis, scabies, and pediculosis. Recent findings indicate that IVM may reach other pharmacological targets, which accounts for its proven anti-inflammatory/immunomodulatory, cytostatic, and antiviral effects. However, little is known about the assessment of alternative drug formulations for human use. **Objective:** To compare the systemic availability and disposition kinetics of IVM orally administered as different pharmaceutical formulations (tablet, solution, or capsule) to healthy adults. **Experimental design/main findings:** Volunteers were randomly assigned to 1 of 3 experimental groups and orally treated with IVM as either, a tablet, solution, or capsules at 0.4 mg/kg in a three-phase crossover design. Blood samples were taken as dried blood spots (DBS) between 2 and 48 h post-treatment and IVM was analyzed by HPLC with fluorescence detection. IVM C_{max} value was higher ($P < 0.05$) after the administration of the oral solution compared to treatments with both solid preparations. The oral solution resulted in a significantly higher IVM systemic exposure (AUC: 1653 ng h/mL) compared to the tablet (1056 ng h/mL) and capsule (996 ng h/mL) formulations. The simulation of a 5-day repeated administration for each formulation did not show a significant systemic accumulation. **Conclusion:** Beneficial effects against systemically located parasitic infections as well as in any other potential therapeutic field of IVM application would be expected from its use in the form of oral solution. This pharmacokinetic-based therapeutic advantage without the risk of excessive accumulation needs to be corroborated in clinical trials specifically designed for each purpose.

Spatio-temporal and transmission dynamics of sarcoptic mange in an endangered New World kit fox.

Foley P, Foley J, Rudd J, Clifford D, Westall T, Cypher B.

16-02-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36795734/>

Case of concurrence of bullous pemphigoid and Norwegian scabies.

Wang X, Liu Y, Li J, Bao F, Chen M.

Mar-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36645298/>

Morsures de serpent

[Incidence of snakebites in rural communities living in the Paoua savannah and Mbaiki forest areas in Central African Republic].

Zarambaud R, Piamale G, Longo JD, Diemer HS, Gresenguet G.

27-10-2022

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/36815179/>

National snakebite project on capacity building of health system on prevention and management of snakebite envenoming including its complications in selected districts of Maharashtra and Odisha in India: A study protocol.

Gajbhiye RK, Chaaithanya IK, Munshi H, Prusty RK, Mahapatra A, Palo SK, Pati S, Yadav A, Bansode M, Shambharkar S, Madavi K, Bawaskar HS, Mahale SD.

17-02-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/36800356/>

Background: Snakebite envenoming (SBE) is an acute, life-threatening emergency in tropical and subtropical countries. It is an occupational hazard and a major socioeconomic determinant. Limited awareness, superstitions, lack of trained health providers, poor utilization of anti-venom results in high mortality and morbidity. India is the snakebite capital of the world. Yet, information on awareness, knowledge, and perceptions about snakebite is limited. Data on capacity building of health systems and its potential impact is lacking. Recommended by the National Task Force on snakebite research in India, this protocol describes the National Snakebite Project aiming for capacity building of health systems on prevention and management of snakebite envenomation in Maharashtra and Odisha states. **Methods:** A cross-sectional, multi-centric study will be carried out in Shahapur, Aheri blocks of Maharashtra, and Khordha, Kasipur blocks of Odisha. The study has five phases: Phase I involves the collection of retrospective baseline data of snakebites, facility surveys, and community focus group discussions (FGDs). Phase II involves developing and implementing educational intervention programs for the community. Phase III will assess the knowledge and practices of the healthcare providers on snakebite management followed by their training in Phase IV. Phase V will evaluate the impact of the interventions on the community and healthcare system through FGDs and comparison of prospective and baseline data. **Discussion:** The National Snakebite Project will use a multi-sectoral approach to reduce the burden of SBE. It intends to contribute to community empowerment and capacity building of the public healthcare system on the prevention and management of SBE. The results could be useful for upscaling to other Indian states, South Asia and

other tropical countries. The findings of the study will provide critical regional inputs for the revision of the National Snakebite Treatment protocol.

surveillance system, which should be made a priority in countries facing similar public health challenges.

Snakebite envenoming in Brazilian children: clinical aspects, management and outcomes.

Oliveira IS, Pucca MB, Cerni FA, Vieira S, Sachett J, Seabra de Farias A, Lacerda M, Murta F, Baia-da-Silva D, Rocha TAH, Silva LL, Bassat Q, Vissoci JRN, Gerardo CJ, Sampaio VS, Wen FH, Bernarde PS, Monteiro WM.

06-02-2023

J Trop Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36795080/>

A generalized framework for estimating snakebite underreporting using statistical models: A study in Colombia.

Bravo-Vega C, Renjifo-Ibañez C, Santos-Vega M, León Nuñez LJ, Angarita-Sierra T, Cordovez JM.

06-02-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36745647/>

Background: Snakebite envenoming is a neglected tropical disease affecting deprived populations, and its burden is underestimated in some regions where patients prefer using traditional medicine, case reporting systems are deficient, or health systems are inaccessible to at-risk populations. Thus, the development of strategies to optimize disease management is a major challenge. We propose a framework that can be used to estimate total snakebite incidence at a fine political scale.

Methodology/principal findings: First, we generated fine-scale snakebite risk maps based on the distribution of venomous snakes in Colombia. We then used a generalized mixed-effect model that estimates total snakebite incidence based on risk maps, poverty, and travel time to the nearest medical center. Finally, we calibrated our model with snakebite data in Colombia from 2010 to 2019 using the Markov-chain-Monte-Carlo algorithm. Our results suggest that 10.19% of total snakebite cases (532.26 yearly envenomings) are not reported and these snakebite victims do not seek medical attention, and that populations in the Orinoco and Amazonian regions are the most at-risk and show the highest percentage of underreporting. We also found that variables such as precipitation of the driest month and mean temperature of the warmest quarter influences the suitability of environments for venomous snakes rather than absolute temperature or rainfall.

Conclusions/significance: Our framework permits snakebite underreporting to be estimated using data on snakebite incidence and surveillance, presence locations for the most medically significant venomous snake species, and openly available information on population size, poverty, climate, land cover, roads, and the locations of medical centers. Thus, our algorithm could be used in other countries to estimate total snakebite incidence and improve disease management strategies; however, this framework does not serve as a replacement for a