



Veille scientifique

Maladies tropicales négligées

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31 juillet au 06 août 2023

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Cysticercose

The prevalence and molecular detection of bovine cysticercosis and its impact on slaughtered cattle in Egypt.

El-Dakhly KM, Hany SA, Arafa WM, Abdel-Fatah OR, Abdel-Atty NS, El-Nahass ES.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520208/>

Cysticercus bovis is the metacestode of the commonly defined foodborne cestode, *Taenia saginata*. It infects heart, masseter muscles and other muscular sites of cattle causing bovine cysticercosis. So, a retrospective study using archival documents from authorized agencies is done during the period of 2018-2020 with estimating economic losses. Cysts were collected from municipal Beni-Suef and Basatin abattoirs. Molecular approach including cPCR and sequencing analysis is used to prove the species. The prevalence was 0.34% in Beni-Suef abattoir and 5.70% in Basatin abattoir including heads, hearts or all carcasses condemned. Among 27 provinces surveyed, the highest prevalence was recorded in Aswan followed by Cairo, Suez and Red Sea. Moreover, 19 provinces (Cairo, Alexandria, Suez, Dakahlia, Sharkia, Qalyobia, Kafrelsheikh, Gharbia, Menofiya, Ismailia, Giza, Beni-Suef, Assiut, Sohag, Qena, Aswan, Red Sea, South Sinai and El-Wadi El-Gadid) recorded bovine cysticercosis in 2018, 2019 and 2020. On the other hand, Luxor and North Sinai had no infections. The percentages of condemnation among slaughtered cattle were 1.38, 1.49 and 0.87% in 2018, 2019 and 2020, respectively. Condemnations significantly varied among north, middle and south districts of Egypt, and also varied annually. Molecularly, a diagnostic band at an amplicon size 253 bp targeting the COI gene specific for *Cysticercus bovis* was revealed. The obtained sequences showed 100% identity with the different *Taenia saginata* COI GB sequence isolates in many countries worldwide. The phylogenetic analysis method showed that the obtained sequences originating from the same clade of *Taenia saginata* GB isolates globally. Careful meat inspection as well as strict hygienic measures is recommended for both veterinarians and public.

Community Health-Education Intervention Trial against Human *Taenia solium* Taeniasis/Cysticercosis in Central and Southern Zones of Tanzania.

Makingi G, Ngowi B, Mkupasi E, Wilson C, Winkler AS, Nzalawahe J, Ngowi H.

20-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513802/>

Poor knowledge of human *T. solium* taeniasis/cysticercosis and insufficient sanitary and hygienic practices have been associated with the persistence of human *T. solium* infections in endemic areas. Community health education intervention measures were implemented in 42 villages of Kongwa and Songwe Districts to increase knowledge,

improve good practices against infection and reduce incidences of human cysticercosis transmission using a health education package. The health education package comprised of leaflet, poster and a booklet. The 42 villages were allocated into intervention group and control group, and each group consisted of 21 villages. Baseline and post-intervention information on social demography, knowledge, safe practices and incidences of human cysticercosis was collected from both village groups. The impact of the intervention was evaluated by comparing changes in knowledge, preventive practices related to human *T. solium* infections and the cumulative incidence of human cysticercosis between intervention and control villages. There was no significant difference in mean knowledge scores and preventive practice mean scores between the control and intervention groups at baseline. However, there were significantly higher knowledge mean scores in the intervention group compared to the control group at one year post-intervention (2.06 ± 1.45 vs. 0.94 ± 1.18 , $p < 0.001$). There was no significant difference in the mean practice scores between the intervention and the control group at one year post-intervention (2.49 ± 1.13 vs. 2.40 ± 1.13 , $p = 0.31$). Furthermore, there was no significant difference in the prevalence of human *T. solium* cysticercosis between the intervention and the control group at the baseline (1.4% vs. 1.4%, $p = 0.97$) by Ag-Elisa, and at one year post-intervention the cumulative incidence of human cysticercosis was 1.9 and 1.2 per cent in the control and intervention group, respectively. There was no significant difference in the cumulative incidence of human cysticercosis between the intervention and the control group at one year post-intervention ($p > 0.05$). Community health-education intervention is effective at improving the knowledge of human *T. solium* infections. The improvement in preventive practices and reduction in incidences of human cysticercosis are a gradual process, they may require sanitary and hygienic improvement and more time after the intervention to see improved changes. The study recommends a sustainable public health education on *T. solium* infections using the health education package through one health approach.

A meta-analysis on the prevalence of *Taenia solium* and *Taenia saginata* infections in India.

Balodhi A, Jain K, Gupta P, Deebea F, Salam N.

03-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37076247/>

Dengue, chikungunya et maladie à virus Zika

A point-of-care microfluidic biosensing system for rapid and ultrasensitive nucleic acid detection from clinical samples.

Zhang Y, Song Y, Weng Z, Yang J, Avery L, Dieckhaus KD, Lai RY, Gao X, Zhang Y.

04-08-2023

Lab Chip.

<https://pubmed.ncbi.nlm.nih.gov/37539483/>

Rapid and ultrasensitive point-of-care RNA detection plays a critical role in the diagnosis and management of various infectious diseases. The gold-standard detection method of reverse transcription-quantitative polymerase chain reaction (RT-qPCR) is ultrasensitive and accurate yet limited by the lengthy turnaround time (1-2 days). On the other hand, an antigen test offers rapid at-home detection (typically ~15 min) but suffers from low sensitivity and high false-negative rates. An ideal point-of-care diagnostic device would combine the merits of PCR-level sensitivity and rapid sample-to-result workflow comparable to antigen testing. However, the existing detection platforms typically possess superior sensitivity or rapid sample-to-result time, but not both. This paper reports a point-of-care microfluidic device that offers ultrasensitive yet rapid detection of viral RNA from clinical samples. The device consists of a microfluidic chip for precisely manipulating small volumes of samples, a miniaturized heater for viral lysis and ribonuclease inactivation, a Cas13a-electrochemical sensor for target preamplification-free and ultrasensitive RNA detection, and a smartphone-compatible potentiostat for data acquisition. As demonstrations, the devices achieve the detection of heat-inactivated SARS-CoV-2 samples with a limit of detection down to 10 aM within 25 minutes, which is comparable to the sensitivity of RT-PCR and rapidness of an antigen test. The platform also successfully distinguishes all nine positive unprocessed clinical SARS-CoV-2 nasopharyngeal swab samples from four negative samples within 25 minutes of sample-to-result time. Together, this device provides a point-of-care solution that can be deployed in diverse settings beyond laboratory environments for rapid and accurate detection of RNA from clinical samples. The device can potentially be expandable to detect other viral targets, such as human immunodeficiency virus self-testing and Zika virus, where rapid and ultrasensitive point-of-care detection is required.

Human footprint is associated with shifts in the assemblages of major vector-borne diseases.

Skinner EB, Glidden CK, MacDonald AJ, Mordecai EA.

Juin-2023

Nat Sustain.

<https://pubmed.ncbi.nlm.nih.gov/37538395/>

Erste Impfung gegen Dengue-Fieber.

Blume T.

Août-2023

MMW Fortschr Med.

<https://pubmed.ncbi.nlm.nih.gov/37537467/>

MAVS signaling is required for preventing persistent chikungunya heart infection and chronic vascular tissue inflammation.

Noval MG, Spector SN, Bartnicki E, Izzo F, Narula N, Yeung ST, Damani-Yokota P, Dewan MZ, Mezzano V,

Rodriguez-Rodriguez BA, Loomis C, Khanna KM, Stapleford KA.

03-08-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37537212/>

Chikungunya virus (CHIKV) infection has been associated with severe cardiac manifestations, yet, how CHIKV infection leads to heart disease remains unknown. Here, we leveraged both mouse models and human primary cardiac cells to define the mechanisms of CHIKV heart infection. Using an immunocompetent mouse model of CHIKV infection as well as human primary cardiac cells, we demonstrate that CHIKV directly infects and actively replicates in cardiac fibroblasts. In immunocompetent mice, CHIKV is cleared from cardiac tissue without significant damage through the induction of a local type I interferon response from both infected and non-infected cardiac cells. Using mice deficient in major innate immunity signaling components, we found that signaling through the mitochondrial antiviral-signaling protein (MAVS) is required for viral clearance from the heart. In the absence of MAVS signaling, persistent infection leads to focal myocarditis and vasculitis of the large vessels attached to the base of the heart. Large vessel vasculitis was observed for up to 60 days post infection, suggesting CHIKV can lead to vascular inflammation and potential long-lasting cardiovascular complications. This study provides a model of CHIKV cardiac infection and mechanistic insight into CHIKV-induced heart disease, underscoring the importance of monitoring cardiac function in patients with CHIKV infections.

Corrigendum to "Nasopharyngeal swabs as alternative specimens for the diagnosis of dengue virus infection" [J Infect 87 (2023) 145-147].

Maia AC, Quintão TSC, de Oliveira PM, Cassemiro ÉM, Cilião-Alves DC, Alves PPM, Martins FDAP, Araújo ELL, da Costa Gurgel H, Noronha EF, Ramalho WM, Pereira AL, Slavov SN, de Araújo WN, Haddad R.

01-08-2023

J Infect.

<https://pubmed.ncbi.nlm.nih.gov/37537009/>

How climate change is changing dengue fever.

Bashir A.

03-08-2023

BMJ.

<https://pubmed.ncbi.nlm.nih.gov/37536724/>

Population genetic characterization of (*Aedes albopictus*) mosquitoes (Diptera: Culicidae) from the Yangtze River Basin of China based on rDNA-ITS2.

Ma Z, Xing D, Liu Q, Gao J, Wang G, Li C, Guo X, Jiang Y, Zhao T, Zhou X, Zhang H, Zhao T.

01-08-2023

Infect Genet Evol.

<https://pubmed.ncbi.nlm.nih.gov/37536530/>

A comparison of changes in venous lactate and haematocrit during fluid resuscitation of dengue haemorrhagic fever.

Priyankara WDD, Samarutilake DGN, Viswakula S, Manoj EM, Wijewickrama A, Perera N, Wanigasuriya JKP.

03-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37534814/>

Background: Judicious fluid resuscitation and stringent monitoring of clinical parameters improve the outcome of dengue haemorrhagic fever (DHF). The usefulness of serum lactate to monitor adequate fluid therapy has not been adequately explored. **Methods:** An observational study was conducted in Sri Lanka, recruiting 162 DHF patients within 12 h of diagnosis of the critical phase. Venous lactate level was measured at each time of performing haematocrit (HCT), using a prevalidated handheld lactate analyser. **Results:** The median venous lactate level was 1.3 (range 0.3-6) mmol/L in the study population and 154 (95.2%) patients had median lactate levels of <2 mmol/L. The HCT values in the study participants ranged from 28 to 62, with a median value of 43. There was no statistically significant correlation between the lactate and HCT values obtained at the same time. A significant reduction in venous lactate was not observed following the administration of fluid boluses. The expected reduction in HCT was seen following the administration of dextran and crystalloid/dextran combination. The maximum recorded lactate level positively correlated with the duration of hospital stay. **Conclusions:** This study concludes that venous lactate is not an appropriate parameter with which to monitor the response to fluid therapy in uncomplicated DHF.

Differential localization of dengue virus protease affects cell homeostasis and triggers to thrombocytopenia.

Gandhi L, Maisnam D, Rathore D, Chauhan P, Bonagiri A, Venkataramana M.

05-06-2023

iScience.

<https://pubmed.ncbi.nlm.nih.gov/37534186/>

Thrombocytopenia is one of the symptoms of many virus infections which is the "hallmark" in the case of dengue virus. In this study, we show the differential localization of existing two forms of dengue virus protease, i.e., NS2BNS3 to the nucleus and NS3 to the nucleus and mitochondria. We also report a nuclear transcription factor, erythroid differentiation regulatory factor 1 (EDRF1), as the substrate for this protease. EDRF1 regulates the expression and activity of GATA1, which in turn controls spectrin synthesis. Both GATA1 and spectrins are required for platelet formation. On the other hand, we found that the mitochondrial activities will be damaged by NS3 localization which cleaves GrpEL1, a co-chaperone of mitochondrial Hsp70. Levels of both EDRF1 and GrpEL1 were found to deteriorate in dengue virus-infected clinical samples. Hence, we conclude that NS2BNS3-mediated EDRF1 cleavage and the NS3-led mitochondrial dysfunction account for thrombocytopenia.

Isogenic human trophectoderm cells demonstrate the role of NDUF4 and associated variants in ZIKV infection.

Yang L, Han Y, Zhou T, Lacko LA, Saeed M, Tan C, Danziger R, Zhu J, Zhao Z, Cahir C, Giani AM, Li Y, Dong X, Moroziewicz D; NYSCF Global Stem Cell Array® Team; Paull D, Chen Z, Zhong A, Noggle SA, Rice CM, Qi Q, Evans T, Chen S.

29-05-2023

iScience.

<https://pubmed.ncbi.nlm.nih.gov/37534130/>

A Phase 1, double-blind, randomized, placebo-controlled study to evaluate the safety and immunogenicity of a tetravalent live attenuated dengue vaccine in adults.

Gunale B, Farinola N, Yeolekar L, Shrivastava S, Girgis H, Poonawalla CS, Dhere RM, Arankalle V, Chandra Mishra A, Mehla R, Kulkarni PS.

31-07-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37532611/>

Leucine to tryptophane substitution in the pore helix IIP1 confer sodium channel resistance to pyrethroids and DDT.

Wu H, Qian J, Xu Z, Yan R, Zhu G, Wu S, Chen M.

Aug-2023

Pestic Biochem Physiol.

<https://pubmed.ncbi.nlm.nih.gov/37532317/>

Aedes aegypti is responsible for transmitting a variety of arboviral infectious diseases such as dengue and chikungunya. Insecticides, particularly pyrethroids, are used widely for mosquito control. However, intensive use of pyrethroids has led to the selection of *kdr* mutations on sodium channels. L982W, located in the PyR1 (Pyrethroid receptor site 1), was first reported in *Ae. aegypti* populations collected from Vietnam. Recently, the high frequency of L982W was detected in pyrethroid-resistant populations of Vietnam and Cambodia, and also concomitant mutations L982W + F1534C was detected in both countries. However, the role of L982W in pyrethroid resistance remains unclear. In this study, we examined the effects of L982W on gating properties and pyrethroid sensitivity in *Xenopus* oocytes. We found that mutations L982W and L982W + F1534C shifted the voltage dependence of activation in the depolarizing direction, however, neither mutations altered the voltage dependence of inactivation. L982W significantly reduced channel sensitivity to Type I pyrethroids, permethrin and bifenthrin, and Type II pyrethroids, deltamethrin and cypermethrin. No enhancement was observed when synergized with F1534C. In addition, L982W and L982W + F1534C mutations reduced the channel sensitivity to DDT. Our results illustrate the molecular basis of resistance mediated by L982W mutation, which will be helpful to understand the interactions of pyrethroids or DDT with sodium channels and develop molecular markers for monitoring pest resistance to pyrethroids and DDT.

Tarsal exposure to atovaquone inhibits chikungunya virus transmission by Aedes aegypti mosquitoes, but not the transmission of Zika virus.

Wang L, Sanon A, Khoiriyah Z, Verwimp S, Abdelnabi R, Delang L.

31-07-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/37532005/>

The antimalarial drug atovaquone was recently reported to inhibit the in vitro replication of different arboviruses, including chikungunya virus (CHIKV) and Zika virus (ZIKV). Furthermore, atovaquone was shown to block Plasmodium parasite transmission by Anopheles mosquitoes when the mosquitoes were exposed to low concentrations on treated surfaces (i.e. tarsal exposure). Therefore, we evaluated the anti-CHIKV and -ZIKV effects of atovaquone via tarsal exposure in Aedes aegypti mosquitoes. We first confirmed that atovaquone exerted a dose-dependent antiviral effect on CHIKV and ZIKV replication in mosquito-derived cells. The modest antiviral effect could be rescued by adding exogenous uridine. Next, we assessed the effect of tarsal exposure to atovaquone on the fitness of Ae. aegypti. Concentrations up to 100 $\mu\text{mol}/\text{m}^2$ did not affect the fecundity and egg-hatching rate. No significant effect on mosquito survival was observed when mosquitoes were exposed to concentrations up to 25 $\mu\text{mol}/\text{m}^2$. To evaluate the antiviral effect of atovaquone against CHIKV, we exposed female mosquitoes to 100 $\mu\text{mol}/\text{m}^2$ atovaquone for 1h, after which the mosquitoes were immediately infected with CHIKV or ZIKV via bloodmeal. Atovaquone did not significantly reduce ZIKV or CHIKV infection in Ae. aegypti, but successfully blocked the transmission of CHIKV in saliva. Tarsal exposure to antiviral drugs could therefore be a potential new strategy to reduce virus transmission by mosquitoes.

Chikungunya virus infection in the southernmost state of Brazil was characterised by self-limited transmission (2017-2019) and a larger 2021 outbreak.

Gregianini TS, Salvato RS, Barcellos RB, Godinho FM, Ruivo AP, de Melo VH, Schroder JA, Martiny FL, Möllmann EB, Favreto C, Baethgen LF, Ferreira VP, de Lima LE, Piazza CF, Machado TRM, Becker IM, Ramos RR, Frölich GC, Rossetti AF, Almeida LDC, Rodrigues TMA, Bragança IT, Campos AAS, Manzoni VB, Machado LC, da Silva LMI, de Oliveira ALS, Paiva MHS, Nunes ZMA, de Almeida PR, Demoliner M, Gualarte JS, da Silva MS, Filippi M, Pereira VMAG, Spilki FR, da Veiga ABG, Wallau GL.

31-07-2023

Mem Inst Oswaldo Cruz.

<https://pubmed.ncbi.nlm.nih.gov/37531506/>

A specific and low background nucleic acids sensing strategy based on rolling circle amplification coupled with a magnetic DNA machine.

Lai X, Zhao X, Peng Y, Zhang R, Pang H, Gao Z, Li D, Cao P, Pu Q, Qiao B, Pei H, Wu Q.

02-08-2023

Chem Commun (Camb).

<https://pubmed.ncbi.nlm.nih.gov/37530562/>

Peptidomimetic Oligomers Targeting Membrane Phosphatidylserine Exhibit Broad Antiviral Activity.

Tate PM, Mastrodomenico V, Cunha C, McClure J, Barron AE, Diamond G, Mounce BC, Kirshenbaum K.

02-08-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37530426/>

The development of durable new antiviral therapies is challenging, as viruses can evolve rapidly to establish resistance and attenuate therapeutic efficacy. New compounds that selectively target conserved viral features are attractive therapeutic candidates, particularly for combating newly emergent viral threats. The innate immune system features a sustained capability to combat pathogens through production of antimicrobial peptides (AMPs); however, these AMPs have shortcomings that can preclude clinical use. The essential functional features of AMPs have been recapitulated by peptidomimetic oligomers, yielding effective antibacterial and antifungal agents. Here, we show that a family of AMP mimetics, called peptoids, exhibit direct antiviral activity against an array of enveloped viruses, including the key human pathogens Zika, Rift Valley fever, and chikungunya viruses. These data suggest that the activities of peptoids include engagement and disruption of viral membrane constituents. To investigate how these peptoids target lipid membranes, we used liposome leakage assays to measure membrane disruption. We found that liposomes containing phosphatidylserine (PS) were markedly sensitive to peptoid treatment; in contrast, liposomes formed exclusively with phosphatidylcholine (PC) showed no sensitivity. In addition, chikungunya virus containing elevated envelope PS was more susceptible to peptoid-mediated inactivation. These results indicate that peptoids mimicking the physicochemical characteristics of AMPs act through a membrane-specific mechanism, most likely through preferential interactions with PS. We provide the first evidence for the engagement of distinct viral envelope lipid constituents, establishing an avenue for specificity that may enable the development of a new family of therapeutics capable of averting the rapid development of resistance.

Atypical clinical presentation of Zika virus from India.

Shukla S, Yadav PD, Patil S, Jain A, Aggarawal V.

Juil-Sept 2023

Indian J Pathol Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37530371/>

Spontaneous bacterial peritonitis: A rare manifestation of expanded dengue syndrome.

Kaur J, Singh J, Cheema YS.

28-09-2023

Turk J Emerg Med.

<https://pubmed.ncbi.nlm.nih.gov/37529785/>

Identification of Zika virus NS2B-NS3 protease and NS5 polymerase inhibitors by structure-based virtual screening of FDA-approved drugs.

Ezzemani W, Altawalah H, Windisch M, Ouladlarsen A, Saile R, Kettani A, Ezzikouri S.

01-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37528667/>

Identification of a small chemical as a lysosomal calcium mobilizer and characterization of its ability to inhibit autophagy and viral infection.

Zhang K, Huang L, Cai Y, Zhong Y, Chen N, Gao F, Zhang L, Li Q, Liu Z, Zhang R, Zhang L, Yue J.

01-08-2023

FEBS J.

<https://pubmed.ncbi.nlm.nih.gov/37528513/>

We previously identified glyceraldehyde 3-phosphate dehydrogenase (GAPDH) as one of the cyclic adenosine diphosphoribose (cADPR)'s binding proteins and found that GAPDH participates in cADPR-mediated Ca^{2+} release from endoplasmic reticulum via ryanodine receptors (RyRs). Here, we aimed to chemically synthesise and pharmacologically characterise novel cADPR analogues. Based on the simulated cADPR-GAPDH complex structure, we performed the structure-based drug screening, identified several small chemicals with high docking scores to cADPR's binding pocket in GAPDH and showed that two of these compounds, C244 and C346, are potential cADPR antagonists. We further synthesised several analogues of C346 and found that its analogue, G42, also mobilised Ca^{2+} release from lysosomes. G42 alkalinised lysosomal pH and inhibited autophagosome-lysosome fusion. Moreover, G42 markedly inhibited Zika virus (ZIKV, a flavivirus) or murine hepatitis virus (MHV, a β -coronavirus) infections of host cells. These results suggest that G42 inhibits virus infection, likely by triggering lysosomal Ca^{2+} mobilisation and inhibiting autophagy.

Ophthalmic complications during the dengue epidemic in Reunion Island in 2020: a case series and review of the literature.

Mbu-Nyamsi D, Vincent M, Perez-Fontana M, Best AL, Mesnard C, Villeroy F, Foucher A, Raffray L, Terrier CS, Bertolotti A.

02-08-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37528344/>

Introduction: Dengue is an arboviral disease transmitted by the dengue virus, whose vectors are *Aedes aegypti* and *Aedes albopictus*. The acute phase with its cohort of well-known symptoms is usually spontaneously favorable. Since 2020 in Reunion Island, a new symptom has

appeared: the ocular damage of dengue fever, which has already been described in South Asia and South-East Asia. We therefore decided to describe the clinical, biological, ophthalmological, therapeutic, and outcomes of patients with ocular manifestations during dengue fever in Reunion Island in 2020. **Patients and methods:** This was a retrospective observational study. Patients were included from January 2020 to August 2020 and then reassessed by teleconsultation 1 year later. The patients were identified from the French public health surveillance network by all ophthalmologists on the island. Medical data were collected directly from medical records. **Results:** Twenty-eight patients were included. The mean age was 41.9 years. Ocular involvement occurred approximately 9.2 days after the onset of dengue symptoms. The main symptoms were scotoma (71.4%) and sudden decrease of visual acuity (39.2%). Eighteen patients (64.2%) had macular involvement. Fourteen patients were treated with oral or intravenous corticosteroids. Twenty-two (78.5%) patients were evaluated by telephone one year later. Scotoma and decreased visual acuity persisted in 15 patients. Thirteen patients (59%) were bothered by night driving, 32% of patients had reading difficulties and 27% of patients became sensitive to prolonged exposure to screens. **Conclusion:** Ocular complications of dengue require early and collegial management to limit the risk of long-term sequelae. Further studies on the characteristics and complications of dengue fever are needed to better understand this disease.

Synthesis of Isolated DNA Aptamer and Its Application of AC-Electrothermal Flow-Based Rapid Biosensor for the Detection of Dengue Virus in a Spiked Sample.

Park H, Lee H, Lee M, Baek C, Park JA, Jang M, Kwon Y, Min J, Lee T.

01-08-2023

Bioconjug Chem.

<https://pubmed.ncbi.nlm.nih.gov/37527337/>

Development of a novel multi-epitope vaccine based on capsid and envelope protein against Chikungunya virus.

Ma S, Zhu F, Wen H, Rao M, Zhang P, Peng W, Cui Y, Yang H, Tan C, Chen J, Pan P.

01-08-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37526203/>

Chikungunya virus (CHIKV), a type A virus borne by mosquitoes that can cause major clinical manifestations including rash, fever and debilitating arthritis, grown into a reemerging serious public health issue. Currently, there is no licensed therapy or vaccine available for CHIKV, although the most promising form of treatment appears to be immunotherapy. Neutralizing antibodies for CHIKV can provide high protection for all CHIKV strains, as well as other alphaviruses. Development of a protective vaccine may be an effective strategy to prevent the outbreak of CHIKV and provide protection for travelers. In this study, we designed a multi-epitope vaccine with a 543-amino-

acid structure based on the E1, E2 and capsid proteins of CHIKV, including 6 CTL epitopes, 6 HTL epitopes, 12 linear B epitopes, along with the adjuvant β -defensin III. All T-cell epitopes were docked with their corresponding MHC alleles to validate their effect on inducing immune responses, and the vaccine's sequence was proven to have acceptable physicochemical properties. Further, the developed vaccine was docked with TLR3 and TLR8, both of which play an important role in recognizing RNA viruses. Basic analyses of the docked complexes and molecular dynamic simulations revealed that the vaccine interacted strongly with TLRs. Immunological simulations indicated that the vaccine could induce both cellular and humoral immunity. Hopefully, this proposed vaccine structure can serve as a viable candidate against CHIKV infection. Communicated by Ramaswamy H. Sarma.

Investigation of the impact of AXL, TLR3, and STAT2 in congenital Zika syndrome through genetic polymorphisms and protein-protein interaction network analyses.

Gomes JA, Sgarioni E, Boquett JA, Kowalski TW, Fraga LR, Terças-Trettel ACP, da Silva JH, Ribeiro BFR, Galera MF, de Oliveira TM, Carvalho de Andrade MDF, Carvalho IF, Schüler-Faccini L, Vianna FSL.

01-08-2023

Birth Defects Res.

<https://pubmed.ncbi.nlm.nih.gov/37526179/>

Introduction: Zika virus (ZIKV) is a human teratogen that causes congenital Zika syndrome (CZS). AXL, TLR3, and STAT2 are proteins involved in the ZIKV's entry into cells (AXL) and host's immune response (TLR3 and STAT2). In this study, we evaluated the role of genetic polymorphisms in these three genes as risk factors to CZS, and highlighted which proteins that interact with them could be important for ZIKV infection and teratogenesis.

Materials and methods: We evaluate eighty-eight children exposed to ZIKV during the pregnancy, 40 with CZS and 48 without congenital anomalies. The evaluated polymorphisms in AXL (rs1051008), TLR3 (rs3775291), and STAT2 (rs2066811) were genotyped using TaqMan® Genotyping Assays. A protein-protein interaction network was created in STRING database and analyzed in Cytoscape software. **Results:** We did not find any statistical significant association among the polymorphisms and the occurrence of CZS. Through the analyses of the network composed by AXL, TLR3, STAT2 and their interactions targets, we found that EGFR and SRC could be important proteins for the ZIKV infection and its teratogenesis.

Conclusion: In summary, our results demonstrated that the evaluated polymorphisms do not seem to represent risk factors for CZS; however, EGFR and SRC appear to be important proteins that should be investigated in future studies.

Evaluation of Dengue, Zika virus, and Chikungunya virus transmission by blood components in recipients of haematopoietic stem cell transplantation.

de Oliveira FN, Ferreira SC, Nishiya AS, Mendrone-Junior A, Batista MV, Rocha V, Costa SF.

01-08-2023

Transfus Med.

<https://pubmed.ncbi.nlm.nih.gov/37525935/>

Background: Brazil has a high prevalence of arboviruses, especially Dengue (DENV), Zika (ZKV), and Chikungunya (CHKV). **Objectives:** To study the risk of DENV, ZKV, and CHKV transmission by blood components in the haematopoietic stem cell transplantation (HSCT) population. **Methods:** Prospective cohort of HSCT recipients and donors performed at the Hospital das Clínicas da FMUSP, São Paulo-Brazil. Patients were evaluated by serology and RT-PCR for DENV, ZKV, and CHKV pre-transplantation and once a week until neutrophil grafting. In positive cases (positive RT-PCR and/or serology conversion), an investigation was carried out on the blood components that the patient received to evaluate the possibility of it being transfusion transmitted. **Results:** A total of 93 patients were included during the study period. The mean age was 52 years with a predominance of males (56.9%). We considered five (5.3%) DENV cases positive by seroconversion in our study. One patient had IgM seroconversion and the other four presented IgG seroconversion to DENV. In the investigation of the blood components, 145 individual samples were analysed. None of the investigated blood components showed a positive RT-PCR. **Conclusion:** We observed a low prevalence of DENV, ZKV, and CHKV in HSCT donors and recipients by serology and RT-PCR, and no case of blood transfusion transmission by RT-PCR.

[Second Sogupit Congress "emerging and re-emerging infectious diseases in Africa: governance, challenges and prospects". 13 - 14 October 2022, Conakry, Guinea].

Sow MS, Desclaux A, Keita AK, Makanera A, Traore MA, Traore A, Toure A, Sagnon M, Diop M, Barry AO, Diallo MOS, Camara A, Delamou A, LE Marcis F, Fortes Denguenovo L, Poda A, Alhassane A, Mohamed B, Savadogo M, Tolno A, Diakite D, Oury Keita M, Cissoko Y.

29-06-2023

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/37525678/>

Assessing the Relationship between Annual Surface Temperature Changes and the Burden of Dengue: Implications for Climate Change and Global Health Outcomes.

Mendoza-Cano O, Trujillo X, Huerta M, Ríos-Silva M, Lugo-Radillo A, Benites-Godínez V, Bricio-Barrios JA, Ríos-Bracamontes EF, Uribe-Ramos JM, Baltazar-Rodríguez GM, Murillo-Zamora E.

02-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505647/>

Maximizing the Potential of Attractive Targeted Sugar Baits (ATSBs) for Integrated Vector Management.

Njoroge TM, Hamid-Adiamoh M, Duman-Scheel M.

28-06-2023

Insects.

<https://pubmed.ncbi.nlm.nih.gov/37504591/>

Due to the limitations of the human therapeutics and vaccines available to treat and prevent mosquito-borne diseases, the primary strategy for disease mitigation is through vector control. However, the current tools and approaches used for mosquito control have proven insufficient to prevent malaria and arboviral infections, such as dengue, Zika, and lymphatic filariasis, and hence, these diseases remain a global public health threat. The proven ability of mosquito vectors to adapt to various control strategies through insecticide resistance, invasive potential, and behavioral changes from indoor to outdoor biting, combined with human failures to comply with vector control requirements, challenge sustained malaria and arboviral disease control worldwide. To address these concerns, increased efforts to explore more varied and integrated control strategies have emerged. These include approaches that involve the behavioral management of vectors. Attractive targeted sugar baits (ATSBs) are a vector control approach that manipulates and exploits mosquito sugar-feeding behavior to deploy insecticides. Although traditional approaches have been effective in controlling malaria vectors indoors, preventing mosquito bites outdoors and around human dwellings is challenging. ATSBs, which can be used to curb outdoor biting mosquitoes, have the potential to reduce mosquito densities and clinical malaria incidence when used in conjunction with existing vector control strategies. This review examines the available literature regarding the utility of ATSBs for mosquito control, providing an overview of ATSB active ingredients (toxicants), attractants, modes of deployment, target organisms, and the potential for integrating ATSBs with existing vector control interventions.

Peptide aptamer-based time-resolved fluoroimmunoassay for CHIKV diagnosis.

Liu T, Gao C, Wang J, Song J, Chen X, Chen H, Zhao X, Tang H, Gu D.

27-07-2023

Viral J.

<https://pubmed.ncbi.nlm.nih.gov/37501131/>

A spatial analysis of co-circulating dengue and chikungunya virus infections during an epidemic in a region of Northeastern Brazil.

de Mendonça MFS, Silva APSC, Lacerda HR.

2023

Spat Spatiotemporal Epidemiol.

<https://pubmed.ncbi.nlm.nih.gov/37500226/>

The aim of this study was to describe, through spatial analysis, the cases of arboviruses (dengue and

chikungunya), including deaths, during the first epidemic after the circulation of the chikungunya virus (CHIKV) in the state of Pernambuco, Northeastern Brazil. This was an ecological study in both Pernambuco and the state capital, Recife, from 2015 to 2018. The odds ratios (OR) were estimated, and the statistical significance was considered $p \leq 0.05$. For the spatial analysis, Kulldorff's space-time scan statistics method was adopted to identify spatial clusters and to provide the relative risk (RR). In order to assess the significance at a level of $p < 0.01$ of the model, the number of Monte Carlo replications was 999 times. To perform the scan statistics we used the Poisson probability model, with a circular scanning window; annual temporal precision and retrospective analysis. A total of 227 deaths and 158,728 survivors from arboviruses was reported during the study period, with 100 deaths from dengue and 127 from CHIKV. The proportion of deaths from dengue was 0.08% and from chikungunya was 0.35%. The proportion of all those infected (deaths plus survivors) with dengue was 77.42% and with chikungunya was 22.58%. Children aged 0 to 9 years were around 3 times more likely to die than the reference group (OR 2.84; CI95% 1.16-5.00). From the age of 40, the chances of death increased significantly: 40-49 (OR 2.52; CI95% 1.19-5.29), 50-59 (OR 5.55; CI95% 2.76-11.17) and 60 or more (OR 14.90; CI95% 7.79-28.49). Males were approximately twice as likely to die as females (OR 1.77; CI95% 1.36-2.30). White-skinned people were less likely to die compared to non-white (OR 0.60; CI95% 0.41-0.87). The space-time analysis of prevalence in the state of Pernambuco revealed the presence of four clusters in the years 2015 and 2016, highlighting the Metropolitan Macro-region with a relative risk=4 and the Agreste and Hinterland macro-regions with a relative risk=3.3. The spatial distribution of the death rate in the municipality of Recife smoothed by the local empirical Bayesian estimator enabled a special pattern to be identified in the southwest and northeast of the municipality. The spatiotemporal analysis of the death rate revealed the presence of two clusters in the year 2015. In the primary cluster, it may be noted that the aforementioned aggregate presented a $RR=7.2$, and the secondary cluster presented a $RR=6.0$. The spatiotemporal analysis with Kulldorff's space-time scan statistics method, proved viable in identifying the risk areas for the occurrence of arboviruses, and could be included in surveillance routines so as to optimize prevention strategies during future epidemics.

A comprehensive protein interaction map and druggability investigation prioritized dengue virus NS1 protein as promising therapeutic candidate.

Farooq QUA, Aiman S, Ali Y, Shaukat Z, Ali Y, Khan A, Samad A, Wadood A, Li C.

27-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37498862/>

Travel-Associated Dengue Cases - United States, 2010-2021.

Wong JM, Rivera A, Volkman HR, Torres-Velasquez B, Rodriguez DM, Paz-Bailey G, Adams LE.

Juil-2023

MMWR Morb Mortal Wkly Rep.

<https://pubmed.ncbi.nlm.nih.gov/37498793/>

Splenic macrophages escalate dengue disease.

Dunagan MM, Fox JM.

Août-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37488257/>

High-resolution mapping reveals the mechanism and contribution of genome insertions and deletions to RNA virus evolution.

Aguilar Rangel M, Dolan PT, Taguwa S, Xiao Y, Andino R, Frydman J.

Août-2023

Proc Natl Acad Sci U S A.

<https://pubmed.ncbi.nlm.nih.gov/37487061/>

RNA viruses rapidly adapt to selective conditions due to the high intrinsic mutation rates of their RNA-dependent RNA polymerases (RdRps). Insertions and deletions (indels) in viral genomes are major contributors to both deleterious mutational load and evolutionary novelty, but remain understudied. To characterize the mechanistic details of their formation and evolutionary dynamics during infection, we developed a hybrid experimental-bioinformatic approach. This approach, called MultiMatch, extracts insertions and deletions from ultradeep sequencing experiments, including those occurring at extremely low frequencies, allowing us to map their genomic distribution and quantify the rates at which they occur. Mapping indel mutations in adapting poliovirus and dengue virus populations, we determine the rates of indel generation and identify mechanistic and functional constraints shaping indel diversity. Using poliovirus RdRp variants of distinct fidelity and genome recombination rates, we demonstrate tradeoffs between fidelity and Indel generation. Additionally, we show that maintaining translation frame and viral RNA structures constrain the Indel landscape and that, due to these significant fitness effects, Indels exert a significant deleterious load on adapting viral populations. Conversely, we uncover positively selected Indels that modulate RNA structure, generate protein variants, and produce defective interfering genomes in viral populations. Together, our analyses establish the kinetic and mechanistic tradeoffs between misincorporation, recombination, and Indel rates and reveal functional principles defining the central role of Indels in virus evolution, emergence, and the regulation of viral infection.

Human FcγRIIIa activation on splenic macrophages drives dengue pathogenesis in mice.

Yamin R, Kao KS, MacDonald MR, Cantaert T, Rice CM, Ravetch JV, Bournazos S.

Août-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37429907/>

Although dengue virus (DENV) infection typically causes asymptomatic disease, DENV-infected patients can experience severe complications. A risk factor for symptomatic disease is pre-existing anti-DENV IgG antibodies. Cellular assays suggested that these antibodies can enhance viral infection of Fcγ receptor (FcγR)-expressing myeloid cells. Recent studies, however, revealed more complex interactions between anti-DENV antibodies and specific FcγRs by demonstrating that modulation of the IgG Fc glycan correlates with disease severity. To investigate the in vivo mechanisms of antibody-mediated dengue pathogenesis, we developed a mouse model for dengue disease that recapitulates the unique complexity of human FcγRs. In in vivo mouse models of dengue disease, we discovered that the pathogenic activity of anti-DENV antibodies is exclusively mediated through engagement of FcγRIIIa on splenic macrophages, resulting in inflammatory sequelae and mortality. These findings highlight the importance of IgG-FcγRIIIa interactions in dengue, with important implications for the design of safer vaccination approaches and effective therapeutic strategies.

Identification of alpha-linolenic acid as a broad-spectrum antiviral against zika, dengue, herpes simplex, influenza virus and SARS-CoV-2 infection.

Feng Y, Yang Y, Zou S, Qiu S, Yang H, Hu Y, Lin G, Yao X, Liu S, Zou M.

Août-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/37429528/>

Inhibiting immunoregulatory amidase NAAA blocks ZIKV maturation in Human Neural Stem Cells.

Lai M, La Rocca V, Iacono E, Filipponi C, De Carli A, Favaro D, Fonnesu R, Filippini F, Spezia PG, Amato R, Catelli E, Matteo B, Lottini G, Onorati M, Clementi N, Freer G, Piomelli D, Pistello M.

Août-2023

Antiviral Res.

<https://pubmed.ncbi.nlm.nih.gov/37414288/>

Recent evidence suggests that lipids play a crucial role in viral infections beyond their traditional functions of supplying envelope and energy, and creating protected niches for viral replication. In the case of Zika virus (ZIKV), it alters host lipids by enhancing lipogenesis and suppressing β-oxidation to generate viral factories at the endoplasmic reticulum (ER) interface. This discovery prompted us to hypothesize that interference with lipogenesis could serve as a dual antiviral and anti-inflammatory strategy to combat the replication of positive sense single-stranded RNA (ssRNA+) viruses. To test this hypothesis, we examined the impact of inhibiting N-Acylethanolamine acid amidase (NAAA) on ZIKV-infected human Neural Stem Cells. NAAA is responsible for the hydrolysis of palmitoylethanolamide (PEA) in lysosomes and endolysosomes. Inhibition of NAAA results in PEA accumulation, which activates peroxisome

proliferator-activated receptor- α (PPAR- α), directing β -oxidation and preventing inflammation. Our findings indicate that inhibiting NAAA through gene-editing or drugs moderately reduces ZIKV replication by approximately one log₁₀ in Human Neural Stem Cells, while also releasing immature virions that have lost their infectivity. This inhibition impairs furin-mediated prM cleavage, ultimately blocking ZIKV maturation. In summary, our study highlights NAAA as a host target for ZIKV infection.

Adenovirus vector produced Zika virus-like particles induce a long-lived neutralising antibody response in mice.

Carrera J, Aktepe TE, Earnest L, Christiansen D, Wheatley AK, Tan HX, Chung AW, Collett S, McPherson K, Torresi J, Mackenzie JM, Simmons CP.

25-07-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37391311/>

The Density of Aedes albopictus in a High-Latitude and High-Risk Dengue Fever Transmission Region in Shandong Province, Northern China.

Huang X, Liu L, Liu S, Cheng P, Gong M, Wang X, Liu H.

AOÛT-2023

Vector Borne Zoonotic Dis.

<https://pubmed.ncbi.nlm.nih.gov/37389829/>

Molecular Detection of Dengue Virus, Zika Virus, and Chikungunya Virus Arboviruses in Neotropical Bats.

Hernández-Aguilar I, Lorenzo C, Ramírez-Palacios LR, Santos-Moreno A, Naranjo EJ.

AOÛT-2023

Vector Borne Zoonotic Dis.

<https://pubmed.ncbi.nlm.nih.gov/37389819/>

Background: The dengue, Zika, and Chikungunya arboviruses have spread in America in the past year, thus becoming global health issues. These viruses are maintained in nature in two transmission cycles: an urban cycle, transmitted from hematophagous mosquitoes to humans, and a wild cycle, recorded only in Africa and Asia, involving mosquitoes and nonhuman primates as natural hosts. The evidence shows that these arboviruses infect other wild mammals in America, such as rodents, marsupials, and bats. This study aimed to determine the potential natural infection of arboviruses in bats captured in contrasting sites (tropical forests, urban areas, and caves) in Oaxaca, Mexico. **Materials and Methods:** Liver samples were collected from some bats and tested for RNA from dengue, Zika, and Chikungunya with the quantitative real-time PCR assay. We analyzed 162 samples that encompassed 23 bat species. **Results:** No natural infection with any of the three arboviruses was detected in any sample tested. **Conclusion:** The existence of a wild cycle of the three arboviruses in the American continent is not ruled out. However, owing to the low or zero prevalence recorded in other studies and the present

study, bats are likely involved in the arbovirus transmission cycle as accidental hosts.

Prevalence and Predictors of COVID-19 Long-Term Symptoms: A Cohort Study from the Amazon Basin.

Silva KM, Freitas DCA, Medeiros SS, Miranda LVA, Carmo JBM, Silva RG, Becker LL, Abreu ES, Buranello L, Souza MSM, Nadruz W, Fernandes-Silva MM, Maguire JH, Toledo-Cornell C, Silvestre OM.

26-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37364863/>

It remains unclear whether a previous history of tropical infectious diseases and a second SARS-CoV-2 infection may influence the likelihood of later symptoms. In this prospective cohort study, individuals infected with SARS-CoV-2 were followed up by telephone shortly after diagnosis of COVID-19 and again 12 months later. Poisson regression was used to identify the predictors of the highest number of symptoms in the post-COVID-19 syndrome. A total of 1,371 patients with COVID-19, with a mean age of 39.7 \pm 11.7 years and 50% female, were followed for 12 months. Reinfection was found in 32 (2.3%) participants, and 806 (58.8%) individuals reported a previous history of dengue, malaria, Zika, chikungunya, leprosy, and visceral leishmaniasis. Eight hundred seventy-seven (63.9%) participants reported late symptoms related to COVID-19. After adjusting for multiple factors, female sex, non-White race, number of acute-phase symptoms, body mass index, and reinfection were independent predictors of higher number of symptoms in post-COVID-19 syndrome. Female sex, non-White race, number of acute-phase symptoms, body mass index, and reinfection, but not previous endemic tropical diseases, were associated with long-term symptoms.

Prevalence, Characteristics, and Outcomes Associated with Acute Kidney Injury among Adult Patients with Severe Dengue in Mainland China.

Wang C, Hong W, Ou Z, Yang H, Zhao L, Zhang Z, Zhang F.

26-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37364862/>

Acute kidney injury (AKI) can occur in adult patients with severe dengue (SD) and have serious clinical outcomes. This study aimed to determine the prevalence, characteristics, risk factors, and clinical outcomes of AKI in adult patients with SD; the correlation of dengue virus (DENV) serological and virological profiles with AKI; and the clinical features of patients with severe AKI who received renal replacement treatment (RRT). This multicenter study was conducted in Guangdong Province, China, between January 2013 and November 2019. A total of 242 patients were evaluated, of which 85 (35.1%) developed AKI and 32 (13.2%) developed severe AKI (stage 3). Patients with AKI had a higher fatality rate (22.4% versus 5.7%; $P < 0.001$) and longer length of hospital stay (median: 13 versus 9 days; $P < 0.001$). Independent risk factors for AKI were hypertension (odds ratio [OR]: 2.03;

95% CI: 1.10-3.76), use of nephrotoxic drugs (OR: 1.90; 95% CI: 1.00-3.60), respiratory distress (OR: 4.15; 95% CI: 1.787-9.632), high international normalized ratio (INR) levels (OR: 6.44; 95% CI: 1.89-21.95), and hematuria (OR: 2.12; 95% CI: 1.14-3.95). There was no significant association between DENV serological and virological profiles and the presence or absence of AKI. Among patients with severe AKI, those who received RRT had a longer length of hospital stay and similar fatality rate. Hence, adult patients with SD should be closely monitored for the development of AKI to enable timely and appropriate therapy.

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

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

20-06-2023

Am J Trop Med Hyg.

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

Identification and validation of the first EST-SSR markers based on transcriptome of *Anopheles darlingi*, the primary transmitter of malaria in Brazil.

de Souza AT, Batista JS, Guimarães-Marques GM, Cunha-Machado AS, Rafael MS.

Août-2023

Mol Biol Rep.

<https://pubmed.ncbi.nlm.nih.gov/37314602/>

Previous Dengue Infection among Children in Puerto Rico and Implications for Dengue Vaccine Implementation.

Adams LE, Hitchings MDT, Medina FA, Rodriguez DM, Sánchez-González L, Moore H, Whitehead SS, Muñoz-Jordán JL, Rivera-Amill V, Paz-Bailey G.

12-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37308104/>

Longitudinal evolution of electroencephalogram (EEG): Findings over five years of follow-up in children with Zika-related microcephaly from the Microcephaly Epidemic Research Group Pediatric Cohort (2015-2020).

Carvalho MDCG, Ximenes RAA, Andrade-Valença LPA, Montarroyos UR, Diniz GTN, Rodrigues LC, Brickley EB, Eickmann SH, de Araujo TVB, Martelli CMT, da Silva PFS, Miranda-Filho DB; Microcephaly Epidemic Research Group (MERG).

Août-2023

Seizure.

<https://pubmed.ncbi.nlm.nih.gov/37302158/>

Objective: To assess the longitudinal evolution of EEG findings in children with Zika related-microcephaly (ZRM) and to evaluate the associations of these patterns with the children's clinical and neuroimaging characteristics.

Methods: As part of the follow-up of the Microcephaly Epidemic Research Group Pediatric Cohort (MERG-PC) in Recife, Brazil, we performed serial EEG recordings in a subgroup of children with ZRM to evaluate changes in background rhythms and epileptiform activity (EA). Latent class analysis was used to identify patterns in the evolution of EA over time; clinical and neuroimaging findings were compared across the identified groups. **Results:** Out of the 72 children with ZRM who were evaluated during 190 EEGs/videoEEGs, all participants presented with abnormal background activity, 37.5% presented with an alpha-theta rhythmic activity, and 25% presented with sleep spindles, which were less commonly observed in children with epilepsy. EA changed over time in 79.2% of children, and three distinct trajectories were identified: (i) multifocal EA over time, (ii) no discharges/focal EA evolving to focal/multifocal EA, and (iii) focal/multifocal EA evolving to epileptic encephalopathy patterns (e.g., hypsarrhythmia or continuous EA in sleep). The multifocal EA over time trajectory was associated with periventricular and thalamus/basal ganglia calcifications, brainstem and corpus callosum atrophy and had less focal epilepsy, whereas the children in the trajectory which evolved to epileptic encephalopathy patterns had more frequently focal epilepsy. **Significance:** These findings suggest that, in most children with ZRM, trajectories of changes in EA can be identified and associated with neuroimaging and clinical features.

A meta-analysis reveals that dragonflies and damselflies can provide effective biological control of mosquitoes.

Priyadarshana TS, Slade EM.

Août-2023

J Anim Ecol.

<https://pubmed.ncbi.nlm.nih.gov/37272224/>

Measuring the effects of typhoon trajectories on dengue outbreaks in tropical regions of Taiwan: 1998-2019.

Kao B, Lin CH, Wen TH.

Août-2023

Int J Biometeorol.

<https://pubmed.ncbi.nlm.nih.gov/37266834/>

Dengue fever is a rapidly spreading mosquito-borne contagion. However, the effects of extreme rainfall events on dengue occurrences have not been widely evaluated. With their immense precipitation and high winds, typhoons may have distinct effects on dengue occurrence from those during other heavy rain events. Frequented by typhoons and situated in the tropical climate zone, southern Taiwan is an appropriate study area due to its isolated geographic environment. Each subject to distinct orographic effects on typhoon structure and typhoon-induced precipitation, 9 typhoon trajectories around Taiwan have not been observed until now. This study analyzes typhoon-induced precipitation and examines historical typhoon events by trajectory to determine the effects of typhoons on dengue occurrences in different urban contexts of Tainan and Kaohsiung in high-epidemic southern Taiwan. We employed data from 1998 to 2019

and developed logistic regression models for modeling dengue occurrence while taking 28-day lag effects into account. We considered factors including typhoon trajectory, occurrence, and typhoon-induced precipitation to dengue occurrences. Our results indicate that typhoon trajectories are a significant risk factor for dengue occurrence. Typhoons affect dengue occurrence differently by trajectory. One out of four northbound (along the Taiwan Strait) and four out of five westbound (across Taiwan) typhoons were found to be positively correlated with dengue occurrences in southern Taiwan. We observe that typhoon-induced precipitation is not associated with dengue occurrence in southern Taiwan, which suggests that wind destruction during typhoon events may serve as the primary cause for their positive effects by leaving debris suitable for mosquito habitats. Our findings provide insights into the impact of typhoons by trajectory on dengue occurrence, which can improve the accuracy of future dengue forecasts in neighboring regions with similar climatic contexts.

Epidemiological and clinical features of the 2016-2018 Zika virus outbreak in northern Argentina.

Byrne AB, Bonnin FA, Bruno A, Bono MM, Contrini MM, López EL, Quipildor MO, Talarico LB.
03-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37026534/>

Routine blood parameters of dengue infected children and adults. A meta-analysis.

Low GK, Jiee SF, Masilamani R, Shanmuganathan S, Rai P, Manda M, Omosumwen OF, Kagize J, Gavino AI, Azahar A, Jabbar MA.

Sept-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36593636/>

No room for complacency to control dengue in Nepal.

Subedi D, Subedi S, Acharya KP, Sah R.

28-07-2023

QJM.

<https://pubmed.ncbi.nlm.nih.gov/36448704/>

Applicability of the Mexican ovitrap system for Aedes vector surveillance in Colombia.

Wright E, Carrillo MA, Matamoros D, Sanchez RC, Yañez J, Di Lorenzo G, Villa JM, Kroegeer A.

Sept-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36384430/>

Ovitrap can detect Aedes vectors at an early stage and can serve as an alarm indicator for outbreak prediction. This study aimed to summarize the available literature about the ovitrap system and to determine its feasibility, required resources and costs when installing and

maintaining this vector surveillance system in the municipality of Los Patios, Colombia. A scoping review to assess the role of ovitraps as a tool for Aedes vector surveillance was conducted. The subsequent fieldwork consisted of mapping the municipality, manufacturing, and installing 40 ovitraps in 10 blocks, revising them weekly for 4 weeks by two half-time employed vector control technicians, and carrying out a cost analysis. A total of 38 studies were included in this review showing that ovitraps had a better performance than other entomological surveillance methods and a positive correlation with other entomological and disease variables. From the field results over 4 weeks, a high proportion of positive ovitraps (80%, 90%, 75%, 97.5%) and positive blocks (100%) as well as a good acceptance by house owners (76.9%), were identified. Operational indicators such as average installation time of the ovitraps (10h15 m), weekly reading and reinstallation (on average 7h27 m) and the cost of the intervention (COL\$1,142,304.47/US\$297) were calculated. Literature shows that ovitraps are sensitive to detect the presence of Aedes mosquitoes, providing data efficiently and timely for outbreak prediction. The field testing showed it is an affordable and feasible method in the context of a Colombian municipality and similar endemic areas.

Role of air pollutants in dengue fever incidence: evidence from two southern cities in Taiwan.

Lu HC, Lin FY, Huang YH, Kao YT, Loh EW.

Sept-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36262027/>

Air pollution may be involved in spreading dengue fever (DF) besides rainfalls and warmer temperatures. While particulate matter (PM), especially those with diameter of 10 µm (PM10) or 2.5 µm or less (PM2.5), and NO2 increase the risk of coronavirus 2 infection, their roles in triggering DF remain unclear. We explored if air pollution factors predict DF incidence in addition to the classic climate factors. Public databases and DF records of two southern cities in Taiwan were used in regression analyses. Month order, PM10 minimum, PM2.5 minimum, and precipitation days were retained in the enter mode model, and SO2 minimum, O3 maximum, and CO minimum were retained in the stepwise forward mode model in addition to month order, PM10 minimum, PM2.5 minimum, and precipitation days. While PM2.5 minimum showed a negative contribution to the monthly DF incidence, other variables showed the opposite effects. The sustain of month order, PM10 minimum, PM2.5 minimum, and precipitation days in both regression models confirms the role of classic climate factors and illustrates a potential biological role of the air pollutants in the life cycle of mosquito vectors and dengue virus and possibly human immune status. Future DF prevention should concern the contribution of air pollution besides the classic climate factors.

Rapid Generation of Recombinant Flaviviruses Using Circular Polymerase Extension Reaction.

Dong HL, He MJ, Wang QY, Cui JZ, Chen ZL, Xiong XH, Zhang LC, Cheng H, Xiong GQ, Hu A, Lu YY, Cheng CL, Meng ZX, Zhu C, Zhao G, Liu G, Chen HP.

17-07-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37515065/>

The genus *Flavivirus* is a group of arthropod-borne single-stranded RNA viruses, which includes important human and animal pathogens such as Japanese encephalitis virus (JEV), Zika virus (ZIKV), Dengue virus (DENV), yellow fever virus (YFV), West Nile virus (WNV), and Tick-borne encephalitis virus (TBEV). Reverse genetics has been a useful tool for understanding biological properties and the pathogenesis of flaviviruses. However, the conventional construction of full-length infectious clones for flavivirus is time-consuming and difficult due to the toxicity of the flavivirus genome to *E. coli*. Herein, we applied a simple, rapid, and bacterium-free circular polymerase extension reaction (CPER) method to synthesize recombinant flaviviruses in vertebrate cells as well as insect cells. We started with the de novo synthesis of the JEV vaccine strain SA-14-14-2 in Vero cells using CPER, and then modified the CPER method to recover insect-specific flaviviruses (ISFs) in mosquito C6/36 cells. Chimeric Zika virus (ChinZIKV) based on the Chaoyang virus (CYV) backbone and the *Culex* flavivirus reporter virus expressing green fluorescent protein (CxFV-GFP) were subsequently rescued in C6/36 cells. CPER is a simple method for the rapid generation of flaviviruses and other potential RNA viruses. A CPER-based recovery system for flaviviruses of different host ranges was established, which would facilitate the development of countermeasures against flavivirus outbreaks in the future.

A Review: Understanding Molecular Mechanisms of Antibody-Dependent Enhancement in Viral Infections.

Sawant J, Patil A, Kurle S.

14-07-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37515055/>

A Lateral Flow Assay for the Detection of *Leptospira* lipL32 Gene Using CRISPR Technology.

Natarajan S, Joseph J, Vinayagamurthy B, Estrela P.

20-07-2023

Sensors (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37514838/>

Increased In Vivo Exposure of N-(4-Hydroxyphenyl) Retinamide (4-HPR) to Achieve Plasma Concentrations Effective against Dengue Virus.

Martin AJ, Shackelford DM, Charman SA, Wagstaff KM, Porter CJH, Jans DA.

18-07-2023

Pharmaceutics.

<https://pubmed.ncbi.nlm.nih.gov/37514160/>

N-(4-hydroxyphenyl) retinamide (4-HPR, or fenretinide) has promising in vitro and in vivo antiviral activity against a range of flaviviruses and an established safety record, but there are challenges to its clinical use. This study evaluated the in vivo exposure profile of a 4-HPR dosage regime previously shown to be effective in a mouse model of severe dengue virus (DENV) infection, comparing it to an existing formulation for human clinical use for other indications and developed/characterised self-emulsifying lipid-based formulations of 4-HPR to enhance 4-HPR in vivo exposure. Pharmacokinetic (PK) analysis comprising single-dose oral and IV plasma concentration-time profiles was performed in mice; equilibrium solubility testing of 4-HPR in a range of lipids, surfactants and cosolvents was used to inform formulation approaches, with lead formulation candidates digested in vitro to analyse solubilisation/precipitation prior to in vivo testing. PK analysis suggested that effective plasma concentrations could be achieved with the clinical formulation, while novel lipid-based formulations achieved > 3-fold improvement. Additionally, 4-HPR exposure was found to be limited by both solubility and first-pass intestinal elimination but could be improved through inhibition of cytochrome P450 (CYP) metabolism. Simulated exposure profiles suggest that a b.i.d dosage regime is likely to maintain 4-HPR above the minimum effective plasma concentration for anti-DENV activity using the clinical formulation, with new formulations/CYP inhibition viable options to increase exposure in the future.

Whole Yeast Vaccine Displaying ZIKV B and T Cell Epitopes Induces Cellular Immune Responses in the Murine Model.

Silva AJD, de Jesus ALS, Leal LRS, de Macêdo LS, da Silva Barros BR, de Sousa GF, da Paz Leôncio Alves S, Pena LJ, de Melo CML, de Freitas AC.

06-07-2023

Pharmaceutics.

<https://pubmed.ncbi.nlm.nih.gov/37514084/>

Novel Lipophilic Hydroxamates Based on Spirocarbocyclic Hydantoin Scaffolds with Potent Antiviral and Trypanocidal Activity.

Pardali V, Giannakopoulou E, Mpekoulis G, Tsopela V, Panos G, Taylor MC, Kelly JM, Vassilaki N, Zoidis G.

24-07-2023

Pharmaceutics (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37513957/>

Galactoside-Based Molecule Enhanced Antimicrobial Activity through Acyl Moiety Incorporation: Synthesis and In Silico Exploration for Therapeutic Target.

Ahmed F, Al-Mijalli SH, Abdallah EM, Eissa IH, Ali F, Bhat AR, Jamalis J, Ben Hadda T, Kawsar SMA.

13-07-2023

Pharmaceutics (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37513910/>

In this study, a series of galactoside-based molecules, compounds of methyl β -D-galactopyranoside (MDGP, **1**), were selectively acylated using 2-bromobenzoyl chloride to obtain 6-O-(2-bromobenzoyl) substitution products, which were then transformed into 2,3,4-tri-O-6-(2-bromobenzoyl) compounds (**2-7**) with various nontraditional acyl substituents. The chemical structures of the synthesized analogs were characterized by spectroscopic methods and physicochemical and elemental data analyses. The antimicrobial activities of the compounds against five human pathogenic bacteria and two phyto-fungi were evaluated in vitro and it was found that the acyl moiety-induced synthesized analogs exhibited varying levels of antibacterial activity against different bacteria, with compounds **3** and **6** exhibiting broad-spectrum activity and compounds **2** and **5** exhibiting activity against specific bacteria. Compounds **3** and **6** were tested for MIC (minimum inhibitory concentration) and MBC (minimum bactericidal concentration) based on their activity. The synthesized analogs were also found to have potential as a source of new antibacterial agents, particularly against gram-positive bacteria. The antifungal results suggested that the synthesized analogs could be a potential source of novel antifungal agents. Moreover, cytotoxicity testing revealed that the compounds are less toxic. A structure-activity relationship (SAR) investigation revealed that the lauroyl chain [$\text{CH}_3(\text{CH}_2)_{10}\text{CO}-$] and the halo-aromatic chain [$3(4)-\text{Cl.C}_6\text{H}_4\text{CO}-$] in combination with sugar, had the most potent activity against bacterial and fungal pathogens. Density functional theory (DFT)-calculated thermodynamic and physicochemical parameters, and molecular docking, showed that the synthesized molecule may block dengue virus 1 NS2B/NS3 protease (3L6P). A 150 ns molecular dynamic simulation indicated stable conformation and binding patterns in a stimulating environment. In silico ADMET calculations suggested that the designed (MDGP, **1**) had good drug-likeness values. In summary, the newly synthesized MDGP analogs exhibit potential antiviral activity and could serve as a therapeutic target for dengue virus 1 NS2B/NS3 protease.

Coinfections and Superinfections Associated with COVID-19 in Colombia: A Narrative Review.

Dueñas D, Daza J, Liscano Y.

20-07-2023

Medicina (Kaunas).

<https://pubmed.ncbi.nlm.nih.gov/37512147/>

The COVID-19 pandemic has had significant impacts on healthcare systems around the world, including in Latin America. In Colombia, there have been over 23,000 confirmed cases and 100 deaths since 2022, with the highest number of cases occurring in females and the highest number of deaths in males. The elderly and those with comorbidities, such as arterial hypertension, diabetes mellitus, and respiratory diseases, have been particularly affected. Coinfections with other microorganisms, including dengue virus, *Klebsiella pneumoniae*, and *Mycobacterium tuberculosis*, have also been a significant factor in increasing morbidity and mortality rates in COVID-19 patients. It is important for surveillance systems

to be improved and protocols to be established for the early detection and management of coinfections in COVID-19. In addition to traditional treatments, alternatives such as zinc supplementation and nanomedicine may have potential in the fight against COVID-19. It is also crucial to consider the social, labor, educational, psychological, and emotional costs of the pandemic and to address issues such as poverty and limited access to potable water in order to better prepare for future pandemics.

Multidimensional Machine Learning Model to Calculate a COVID-19 Vulnerability Index.

Rosero Perez PA, Realpe Gonzalez JS, Salazar-Cabrera R, Restrepo D, López DM, Blobel B.

15-07-2023

J Pers Med.

<https://pubmed.ncbi.nlm.nih.gov/37511754/>

Repurposing Anti-Dengue Compounds against Monkeypox Virus Targeting Core Cysteine Protease.

Imran M, Abida, Alotaibi NM, Thabet HK, Alruwaili JA, Eltaib L, Alshehri A, Alsaiari AA, Kamal M, Alshammari AMA.

18-07-2023

Biomedicines.

<https://pubmed.ncbi.nlm.nih.gov/37509664/>

The monkeypox virus (MPXV) is an enveloped, double-stranded DNA virus belonging to the genus Orthopox viruses. In recent years, the virus has spread to countries where it was previously unknown, turning it into a worldwide emergency for public health. This study employs a structural-based drug design approach to identify potential inhibitors for the core cysteine proteinase of MPXV. During the simulations, the study identified two potential inhibitors, compound CHEMBL32926 and compound CHEMBL4861364, demonstrating strong binding affinities and drug-like properties. Their docking scores with the target protein were -10.7 and -10.9 kcal/mol, respectively. This study used ensemble-based protein-ligand docking to account for the binding site conformation variability. By examining how the identified inhibitors interact with the protein, this research sheds light on the workings of the inhibitors' mechanisms of action. Molecular dynamic simulations of protein-ligand complexes showed fluctuations from the initial docked pose, but they confirmed their binding throughout the simulation. The MMGBSA binding free energy calculations for CHEMBL32926 showed a binding free energy range of (-9.25 to -9.65) kcal/mol, while CHEMBL4861364 exhibited a range of (-41.66 to -31.47) kcal/mol. Later, analogues were searched for these compounds with 70% similarity criteria, and their IC_{50} was predicted using pre-trained machine learning models. This resulted in identifying two similar compounds for each hit with comparable binding affinity for cysteine proteinase. This study's structure-based drug design approach provides a promising strategy for identifying new drugs for treating MPXV infections.

Multicenter study of the natural history and therapeutic responses of patients with chikungunya, focusing on acute and chronic musculoskeletal manifestations - a study protocol from the clinical and applied research in Chikungunya (REPLICK network).

da Silva Duarte G, Jones AD, de Goes Cavalcanti LP, de Melo Rêgo MJB, Ribeiro GS, Boyton RJ, Pereira DB, Croda JHR, Costa FTM, Duarte AP, Consolaro MEL, Stabeli RG, Negrão FJ, Proença-Modena JL, Villalobos-Salcedo JM, da Rocha Castelar Pinheiro G, de Barros Albuquerque AP, de Almeida Barreto FK, Moreira J, Ferrari IC, Évora PM, da Silva VRS, Lacerda MVG, Altmann DM; REPLICK network; Siqueira AM.

28-07-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37507666/>

Background: Chikungunya is associated with high morbidity and the natural history of symptomatic infection has been divided into three phases (acute, post-acute, and chronic) according to the duration of musculoskeletal symptoms. Although this classification has been designed to help guide therapeutic decisions, it does not encompass the complexity of the clinical expression of the disease and does not assist in the evaluation of the prognosis of severity nor chronic disease. Thus, the current challenge is to identify and diagnose musculoskeletal disorders and to provide the optimal treatment in order to prevent perpetuation or progression to a potentially destructive disease course. **Methods:** The study is the first product of the Clinical and Applied Research Network in Chikungunya (REPLICK). This is a prospective, outpatient department-based, multicenter cohort study in Brazil. Four work packages were defined: i. Clinical research; ii) Translational Science - comprising immunology and virology streams; iii) Epidemiology and Economics; iv) Therapeutic Response and clinical trials design. Scheduled appointments on days 21 (D21) \pm 7 after enrollment, D90 \pm 15, D120 \pm 30, D180 \pm 30; D360 \pm 30; D720 \pm 60, and D1080 \pm 60 days. On these visits a panel of blood tests are collected in addition to the clinical report forms to obtain data on socio-demographic, medical history, physical examination and questionnaires devoted to the evaluation of musculoskeletal manifestations and overall health are performed. Participants are asked to consent for their specimens to be maintained in a biobank. Aliquots of blood, serum, saliva, PAXgene, and when clinically indicated to be examined, synovial fluid, are stored at -80° C. The study protocol was submitted and approved to the National IRB and local IRB at each study site. **Discussion:** Standardized and harmonized patient cohorts are needed to provide better estimates of chronic arthralgia development, the clinical spectra of acute and chronic disease and investigation of associated risk factors. This study is the largest evaluation of the long-term sequelae of individuals infected with CHIKV in the Brazilian population focusing on musculoskeletal manifestations, mental health, quality of life, and chronic pain. This information will both define disease burden and costs associated with CHIKV infection, and better inform therapeutic guidelines.

Knowledge, Attitudes and Practices About Zika Virus Infection Among Women of Reproductive Age in Central Brooklyn, New York City, USA.

Dowling R, Thompson AB, Kolokotronis SO.

28-07-2023

J Community Health.

<https://pubmed.ncbi.nlm.nih.gov/37507524/>

Imported and autochthonous dengue in Spain.

Herrero-Martínez JM, Sánchez-Ledesma M, Ramos-Rincón JM.

26-07-2023

Rev Clin Esp (Barc).

<https://pubmed.ncbi.nlm.nih.gov/37507047/>

Dengue is globally the most important arboviral infection. It is caused by the dengue virus and it is generally transmitted by Aedes mosquitoes' bites (Ae aegypti or Ae albopictus). In Spain it was initially eradicated in the 20th century, together with the Ae aegypti vector, and currently most of the cases reported in Spain are imported by travelers from countries with dengue transmission (imported dengue). However, in recent years, cases of dengue have been described in people residing in Spain who had not traveled to areas with known transmission (autochthonous dengue), transmitted by Aedes albopictus (the so-called tiger mosquito), present especially in the Mediterranean basin. Therefore, a good knowledge of this potentially severe disease is required, so that it can be diagnosed early, and managed correctly, thus reducing its mortality, as well as its eventual autochthonous transmission.

Liang-Ge-San inhibits dengue virus serotype 2 infection by reducing caveolin1-induced cytoplasmic heat shock protein 70 translocation into the plasma membrane.

Chen X, Yang JB, Cao HH, Fang XC, Liu SH, Zou LF, Yu JH, Zuo JP, Zhao W, Lu ZB, Liu JS, Yu LZ.

18-07-2023

Phytomedicine.

<https://pubmed.ncbi.nlm.nih.gov/37506573/>

Background: Dengue virus (DENV) is a major public health threat. However, there are no specific therapeutic drugs for DENV. Many Chinese heat-cleaning formulas, such as Liang-Ge-San (LGS), have been frequently used in the virus-induced diseases. The antiviral effect of LGS has not been reported yet. **Purpose:** In this study, the effect of LGS on the inhibition of dengue virus serotype 2 (DENV-2) was investigated and the relevant mechanism was explored. **Methods:** High-performance liquid chromatography was applied to analyze the chemical characterization of LGS. The in vitro antiviral activities of LGS against DENV-2 were evaluated by time-of-drug-addition assay. The binding of heat shock protein 70 (Hsp70) and envelope (E) protein or caveolin1 (Cav1) were analyzed by immunofluorescence and immunoprecipitation assays. Then the role of Cav1 in the anti-DENV-2 effects of LGS was further examined.

DENV-2 infected Institute of Cancer Research suckling mice (n = 10) and AG129 mice (n = 8) were used to examine the protective effects of LGS. **Results:** It was found that geniposide, liquiritin, forsythenside A, forsythin, baicalin, baicalein, rhein, and emodin maybe the characteristic components of LGS. LGS inhibited the early stage of DENV-2 infection, decreased the expression levels of viral E and non-structural protein 1 (NS1) proteins. LGS also reduced E protein and Hsp70 binding and attenuated the translocation of Hsp70 from cytoplasm to the cell membrane. Moreover, LGS decreased the binding of Hsp70 to Cav1. Further study showed that the overexpression of Cav1 reversed LGS-mediated E protein and Hsp70 inhibition in the plasma membrane. In the in vivo study, LGS was highly effective in prolonging the survival time, reducing viral loads. **Conclusion:** This work demonstrates for the first time that LGS exerts anti-DENV-2 activity in vitro and in vivo. LGS decreases DENV-2-stimulated cytoplasmic Hsp70 translocation into the plasma membrane by Cav1 inhibition, thereby inhibiting the early stage of virus infection. These findings indicate that LGS may be a candidate for the treatment of DENV.

Quinazolinone Compounds Have Potent Antiviral Activity against Zika and Dengue Virus.

Ashraf-Uz-Zaman M, Li X, Yao Y, Mishra CB, Moku BK, Song Y.

28-07-2023

J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37506506/>

Brain MRI segmentation of Zika-Exposed normocephalic infants shows smaller amygdala volumes.

Ghosh S, Salan T, Riotti J, Ramachandran A, Gonzalez IA, Bandstra ES, Reyes FL, Andreansky SS, Govind V, Saigal G.

28-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37506075/>

Chikungunya Virus Diagnosis: A Review of Current Antigen Detection Methods.

Simo FBN, Burt FJ, Makoah NA.

17-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505661/>

Chikungunya is a mosquito-borne viral disease caused by the chikungunya virus (CHIKV). CHIKV is expanding at an alarming rate, potentially spreading and establishing endemicity in new areas where competent vectors are present. The dramatic spread of CHIKV in recent years highlights the urgent need to take precautionary measures and investigate options for control. It is crucial in developing nations where diagnostic tools are limited, and symptoms are similar to other prevalent diseases such as malaria and dengue. The most reliable method for diagnosing chikungunya virus is viral gene detection by RT-PCR. Alternative methods like detecting human antibody and viral antigen can also be used, especially in areas

where resources are limited. In this review, we summarize the limited data on antigen detection immunoassays. We further explain the essential structural elements of the virus to help comprehend the scientific concepts underlying the testing methods, as well as future methods and diagnostic approaches under investigation.

Risk Stratification to Guide Prevention and Control Strategies for Arboviruses Transmitted by *Aedes aegypti*.

Espinosa MO, Andreo V, Paredes G, Leaplaza C, Heredia V, Periago MV, Abril M.

14-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505658/>

Modelling Differential Diagnosis of Febrile Diseases with Fuzzy Cognitive Map.

Obot O, John A, Udo I, Attai K, Johnson E, Udoh S, Nwokoro C, Akwaowo C, Dan E, Umoh U, Uzoka FM.

03-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505648/>

Codetection of *Plasmodium falciparum* in Children Hospitalized With Dengue Fever in the Dominican Republic.

Teoh Z, Simpson BN, Howard T, McElhinney K, Ware R, Mena R, Schlaudecker EP.

31-07-2023

Pediatr Infect Dis J.

<https://pubmed.ncbi.nlm.nih.gov/37523515/>

Prevalence and factors associated with long COVID and mental health status among recovered COVID-19 patients in southern Thailand.

Phu DH, Maneerattanasak S, Shohaimi S, Trang LTT, Nam TT, Kuning M, Like A, Torpor H, Suwanbamrung C.

31-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37523396/>

Mental health disorders have become a growing public health concern among individuals recovering from COVID-19. Long COVID, a condition where symptoms persist for an extended period, can predict psychological problems among COVID-19 patients. This study aimed to investigate the prevalence of long COVID and mental health status among Thai adults who had recovered from COVID-19, identify the association between the mental health status and long COVID symptoms, and investigate the risk factors associated with the correlation between long COVID and mental health outcomes. A cross-sectional study was conducted among 939 randomly selected participants in Nakhon Si Thammarat province, southern Thailand. The Depression, Anxiety, and Stress Scale-21 was used to investigate mental health symptoms, and a checklist comprised of thirteen common symptoms was used to identify the long COVID among participants. Logistic

regression models were used to investigate the risk factors associated with mental health status and long COVID symptoms among participants. Among the 939 participants, 104 (11.1%) had depression, 179 (19.1%) had anxiety, and 42 (4.8%) were stressed. A total of 745 participants (79.3%) reported experiencing at least one symptom of long COVID, with fatigue (72.9%, SE±0.02), cough (66.0%, SE±0.02), and muscle pain (54.1%, SE±0.02) being the most frequently reported symptoms. All long COVID symptoms were significantly associated with mental health status. Shortness of breath, fatigue, and chest tightness were the highest risk factors for mental health status among COVID-19 patients. The final multivariable model indicated that female patients (OR = 1.89), medical history (OR = 1.92), and monthly income lower than 5,000 Thai baht (OR = 2.09) were associated with developing long COVID symptoms and mental health status (all $p < 0.01$). This study provides valuable insights into the potential long-term effects of COVID-19 on mental health and enhances understanding of the mechanisms underlying the condition for predicting the occurrence of mental health issues in Thai COVID-19 patients.

Genomic epidemiology of dengue in Shantou, China, 2019.

Tian L, Liang C, Huang X, Liu Z, Su J, Guo C, Zhu G, Sun J.
13-07-2023

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37522010/>

Objectives: Dengue has been endemic in Southeast Asian countries for decades. There are few reports tracing the dynamics of dengue in real time. In this study, we generated hundreds of pathogen genomes to understand the genomic epidemiology of an outbreak in a hyper-endemic area of dengue. **Methods:** We leveraged whole-genome short-read sequencing (PE150) to generate genomes of the dengue virus and investigated the genomic epidemiology of a dengue virus transmission in a mesoscale outbreak in Shantou, China, in 2019. **Results:** The outbreak was sustained from July to December 2019. The total accumulated number of laboratory-confirmed cases was 944. No gender bias or fatalities were recorded. Cambodia and Singapore were the main sources of imported dengue cases (74.07%, $n = 20$). A total of 284 dengue virus strains were isolated, including 259 DENV-1, 24 DENV-2, and 1 DENV-3 isolates. We generated the entire genome of 252 DENV isolates (229 DENV-1, 22 DENV-2, and 1 DENV-3), which represented 26.7% of the total cases. Combined epidemiological and phylogenetic analyses indicated multiple independent introductions. The internal transmission evaluations and transmission network reconstruction supported the inference of phylodynamic analysis, with high Bayes factor support in BSSVS analysis. Two expansion founders and transmission chains were detected in CCH and LG of Shantou. **Conclusions:** We observed the instant effects of genomic epidemiology in monitoring the dynamics of DENV and highlighted its prospects for real-time tracing of outbreaks of other novel agents in the future.

Correction to: Molecular evolution of dengue virus: a Bayesian approach using 1581 whole-genome sequences from January 1944 to July 2022.

Wolf J, Souza AP, Schardosim RFC, Pille A, Maccari JG, Mutlaq MP, Nasi LA.

31-07-2023

Arch Virol.

<https://pubmed.ncbi.nlm.nih.gov/37518501/>

The viral protein K7 inhibits biochemical activities and condensate formation by the DEAD-box helicase DDX3X.

L Venus S, Tandjigora K, Jankowsky E.

28-07-2023

J Mol Biol.

<https://pubmed.ncbi.nlm.nih.gov/37517790/>

Arboviral vaccines for use in pregnant travelers.

Hills SL, Wong JM, Staples JE.

28-07-2023

Travel Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37517630/>

Role of endoplasmic reticulum stress-related unfolded protein response and its implications in dengue virus infection for biomarker development.

Das B, Samal S, Hamdi H, Pal A, Biswas A, Behera J, Singh G, Behera CK, Sahoo DP, Pati S.

28-07-2023

Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/37517582/>

Epidemiological evidence of acute transmission of Zika virus infection in dengue suspected patients in Sri-Lanka.

Ngwe Tun MM, Raini SK, Fernando L, Gunawardene Y, Inoue S, Takamatsu Y, Urano T, Muthugala R, Hapugoda M, Morita K.

23-07-2023

J Infect Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37517370/>

Background: Zika Virus (ZIKV) is a re-emerging, arthropod-borne flavivirus transmitted by Aedes mosquitoes (Ae. aegypti and Ae. albopictus). The coexistence of dengue virus (DENV) and ZIKV concurrently has been associated with a wide array of neurological complications, which may influence the clinical outcomes of infections. Sri Lanka witnessed a severe dengue epidemic in 2017, characterized by extraordinary and severe disease manifestations with considerable morbidity. Therefore, this study assessed the potential occurrence of ZIKV infection during DENV outbreak in Sri Lanka from 2017 to 2019, which could bear substantial implications for public health.

Methods: Five hundred ninety-five serum samples were procured from individuals suspected of dengue and

admitted to Kandy National Hospital between 2017 and 2018 and the Negombo District General Hospital between 2018 and 2019. These samples underwent quantitative real-time RT-PCR (qRT-PCR) to identify the presence of the ZIKV gene, while enzyme-linked immunosorbent assay was employed to detect ZIKV-specific IgM and IgG antibodies. Focus reduction neutralization tests were subsequently conducted to confirm ZIKV infection.

Results: Among the 595 serum samples, 6 (1.0%) tested positive for ZIKV using qRT-PCR. Anti-ZIKV IgM and IgG were identified in 18.0% and 38.6% patients. Sixty-six (11.0%) samples demonstrated the presence of anti-ZIKV IgM and IgG. Within ZIKV IgM-positive samples, 2.2% exhibited neutralizing antibodies against ZIKV. Through the implementation of qRT-PCR, ZIKV IgM detection, and neutralization testing, 2% and 3.7% cases of ZIKV infections were confirmed in the Kandy and Negombo regions, respectively.

Conclusion: This study is the inaugural endeavor to substantiate the existence of ZIKV infection in Sri Lanka utilizing molecular and serological analysis. The findings of this investigation imply that ZIKV was circulating throughout the 2017-2019 DENV outbreak. These results underscore the necessity for improved preparedness for future outbreaks, fortifying governmental policies on public health, and establishing effective early warning systems regarding the emergence of these viruses.

An in-silico receptor-pharmacophore based multistep molecular docking and simulation study to evaluate the inhibitory potentials against NS1 of DENV-2.

Roy A, Paul I, Paul T, Hazarika K, Dihidar A, Ray S.
30-07-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37517062/>

DENV-2 strain is the most fatal and infectious of the five dengue virus serotypes. The non-structural protein NS1 encoded by its genome is the most significant protein required for viral pathogenesis and replication inside the host body. Thus, targeting the NS1 protein and designing an inhibitor to limit its stability and secretion is a propitious attempt in our fight against dengue. Four novel inhibitors are designed to target the conserved cysteine residues (C55, C313, C316, and C329) and glycosylation sites (N130 and N207) of the NS1 protein in an attempt to halt the spread of the dengue infection in the host body altogether. Numerous computer-aided drug designing techniques including molecular docking, molecular dynamics simulation, virtual screening, principal component analysis, and dynamic cross-correlation matrix were employed to determine the structural and functional activity of the NS1-inhibitor complexes. From our analysis, it was evident that the extent of structural and atomic level fluctuations of the ligand-bound protein exhibited a declining trend in contrast to unbound protein which was prominently noticeable through the RMSD, RMSF, R_g , and SASA graphs. The ADMET analysis of the four ligands revealed a promising pharmacokinetics and pharmacodynamic profile, along with good bioavailability

and toxicity properties. The proposed drugs when bound to the targeted cavities resulted in stable conformations in comparison to their unbound state, implying they have good affinity promising effective drug action. Thus, they can be tested *in vitro* and used as potential anti-dengue drugs. Communicated by Ramaswamy H. Sarma.

WTAP-mediated m6A modification of IFNE is required for antiviral defense in condyloma acuminata.

Gu Z, Liu J, Qin L, Zhang Y, Cui W, Huang H, Liu L, Cao Y, Zhang H.

20-07-2023

J Dermatol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37516644/>

Seroprevalence of Alphaviruses (Togaviridae) among Urban Population in Nouakchott, Mauritania, West Africa.

Abdoullah B, Durand GA, Basco LK, El Bara A, Bollahi MA, Bosio L, Geulen M, Briolant S, Boukhary AOMS.

20-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515274/>

The presence of alphaviruses, such as chikungunya virus (CHIKV), has never been reported in Mauritania. We assessed the seroprevalence of CHIKV among Nouakchott residents. A cross-sectional study involving 1300 non-febrile patients consulting at the Nouakchott hospital center was conducted between January and June 2021. The presence of anti-CHIKV IgG and neutralizing antibodies against CHIKV, O'nyong-nyong virus (ONNV), and Semliki Forest virus (SFV) was determined by an enzyme-linked immunosorbent assay (ELISA) and a serum neutralization test, respectively, and the associated risk factors were investigated. Of the 1300 study participants, serological evidence of previous exposure to CHIKV was observed in 37 individuals (2.8%). Sex, age, reported use of repellants, and bed net ownership and usage were not associated with CHIKV seropositivity. Our results showed the co-circulation of two other alphaviruses, ONNV and SFV, in Nouakchott in 30 (2.3%) individuals. This is the first study that documents the co-circulation of CHIKV, ONNV, and SFV in Mauritania, albeit at low prevalence. Surveillance and routine testing for alphaviruses and other arboviruses in symptomatic patients should be implemented in health facilities to assess the health burden associated with these viruses. Efforts should also be made to strengthen the vector control measures.

Antiviral Activity of an Indole-Type Compound Derived from Natural Products, Identified by Virtual Screening by Interaction on Dengue Virus NS5 Protein.

García-Ariza LL, González-Rivillas N, Díaz-Aguirre CJ, Rocha-Roa C, Padilla-Sanabria L, Castaño-Osorio JC.

17-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515249/>

The Importance of Including Non-Household Environments in Dengue Vector Control Activities.

Peña-García VH, Mutuku FM, Ndenga BA, Mbakaya JO, Ndire SO, Agola GA, Mutuku PS, Malumbo SL, Ng'ang'a CM, Andrews JR, Mordecai EA, LaBeaud AD.

14-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515236/>

Investigating the Mechanism of Action of Anti-Dengue Compounds as Potential Binders of Zika Virus RNA-Dependent RNA Polymerase.

Alandijany TA, El-Daly MM, Tolah AM, Bajrai LH, Khateb AM, Alsaady IM, Altwaim SA, Dubey A, Dwivedi VD, Azhar EI.

04-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515188/>

The World Health Organization (WHO) has designated the Zika virus (ZIKV) as a significant risk to the general public's health. Currently, there are no vaccinations or medications available to treat or prevent infection with the Zika virus. Thus, it is urgently required to develop a highly efficient therapeutic molecule. In the presented study, a computationally intensive search was carried out to identify potent compounds that have the potential to bind and block the activity of ZIKV NS5 RNA-dependent RNA polymerase (RdRp). The anti-dengue chemical library was subjected to high-throughput virtual screening and MM/GBSA analysis in order to rate the potential candidates. The top three compounds were then chosen. According to the MM/GBSA analysis, compound 127042987 from the database had the highest binding affinity to the protein with a minimum binding free energy of -77.16 kcal/mole. Compound 127042987 had the most stable RMSD trend and the greatest number of hydrogen bond interactions when these chemical complexes were evaluated further under a 100 ns molecular dynamics simulation. Compound 127042987 displayed the best binding free energy (GBind) of -96.50 kcal/mol, surpassing the native ligand binding energy (-66.17 kcal/mole). Thereafter, an MM/GBSA binding free energy study was conducted to validate the stability of selected chemical complexes. Overall, this study illustrated that compound 127042987 showed preferred binding free energies, suggesting a possible inhibitory mechanism against ZIKV-RdRp. As per this study, it was proposed that compound 127042987 could be used as a therapeutic option to prevent Zika virus infection. These compounds need to be tested in experiments for further validation.

Spatio-Temporal Cluster Detection of Dengue, Chikungunya, and Zika Viruses' Infection in Rio de Janeiro State from 2010 to 2019.

Almeida PMP, Câmara DCP, Nobre AA, Ayllón T, Ribeiro MS, Dias CMG, Peixoto EM, Rocha MMD, Carvalho S, Honório NA.

01-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515183/>

Dengue (DENV), chikungunya (CHIKV), and Zika (ZIKV) virus infections are widespread throughout the Rio de Janeiro state. The co-circulation of these emergent arboviruses constitutes a serious public health problem, resulting in outbreaks that can spatially and temporally overlap. Environmental conditions favor the presence, maintenance, and expansion of *Aedes aegypti*, the primary vector of these urban arboviruses. This study assessed the detection of clusters of urban arboviruses in the Rio de Janeiro state from 2010 to 2019. Notified cases of dengue, chikungunya, and Zika were grouped by year according to the onset of symptoms and their municipality of residence. The study period recorded the highest number of dengue epidemics in the state along with the simultaneous circulation of chikungunya and Zika viruses. The analyzes showed that the central municipalities of the metropolitan regions were associated with higher risk areas. Central municipalities in metropolitan regions were the first most likely clusters for dengue and Zika, and the second most likely cluster for chikungunya. Furthermore, the northwest and north regions were comprised clusters with the highest relative risk for the three arboviruses, underscoring the impact of these arboviruses in less densely populated regions of Brazil. The identification of high-risk areas over time highlights the need for effective control measures, targeted prevention and control interventions for these urban arboviral diseases.

Equine Polyclonal Antibodies Prevent Acute Chikungunya Virus Infection in Mice.

Barker D, Han X, Wang E, Dagley A, Anderson DM, Jha A, Weaver SC, Julander J, Nykiforuk C, Kodihalli S.

29-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515166/>

Cholesterol-Lowering Drugs as Potential Antivirals: A Repurposing Approach against Flavivirus Infections.

Osuna-Ramos JF, Farfan-Morales CN, Cordero-Rivera CD, De Jesús-González LA, Reyes-Ruiz JM, Hurtado-Monzón AM, Palacios-Rápalo SN, Jiménez-Camacho R, Meraz-Ríos MA, Del Ángel RM.

28-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515153/>

Targeting Inflammasome Activation in Viral Infection: A Therapeutic Solution?

Deng CH, Li TQ, Zhang W, Zhao Q, Wang Y.

27-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515138/>

Inflammasome activation is exclusively involved in sensing activation of innate immunity and inflammatory response during viral infection. Accumulating evidence suggests that the manipulation of inflammasome assembly or its

interaction with viral proteins are critical factors in viral pathogenesis. Results from pilot clinical trials show encouraging results of NLRP3 inflammasome suppression in reducing mortality and morbidity in SARS-CoV-2-infected patients. In this article, we summarize the up-to-date understanding of inflammasomes, including NLRP3, AIM2, NLRP1, NLRP6, and NLRC4 in various viral infections, with particular focus on RNA viruses such as SARS-CoV-2, HIV, IAV, and Zika virus and DNA viruses such as herpes simplex virus 1. We also discuss the current achievement of the mechanisms involved in viral infection-induced inflammatory response, host defense, and possible therapeutic solutions.

Identification of the Tembusu Virus in Mosquitoes in Northern Thailand.

Hamel R, Vargas REM, Rajonhson DM, Yamanaka A, Jaroenpool J, Wichit S, Missé D, Kritiyakan A, Chaisiri K, Morand S, Pompon J.

27-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515135/>

Proposal of Model for Evaluation of Viral Kinetics of African/Asian/Brazilian-Zika virus Strains (Step Growth Curve) in Trophoblastic Cell Lines.

Barbosa MD, Costa A, Prieto-Oliveira P, Andreata-Santos R, Peter CM, Zanotto PMA, Janini LMR.

27-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515134/>

Dengue Virus Infection Alters Inter-Endothelial Junctions and Promotes Endothelial-Mesenchymal-Transition-Like Changes in Human Microvascular Endothelial Cells.

Escudero-Flórez M, Torres-Hoyos D, Miranda-Brand Y, Gallego-Gómez JC, Vicente-Manzanares M.

27-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515125/>

Dengue virus (DENV) is a pathogenic arbovirus that causes human disease. The most severe stage of the disease (severe dengue) is characterized by vascular leakage, hypovolemic shock, and organ failure. Endothelial dysfunction underlies these phenomena, but the causal mechanisms of endothelial dysfunction are poorly characterized. This study investigated the role of c-ABL kinase in DENV-induced endothelial dysfunction. Silencing c-ABL with artificial miRNA or targeting its catalytic activity with imatinib revealed that c-ABL is required for the early steps of DENV infection. DENV-2 infection and conditioned media from DENV-infected cells increased endothelial expression of c-ABL and CRKII phosphorylation, promoted expression of mesenchymal markers, e.g., vimentin and N-cadherin, and decreased the levels of endothelial-specific proteins, e.g., VE-cadherin and ZO-1. These effects were reverted by silencing or inhibiting c-ABL. As part of the acquisition of a mesenchymal phenotype, DENV infection

and treatment with conditioned media from DENV-infected cells increased endothelial cell motility in a c-ABL-dependent manner. In conclusion, DENV infection promotes a c-ABL-dependent endothelial phenotypic change that leads to the loss of intercellular junctions and acquisition of motility.

Kunjin Virus, Zika Virus, and Yellow Fever Virus Infections Have Distinct Effects on the Coding Transcriptome and Proteome of Brain-Derived U87 Cells.

Brand C, Deschamps-Francoeur G, Bullard-Feibelman KM, Scott MS, Geiss BJ, Bisaillon M.

23-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515107/>

Dengue Virus Infection of Human Retinal Müller Glial Cells.

Oliver GF, Ashander LM, Dawson AC, Ma Y, Carr JM, Williams KA, Smith JR.

21-06-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515098/>

Retinopathy is a recently recognized complication of dengue, affecting up to 10% of hospitalized patients. Research on the pathogenesis has focused largely on effects of dengue virus (DENV) at the blood-retinal barrier. Involvement of retinal Müller glial cells has received little attention, although this cell population contributes to the pathology of other intraocular infections. The goal of our work was to establish the susceptibility of Müller cells to infection with DENV and to identify characteristics of the cellular antiviral, inflammatory, and immunomodulatory responses to DENV infection in vitro. Primary human Müller cell isolates and the MIO-M1 human Müller cell line were infected with the laboratory-adapted Mon601 strain and DENV serotype 1 and 2 field isolates, and cell-DENV interactions were investigated by immunolabelling and quantitative real-time polymerase chain reaction. Müller cells were susceptible to DENV infection, but experiments involving primary cell isolates indicated inter-individual variation. Viral infection induced an inflammatory response (including tumour necrosis factor- α , interleukin [IL]-1 β , and IL-6) and an immunomodulatory response (including programmed death-ligand [PD-L]1 and PD-L2). The type I interferon response was muted in the Müller cell line compared to primary cell isolates. The highest infectivity and cell responses were observed in the laboratory-adapted strain, and overall, infectivity and cell responses were stronger in DENV2 strains. This work demonstrates that Müller cells mount an antiviral and immune response to DENV infection, and that this response varies across cell isolates and DENV strain. The research provides a direction for future efforts to understand the role of human retinal Müller glial cells in dengue retinopathy.

Genomic Surveillance of Recent Dengue Outbreaks in Colombo, Sri Lanka.

Maduranga S, Valencia BM, Sigera C, Adikari T, Weeratunga P, Fernando D, Rajapakse S, Lloyd AR, Bull RA, Rodrigo C.
21-06-2023
Viruses.
<https://pubmed.ncbi.nlm.nih.gov/37515097/>

Obesity as a clinical predictor for severe manifestation of dengue: a systematic review and meta-analysis.

Chen CY, Chiu YY, Chen YC, Huang CH, Wang WH, Chen YH, Lin CY.
31-07-2023
BMC Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37525106/>

TMEM120A/TACAN: A putative regulator of ion channels, mechanosensation, and lipid metabolism.

Gabrielle M, Rohacs T.
Déc-2023
Channels (Austin).
<https://pubmed.ncbi.nlm.nih.gov/37523628/>

TMEM120A (TACAN) is an enigmatic protein with several seemingly unconnected functions. It was proposed to be an ion channel involved in sensing mechanical stimuli, and knockdown/knockout experiments have implicated that TMEM120A may be necessary for sensing mechanical pain. TMEM120A's ion channel function has subsequently been challenged, as attempts to replicate electrophysiological experiments have largely been unsuccessful. Several cryo-EM structures revealed TMEM120A is structurally homologous to a lipid modifying enzyme called Elongation of Very Long Chain Fatty Acids 7 (ELOVL7). Although TMEM120A's channel function is debated, it still seems to affect mechanosensation by inhibiting PIEZO2 channels and by modifying tactile pain responses in animal models. TMEM120A was also shown to inhibit polycystin-2 (PKD2) channels through direct physical interaction. Additionally, TMEM120A has been implicated in adipocyte regulation and in innate immune response against Zika virus. The way TMEM120A is proposed to alter each of these processes ranges from regulating gene expression, acting as a lipid modifying enzyme, and controlling subcellular localization of other proteins through direct binding. Here, we examine TMEM120A's structure and proposed functions in diverse physiological contexts.

Investigating and combatting the key drivers of viral zoonoses in Africa: an analysis of eight epidemics.

Isibor PO, Onwaeze OO, Kayode-Edwards II, Agbontaen DO, Ifebem-Ezima IM, Bilewu O, Onuselogu C, Akinniyi AP, Obafemi YD, Oniha MI.
28-07-2023
Braz J Biol.
<https://pubmed.ncbi.nlm.nih.gov/37531478/>

Investigating the interplay of factors that result in a viral zoonotic outbreak is difficult, though it is increasingly important. As anthropogenic influences shift the delicate balance of ecosystems, new zoonoses emerge in humans. Sub-Saharan Africa is a notable hotspot for zoonotic disease due to abundant competent mammalian reservoir hosts. Furthermore, poverty, corruption, and an overreliance on natural resources play considerable roles in depleting biological resources, exacerbating the population's susceptibility. Unsurprisingly, viral zoonoses have emerged in Africa, including HIV/AIDS, Ebola, Avian influenza, Lassa fever, Zika, and Monkeypox. These diseases are among the principal causes of death in endemic areas. Though typically distinct in their manifestations, viral zoonoses are connected by underlying, definitive factors. This review summarises vital findings on viral zoonoses in Africa using nine notable case studies as a benchmark for future studies. We discuss the importance of ecological recuperation and protection as a central strategy to control zoonotic diseases. Emphasis was made on moderating key drivers of zoonotic diseases to forestall future pandemics. This is in conjunction with attempts to redirect efforts from reactive to pre-emptive through a multidisciplinary "one health" approach.

Secretory pathways and multiple functions of nonstructural protein 1 in flavivirus infection.

Zhang S, He Y, Wu Z, Wang M, Jia R, Zhu D, Liu M, Zhao X, Yang Q, Wu Y, Zhang S, Huang J, Ou X, Gao Q, Sun D, Zhang L, Yu Y, Chen S, Cheng A.
13-07-2023
Front Immunol.
<https://pubmed.ncbi.nlm.nih.gov/37520540/>

A stochastic B cell affinity maturation model to characterize mechanisms of protection for tetravalent dengue vaccine constructs.

Pannala VR, Nguyen HD, Wallqvist A.
14-07-2023
Front Mol Biosci.
<https://pubmed.ncbi.nlm.nih.gov/37520320/>

Efficient reverse genetics approach involving infectious subgenomic amplicon for engineering dengue virus.

Park CJ, Lee YA, Yoo SM, Kim GA, Lee MS, Park C.
Août-2023
J Med Virol.
<https://pubmed.ncbi.nlm.nih.gov/37515534/>

Dengue virus, which belongs to the Flaviviridae family, can induce a range of symptoms from mild to severe, including dengue fever, dengue hemorrhagic fever, and dengue shock syndrome. While infectious cloning technology is a useful tool for understanding viral pathogenesis and symptoms, it exhibits limitations when constructing the entire Flavivirus genome. The instability and toxicity of the genome to bacteria make its full-length construction in bacterial vectors a time-consuming and laborious process. To address these challenges, we employed the modified

infectious subgenomic amplicon (ISA) method in this study, which can potentially be a superior tool for reverse genetic studies on the dengue virus. Using ISA, we generated recombinant dengue viruses de novo and validated their robust replication in both human and insect cell lines, which was comparable to that of the original strains. Moreover, the efficiency of ISA in genetically modifying the dengue virus was elucidated by successfully inserting the gene for green fluorescence protein into the genome of dengue virus serotype 4. Overall, this study highlighted the effectiveness of ISA for genetically engineering the dengue virus and provided a technical basis for a convenient reverse genetics system that could expedite investigations into the dengue virus.

Dracunculose

Participating in eradication: how Guinea worm redefined eradication, and eradication redefined Guinea worm, 1985-2022.

Roberts JD.

Avr-2023

Med Hist.

<https://pubmed.ncbi.nlm.nih.gov/37525460/>

Transcriptome Profiling Reveals Differential Gene Expression during the Process of Microtuber Formation in *Pinellia ternata*.

Bo C, Su C, Teng J, Sheng W, Xue T, Zhu Y, Xue J.

18-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37511363/>

Using petiole material as explants and directly inducing the formation of microtubers without going through the callus stage is an essential way to rapidly expand scarce medical plants such as *Pinellia ternata*. However, the early molecular mechanism underlying the formation of the microtuber is largely elusive. Here, we conducted cytology and dynamic transcriptome analyses of inchoate microtubers in *Pinellia* explants and identified 1092 differentially expressed genes after their cultivation in vitro for 0, 5, and 15 days. Compared with 0 day, the number and size of the microtuber cells were larger at 5 and 15 days of culture. Detailed categorization revealed that the differentially expressed genes were mainly related to responses to stimulus, biological regulation, organelles, membranes, transcription factor activity, and protein binding. Further analysis revealed that the microtuber at different incubation days exhibited quite a difference in both hormone signaling pathway transduction and the regulation pattern of transcription factors. Therefore, this study contributes to a better understanding of the early molecular regulation during the formation of the microtuber and provides new insights for the study of the rapid expansion of *P. ternata* and other medical plants.

Impact of mercury on photosynthetic performance of *Lemna minor*: a chlorophyll fluorescence analysis.

Singh H, Kumar D, Soni V.

27-07-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37500693/>

The purpose of this study was to evaluate the effectiveness of chlorophyll fluorescence analysis in detecting the effects of mercury (Hg) treatment in duckweed species *Lemna minor*. The results showed that Hg treatment (ranging from 0.0 to 0.4 μ M) significantly impacted the plant's photosynthetic ability, with a decrease in variable chlorophyll fluorescence, energy fluxes, density of reaction centers, and performance index. Complete inhibition of electron transport was observed in plants treated with high Hg concentrations, and the quantum yield of primary photochemistry and the ratio of dissipated energy to absorption both decreased with increasing Hg concentrations. Performance Index (PI) was significantly affected by the Hg concentrations, reaching zero in plants treated with the highest Hg concentration. Overall, JIP analysis was found to be an effective tool for detecting deleterious effects of Hg in plants.

Mulberry leaf and konjac compound powder improves the metabolic capacity of old mice on a high-protein diet by regulating the structure of the intestinal microbiota.

Deng L, Zhong G, Peng Y, Zhu Z.

Sept-2023

J Sci Food Agric.

<https://pubmed.ncbi.nlm.nih.gov/37127926/>

Echinococcosis

Management of hydatid cyst in a centre with high prevalence. Descriptive series.

García-Redondo M, González Sánchez D, Cabañó-Muñoz D, Rico-Morales MDM, Rodríguez-Perdomo MJ, López-Fernández J, Torres-Melero J, Reina-Duarte Á.

04-08-2023

Rev Esp Enferm Dig.

<https://pubmed.ncbi.nlm.nih.gov/37539541/>

Hydatidosis is a zoonosis caused by the larval stage of the genus *Echinococcus*. Humans are an accidental intermediate host. The main organ affected is the liver (70%). The incidence increases in endemic regions such as North Africa, Eastern Europe and South America. We present a descriptive series of cases treated in our hospital in the last 5 years. Demographic variables, cyst characteristics, as well as preoperative and postoperative variables are collected.

Characterisation of extracellular vesicles isolated from hydatid cyst fluid and evaluation of immunomodulatory effects on human monocytes.

Khosravi M, Mohammad Rahimi H, Nazari A, Baghaei K, Asadzadeh Aghdai H, Shahrokh S, Sharifdini M, Torrecilhas AC, Mehryab F, Mirjalali H, Shekari F, Zali MR.

02-08-2023

J Cell Mol Med.

<https://pubmed.ncbi.nlm.nih.gov/37530547/>

Hydropneumothorax caused by complete rupture of a pulmonary hydatid cyst: A rare case report.

Almoussa M, Alhadla A, Aljomaa M, Abdalrazzak T.

30-07-2023

Clin Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37529137/>

NOVEL REPORT OF THE EUROPEAN VARIANT OF ECHINOCOCCUS MULTILOCULARIS IN COYOTES (CANIS LATRANS) IN NEW YORK STATE.

Conlon CL, Schuler KL, Lejeune M, Whipps CM.

01-07-2023

J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37527278/>

Echinococcus multilocularis is a zoonotic cestode that can infect wildlife, domestic animals, and humans. In humans, infection with the larval stage of the parasite causes the disease alveolar echinococcosis, which can be fatal if left untreated. Surveillance for the parasite in New York State occurred during the 2021-2022 coyote (Canis latrans) hunting season. Fecal samples and the gastrointestinal tracts (GIT) from 43 coyote carcasses were collected from hunters and trappers across 8 counties. Fecal samples were screened for E. multilocularis DNA using a multiplex PCR. Three samples tested positive for E. multilocularis DNA. Subsequently, adult cestodes were collected from GIT samples using the sedimentation, filtration, and counting technique. Phylogenetic analysis of DNA sequences from the nad2 and cob genes from individual worms indicated these New York sequences cluster with E. multilocularis sequences from Europe. This is the first report of adult E. multilocularis cestodes in New York State, as well as the first detection of the European haplotype of E. multilocularis in wildlife in the northeastern United States.

Palliative Treatment for the Management of Advanced Pelvic Hydatid Bone Disease.

Luan H, Liu K, Tian Q, Chen Y, Peng C, Sun X, Song X.

31-07-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37524327/>

Hydatid bone disease is a zoonotic parasitic infection that is caused primarily by the tapeworm Echinococcus granulosus, and it continues to be a major public health concern in pastoral regions. The reconstruction of limb function after limb salvage surgery remains a challenge for clinicians. The purpose of this study was to determine the

clinical efficacy of palliative treatment of the management of advanced pelvic hydatid bone disease. From March 2005 to December 2018, medical records and images of patients with advanced pelvic hydatid bone disease treated with surgery combined with antiparasitic chemotherapy were evaluated retrospectively. The Enneking classification was applied to determine the location of the lesion, and the Musculoskeletal Tumor Society score system was used for outcome evaluation. Fifteen patients who met the criteria were included in this study, with a mean follow-up of 4.40 ± 1.76 years. All patients received treatment with surgery combined with antiparasitic chemotherapy. The mean number of surgical interventions per patient for pelvic cystic echinococcosis was 5.3 (range, 2-9 interventions per patient). Recurrence of pelvic hydatid bone disease occurred in 5 patients and was managed successfully through repeated debridement procedures. Palliative treatment with limb salvage surgery was an effective and practical approach to the management of advanced pelvic hydatid bone disease. Standard antiparasitic chemotherapy, which included albendazole at a dose of 10 mg/kg/day administered in two daily doses for 3 to 6 months, was also considered an essential part of the overall treatment strategy.

Editorial: "You shall not pass" or "Let's make a deal" - crosstalk between helminths and the host immune system.

Bąska P, Schabussova I, Zawistowska-Deniziak A.

14-07-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37520436/>

Diagnosis and treatment of mycotic aneurysms secondary to cardiac hydatid cyst: An unusual cause of multiple cerebral strokes in a 23-year-old female.

Malih SE, Ezzahi M, Ismail O, Akammar A, Bouardi NE, Haloua M, Alami B, Boubbou M, Maaroufi M, Lamrani MYA.

07-07-2023

Radiol Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37520388/>

Report of a two-headed protoscolex of Echinococcus granulosus revealed by phase contrast microscopy in Shiraz, Iran.

Karpisheh E, Sadjjadi SM.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520207/>

Echinococcus granulosus sensu lato can produce cystic echinococcosis (CE)/hydatidosis in different hosts. Each CE cyst can produce numerous protoscoleces by its germinal layer in two forms: evaginated and invaginated. Usually, each protoscolex has one head consisting of a rostellum with two rows of hooks and four suckers. During a study of protoscolicidal agents on sheep Echinococcus granulosus protoscoleces, and investigations on their microscopic changes using Phase contrast microscopy, we observed a

case of two-headed evaginated protoscolex. Two heads were attached to a unique bigger size of protoscolex body. Morphological observations showed its dimension around two times of usual protoscolex. There was no space between the bodies, hence one fused body was observed which was clearly shown by Phase contrast microscopy. Each head possessed two rows of hooks. Using micrometry all parts of the two-headed protoscolex, especially hooks were measured and photographed showing all aspects of its morphology including tegument, hooks, and two heads. Specific parts of two-headed protoscolex including suckers, hooks, also calcareous corpuscles were measured. The measurements on the two-headed protoscolex showed that the small hook blade length (SBL) and large hook blade length (LBL) were almost longer than one head protoscolex. A total of 120 calcareous corpuscles in two-headed-protoscolex is much higher than one head protoscolexes.

Primary intramuscular thigh hydatid cyst: A case report.

Siraj S, Nijrabi MM, Hakimi A, Zaki A, Hares R.

27-07-2023

Int J Surg Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37517254/>

Primary pleural hydatidosis presenting as an isolated cough: A rare case report.

George MS, Jagannath P, Byuzandyan T, Baghumyan N, Khanoyan A, Hashmi MF.

26-06-2023

Int J Surg Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37517250/>

Characterization of protein cargo of Echinococcus granulosus extracellular vesicles in drug response and its influence on immune response.

Nicolao MC, Rodrigues CR, Coccimiglio MB, Ledo C, Docena GH, Cumino AC.

29-07-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37516852/>

Background: The *Echinococcus granulosus sensu lato* species complex causes cystic echinococcosis, a zoonotic disease of medical importance. Parasite-derived small extracellular vesicles (sEVs) are involved in the interaction with hosts intervening in signal transduction related to parasite proliferation and disease pathogenesis. Although the characteristics of sEVs from *E. granulosus* protoscolexes and their interaction with host dendritic cells (DCs) have been described, the effect of sEVs recovered during parasite pharmacological treatment on the immune response remains unexplored. **Methods:** Here, we isolated and characterized sEVs from control and drug-treated protoscolexes by ultracentrifugation, transmission electron microscopy, dynamic light scattering, and proteomic analysis. In addition, we evaluated the cytokine response profile induced in murine bone marrow-derived dendritic cells (BMDCs) by qPCR. **Results:** The isolated sEVs, with conventional size between

50 and 200 nm, regardless of drug treatment, showed more than 500 cargo proteins and, importantly, 20 known antigens and 70 potential antigenic proteins, and several integral-transmembrane and soluble proteins mainly associated with signal transduction, immunomodulation, scaffolding factors, extracellular matrix-anchoring, and lipid transport. The identity and abundance of proteins in the sEV-cargo from metformin- and albendazole sulfoxide (ABZSO)-treated parasites were determined by proteomic analysis, detecting 107 and eight exclusive proteins, respectively, which include proteins related to the mechanisms of drug action. We also determined that the interaction of murine BMDCs with sEVs derived from control parasites and those treated with ABZSO and metformin increased the expression of pro-inflammatory cytokines such as IL-12 compared to control cells. Additionally, protoscolex-derived vesicles from metformin treatments induced the production of IL-6, TNF- α , and IL-10. However, the expression of IL-23 and TGF- β was downregulated. **Conclusions:** We demonstrated that sEV-cargo derived from drug-treated *E. granulosus* protoscolexes have immunomodulatory functions, as they enhance DC activation towards a type 1 pro-inflammatory profile against the parasite, and therefore support the proposal of a new approach for the prevention and treatment of secondary echinococcosis.

Helminths in Invasive Raccoons (Procyon lotor) from Southwest Germany.

Reinhardt NP, Wassermann M, Härle J, Romig T, Kurzrock L, Arnold J, Großmann E, Mackenstedt U, Straubinger RK.

08-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513766/>

As hosts of numerous zoonotic pathogens, the role of raccoons needs to be considered in the One Health context. Raccoons progressively expand their range as invasive alien species in Europe. This study aimed to investigate the intestinal helminth fauna of raccoons in Baden-Wuerttemberg, Germany, as no such screening had ever been conducted there. In total, we obtained 102 animals from hunters in 2019 and 2020. Intestinal helminths were retrieved using the SSCT (segmented sedimentation and counting technique) and identified morphologically and by PCR-based Sanger sequencing. Fecal samples were assessed using the ELISA PetChek™ IP assay (IDEXX, Germany) and flotation technique. The artificial digestion method was employed for analyzing muscle tissue. We detected species of four nematode genera (*Baylisascaris procyonis*, *Toxocara canis*, *Capillaria* spp., and *Trichuris* spp.), three cestode genera (*Atriotaenia* cf. *incisa/procyonis*, *Taenia martis*, and *Mesocostoides* spp.), and three trematode genera (*Isthmiophora hortensis/melis*, *Plagiorchis muris*, and *Brachylaima* spp.). *Echinococcus* spp. and *Trichinella* spp. were not found. The invasive behavior and synanthropic habits of raccoons may increase the infection risk with these helminths in wildlife, domestic and zoo animals, and humans by serving as a connecting link. Therefore, it is crucial to initiate additional studies assessing these risks.

Parasites as potential targets for cancer immunotherapy.

Yousefi M, Akbari M, Hadipour M, Dehkordi AB, Farahbakhsh Z, Darani HY.

Aug-2023

J Cancer Res Clin Oncol.

<https://pubmed.ncbi.nlm.nih.gov/36949175/>

Filariose lymphatique

Substance P promote macrophage M2 polarization to attenuate secondary lymphedema by regulating NF- κ B/NLRP3 signaling pathway.

Zhou Z, Sui X, Cao Z, Li X, Qing L, Tang J.

26-07-2023

Peptides.

<https://pubmed.ncbi.nlm.nih.gov/37507091/>

Secondary lymphedema often occurs after filariasis, trauma, lymph node dissection and radiation therapy, which is manifested by infiltration of inflammatory cells and fibrosis formation in pathologically. Substance P is a widely used neuropeptide in the field of tissue repair, while the regenerative potential of the substance P has not been proven in the secondary lymphedema. In this study, animal model of secondary lymphedema was constructed by excising the skin and subcutaneous lymphatic network in the tail of mice, and the degree of swelling in the tail of mice was evaluated after 6 weeks under the treatment with substance P. Immunofluorescence staining was also performed to assess immune cell infiltration, subcutaneous fibrosis and lymphangiogenesis. The results revealed that substance P significantly alleviated post-surgical lymphedema in mice. Furthermore, we found that substance P promoted macrophages M2 polarization, a process associated with downregulation of the NF- κ B/NLRP3 pathway. After application of disodium clodronate (macrophage scavenger, CLO), the positive effect of substance P in lymphedema is significantly inhibited. In vitro experiments, we further demonstrated the polarizing effect of substance P on bone marrow-derived macrophages (BMDMs), while substance P inhibited the activation of the NF- κ B/NLRP3 pathway in BMDMs after the treatment of lipopolysaccharide (LPS). In addition, polarized macrophages were demonstrated to promote the proliferation, tube-forming and migratory functions of human lymphatic endothelial cells (hLEC). In conclusion, our study provides preliminary evidence that substance P alleviates secondary lymphedema by promoting macrophage M2 polarization, and this therapeutic effect may be associated with downregulation of the NF- κ B/NLRP3 pathway.

Lymphatic Filariasis Elimination Status: *Wuchereria bancrofti* Infections in Human Populations after Five Effective Rounds of Mass Drug Administration in Zambia.

Matapo BB, Mpabalwani EM, Kaonga P, Simuunza MC, Bakyaite N, Masaninga F, Siyumbwa N, Siziya S, Shamilimo F, Muzongwe C, Mwase ET, Sikasunge CS.

22-06-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505629/>

Lymphatic filariasis (LF), also commonly known as elephantiasis, is a neglected tropical disease (NTD) caused by filarial parasites. The disease is transmitted via a bite from infected mosquitoes. The bites of these infected mosquitoes deposit filarial parasites, *Wuchereria* or *Brugia*, whose predilection site is the lymphatic system. The damage to the lymph system causes swelling in the legs, arms, and genitalia. A mapping survey conducted between 2003 and 2011 determined LF as being endemic in Zambia in 96 out of 116 districts. Elimination of LF is known to be possible by stopping the spread of the infection through large-scale preventive chemotherapy. Therefore, mass drug administration (MDA) with diethylcarbamazine citrate (DEC) (6 mg/kg) and Albendazole (400 mg) for Zambia has been conducted and implemented in all endemic districts with five effective rounds. In order to determine whether LF prevalence has been sufficiently reduced to levels less than 2% antigenemia and less than 1% microfilariaemia, a pre-transmission assessment survey (pre-TAS) was conducted. Therefore, post-MDA pre-TAS was conducted between 2021 and 2022 in 80 districts to determine the LF prevalence. We conducted a cross-sectional seroprevalence study involving 600 participants in each evaluation unit (EU) or each district. The study sites (sentinel and spot-check sites) were from districts that were the implementation units (IUs) of the LF MDA. These included 80 districts from the 9 provinces. A total of 47,235 people from sentinel and spot-check locations were tested. Of these, valid tests were 47,052, of which 27,762 (59%) were females and 19,290 (41%) were males. The survey revealed in the 79/80 endemic districts a prevalence of *Wb* antigens of 0.14% and 0.0% prevalence of microfilariae. All the surveyed districts had an optimum prevalence of less than 2% for antigenaemia, except for Chibombo district. The majority of participants that tested positive for *Wuchereria bancrofti* (*Wb*) Antigens (Ag) were those that had 2, 3, and 4 rounds of MDA. Surprisingly, individuals that had 1 round of MDA were not found to have circulating antigens of *Wb*. The study showed that all the surveyed districts, except for Chibombo, passed pre-TAS. This further implies that there is a need to conduct transmission assessment surveys (TASs) in these districts.

Maximizing the Potential of Attractive Targeted Sugar Baits (ATSBs) for Integrated Vector Management.

Njoroge TM, Hamid-Adiamoh M, Duman-Scheel M.

28-06-2023

Insects.

<https://pubmed.ncbi.nlm.nih.gov/37504591/>

Individual longitudinal compliance to neglected tropical disease mass drug administration programmes, a systematic review.

Maddren R, Phillips A, Rayment Gomez S, Forbes K, Collyer BS, Kura K, Anderson R.
17-07-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37459369/>

A meta-analysis reveals that dragonflies and damselflies can provide effective biological control of mosquitoes.

Priyadarshana TS, Slade EM.

Aug-2023

J Anim Ecol.

<https://pubmed.ncbi.nlm.nih.gov/37272224/>

Dragonfly/damselfly naiads have the potential to control mosquitoes, and indirectly the diseases they carry, due to their extensive predation on mosquito larvae. Experimental studies have measured the effectiveness of individual dragonfly/damselfly naiads in controlling mosquitoes by introducing them to mosquito larvae and counting the number of larvae eaten in a given time period (i.e. predation success). Without a quantitative synthesis, however, such individual measures are unable to provide a generalized estimation about the effectiveness of dragonflies/damselflies as biological mosquito control agents. To achieve this, we assembled a database containing 485 effect sizes across 31 studies on predation successes of 47 species of commonly found dragonfly/damselfly naiads on nine species of mosquito larvae belonging to *Aedes*, *Anopheles* and *Culex*. These studies covered 14 countries across Asia, Africa and South and North America, where mosquitoes are the vectors of Chikungunya, Dengue, Japanese encephalitis, Lymphatic filariasis, Malaria, Rift Valley fever, West Nile fever, Yellow fever and Zika. Using this database, we conducted a meta-analysis to estimate the average predation success per day by a single individual dragonfly/damselfly naiad on these mosquito larvae as a generalized measure of the effectiveness of dragonflies/damselflies for mosquito control. We also built an interaction network for predator-dragonflies/damselflies and prey-mosquitoes and the diseases they vector to understand the functioning of this important predator-prey network. Our results showed that mosquito larvae were significantly reduced through predation by dragonfly/damselfly naiads. Within experimental containers, a single individual dragonfly/damselfly naiad can eat on average 40 (95% confidence intervals [CIs] = 20, 60) mosquito larvae per day, equivalent to a reduction of the mosquito larval population by 45% (95% CIs = 30%, 59%) per day. The average predation success did not significantly vary among *Aedes*, *Anopheles* and *Culex* mosquitoes or among the four (I-IV) mosquito larval stages. These results provide strong evidence that dragonflies/damselflies can be effective biological control agents of mosquitoes, and environmental planning to promote them could lower the risk of spreading mosquito-borne diseases in an environmentally friendly and cost-effective manner.

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

Meuti ME, Siperstein A, Wolkoff M.

01-08-2023

Cold Spring Harb Protoc.

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

Gale

Treatment of permethrin-resistant scabies with pyrethrins/piperonyl butoxide foam.

Veraldi S, Schianchi R, Nazzaro G.

Déc-2023

J Dermatolog Treat.

<https://pubmed.ncbi.nlm.nih.gov/37526055/>

A linear cob-led torch may become a new dermatological tool for scabies diagnosis.

Scanni G.

Juil-2023

Skin Res Technol.

<https://pubmed.ncbi.nlm.nih.gov/37522503/>

Plantar keratoderma-like crusted scabies in an immunocompetent infant after topical steroids.

Segado Sánchez M, Lova Navarro M, Martínez Ortega FJ, Parra García JJ, López Martínez D, Sánchez-Pedreño Guillén P.

30-07-2023

Pediatr Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37518420/>

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

Unambiguous identification of Ancylostoma caninum and Uncinaria stenocephala in Australian and New Zealand dogs from faecal samples.

Stocker T, Scott I, Šlapeta J.

03-08-2023

Aust Vet J.

<https://pubmed.ncbi.nlm.nih.gov/37537874/>

Hookworms (Ancylostomatidae) are well-known parasites in dogs due to their health impacts and zoonotic potential. While faecal analysis is the traditional method for detection, improvements in husbandry and deworming have decreased their prevalence in urban owned dogs. Drug resistance in *Ancylostoma caninum* is becoming a discussion point in small animal practices across the region. This study aimed to identify hookworm species present in Australian and New Zealand dogs using molecular techniques. The ITS-2 and isotype-1 β -tubulin

assays were used to identify and quantify hookworm species. Results showed absence of coinfection in Australian samples from Greater Sydney region belonging either to *A. caninum* or *Uncinaria stenocephala*, while New Zealand samples were a mixture of *A. caninum* and *U. stenocephala*. The amplified isotype-1 β -tubulin sequences exhibited susceptibility to benzimidazole drugs. Rare mutations were identified in *A. caninum* and *U. stenocephala* sequences, representing a small percentage of reads. This study highlights the importance of molecular techniques in accurately identifying and quantifying hookworm species in dog populations.

Prevalence of gastro-intestinal and haemoparasitic infections among domestic cats of Kerala.

Vincy P, Tresamol PV.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520191/>

The population of domesticated cats has drastically increased during the last decades. With the recently identified rise in cat population an upsurge in the parasitic infections associated with domestic cats is evident. A total of 122 domestic cats were screened for gastro-intestinal and haemoparasites. Screening for gastro-intestinal parasites revealed an overall prevalence of 19 per cent (23/122). *Ancylostoma* spp. was the major gastro-intestinal parasite noticed (61 per cent) followed by *Toxocara cati* (13.04 per cent), *Isospora* spp. (8.7 per cent), *Dipyllobothrium latum* (4.35 per cent) and mixed infection of these (13 per cent). Blood smear examination revealed *Cytauxzoon* spp. in three cats (2.46 per cent) and *Babesia* spp. in two cats (1.6 per cent). None of the cats were positive for gamonts of *Hepatozoon* spp. Molecular analysis revealed *Hepatozoon* spp. infection in seven cats (5.7 per cent), *Cytauxzoon* spp. in 29 cats (23.8 per cent) and *Babesia* spp. in two cats (1.6 per cent). Present study highlights the inevitability of molecular techniques in the identification of haemoparasites. Establishment of proper preventive measures are required to control parasitic infection among domestic cats.

A coprological survey on helminths of Jackal *Canis aureus* Linnaeus 1758 in Kashmir Himalaya.

Sheikh MM, Tak H, Fazili MF, Wani IN.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520190/>

Cytokine Responses during *Mycobacterium tuberculosis* H37Rv and *Ascaris lumbricoides* Costimulation Using Human THP-1 and Jurkat Cells, and a Pilot Human Tuberculosis and Helminth Coinfection Study.

Bhengu KN, Singh R, Naidoo P, Mpaka-Mbatha MN, Nembu-Mafa N, Mkhize-Kwitshana ZL.

21-07-2023

Microorganisms.

<https://pubmed.ncbi.nlm.nih.gov/37513018/>

Background: Helminth infections are widespread in tuberculosis-endemic areas and are associated with an increased risk of active tuberculosis. In contrast to the pro-inflammatory Th1 responses elicited by *Mycobacterium tuberculosis* (Mtb) infection, helminth infections induce anti-inflammatory Th2/Treg responses. A robust Th2 response has been linked to reduced tuberculosis protection. Several studies show the effect of helminth infection on BCG vaccination and TB, but the mechanisms remain unclear. **Aim:** To determine the cytokine response profiles during tuberculosis and intestinal helminth coinfection. **Methods:** For the in vitro study, lymphocytic Jurkat and monocytic THP-1 cell lines were stimulated with Mtb H37Rv and *Ascaris lumbricoides* (*A. lumbricoides*) excretory-secretory protein extracts for 24 and 48 h. The pilot human ex vivo study consisted of participants infected with Mtb, helminths, or coinfecting with both Mtb and helminths. Thereafter, the gene transcription levels of IFN- γ , TNF- α , granzyme B, perforin, IL-2, IL-17, NFATC2, Eomesodermin, IL-4, IL-5, IL-10, TGF- β and FoxP3 in the unstimulated/uninfected controls, singly stimulated/infected and costimulated/coinfecting groups were determined using RT-qPCR. **Results:** TB-stimulated Jurkat cells had significantly higher levels of IFN- γ , TNF- α , granzyme B, and perforin compared to unstimulated controls, LPS- and *A. lumbricoides*-stimulated cells, and *A. lumbricoides* plus TB-costimulated cells ($p < 0.0001$). IL-2, IL-17, Eomes, and NFATC2 levels were also higher in TB-stimulated Jurkat cells ($p < 0.0001$). Jurkat and THP-1 cells singly stimulated with TB had lower IL-5 and IL-4 levels compared to those singly stimulated with *A. lumbricoides* and those costimulated with TB plus *A. lumbricoides* ($p < 0.0001$). *A. lumbricoides*-singly stimulated cells had higher IL-4 levels compared to TB plus *A. lumbricoides*-costimulated Jurkat and THP-1 cells ($p < 0.0001$). TGF- β levels were also lower in TB-singly stimulated cells compared to TB plus *A. lumbricoides*-costimulated cells ($p < 0.0001$). IL-10 levels were lower in TB-stimulated Jurkat and THP-1 cells compared to TB plus *A. lumbricoides*-costimulated cells ($p < 0.0001$). Similar results were noted for the human ex vivo study, albeit with a smaller sample size. **Conclusions:** Data suggest that helminths induce a predominant Th2/Treg response which may downregulate critical Th1 responses that are crucial for tuberculosis protection.

Multiple anthelmintic drug resistant *Ancylostoma caninum* in foxhounds.

Balk JD, Mitchell ND, Hughes J, Soto Nauto P, Rossi J, Ramirez-Barrios R.

Aug-2023

Int J Parasitol Drugs Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37481894/>

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

Marsh AE, Lakritz J.

Aug-2023

Int J Parasitol Drugs Drug Resist.
<https://pubmed.ncbi.nlm.nih.gov/37229949/>

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

Leishmaniose

Antimicrobial and in silico studies of the triterpenoids of *Dichapetalum albidum*.

Chama MA, Dziwornu GA, Popli E, Mas-Claret E, Egyir B, Ayine-Tora DM, Owusu KB, Reid DG, Osei-Safo D, Duer M, Mulholland D, Bender A.

14-07-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37539285/>

Here we report a new polyhydroxylated triterpene, 2 β ,6 β ,21 α -trihydroxyfriedelan-3-one (**4**) isolated from the root and stem bark of *Dichapetalum albidum* A. Chev (Dichapetalaceae), along with six known triterpenoids (**1-3**, **5**, **6**, **8**), sitosterol-3 β -O-D-glucopyranoside (**9**), a dipeptide (**7**), and a tyramine derivative of coumaric acid (**10**). Friedelan-3-one (**2**) showed an antimicrobial activity (IC₅₀) of 11.40 μ g/mL against *Bacillus cereus*, while friedelan-3 α -ol (**1**) gave an IC₅₀ of 13.07 μ g/mL against *Staphylococcus aureus* with ampicillin reference standard of 19.52 μ g/mL and 0.30 μ g/mL respectively. 3 β -Acetyl tormentic acid (**5**) showed an IC₅₀ of 12.50 μ g/mL against *Trypanosoma brucei brucei* and sitosterol-3 β -O-d-

glucopyranoside (**9**) showed an IC₅₀ of 5.06 μ g/mL against *Leishmania donovani* with respective reference standards of IC₅₀ 5.02 μ g/mL for suramin and IC₅₀ 0.27 μ g/mL for amphotericin B. Molecular docking of the isolated compounds on the enzyme glucose-6-phosphate dehydrogenase (G6PDH) suggested 3 β -acetyl tormentic acid (**5**) and sitosterol-3 β -O-D-glucopyranoside (**9**) as plausible inhibitors of the enzyme in accordance with the experimental biological results observed.

Cutaneous leishmaniasis in a newly established treatment centre in the Lay Gayint district, Northwest Ethiopia.

Yizengaw E, Nibret E, Yismaw G, Gashaw B, Tamiru D, Munshea A, Takele Y, Müller I, Chapman L, Weller R, Cotton JA, Kropf P.

17-03-2023

Skin Health Dis.

<https://pubmed.ncbi.nlm.nih.gov/37538321/>

Background: Cutaneous leishmaniasis (CL) is a neglected tropical disease that primarily affects the most vulnerable populations. In Ethiopia, where this study took place, CL is an important health problem, however, the incidence of CL is poorly monitored. **Objectives:** This study took place in a recently established CL treatment centre, at Nefas Mewcha Hospital, Lay Gayint. This area was considered to be endemic for CL, however, no cases of CL from Lay Gayint had previously been officially reported to the Amhara Regional Health Bureau. **Methods:** Following a CL awareness campaign, a retrospective data review was performed of patients presenting to this centre between July 2019 and March 2021. Basic demographic and clinical data were collected by a nurse and recorded in the logbook of the CL treatment centre. **Results:** Two hundred and one patients presented for diagnosis and treatment. The age of the patients ranged from 2 to 75 years and 63.2% were males. Most patients were between 10- and 19-years-old. The majority (79.1%) of the patients presented with localised cutaneous leishmaniasis and 20.9% with mucocutaneous leishmaniasis. 98% of the patients tested positive for *Leishmania* parasites by microscopy. **Conclusions:** This work underpinned how CL is a major public health problem in the Lay Gayint district. It also shows that raising awareness about CL in the community and providing diagnosis and treatment encouraged patients to travel to seek diagnosis and treatment.

Antileishmanial activity of 2-aminothiophene derivative SB-200.

Sousa JPA, Sousa JMS, Rodrigues RRL, Nunes TAL, Machado YAA, Araujo AC, da Silva IGM, Barros-Cordeiro KB, Bão SN, Alves MMM, Mendonça-Junior FJB, Rodrigues KADF.

01-08-2023

Int Immunopharmacol.

<https://pubmed.ncbi.nlm.nih.gov/37536181/>

Organogold(III)-dithiocarbamate compounds and their coordination

analogues as anti-tumor and anti-leishmanial metallodrugs.

de Andrade Querino AL, de Sousa AM, Thomas SR, de Lima GM, Dittz D, Casini A, do Monte-Neto RL, Silva H.
29-07-2023

J Inorg Biochem.

<https://pubmed.ncbi.nlm.nih.gov/37536162/>

Evaluating leishmanicidal effects of *Lucilia sericata* products in combination with *Apis mellifera* honey using an in vitro model.

Sherafati J, Dayer MS, Ghaffarifar F, Akbarzadeh K, Pirestani M.

03-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37535629/>

Leishmaniasis is a zoonotic disease caused by an intracellular parasite from the genus *Leishmania*. Lack of safe and effective drugs has increasingly promoted researches into new drugs of natural origin to cure the disease. The study, therefore, aimed to investigate the anti-leishmanial effects of *Lucilia sericata* larval excretion/secretion (ES) in combination with *Apis mellifera* honey as a synergist on *Leishmania major* using an in vitro model. Various concentrations of honey and larval ES fractions were tested against promastigotes and intracellular amastigotes of *L. major* using macrophage J774A.1 cell line. The inhibitory effects and cytotoxicity of ES plus honey were evaluated using direct counting method and MTT assay. To assess the effects of larval ES plus honey on the amastigote form, the rate of macrophage infection and the number of amastigotes per infected macrophage cell were estimated. The 50% inhibitory concentration (IC₅₀) values were 21.66 µg/ml, 43.25 µg/ml, 52.58 µg/ml, and 70.38 µg/ml for crude ES plus honey, ES >10 kDa plus honey, ES <10 kDa plus honey, and honey alone, respectively. The IC₅₀ for positive control (glucantime) was 27.03 µg/ml. There was a significant difference between viability percentages of promastigotes exposed to different doses of applied treatments compared to the negative control ($p \leq 0.0001$). Microscopic examination of amastigote forms revealed that dosages applied at 150 to 300 µg/ml significantly reduced the rate of macrophage infection and the number of amastigotes per infected macrophage cell. Different doses of larval products plus honey did not show a significant toxic effect against macrophage J774 cells. The larval ES fractions of *L. sericata* in combination with *A. mellifera* honey acted synergistically against *L. major*.

Serum Zinc Level and Efficacy of Zinc Therapy in Cutaneous Leishmaniasis: a Systematic Review and Meta-analysis.

Pal B, Mishra AK, Raj H, Chaudhary V, Khurana N, Azharuddin M, Kumari S.

03-08-2023

Biol Trace Elem Res.

<https://pubmed.ncbi.nlm.nih.gov/37535217/>

Cutaneous leishmaniasis is a parasitic skin disease prevalent in many parts of the world. Zinc has been investigated for its potential role in the immune response against *Leishmania* parasites. This study aimed to systematically review the literature and conduct meta-analyses to evaluate the serum zinc level and efficacy of zinc therapy in cutaneous leishmaniasis. A comprehensive search of electronic databases was performed to find studies reporting serum zinc levels and the efficacy of zinc therapy in cutaneous leishmaniasis. Meta-analyses were conducted using RevMan software (version 5.4), calculating the mean difference for serum zinc levels and risk ratio for the efficacy of zinc therapy. A total of 11 studies with 1009 participants were evaluated. Five of these studies, comprising 637 participants, examined serum zinc levels; the remaining six, involving 372 individuals, examined the effectiveness of zinc therapy in treating cutaneous leishmaniasis. The results showed that the serum zinc level was significantly lower in cutaneous leishmaniasis patients compared to controls (MD: - 26.65; 95% CI: [- 42.74, - 10.57]; $p = 0.001$). However, zinc therapy did not demonstrate a significant clinical improvement compared to standard treatment (RR: 0.96; 95% CI: [0.74, 1.23], $p = 0.73$).

Nucleoside hydrolase immobilized on magnetic particles as a tool for onflow screening and characterization of inhibitors.

de Oliveira PCO, Ceroulo MS, Dos Santos MB, Medeiros PRC, Marques BCB, Tinoco LW, de Souza MCBV, da Costa Santos Boechat F, de Moraes MC.

20-07-2023

J Pharm Biomed Anal.

<https://pubmed.ncbi.nlm.nih.gov/37531732/>

Nucleoside Hydrolases (NH) are considered a target for the development of new antiprotozoal agents. The development of new and automated screening assays for the identification of NH inhibitors can accelerate the first stages of the drug discovery process. In this work, NH from *Leishmania donovani* (LdNH) was covalently immobilized onto magnetic particles (LdNH-MPs) and trapped by magnets into a TFE tube to yield an immobilized enzyme reactor (IMER). For an automated assay, the LdNH-MP-IMER was connected in-line to an analytical column in an HPLC-DAD system to monitor the enzyme activity through quantification of the product hypoxanthine. Kinetic studies provided a K_M value of $2079 \pm 87 \mu\text{mol.L}^{-1}$ for the inosine substrate. Validation of the LdNH-MP-IMER for onflow screening purposes was performed with a library containing 12 quinolone ribonucleosides. Among them, three were identified as new competitive LdNH inhibitors, with K_i values between 83.5 and $169.4 \mu\text{mol.L}^{-1}$. This novel in-line screening assay has proven to be reliable, fast, low cost, and applicable to large libraries of compounds.

[Elucidating and characterizing the dynamic biological processes that account for the sustainability of *Leishmania* populations].

Giraud É, Milon G.

05-06-2023

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/37525683/>

Fever of unknown origin and splenomegaly: a case report of visceral leishmaniasis diagnosed by metagenomic next-generation sequencing.

Li LQ, He Y, Liu T, Zhou J, Chen EQ.

31-07-2023

Future Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37522175/>

Plasma metagenomics reveals regional variations of emerging and re-emerging pathogens in Chinese blood donors with an emphasis on human parvovirus B19.

Mengyi Z, Yuhui L, Zhan G, Anqing L, Yujia L, Shilin L, Lei G, Yue L, Mei H, Jianhua W, Weilan H, Wei M, Jie C, Jingyu Z, Yijing Y, Yanli G, Qiulei Z, Yang H, Limin C, Zhenxin F, Miao H.

13-07-2023

One Health.

<https://pubmed.ncbi.nlm.nih.gov/37520848/>

At present, many infectious pathogens, especially emerging/re-emerging pathogens, exist in the blood of voluntary blood donors and may be transmitted through blood transfusions. However, most of Chinese blood centers only routinely screen for HBV, HCV, HIV, and syphilis. We employed metagenomic next-generation sequencing (mNGS) to investigate the microbiome in healthy voluntary blood donors to help assess blood safety in China by identifying infectious pathogens presented in donations that could lead to transfusion-acquired infections. We collected 10,720 plasma samples from voluntary blood donors from seven blood centers in different cities during 2012-2018 in China. A total of 562 GB of clean data was obtained. By analyzing the sequencing data, it was found that the most commonly identified bacteria found in the healthy blood were *Serratia spp.* (5.0176%), *Pseudomonas spp.* (0.6637%), and *Burkholderia spp.* (0.5544%). The principal eukaryote were *Leishmania spp.* (1.3723%), *Toxoplasma gondii* (0.6352%), and *Candida dubliniensis* (0.1848%). Among viruses, Human Parvovirus B19 (B19V) accounts for the highest proportion (0.1490%), followed by Torque teno midi virus (0.0032%) and Torque teno virus (0.0015%). Since that B19V is a non-negligible threat to blood safety, we evaluated the positive samples for B19V tested by mNGS using quantitative polymerase chain reaction, Sanger sequencing, and phylogenetic analysis to achieve a better understanding of B19V in Chinese blood donors. Subsequently, 9 (0.07%) donations were positive for B19V DNA. The quantitative DNA levels ranged from 5.58×10^2 to 7.24×10^4 IU/ml. The phylogenetic analyses showed that prevalent genotypes belonged to the B19-1A subtype, which disclosed previously unknown regional variability in the B19V positivity rate. The investigation revealed that many microbes dwell in the blood of healthy donors, including some pathogens that may be dormant in the

blood and only cause disease under specific conditions. Thus, investigating the range and nature of potential pathogens in the qualified donations provided a framework for targeted interventions to help prevent emerging and re-emerging infectious diseases.

Intravenous Liposomal Amphotericin B Efficacy and Safety for Cutaneous and Mucosal Leishmaniasis: A Systematic Review and Meta-analysis.

Chivinski J, Nathan K, Naeem F, Ekmekjian T, Libman MD, Barkati S.

11-07-2023

Open Forum Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520422/>

Novel Schiff bases of Vanillin: potent inhibitors of macrophage harbored *Leishmania tropica*.

Ur Rahman M, Khan M, Khan SW, Khan RU, Sohail A, Zaman A, Alam N.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520206/>

In vitro screening of natural product-based compounds for leishmanicidal activity.

Tandon S, Puri M, Bharath Y, Choudhury UM, Mohapatra DK, Muthuswami R, Madhubala R.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520198/>

Leishmaniasis is one of the major parasitic diseases, caused by obligate intracellular protozoa *Leishmania*, having high mortality as well as morbidity rate. As there is no human licensed vaccine available against leishmaniasis, chemotherapy remains the major way of combating this disease. Many disadvantages are known to be associated with the current drug regime including severe side effects and toxicity, long duration and expensive treatment, and the emergence of resistance. An alternative approach is being utilized to search for active molecules using natural sources, rather than relying on synthetic drugs. Many plant-derived secondary metabolites like phenolic compounds, steroids, quinones, etc. are being extensively investigated for their anti-leishmanial potential. One such group of complex phenolic compounds are diarylheptanoids. These compounds have been shown to exhibit anti-inflammatory, anti-parasitic, anti-fungal, and other pharmacological activities. In the present study, a set of sixteen tetrahydropyran derivatives including three natural products were obtained in lyophilized form. These compounds with *trans*-2,6-disubstituted tetrahydropyrans, Diospongin A, Diospongin B (isolated from *Dioscorea spongiosa*) and Centrolobine (*Centrolobium sclerophyllum*) as parent compounds were synthesized by the reaction of 1-phenyl-1-trimethylsiloxyethylene with six-membered cyclic hemiacetals in the presence of iodine as a catalyst. All the sixteen synthesized tetrahydropyran derivatives were

used for toxicity analysis against *L. donovani* promastigotes, amastigotes and THP-1-derived human macrophages. IC₅₀ values and selectivity index were calculated for all the compounds. Out of these sixteen, five compounds showed the best effect in vitro in terms of both leishmanicidal activity and non-toxicity to human macrophages.

In vitro evaluation of herbal based Lesh Nat B cream against *Leishmania tropica*.

Gul S, Khan M, Amin A, Zaman A, Said A, Iqbal A, Muhammad S, Khan RU.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520195/>

Leishmaniasis in a tropical area of Brazil: a spatio-temporal analysis.

Filho CRCU, Lima TARF, de Barros LSS, Giannelli A, Alves LC, de Carvalho GA, Ramos RAN.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520193/>

Leishmaniasis are a group of tropical and neglected diseases caused by the protozoa of the genus *Leishmania* which are transmitted by insect sandflies. Despite of the major efforts undertaken at global level for the control of these diseases, a recent spreading to non-endemic areas been observed. In this study we analyzed the spatio-temporal distribution of Visceral Leishmaniasis (VL) and Tegumentary Leishmaniasis (TL) cases notified in a tropical region of Brazil. A retrospective evaluation was carried out using secondary data (e.g., demographics, origin, age and area of occurrence) of human patients obtained from 2009 to 2019. Choropleth maps with levels of color intensity represented the spatial distribution of VL and TL cases. Overall, 116 (10.5 ± 8.5) cases of leishmaniasis were registered in the study area during the whole period. Of those, 61 (5.5 ± 5.5) and 55 (5 ± 4.3) were diagnosed as VL and TL, respectively. VL cases were recorded in 61.9% (13/21) and TL cases in 42.8% (9/21) of the municipalities. Most of the cases were predominantly notified in men from rural areas, and specifically for TL with an age range of 30-59 years old. These findings will be useful to drive strategies of control (e.g., vector control, dog surveillance and notification of suspected cases) against these neglect diseases, preventing the spreading to non-endemic areas.

In vitro and in vivo antileishmanial effects of *Nectaroscordum koelzi* extract against *Leishmania major*.

Alizadegan F, Aghaei M, Kumar SJ, Saadatmand M, Kumar SA.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520187/>

Due to the increasing resistance to common medicinal compounds, the use of medicinal plants has received special attention. Therefore, the current survey was designed to study the antileishmanial effects of

Nectaroscordum koelzi Trautv. methanolic extract against *Leishmania major*. In this study, after preparing the methanolic extract of *N. koelzi*, its effect on the amastigotes of *L. major* and triggering the nitric oxide (NO) were measured. Then, the in vivo effect of the methanol extract on cutaneous leishmaniasis in mice was evaluated. The best anti-amastigote effect was for the methanol extract of *N. koelzi* along with meglumine antimony with 50% inhibitory concentrations value of 17.4 µg/ml ($p < 0.001$). The 50% cytotoxic concentrations values of methanol extract, meglumine antimoniate, and methanol extract + meglumine antimoniate were 596.3, 784.6, and 296.4 µg/ml, respectively. Macrophages treated with the methanolic extract markedly ($p < 0.001$) induced the release of nitric oxide. After 28 days of treatment, lesions were completely ($p < 0.001$) healed in mice treated with the methanolic extract (100 mg/kg) + meglumine antimoniate (25 mg/kg). *N. koelzi* methanolic extract mainly in combination with meglumine antimoniate showed favorable antileishmanial effects on *L. major*, concluding that the methanolic extract of *N. koelzi* can be used for the production of new leishmanicidal agents against cutaneous leishmaniasis. Although we revealed that NO triggering and inhibition of infection in host cells are the antileishmanial mechanism action of *N. koelzi* methanolic extract, more studies must be performed to clear the mechanisms and its safety.

The high expression of glial cell line-derived neurotrophic factor receptor alpha II (GFRA2) as a predictor of poor prognosis in gastric cancer patients: A survival and regression analysis approach.

Yang S, Li J, Cai X.

17-07-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37519699/>

Gastric cancer has high mortality rates worldwide. Therefore, there is a need to identify prognostic biomarkers. This study evaluated the association between *GFRA2* expression levels with clinicopathological features and prognosis in gastric cancer using data extracted from The Cancer Genome Atlas (TCGA) database and a series of algorithms. Survival analysis was performed using the Kaplan-Meier method. Univariate and multivariate Cox regression analyses were used to analyze the association between different clinical features and survival. Single-sample gene set enrichment analysis (GSEA) was used to examine the correlation between *GFRA2* expression and immune infiltration. The results showed that the expression of *GFRA2* in tumor samples was significantly lower than that in normal samples. High expression of *GFRA2* was significantly associated with histological type, histologic grade, and worse overall survival, disease-specific survival, and progression-free survival. The univariate Cox analysis showed that the expression of *GFRA2* was significantly correlated with T stage, N stage, M stage, and age. The multivariate analysis identified *GFRA2* expression as an independent prognostic factor for gastric cancer. GSEA showed that *GFRA2* might regulate the calcium signaling pathway, focus adhesion, olfactory

conduction, the extracellular matrix glycoproteins, and response to the *Leishmania* parasitic infection. *GFRA2* showed a significant moderate positive correlation with the infiltration of mast cells. In summary, a high expression of *GFRA2* may contribute to poor survival in gastric cancer patients and could be used as a potential prognostic biomarker.

Oral immunization with heat-inactivated *Mycobacterium bovis* reduces local parasite dissemination and hepatic granuloma development in mice infected with *Leishmania amazonensis*.

Ferreras-Colino E, Moreno I, Gortázar C, Sevilla I, Agulló-Ros I, Domínguez L, Juste R, Risalde MA, Domínguez M. 26-07-2023

Res Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37517297/>

***Leishmania donovani* persistence and circulation causing cutaneous leishmaniasis in unusual-foci of Nepal.**

Rai T, Shrestha S, Prajapati S, Bastola A, Parajuli N, Ghimire PG, Bhandari P, Pandey K, Jain M, Matlashewski G, Bras-Goncalves R, Manandhar KD. 29-07-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37516780/>

Toll-like receptor 2 selectively modulates Ras isoforms expression in *Leishmania major* infection.

Srivastava A, Nair A, Pandey SP, Kluck GEG, Mesquita I, Ghosh T, Bose A, Baral R, Silvestre R, Bodhale N, Saha B. 27-07-2023

Cytokine.

<https://pubmed.ncbi.nlm.nih.gov/37515982/>

Identification of Immunodominant Proteins of the *Leishmania (Viannia) naiffi* SubProteome as Pan-Specific Vaccine Targets against Leishmaniasis.

Jesus-Oliveira P, Silva-Couto L, Pinho N, Da Silva-Ferreira AT, Saboia-Vahia L, Cuervo P, Da-Cruz AM, Gomes-Silva A, Pinto EF. 21-06-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37514945/>

Leishmaniasis is a wide-spectrum disease caused by parasites from *Leishmania* genus. A well-modulated immune response that is established after the long-lasting clinical cure of leishmaniasis can represent a standard requirement for a vaccine. Previous studies demonstrated that *Leishmania (Viannia) naiffi* causes benign disease and its antigens induce well-modulated immune responses in vitro. In this work we aimed to identify the immunodominant proteins present in the soluble extract of *L. naiffi* (sLnAg) as candidates for composing a pan-specific anti-leishmaniasis vaccine. After immunoblotting using cured patients of cutaneous leishmaniasis sera and

proteomics approaches, we identified a group of antigenic proteins from the sLnAg. In silico analyses allowed us to select mildly similar proteins to the host; in addition, we evaluated the binding potential and degree of promiscuity of the protein epitopes to HLA molecules and to B-cell receptors. We selected 24 immunodominant proteins from a sub-proteome with 328 proteins. Homology analysis allowed the identification of 13 proteins with the most orthologues among seven *Leishmania* species. This work demonstrated the potential of these proteins as promising vaccine targets capable of inducing humoral and cellular pan-specific immune responses in humans, which may in the future contribute to the control of leishmaniasis.

BRCT Domains: Structure, Functions, and Implications in Disease-New Therapeutic Targets for Innovative Drug Discovery against Infections.

Peña-Guerrero J, Fernández-Rubio C, García-Sosa AT, Nguewa PA. 27-06-2023

Pharmaceutics.

<https://pubmed.ncbi.nlm.nih.gov/37514027/>

From Infection to Death: An Overview of the Pathogenesis of Visceral Leishmaniasis.

Costa CHN, Chang KP, Costa DL, Cunha FVM. 24-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513817/>

Kala-azar, also known as visceral leishmaniasis (VL), is a disease caused by *Leishmania infantum* and *L. donovani*. Patients experience symptoms such as fever, weight loss, paleness, and enlarged liver and spleen. The disease also affects immunosuppressed individuals and has an overall mortality rate of up to 10%. This overview explores the literature on the pathogenesis of preclinical and clinical stages, including studies in vitro and in animal models, as well as complications and death. Asymptomatic infection can result in long-lasting immunity. VL develops in a minority of infected individuals when parasites overcome host defenses and multiply in tissues such as the spleen, liver, and bone marrow. Hepatosplenomegaly occurs due to hyperplasia, resulting from parasite proliferation. A systemic inflammation mediated by cytokines develops, triggering acute phase reactants from the liver. These cytokines can reach the brain, causing fever, cachexia and vomiting. Similar to sepsis, disseminated intravascular coagulation (DIC) occurs due to tissue factor overexpression. Anemia, hypergammaglobulinemia, and edema result from the acute phase response. A regulatory response and lymphocyte depletion increase the risk of bacterial superinfections, which, combined with DIC, are thought to cause death. Our understanding of VL's pathogenesis is limited, and further research is needed to elucidate the preclinical events and clinical manifestations in humans.

Neglected Zoonotic Diseases: Advances in the Development of Cell-Penetrating and Antimicrobial Peptides against Leishmaniosis and Chagas Disease.

Robledo SM, Pérez-Silanes S, Fernández-Rubio C, Poveda A, Monzote L, González VM, Alonso-Collado P, Carrión J. 15-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513786/>

In 2020, the WHO established the road map for neglected tropical diseases 2021-2030, which aims to control and eradicate 20 diseases, including leishmaniosis and Chagas disease. In addition, since 2015, the WHO has been developing a Global Action Plan on Antimicrobial Resistance. In this context, the achievement of innovative strategies as an alternative to replace conventional therapies is a first-order socio-sanitary priority, especially regarding endemic zoonoses in poor regions, such as those caused by *Trypanosoma cruzi* and *Leishmania* spp. infections. In this scenario, it is worth highlighting a group of natural peptide molecules (AMPs and CPPs) that are promising strategies for improving therapeutic efficacy against these neglected zoonoses, as they avoid the development of toxicity and resistance of conventional treatments. This review presents the novelties of these peptide molecules and their ability to cross a whole system of cell membranes as well as stimulate host immune defenses or even serve as vectors of molecules. The efforts of the biotechnological sector will make it possible to overcome the limitations of antimicrobial peptides through encapsulation and functionalization methods to obtain approval for these treatments to be used in clinical programs for the eradication of leishmaniosis and Chagas disease.

The Extraordinary Case of a Woman with a 30-Year-Long Diffuse Leishmaniasis Cured with One Single Ampoule of Intranasal Pentavalent Antimoniate.

Gonçalves SVCB, Costa DL, Cantinho-Junior JDJ, Vieira-Junior JN, Ishikawa EAY, Costa RN, Costa-Filho ACG, Araújo RDC, Uliana SRB, Yasunaka JKUY, Coelho AC, Costa JML, Costa CHN. 29-06-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513737/>

Retrospective Long-Term Evaluation of Miltefosine-Allopurinol Treatment in Canine Leishmaniosis.

Gizzarelli M, Foglia Manzillo V, Inglese A, Montagnaro S, Oliva G. 22-06-2032

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513711/>

Miltefosine-Allopurinol (MIL-AL) combination is reported to be one of the most effective treatments for canine leishmaniosis, thanks to its oral administration and MIL-documented low impact on renal function. However, MIL-AL is considered a second-choice treatment when

compared to meglumine-antimoniate-allopurinol combination, mainly due to the risk of earlier relapses. The aim of this study was to evaluate the efficacy of the MIL-AL protocol during a long-term follow-up with an average duration of nine years. Dogs were living in Southern Italy (Puglia, Italy) in an area considered endemic for Canine leishmaniosis (CanL). Inclusion criteria were clinical and/or clinicopathological signs consistent with CanL; positive result to *Leishmania* quantitative ELISA; and negativity to the most frequent canine vector-borne infections. All dogs received 2 mg/kg MIL for 28 days, and 10 mg/kg AL, BID, for a period varying between 2 and 12 months. Ancillary treatments were allowed according to the clinical condition of the dog. A total clinical score and a total clinicopathological score were calculated at each time point by attributing one point to each sign or alteration present and then by adding all points. Improvement after each treatment was defined by the reduction of at least 50% of the total score. A survival analysis (Kaplan-Meier curve) was performed for quantifying the probability of the events occurring during the study follow-up. The following events were considered: decreased and negative ELISA results; improvement/recovery of the clinical and clinicopathological alterations; and relapse of leishmaniasis. One hundred seventy-three dogs (75f and 98m) were retrospectively included in the study by examining their clinical records since the first diagnosis of CanL. One hundred forty-three (83%) dogs were under five years of age. The mean duration of the follow-up period was 5.4 (± 1.1) years with a minimum of 3.2 years and a maximum of 9 years. All dogs received a first treatment of MIL-AL at inclusion; then, during the follow-up course, 30 dogs required a second treatment, 2 dogs required a third treatment and 1 dog required a fourth and a fifth treatment. The mean time interval between the first and the second treatment was 27.2 (± 18.3) months. After the first treatment, all dogs had decreased ELISA levels, in an average interval of 2.6 (± 1.6) months. One hundred seventy dogs (98%) experienced a clinical improvement (mean time 3.0 \pm 4.9 months); 152 (88%) dogs were considered clinically recovered after a mean time of 16.7 \pm 13.5 months. A similar trend was observed for clinicopathological alterations; interestingly, proteinuria decreased in most dogs ($p < 0.0001$ -Chi-square for trends). Thirty dogs experienced relapses, the earliest after 4.8 months. The mean time without relapse was 90.4 (± 2.5) months. In relapsed dogs, the mean time for clinical improvement after the second treatment was 8.6 (± 12.6) months, whereas it was 11.0 (± 15.4) months for clinicopathological alterations. Five dogs had limited gastrointestinal side effects associated with MIL treatment. The present study confirms that the MIL-AL protocol can be considered one of the most effective treatments for CanL therapy, mainly for its capacity to provide a long-time clinical improvement in a large majority of treated dogs. As reported in the literature, the clinical stabilization of dogs does not occur immediately after treatment, probably due to the particular pharmacokinetic properties of MIL. The efficacy of MIL-AL decreases in dogs that need more than one treatment, suggesting the necessity to alternate anti-*Leishmania* drugs for the treatment of relapses. Side effects were

transient and slight, even in dogs that required several treatments.

Is There Any Difference in the In Situ Immune Response in Active Localized Cutaneous Leishmaniasis That Respond Well or Poorly to Meglumine Antimoniate Treatment or Spontaneously Heal?

Leite-Silva J, Oliveira-Ribeiro C, Morgado FN, Pimentel MIF, Lyra MR, Fagundes A, Miranda LFC, Valette-Rosalino CM, Schubach AO, Conceição-Silva F.

22-06-2023

Microorganisms.

<https://pubmed.ncbi.nlm.nih.gov/37512804/>

In Silico Identification and Analysis of Proteins Containing the Phox Homology Phosphoinositide-Binding Domain in Kinetoplastea Protists: Evolutionary Conservation and Uniqueness of Phox-Homology-Domain-Containing Protein Architectures.

Petsana M, Roumia AF, Bagos PG, Boleti H, Braliou GG.

15-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37511280/>

Kinetoplastea are free living and parasitic protists with unique features among Eukaryota. Pathogenic Kinetoplastea parasites (i.e., *Trypanosoma* and *Leishmania* spp.) undergo several developmental transitions essential for survival in their hosts. These transitions require membrane and cytoskeleton reorganizations that involve phosphoinositides (PIs). Phospholipids like PIs are key regulators of vital functions in all eukaryotes including signal transduction, protein transport and sorting, membrane trafficking, and cytoskeleton and membrane remodeling. A large repertoire of PI-metabolizing enzymes and PI-binding proteins/effectors carrying distinct PI-binding modules like the PX (phox homology) module could play significant roles in the life and virulence of pathogenic Kinetoplastea. The aim of this study was to retrieve the entire spectrum of Kinetoplastea protein sequences containing the PX module (PX-proteins), predict their structures, and identify in them evolutionary conserved and unique traits. Using a large array of bioinformatics tools, protein IDs from two searches (based on PFam's pHMM for PX domain (PF00787)) were combined, aligned, and utilized for the construction of a new Kinetoplastea_PX pHMM. This three-step search retrieved 170 PX-protein sequences. Structural domain configuration analysis identified PX, Pkinase, Lipocalin_5, and Vps5/BAR3-WASP domains and clustered them into five distinct subfamilies. Phylogenetic tree and domain architecture analysis showed that some domain architectures exist in proteomes of all Kinetoplastea spp., while others are genus-specific. Finally, amino acid conservation logos of the Kinetoplastea spp. and *Homo sapiens* PX domains revealed high evolutionary conservation in residues forming the critical structural motifs for *PtdIns3P* recognition. This study highlights the

PX-Pkinase domain architecture as unique within *Trypanosoma* spp. and forms the basis for a targeted functional analysis of Kinetoplastea PX-proteins as putative targets for a rational design of anti-parasitic drugs.

Leishmania Seroprevalence in Dogs: Comparing Shelter and Domestic Communities.

Afonso P, Coelho AC, Quintas H, Cardoso L.

19-07-2023

Animals (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37508129/>

Canine leishmaniosis (CanL) is a chronic, systemic, and often severe disease. The main causative agent of CanL is a protozoan parasite, *Leishmania infantum*, with phlebotomine sand flies acting as vectors. In Europe and other continents, *L. infantum* is also responsible for leishmaniosis in other animals, such as cats, horses, and humans. In Portugal, animal and human leishmaniosis is endemic, and high prevalence levels of infections and disease have been reported in dogs. There is a prejudice against stray animals and also those housed in shelters, assuming they have higher levels of infection with vector-borne pathogens, including *L. infantum*, when compared to domestic animals. In northeastern Portugal, serum samples were obtained from March to May 2022 in three shelters ($n = 179$) and thirteen veterinary clinics ($n = 164$), resulting in 343 dogs being analyzed for antibodies to *Leishmania* spp. by the direct agglutination test (DAT). The overall seroprevalence was 9.9%, with 15.2% seroprevalence in domestic dogs and 5.0% in the shelter ones ($p = 0.003$). The fact that shelter dogs had a lower seroprevalence could be explained by more regular veterinary care provided in shelters regarding preventive measures, including insecticides with an antifeeding effect, in comparison with domestic dogs.

Structure-Guided Design and Synthesis of a Pyridazinone Series of Trypanosoma cruzi Proteasome Inhibitors.

Thomas MG, McGonagle K, Rowland P, Robinson DA, Dodd PG, Camino-Díaz I, Campbell L, Cantizani J, Castañeda P, Conn D, Craggs PD, Edwards D, Ferguson L, Fosberry A, Frame L, Goswami P, Hu X, Korczynska J, MacLean L, Martin J, Mutter N, Osuna-Cabello M, Paterson C, Peña I, Pinto EG, Pont C, Riley J, Shishikura Y, Simeons FRC, Stojanovski L, Thomas J, Wrobel K, Young RJ, Zmuda F, Zuccotto F, Read KD, Gilbert IH, Marco M, Miles TJ, Manzano P, De Rycker M.

28-07-2023

J Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37506194/>

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

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

28-07-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37506172/>

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

Anti-Leishmania amazonensis Activity, Cytotoxic Features, and Chemical Profile of Allium sativum (Garlic) Essential Oil.

Garcia AR, Amorim MMB, Amaral ACF, da Cruz JD, Vermelho AB, Nico D, Rodrigues IA.

31-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505671/>

Influence of Testosterone in Neglected Tropical Diseases: Clinical Aspects in Leprosy and In Vitro Experiments in Leishmaniasis.

de Oliveira Rekowsky LL, de Oliveira DT, Cazzaniga RA, Magalhães LS, Albuquerque LF, Araujo JMS, Tenório MDL, Machado TC, Lipscomb MW, Dos Santos PL, Ribeiro de Jesus A, Bezerra-Santos M, da Silva RLL.

10-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505653/>

In Vitro Drug Susceptibility of a Leishmania (Leishmania) infantum Isolate from a Visceral Leishmaniasis Pediatric Patient after Multiple Relapses.

Ferreira BA, Santos GA, Coser EM, Sousa JM, Gama MEA, Júnior LLB, Pessoa FS, Lima MIS, Uliana SRB, Coelho AC.

04-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505650/>

Silver(I) and Copper(II) 1,10-Phenanthroline-5,6-dione Complexes as Promising Antivirulence Strategy against Leishmania: Focus on Gp63 (Leishmanolysin).

Oliveira SSC, Correia CA, Santos VS, da Cunha EFF, de Castro AA, Ramalho TC, Devereux M, McCann M, Branquinha MH, Santos ALS.

30-06-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505644/>

Leishmaniasis, caused by protozoa of the genus *Leishmania*, encompasses a group of neglected diseases with diverse clinical and epidemiological manifestations that can be fatal if not adequately and promptly managed/treated. The current chemotherapy options for this disease are expensive, require invasive administration and often lead to severe side effects. In this regard, our research group has previously reported the potent anti-*Leishmania* activity of two coordination compounds (complexes) derived from 1,10-phenanthroline-5,6-dione (phendione): [Cu(phendione)₃](ClO₄)₂·4H₂O and [Ag(phendione)₂](ClO₄). The present study aimed to evaluate the effects of these complexes on leishmanolysin (gp63), a virulence factor produced by all *Leishmania* species that plays multiple functions and is recognized as a potential target for antiparasitic drugs. The results showed that both Ag-phendione (-74.82 kcal/mol) and Cu-phendione (-68.16 kcal/mol) were capable of interacting with the amino acids comprising the active site of the gp63 protein, exhibiting more favorable interaction energies compared to phendione alone (-39.75 kcal/mol) or 1,10-phenanthroline (-45.83 kcal/mol; a classical gp63 inhibitor) as judged by molecular docking assay. The analysis of kinetic parameters using the fluorogenic substrate Z-Phe-Arg-AMC indicated V_{max} and apparent K_m values of 0.064 μM/s and 14.18 μM, respectively, for the released gp63. The effects of both complexes on gp63 proteolytic activity were consistent with the *in silico* assay, where Ag-phendione exhibited the highest gp63 inhibition capacity against gp63, with an IC₅₀ value of 2.16 μM and the lowest inhibitory constant value (K_i = 5.13 μM), followed by Cu-phendione (IC₅₀ = 163 μM and K_i = 27.05 μM). Notably, pretreatment of live *L. amazonensis* promastigotes with the complexes resulted in a significant reduction in the expression of gp63 protein, including the isoforms located on the parasite cell surface. Both complexes markedly decreased the *in vitro* association indexes between *L. amazonensis* promastigotes and THP-1 human macrophages; however, this effect was reversed by the addition of soluble gp63 molecules to the interaction medium. Collectively, our findings highlight the potential use of these potent complexes in antivirulence therapy against *Leishmania*, offering new insights for the development of effective treatments for leishmaniasis.

Leishmania infantum Axenic Amastigotes Induce Human Neutrophil

Extracellular Traps and Resist NET-Mediated Killing.

Oliveira TKF, Oliveira-Silva J, Linhares-Lacerda L, da Silva Fraga-Junior V, Benjamim CF, Guimaraes-Costa AB, Saraiva EM.

25-06-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505632/>

Biogenic Fabrication of Iron Oxide Nanoparticles from *Leptolyngbya* sp. L-2 and Multiple In Vitro Pharmacogenetic Properties.

Minhas LA, Kaleem M, Minhas MAH, Waqar R, Al Farraj DA, Alsaigh MA, Badshah H, Haris M, Mumtaz AS.

27-06-2023

Toxics.

<https://pubmed.ncbi.nlm.nih.gov/37505527/>

Metallic nanoparticles have received a significant amount of reflection over a period of time, attributed to their electronic, specific surface area, and surface atom properties. The biogenic synthesis of iron oxide nanoparticles (FeONPs) is demonstrated in this study. The green synthesis of metallic nanoparticles (NPs) is acquiring considerable attention due to its environmental and economic superiorities over other methods. *Leptolyngbya* sp. L-2 extract was employed as a reducing agent, and iron chloride hexahydrate ($\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$) was used as a substrate for the biogenic synthesis of FeONPs. Different spectral methods were used for the characterization of the biosynthesized FeONPs, ultraviolet-visible (UV-Vis) spectroscopy gave a surface plasmon resonance (SPR) peak of FeONPs at 300 nm; Fourier transform infrared (FTIR) spectral analysis was conducted to identify the functional groups responsible for both the stability and synthesis of FeONPs. The morphology of the FeONPs was investigated using scanning electron microscopy (SEM), which shows a nearly spherical shape, and an X-ray diffraction (XRD) study demonstrated their crystalline nature with a calculated crystallinity size of 23 nm. The zeta potential (ZP) and dynamic light scattering (DLS) measurements of FeONPs revealed values of -8.50 mV, suggesting appropriate physical stability. Comprehensive in-vitro pharmacogenetic properties revealed that FeONPs have significant therapeutic potential. FeONPs have been reported to have potential antibacterial and antifungal properties. Dose-dependent cytotoxic activity was shown against *Leishmania tropica* promastigotes (IC₅₀: 10.73 µg/mL) and amastigotes (IC₅₀: 16.98 µg/mL) using various concentrations of FeONPs. The cytotoxic potential was also investigated using brine shrimps, and their IC₅₀ value was determined to be 34.19 µg/mL. FeONPs showed significant antioxidant results (DPPH: 54.7%, TRP: 49.2%, TAC: 44.5%), protein kinase (IC₅₀: 96.23 µg/mL), and alpha amylase (IC₅₀: 3745 µg/mL). The biosafety of FeONPs was validated by biocompatibility tests using macrophages (IC₅₀: 918.1 µg/mL) and red blood cells (IC₅₀: 2921 µg/mL). In conclusion, biogenic FeONPs have shown potential biomedical properties and should be the focus of more studies to increase their nano-pharmacological significance for biological applications.

The estimated distribution of autochthonous leishmaniasis by *Leishmania infantum* in Europe in 2005-2020.

Maia C, Conceição C, Pereira A, Rocha R, Ortuño M, Muñoz C, Jumakanova Z, Pérez-Cutillas P, Özbek Y, Töz S, Baneth G, Monge-Maillo B, Gasimov E, Van der Stede Y, Torres G, Gossner CM, Berriatua E.

19-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37467280/>

Case Report: Diffuse Cutaneous Leishmaniasis Successfully Treated with a Combination of Oral Rifampicin and Fluconazole.

Yadav N, Madke B.

10-07-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37429574/>

Diffuse cutaneous leishmaniasis (DCL) is a rare parasitic infection caused by the *Leishmania* species. Diffuse cutaneous leishmaniasis commonly presents as non-ulcerating papules and nodules over the face, neck, and arms. A middle-aged female presented with multiple nodular lesions on her face, neck, and chest region. Histopathology of the lesions showed multiple amastigotes, confirming the diagnosis of DCL. She was successfully treated with a combination course of rifampicin and fluconazole. Here, we report the first case of DCL in north India, a non-endemic area for cutaneous leishmaniasis.

Case Report: Diagnosis and Treatment of Two Clinical Cases of Visceral Leishmaniasis-Related Hemophagocytic Lymphohistiocytosis.

Wang L, Hu M, Wu X, Ma L, Yang H.

10-07-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37429573/>

Leishmania amazonensis infection impairs VLA-4 clustering and adhesion complex assembly at the adhesion site of J774 cells.

Brito R, Hassegawa EM, Camardelli P, Elpidio K, de Menezes J, Figueira CP, Dos-Santos WLC.

17-01-2023

Pathog Dis.

<https://pubmed.ncbi.nlm.nih.gov/37401145/>

Evaluation of murine OX40L-murine IgG1(MM1) fusion protein on immunogenicity against *L. mexicana* infection in BALB/c mice.

Rezvan H, Ali SA, Hamoon Navard S, Rees R.

Aug-2023

Comp Immunol Microbiol Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37393646/>

The majority of OX40L is found on professional antigen-presenting cells (APC), the potency of OX40L to enhance the immunogenicity of potential vaccines against leishmania is not yet fully investigated. There is no report of administration of OX40L on cutaneous leishmaniasis either in therapy or prophylactic immunisation and the present study for the first time reports the effect of OX40L on *L. mexicana* infection. In this study, B9B8E2 cells were transfected with the murine OX40L and IgG1 plasmids, were used to produce the mOX40L-mIgG1 (MM1). The therapeutic effects of MM1 (mOX40L-mIgG1) was tested in a challenge experiment using *L. mexicana* infected BALB/c mice. Mice received two doses of MM1, on day 3 and 7 after the infection. Mice receiving MM1 generated an inflammatory reaction a few days after the injection of the OX40L, which was gradually dampened and finally disappeared 3 weeks later. There was a significant delay in the growth of developing lesions in mice receiving OX40L compared to controls injected with PBS and the size of lesions in the group receiving MM1 was significantly smaller than that of injected with either PBS. 40% of mice given MM1 remained lesion free for two months, when experiments were terminated. The results clearly indicate the high therapeutic effect of mOX40L-mIgG1 fusion protein in *L. mexicana* infection. The effect of OX40L on the enhancement of immunisation, needs to be further investigated for developing new vaccine strategies.

Naïve antibody library derived monoclonal antibody against VP35 of Ebola virus.

Lai JY, Corona A, Ng CL, Tramontano E, Choong YS, Lim TS.

01-08-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37379953/>

Ebola virus is notorious for causing severe and even deadly haemorrhagic fever in infected humans and non-human primates. The high fatality rate of Ebola virus disease (EVD) has highlighted the need for effective diagnosis and treatment. Two monoclonal antibodies (mAbs) have been approved by USFDA for treatment of EVD. Virus surface glycoprotein is the common target for diagnostic and therapy including vaccines. Even so, VP35, a viral RNA polymerase cofactor and interferon inhibitor could be a potential target to curb EVD. The present work describes the isolation of three mAb clones from a phage-displayed human naïve scFv library against recombinant VP35. The clones showed binding against rVP35 in vitro and inhibition of VP35 in luciferase reporter gene assay. Structural modelling analysis was also carried out to identify the binding interactions involved in the antibody-antigen interaction model. This allows some insight into the "fitness" of the binding pocket between the paratope and target epitope which would be useful for the design of new mAbs through in silico means in the future. In conclusion, the information obtained from the 3 isolated mAbs could be potentially useful in the quest to improve VP35 targeting for therapeutic development in the future.

Src- and Abl-family kinases activate spleen tyrosine kinase to maximize phagocytosis and Leishmania infection.

Ullah I, Barrie U, Kernen RM, Mamula ET, Khuong FTH, Booshehri LM, Rhodes EL, Bradford JM, Datta A, Wetzel DM.

15-07-2023

J Cell Sci.

<https://pubmed.ncbi.nlm.nih.gov/37357611/>

A Novel Topical Formulation of the Leishmaniasis Drug Glucantime as a Nanostructured Lipid Carrier-Based Hydrogel.

Dehghani F, Farhadian N, Mashayekhi Goyonlo V, Ahmadi O.

12-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37308100/>

MiR-150 regulates the Leishmania infantum parasitic load and granzyme B levels in peripheral blood mononuclear cells of dogs with canine visceral leishmaniasis.

Soares MF, Costa SF, de Freitas JH, Rebech GT, Dos Santos MO, de Lima VMF.

Août-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37269731/>

Lèpre

Leprosy may now be endemic in Florida, clinicians warn.

Mahase E.

03-08-2023

BMJ.

<https://pubmed.ncbi.nlm.nih.gov/37536721/>

Lapatinib-induced PRIDE complex: a new kid on the block.

Sil A, Sikder B, Biswas SK, Chandra A.

02-08-2023

Postgrad Med J.

<https://pubmed.ncbi.nlm.nih.gov/37535871/>

Leprosy and tuberculosis control scenario of the national program for the improvement of access and quality of primary care in Brazil.

Ferreira GRON, Miranda ALC, Farias VA, Martins MB, Neri DT, Borges WD, Cunha CLF, Dias GAR, Santos DC, Sousa FJD.

02-08-2023

BMC Health Serv Res.

<https://pubmed.ncbi.nlm.nih.gov/37533030/>

Background: In Brazil, despite advances in public health policies aimed at eliminating and controlling infectious and parasitic diseases, the incidence of neglected diseases is still high. The epidemiological scenario in Brazil of diseases such as tuberculosis and leprosy evidences a public policy agenda that has not been resolute in terms of control, nor in terms of elimination. **Objective:** To analyze the actions of diagnosis and treatment of leprosy and tuberculosis in the context of primary health care. **Methods:** In this ecological study, data from the third cycle of the Program for the Improvement of Access and Quality of Primary Care were extracted from electronic address of the Primary Health Care Secretariat of Brazil in the area of Actions, Programs and Strategies. A total of 37,350 primary health care teams that answered the questionnaire were eligible, with variables extracted from leprosy and tuberculosis control actions. The municipalities were grouped according to the characteristic of the Brazilian municipality. The partition chi-square and the Residuals Test were used to assess whether there was a difference in the proportion of tuberculosis and leprosy actions between types of municipalities. Statistics were carried out using Minitab 20 and Bioestat 5.3. **Results:** Regarding the leprosy treatment location, there is a higher proportion of people referred to be treated at the reference in adjacent rural ($p = 0.0097$) and urban ($p < 0.0001$) municipalities; monitoring of people with leprosy referred to the service network ($p = 0.0057$) in remote rural areas. Lower proportion of teams requesting bacilloscopy in remote rural areas ($p = 0.0019$). Rural areas have a higher proportion of teams that diagnose new cases ($p = 0.0004$). Regarding the actions of diagnosis and treatment of tuberculosis. There is a higher proportion of teams that carry out consultations at the unit itself in rural areas when compared to adjacent intermediaries ($p = 0.0099$) and urban ($p < 0.0001$); who requested sputum smear microscopy in adjacent intermediaries ($p = 0.0021$); X-ray in adjacent intermediaries ($p < 0.0001$) and urban ($p < 0.0001$); collection of the first sputum sample in urban ($p < 0.0001$) and adjacent rural areas ($p < 0.0001$); directly observed treatment ($p < 0.0001$) in adjacent rural municipalities. **Conclusion:** There are inequalities in the diagnosis and treatment of leprosy and tuberculosis among the types of municipalities.

The Many Hosts of Mycobacteria 9 (MHM9): A conference report.

Klever AM, Alexander KA, Almeida D, Anderson MZ, Ball RL, Beamer G, Boggiatto P, Buikstra JE, Chandler B, Claey's TA, Concha AE, Converse PJ, Derbyshire KM, Dobos KM, Dupnik KM, Endsley JJ, Endsley MA, Fennelly K, Franco-Paredes C, Hagge DA, Hall-Stoodley L, Hayes D Jr, Hirschfeld K, Hofman CA, Honda JR, Hull NM, Kramnik I, Lacourciere K, Lahiri R, Lamont EA, Larsen MH, Lemaire T, Lesellier S, Lee NR, Lowry CA, Mahfooz NS, McMichael TM, Merling MR, Miller MA, Nagajyothi JF, Nelson E, Nuernberger EL, Pena MT, Perea C, Podell BK, Pyle CJ, Quinn FD, Rajaram MVS, Mejia OR, Rothoff M, Sago SA, Salvador LCM, Simonson AW, Spencer JS, Sreevatsan S, Subbian S, Sunstrum J, Tobin DM, Vijayan KKV, Wright CTO, Robinson RT.

23-07-2023

Tuberculosis (Edinb).

<https://pubmed.ncbi.nlm.nih.gov/37531864/>

Effectiveness of neurolysis as a treatment for complications of leprosy neuritis: a systematic review.

Gonçalves LC, Fuentealba-Torres M, Bolorino N, Ferreira NMA, Freitas FMB, Tirolí CF, Pimenta RA, Arcêncio RA, Pieri FM.

28-07-2023

Rev Soc Bras Med Trop.

<https://pubmed.ncbi.nlm.nih.gov/37531518/>

Inflammation induced by excessive expression of CD4 T-cell lymphocytes & proinflammatory cytokines results in bacterial dissemination in Mycobacterium tuberculosis-infected guinea pig model.

Davuluri KS, Singh SV, Chauhan DS.

02-08-2023

Indian J Med Res.

<https://pubmed.ncbi.nlm.nih.gov/37530232/>

Background & objectives: As CD4+ and CD8+ T lymphocyte numbers decline, the conventional, localized forms of tuberculosis shift to the atypical, disseminated forms. Variations in lymphocyte and immune cell expression levels affect how tuberculosis manifests in disseminated forms. Understanding the relationship between lymphocyte counts (CD4+ and CD8+) and pro-inflammatory cytokines such as tumour necrosis factor- α , interleukin-12 and interferon, we may therefore be able to shed light on how infections spread and suggest potential biomarkers for these immune factors. **Methods:** In this study, 15 guinea pigs were infected with *Mycobacterium tuberculosis* (M.tb) H37Rv strain and grouped into three groups of five each for further investigation. Serum samples and bronchoalveolar lavage (BAL) fluid were examined for the expression of pro-inflammatory cytokines and T-cell subsets in guinea pigs infected with pulmonary tuberculosis and disseminated tuberculosis. **Results:** We found that M.tb escapes macrophages due to pro-inflammatory cytokine dysregulation. Despite the protective immunity created by T-cells and cytokines, M.tb bacilli may spread to other organs due to inflammation induced by these immune components. A high number of T-cells and stimulated cytokine production are involved in triggering inflammation after necrotic tissue develops and tuberculosis spreads. **Interpretation & conclusions:** Our findings imply that increased bacilli in the spleen at the 8th wk of infection may be caused by the overexpression of CD4+ T-cell lymphocyte subsets and cytokines that generated inflammation during the 4th wk of infection. This is a pilot study with a small sample size and less assertive inference. Larger studies would be helpful to validate the results of the present investigation.

Angioma Serpiginosum with Soft Tissue Hypertrophy and Palmar Involvement: A Rare Presentation.

Gupta I, Dayal S, Sahu P, Sen R.

Mai-Juin 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37529470/>

A Tiny Yellowish Growth on the Eyebrow.

Adya KA, Inamadar AC, Palit A, Janagond AB.

Mai-Juin 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37529466/>

Predictability of Nailfold Capillaroscopic Score in Diagnosing Retinopathy in Patients with Type 2 Diabetes Mellitus and its Utility as a Non-Invasive Tool for Differentiating from those Not Having Retinopathy: A Pilot Observational Cross-Sectional Analytical Study.

Raina R, Chhabra N, Barnwal S, Vasisht S, Kansal NK, Kant R.

Mai-Juin 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37529446/>

Uncommon Presentation of Leprosy: A Report of Two Cases.

Supekar BB, Soni R, Bhushan R, Mukhi JI, Singh RP, Bhat D.

Mai-Juin 2023

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37529443/>

Lazarine leprosy is an unusual expression of usually borderline tuberculoid (BT) form characterized by spontaneous ulceration of skin lesions. This is presumably the result of an exaggerated type 1 reaction. It commonly occurs in the BT, borderline lepromatous forms and rarely in the lepromatous forms of leprosy. We report two cases of lazarine leprosy in the BT and BT downgrading to borderline lepromatous spectrum in healthy and immunocompetent males.

Giant gastric GIST with fast-growing mass after intra-tumoral bleeding.

Duguma YM, Seid TA, Shumiye YG, Dinagde TA, Kejela S.

29-07-2023

J Surg Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37525750/>

[Analysis of national leprosy surveillance data in Mauritania from 2009 to 2019].

Boushab BM, Yanogo PK, Barry D, Maham MH, Traoré AMK, Kane EM, Basco L, Meda N.

20-04-2023

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/37525686/>

[Dr Jean Languillon (1912-2003), a major unrecognized leprologist].

Louis JP, Louis F.

19-06-2023

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/37525670/>

Languillon's contribution to the control of leprosy cannot be reduced to the manual of leprology which remains the reference for anyone working on this disease in sub-Saharan Africa. This would mean forgetting his works that established the immunological origin of leprosy and its cutaneous, adverse and neurological complications. Another major aspect, the importance of his contribution to the treatment of the disease, in particular through the development of polychemiotherapy (PCT), which has made Institut Marchoux in Bamako one of the five WHO's collaborating centers in the field of clinical research in leprosy. Languillon was also involved in a holistic approach of the disease by creating the first leprosy surgery unit and implementing physiotherapy, orthopedic care with appropriate equipment, and social rehabilitation... without forgetting preventive aspects of complications through the necessary regular administration of treatments, and control of patients spread over wide territories, by creating a corps of leprosy nurse monitors and leprosy specialists. These will provide essential support to the doctor most often in charge of a huge sector where the need of assistance was obvious. Languillon ended his African career by creating the ILAD, Institute of Applied Leprology in Dakar, which offers the full range of care, as he always advocated. Finally, he did not resist the call of Order of Malta which offered him to share his expertise in the different countries where the Order was involved.

Post skin graft eczematous dermatitis at the donor and recipient sites: a case of Ruocco's immunocompromised district.

Kulkarni S, Adya KA, Inamadar A.

31-07-2023

BMJ Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37524508/>

PGL-III, a Rare Intermediate of Mycobacterium leprae Phenolic Glycolipid Biosynthesis, Is a Potent Mincle Ligand.

Ishizuka S, van Dijk JHM, Kawakita T, Miyamoto Y, Maeda Y, Goto M, Le Calvez G, Groot LM, Witte MD, Minnaard AJ, van der Marel GA, Ato M, Nagae M, Codée JDC, Yamasaki S.

12-07-2023

ACS Cent Sci.

<https://pubmed.ncbi.nlm.nih.gov/37521780/>

Turmeric: The Yellow Allergen.

Palaniappan V, Karthikeyan K.

21-10-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521239/>

Turmeric is the dried rhizome of *Curcuma longa* Linn which is extensively used in Indian culture. Curcumin is its most active pharmaceutical component. Turmeric use is very closely related with the socio-religious life of the population. Topical application of turmeric is a very common practice in the daily lives and auspicious occasions in South India. However, the allergenic potential of this commonly used spice is mentioned in various case reports and studies. The dermatologists and patients should be aware of the possible allergic reactions of this widely used herb. The purpose of this review is to give a brief overview of allergenic potential of this commonly used spice.

A Case of Recalcitrant Prurigo Nodularis with Heightened Expression of STAT 3 and STAT 6 and its Dramatic Response to Tofacitinib.

Agrawal D, Sardana K, Mathachan SR, Ahuja A.
25-05-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521237/>

Staphylococcal Carriage Status: Implications, Mechanisms and Practical Guidelines.

Chakraborty A.

28-06-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521232/>

Which is the Ideal JAK Inhibitor for Alopecia Areata - Baricitinib, Tofacitinib, Ritlecitinib or Ifidancitinib - Revisiting the Immunomechanisms of the JAK Pathway.

Sardana K, Bathula S, Khurana A.

28-06-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521227/>

Genital Ulcer: A Diagnostic Challenge.

Fernandes S, Martis J, Monteiro RC, Almeida JD.

25-05-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521226/>

Chronic Oro-Genital Ulcerations as a Presenting Feature of Chronic Eosinophilic Leukemia: A Case Report.

Padhiyar J, Patel N, Lakum M, Shah H.

25-05-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521217/>

Hypereosinophilia can be primary, including idiopathic hypereosinophilic syndrome (HES) and chronic eosinophilic leukemia, or secondary/reactive to various infective and non-infective stimuli. Chronic oro-genital ulcerations can occur due to various dermatological and

non-dermatological disorders, and many times it serves as a useful indicator of an underlying systemic disorder. Hence, a case presenting with chronic oro-genital ulcerations needs a thorough evaluation. We are reporting an interesting case of a middle-aged male who had chronic oro-genital ulcerations as a presenting feature of chronic eosinophilic leukemia with *FIP1L1-PDGFR* fusion (FIP1-like 1/platelet-derived growth factor receptor alpha). The patient's oro-genital ulcerations responded excellently to imatinib.

A Six-Year Retrospective Analysis of Skin Biopsies in the Pediatric and Adolescent Population Performed at a Tertiary Health Care Center in India.

Vishwanath T, Kharkar V, Gole P, Mahajan S, Chikhalkar S.

28-06-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521215/>

Utility of Dermoscopy in Cutaneous Small Vessel Vasculitis: Preliminary Observations from a Study of 30 Cases.

Kavya RM, Adya KA, Inamadar AC.

25-05-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521212/>

Background: Dermoscopy is a non-invasive diagnostic technique that provides an added advantage to the routine clinical diagnostic exercise. Role of dermoscopy in cutaneous small vessel vasculitis has not been explored well. **Objective:** This study was intended to delineate the dermoscopic features of cutaneous small vessel vasculitis and to correlate them with histopathological findings of the disease. **Materials and methods:** This was a cross-sectional study involving 30 patients with cutaneous small vessel vasculitis confirmed by histopathology and direct immunofluorescence. In each patient, dermoscopic features of early/evolving and established lesions were recorded. Dermoscopic-histopathological correlation was assessed for established lesions. **Results:** On dermoscopy, the early/evolving lesions showed a dull red background in all the 30 (100%) patients, red globules in 8 (26.7%), and red dots in 4 (13.30%) patients. The established lesions showed red background in 28 (93.3%) patients, white and yellow structureless areas in 19 (63.33%) patients each, red globules in 18 (60%), and red dots in 16 (53.3%) patients. A statistically significant association between red globules and red blood cell extravasation was noted ($P=0.01$). White and yellow structureless areas also showed a statistically significant association between sparse ($P=0.023$) and dense ($P=0.007$) perivascular infiltrates, respectively. **Conclusion:** Dermoscopy of cutaneous small vessel vasculitis exhibits fairly reliable and reproducible features correlating well with histopathological aspects of the disease. Hence, inclusion of dermoscopy in the clinical diagnostic protocol for cutaneous small vessel vasculitis is beneficial in complementing the clinical diagnosis and in differentiating from other inflammatory purpuras.

A Clinico-Epidemiological Study of Paederus Dermatitis in a Tertiary Care Center in Puducherry, India.

Palaniappan V, Karthikeyan K.

25-05-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521211/>

Is It EDV?: Diffuse Hypopigmented Keratosis vs Epidermodysplasia Verruciformis: Similar yet Different Entities.

Sane RR, Manoharan K, Gurusamy S, Udhayini KV.

28-06-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521210/>

ChatGPT- Quo Vadis?

Kaliyadan F, Seetharam KA.

28-06-2023

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/37521206/>

Epidemiological clinical profile and closure of chronic plantar ulcers in patients with leprosy sequelae undergoing orthopedic surgery in a municipality in western Amazon.

João FM, Peninni SN, Vasconcelos ZS, da Silva AS, Couceiro KDN, Jorge Brandão AR, Silva MRHDSE, do Vale Filho MF, de Oliveira GMS, Ferreira LS, Mwangi VI, da Silva BM, Barbosa Guerra MDGV, Guerra JAO.

28-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37506098/>

Influence of Testosterone in Neglected Tropical Diseases: Clinical Aspects in Leprosy and In Vitro Experiments in Leishmaniasis.

de Oliveira Rekowsky LL, de Oliveira DT, Cazzaniga RA, Magalhães LS, Albuquerque LF, Araujo JMS, Tenório MDL, Machado TC, Lipscomb MW, Dos Santos PL, Ribeiro de Jesus A, Bezerra-Santos M, da Silva RLL.

10-07-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505653/>

Neglected tropical diseases encompass a group of chronic and debilitating infectious diseases that primarily affect marginalized populations. Among these diseases, leprosy and leishmaniasis are endemic in numerous countries and can result in severe and disfiguring manifestations. Although there have been reports indicating a higher incidence of leprosy and leishmaniasis in males, the underlying factors contributing to this observation remain unclear. Therefore, the objective of this study was to examine both clinical and experimental evidence regarding the role of testosterone in leprosy and leishmaniasis. A prospective clinical study was conducted

to compare the clinical forms of leprosy and assess circulating testosterone levels. Additionally, the impact of testosterone on *Leishmania amazonensis*-infected macrophages was evaluated in vitro. The findings demonstrated that serum testosterone levels were higher in women with leprosy than in the control group, irrespective of the multi- or pauci-bacillary form of the disease. However, no differences in testosterone levels were observed in men when comparing leprosy patients and controls. Interestingly, increasing doses of testosterone in macrophages infected with *L. amazonensis* resulted in a higher proportion of infected cells, decreased CD40 expression on the cell surface, elevated expression of SOCS1, and decreased expression of IRF5. These findings provide biological evidence to support the influence of testosterone on intracellular infections, though the interpretation of clinical evidence remains limited.

Health-Seeking Behavior Regarding Coughs in Urban Slums in Lagos, Nigeria.

Adepoju VA, Oladimeji O, Sokoya OD.

26-06-2023

Medicines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37505059/>

Background: TB is a major cause of morbidity and mortality, with slum residents being disproportionately affected. This study aimed to assess health-seeking behavior among adult residents of slum communities presenting with coughs in Lagos, Nigeria. **Methods:** A community-based, cross-sectional study was conducted across six urban slums in Nigeria as part of community outreaches to mark World TB Day. A structured, pretested questionnaire was used to capture relevant sociodemographic details and questions regarding symptoms of coughs and related symptoms as well as care-seeking behavior. Data were explored, analyzed, and presented using descriptive statistics. **Results:** A total of 632 respondents participated in this study. The majority were 25-34 years old (24.7%), male (65.8%), Christian (55.7%), married (73.7%), with secondary education (37.8%), with 3-4 persons per household (41%) and with 1-2 persons per room (44.5%). In total, 26.6% had had a cough for two weeks or more and were considered as presumptive TB patients. Overall, 37.2% of respondents with a cough visited patent proprietary medicine vendors (PPMVs) as the first port of call. Good health-seeking behavior was exhibited by only 36.2% of respondents. In total, 38.9% delayed seeking care from a health facility (government or private) more than one month after the onset of symptoms. None of the factors included in the multivariate analysis showed a significant association with good health-seeking behavior (i.e., visiting government or private hospitals/clinics). **Conclusions:** The poor health-seeking behavior, delay in seeking TB care and preference for PPMVs emphasizes the need for National tuberculosis programs (NTPs) to further engage these informal providers in TB prevention, diagnosis and treatment services in urban slum communities.

Efficacy and Safety of Naftifine Hydrochloride 2% Gel in Interdigital Tinea Pedis: A Phase III Randomised, Double-Blind, Parallel-Group, Active-Controlled Study in Indian Adult Patients.

Sinha SD, Rajamma A, Bandi MR, Sriramadasu SC, Sahu S, Kothiwala RK, Halder S, Sankerneni A, Panapakam M, Vemireddy VNR, Vattipalli R, Devireddy SR.

Jul-2023

Clin Drug Investig.

<https://pubmed.ncbi.nlm.nih.gov/37462803/>

Case Report: Diffuse Cutaneous Leishmaniasis Successfully Treated with a Combination of Oral Rifampicin and Fluconazole.

Yadav N, Madke B.

10-07-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37429574/>

Prevalence and Predictors of COVID-19 Long-Term Symptoms: A Cohort Study from the Amazon Basin.

Silva KM, Freitas DCA, Medeiros SS, Miranda LVA, Carmo JBM, Silva RG, Becker LL, Abreu ES, Buranello L, Souza MSM, Nadruz W, Fernandes-Silva MM, Maguire JH, Toledo-Cornell C, Silvestre OM.

26-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37364863/>

It remains unclear whether a previous history of tropical infectious diseases and a second SARS-CoV-2 infection may influence the likelihood of later symptoms. In this prospective cohort study, individuals infected with SARS-CoV-2 were followed up by telephone shortly after diagnosis of COVID-19 and again 12 months later. Poisson regression was used to identify the predictors of the highest number of symptoms in the post-COVID-19 syndrome. A total of 1,371 patients with COVID-19, with a mean age of 39.7 ± 11.7 years and 50% female, were followed for 12 months. Reinfection was found in 32 (2.3%) participants, and 806 (58.8%) individuals reported a previous history of dengue, malaria, Zika, chikungunya, leprosy, and visceral leishmaniasis. Eight hundred seventy-seven (63.9%) participants reported late symptoms related to COVID-19. After adjusting for multiple factors, female sex, non-White race, number of acute-phase symptoms, body mass index, and reinfection were independent predictors of higher number of symptoms in post-COVID-19 syndrome. Female sex, non-White race, number of acute-phase symptoms, body mass index, and reinfection, but not previous endemic tropical diseases, were associated with long-term symptoms.

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

Sarath IM, Joseph NM, Jamir I.

20-06-2023

Am J Trop Med Hyg.

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

Case Report: Upper Thoracic Esophageal Paralysis Accompanying a Type 1 Leprosy Reaction.

Zhu J, Shi C, Zhao H, He R, Jing Z, Yang D.

05-06-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37277105/>

Type 1 leprosy reactions (T1LRs) occur mainly in patients with borderline leprosy and an unstable immune status. The main symptoms of T1LRs include aggravated skin lesions and nerve damage. Nerve damage involving the glossopharyngeal and vagus nerves causes dysfunction of the nose, pharynx, larynx, and even the esophagus, which are innervated by these nerves. Here, we report a case of upper thoracic esophageal paralysis caused by vagus nerve involvement in a patient with T1LRs. Although infrequent, this serious emergency merits attention.

Treatment of Acquired Digital Arteriovenous Malformation With Intralesional Bleomycin: An Effective Modality for a Lesser Known Condition.

Khurana A, Mathachan SR, Paliwal P.

01-08-2023

Dermatol Surg.

<https://pubmed.ncbi.nlm.nih.gov/37184505/>

Leprosy and broken bacilli on slit skin smear.

Sukanya G, Manoharan K, Logeswari PT, Naidu DK.

28-07-2023

QJM.

<https://pubmed.ncbi.nlm.nih.gov/37021961/>

Morsures de serpent

Crosstalk of Inflammation and Coagulation in Bothrops Snakebite Envenoming: Endogenous Signaling Pathways and Pathophysiology.

Cavalcante JS, de Almeida DEG, Santos-Filho NA, Sartim MA, de Almeida Baldo A, Brasileiro L, Albuquerque PL, Oliveira SS, Sachett JAG, Monteiro WM, Ferreira RS Jr.

15-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37511277/>

Snakebite envenoming represents a major health problem in tropical and subtropical countries. Considering the elevated number of accidents and high morbidity and mortality rates, the World Health Organization reclassified this disease to category A of neglected diseases. In Latin America, *Bothrops* genus snakes are mainly responsible for snakebites in humans, whose pathophysiology is characterized by local and systemic inflammatory and

degradative processes, triggering prothrombotic and hemorrhagic events, which lead to various complications, organ damage, tissue loss, amputations, and death. The activation of the multicellular blood system, hemostatic alterations, and activation of the inflammatory response are all well-documented in *Bothrops* envenomings. However, the interface between inflammation and coagulation is still a neglected issue in the toxinology field. Thromboinflammatory pathways can play a significant role in some of the major complications of snakebite envenoming, such as stroke, venous thromboembolism, and acute kidney injury. In addition to exacerbating inflammation and cell interactions that trigger vaso-occlusion, ischemia-reperfusion processes, and, eventually, organic damage and necrosis. In this review, we discuss the role of inflammatory pathways in modulating coagulation and inducing platelet and leukocyte activation, as well as the inflammatory production mediators and induction of innate immune responses, among other mechanisms that are altered by *Bothrops* venoms.

Russell Viper Venom: A Journey from the Bedside to the Bench and Back to the Bedside.

Thachil J.

28-07-2023

Semin Thromb Hemost.

<https://pubmed.ncbi.nlm.nih.gov/37506733/>

Russell Viper Venom (RVV) is widely used as a diagnostic test for antiphospholipid syndrome (APS). But the history of how this venom came to be discovered is well known. Dr Patrick Russell is responsible for the identification of the venom during his work on snake bites in India while Dr Robert Macfarlane used it to staunch bleeding in persons with haemophilia. The ability to directly activate factor X led RVV to the laboratory diagnosis of APS. More recently, it has come back to clinical world with a potential for an engineered factor X activator from RVV to be used in the treatment of haemophilia.

Compendium of medically important snakes, venom activity and clinical presentations in Ghana.

Deikumah JP, Biney RP, Awoonor-Williams JK, Gyakobo MK.

28-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37506181/>

A Retrospective Cohort Study of Cobra Envenomation: Clinical Characteristics, Treatments, and Outcomes.

Tansuwannarat P, Tongpoo A, Phongsawad S, Sriapha C, Wananukul W, Trakulsrichai S.

20-07-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37505737/>

Proteomic Profiling of Extracellular Vesicles Isolated from Plasma and Peritoneal Exudate in Mice Induced by *Crotalus scutulatus scutulatus* Crude Venom and Its Purified Cysteine-Rich Secretory Protein (C_{ss}-CRiSP).

Reyes A, Hatcher JD, Salazar E, Galan J, Iliuk A, Sanchez EE, Suntravat M.

02-07-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37505703/>

Increased vascular permeability is a frequent outcome of viperid snakebite envenomation, leading to local and systemic complications. We reported that snake venom cysteine-rich secretory proteins (svCRiSPs) from North American pit vipers increase vascular permeability both in vitro and in vivo. They also induce acute activation of several adhesion and signaling molecules that may play a critical role in the pathophysiology of snakebites. Extracellular vesicles (EVs) have gained interest for their diverse functions in intercellular communication, regulating cellular processes, blood-endothelium interactions, vascular permeability, and immune modulation. They also hold potential as valuable biomarkers for diagnosing, predicting, and monitoring therapeutic responses in different diseases. This study aimed to identify proteins in peritoneal exudate and plasma EVs isolated from BALB/c mice following a 30 min post-injection of *Crotalus scutulatus scutulatus* venom and its purified CRiSP (C_{ss}-CRiSP). EVs were isolated from these biofluids using the EVtrap method. Proteomic analysis of exudate- and plasma-derived EVs was performed using LC-MS/MS. We observed significant upregulation or downregulation of proteins involved in cell adhesion, cytoskeleton rearrangement, signal transduction, immune responses, and vesicle-mediated transports. These findings suggest that svCRiSPs play a crucial role in the acute effects of venom and contribute to the local and systemic toxicity of snakebites.

Incidence of serum sickness following Indian polyvalent antivenom therapy in a cohort of snake-envenomed patients in rural Sri Lanka.

Waidyanatha S, Silva A, Wedasingha S, Siribaddana S, Isbister GK.

Jul-2023

Clin Toxicol (Phila).

<https://pubmed.ncbi.nlm.nih.gov/37486099/>

Introduction: Serum sickness is a poorly reported delayed adverse reaction following snake antivenom therapy. We aimed to assess the frequency of serum sickness associated with administering Indian polyvalent antivenom in Sri Lanka. **Methods:** We recruited patients from the Anuradhapura snakebite cohort who were admitted to a rural tertiary care hospital in Sri Lanka over one year period. Patients were interviewed over the phone 21 to 28 days post-envenoming to collect data on clinical effects: fever/chills, arthralgia/myalgia, rash, malaise, headache, abdominal pain, and nausea/vomiting. The presence of three or more symptoms between the 5th

to 20th days after snake envenoming was defined as serum sickness. **Results:** We were able to contact 98/122 (80%) patients who received antivenom and 423/588 (72%) who did not receive antivenom during the study period. The treated patients received a median dose of 20 vials (interquartile range: 20-30) of Indian polyvalent antivenom and of them, 92 (92%) received premedication. However, 67/98 (68%) developed acute adverse reactions to antivenom, including 19/98 (19%) developing anaphylaxis. Only 4/98 (4%) who received antivenom met the criteria for serum sickness, compared to none who did not receive antivenom therapy. All patients who developed serum sickness were envenomed by Russell's vipers, were premedicated, and received VINS Bioproducts antivenom. Three of them were treated with hydrocortisone in the acute stage, as premedication or as a treatment for acute adverse reactions of antivenom. Although all four patients sought medical advice for their symptoms, only one was clinically suspected to be serum sickness and treated, while the others were treated for infections. **Conclusions:** We confirmed that Indian polyvalent antivenom use in Sri Lanka is associated with high rates of acute adverse reactions. In contrast to studies of other antivenoms only a small proportion of patients developed serum sickness.

Community members and healthcare workers' priorities for the control and prevention of snakebite envenoming in Ghana.

Aglanu LM, Amuasi JH, Prokesh E, Beyuo A, Dari CD, Ravensbergen SJ, Agbogbatey MK, Adobasom-Anane AG, Abass KM, Lalloo DG, Blessmann J, Kreuels B, Stienstra Y.

21-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37478151/>

Introduction: Snakebite is one of the most neglected tropical diseases. In Ghana, there has been a limited interest in snakebite envenoming research despite evidence of high human-snake conflicts. In an effort to meet the World Health Organisation's (WHO) 2030 snakebite targets, the need for research evidence to guide policy interventions is evident. However, in setting the research agenda, community and healthcare workers' priorities are rarely considered. **Methods:** Three categories of focus groups were formed in the Ashanti and Upper West regions of Ghana, comprising of community members with and without a history of snakebite and healthcare workers who manage snakebite patients. Two separate focus group discussions were conducted with each group in each region. Using the thematic content analysis approach, the framework method was adopted for the data analysis. A predefined 15-item list of potential snakebite-associated difficulties and the WHO's 2030 snakebite strategic key activities were ranked in order of priority based on the participants' individual assessment. **Results:** Both acute and chronic effects of snakebite such as bite site management, rehabilitation and mental health were prioritised by the community members. Health system challenges including training, local standard treatment protocols and clinical investigations on the

efficacy of available antivenoms were identified as priorities by the healthcare workers. Notably, all the participant groups highlighted the need for research into the efficacy of traditional medicines and how to promote collaborative strategies between traditional and allopathic treatment practices. **Conclusion:** The prioritisation of chronic snakebite envenoming challenges by community members and how to live and cope with such conditions accentuate the lack of post-hospital treatment follow-ups for both mental and physical rehabilitation. To improve the quality of life of patients, it is essential to involve grassroots stakeholders in the process of developing and prioritising future research agenda.

Healthcare practitioners' knowledge of snakebite management and associated factors in high-burden, low-resource settings in Uganda.

Wafula ST, Mugume IB, Namakula LN, Nalugya A, Naggayi V, Walekhwa AW, Musoke D.

03-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37072287/>

Onchocercose

Epilepsy and nodding syndrome in association with an *Onchocerca volvulus* infection drive distinct immune profile patterns.

Arndts K, Kegele J, Massarani AS, Ritter M, Wagner T, Pfarr K, Lämmer C, Dörmann P, Peisker H, Menche D, Al-Bahra M, Prazeres da Costa C, Schmutzhard E, Matuja W, Hoerauf A, Layland-Heni LE, Winkler AS.

03-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37535695/>

Previous studies have described the association of onchocerciasis (caused by *Onchocerca volvulus*) with epilepsy, including nodding syndrome, although a clear etiological link is still missing. Cases are found in different African countries (Tanzania, South Sudan, Uganda, Democratic Republic of the Congo, Central African Republic and Cameroon). In our study we investigated immunological parameters (cytokine, chemokine, immunoglobulin levels) in individuals from the Mahenge area, Tanzania, presenting with either epilepsy or nodding syndrome with or without *O. volvulus* infection and compared them to *O. volvulus* negative individuals from the same endemic area lacking neurological disorders. Additionally, cell differentiation was performed using blood smears and systemic levels of neurodegeneration markers, leiomodin-1 and N-acetyltyramine-O, β -glucuronide (NATOG) were determined. Our findings revealed that cytokines, most chemokines and neurodegeneration markers were comparable between both groups presenting with epilepsy or nodding syndrome. However, we observed elevated eosinophil percentages within the *O. volvulus* positive epilepsy/nodding syndrome patients accompanied with increased eosinophilic cationic protein (ECP) and antigen-

specific IgG levels in comparison to those without an *O. volvulus* infection. Furthermore, highest levels of NATOG were found in *O. volvulus* positive nodding syndrome patients. These findings highlight that the detection of distinct biomarkers might be useful for a differential diagnosis of epilepsy and nodding syndrome in *O. volvulus* endemic areas. Trial-registration: [NCT03653975](https://pubmed.ncbi.nlm.nih.gov/37507126/).

Adjuvanted Fusion Protein Vaccine Induces Durable Immunity to *Onchocerca volvulus* in Mice and Non-Human Primates.

Ryan NM, Hess JA, Robertson EJ, Tricoche N, Turner C, Davis J, Petrovsky N, Ferguson M, Rinaldi WJ, Wong VM, Shimada A, Zhan B, Bottazzi ME, Makepeace BL, Gray SA, Carter D, Lustigman S, Abraham D.

06-07-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37515028/>

Onchocerciasis remains a debilitating neglected tropical disease. Due to the many challenges of current control methods, an effective vaccine against the causative agent *Onchocerca volvulus* is urgently needed. Mice and cynomolgus macaque non-human primates (NHPs) were immunized with a vaccine consisting of a fusion of two *O. volvulus* protein antigens, Ov-103 and Ov-RAL-2 (Ov-FUS-1), and three different adjuvants: Advax-CpG, alum, and AlT4. All vaccine formulations induced high antigen-specific IgG titers in both mice and NHPs. Challenging mice with *O. volvulus* L3 contained within subcutaneous diffusion chambers demonstrated that Ov-FUS-1/Advax-CpG-immunized animals developed protective immunity, durable for at least 11 weeks. Passive transfer of sera, collected at several time points, from both mice and NHPs immunized with Ov-FUS-1/Advax-CpG transferred protection to naïve mice. These results demonstrate that Ov-FUS-1 with the adjuvant Advax-CpG induces durable protective immunity against *O. volvulus* in mice and NHPs that is mediated by vaccine-induced humoral factors.

Assessing *Onchocerca volvulus* Intensity of Infection and Genetic Diversity Using Mitochondrial Genome Sequencing of Single Microfilariae Obtained before and after Ivermectin Treatment.

Hedtke SM, Choi YJ, Kode A, Chalasani GC, Sirwani N, Jada SR, Hotterbeekx A, Mandro M, Siewe Fodjo JN, Amambo GN, Abong RA, Wanji S, Kuesel AC, Colebunders R, Mitreva M, Grant WN.

24-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513818/>

Mycétome

A surgeon's trial success of curing pedal eumycetoma.

Choudhry B, Mitchell J, Milner S.

28-07-2023

BMJ Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37507126/>

Mycetoma is a chronic infection of underlying fungal (eumycetoma) or bacterial (actinomycetoma) origin. It is characterised by a clinical triad of tumour-like swelling, actively draining sinuses and macroscopic grains of characteristic colours. We the case of a 66-year-old woman on immunosuppressive therapy presenting with eumycetoma of the foot (Madura foot). The fungal organism cultured was *Acrophialophora fusispora*. This case was managed with a combination of extensive surgical debridement, and packing with calcium sulfate (Stimulan) beads impregnated with vancomycin and voriconazole. As far as the authors are aware, this is a novel adjunct to the surgical treatment of deep fungal infection in the foot. Eumycetoma treated with surgery and oral antifungal therapy leads to cure rates of 25%-35%. This novel treatment seems to bear further investigation for the potential to improve cure rates. At 8 months follow-up, our patient appears to be making good progress with no current signs of recurrence.

The First Case of *Fusarium falciforme* Eumycetoma in Sudan and an Extensive Literature Review about Treatment Worldwide.

Siddig EE, Ahmed A, Eltigani HF, Bakhiet SM, van de Sande WWJ, Fahal AH.

06-07-2023

J Fungi (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37504719/>

In search of the ideal periosteal flap for bone non-union: The chimeric fibula-periosteal flap.

Lo S, Yonjan I, Rose A, Roditi G, Drury C, MacLean A.

Août-2023

J Plast Reconstr Aesthet Surg.

<https://pubmed.ncbi.nlm.nih.gov/37285775/>

Vascularised periosteal flaps may increase the union rates in recalcitrant long bone non-union. The fibula-periosteal chimeric flap utilises the periosteum raised on an independent periosteal vessel. This allows the periosteum to be inset freely around the osteotomy site, thereby facilitating bone consolidation. **Patients and methods:** Ten patients underwent fibula-periosteal chimeric flaps (2016-2022) at the Canniesburn Plastic Surgery Unit, UK. Preceding non-union 18.6 months, with mean bone gap of 7.5 cm. Patients underwent preoperative CT angiography to identify the periosteal branches. A case-control approach was used. Patients acted as their own controls, with one osteotomy covered by the chimeric periosteal flap and one without, although in two patients both the osteotomies were covered using a long periosteal flap. **Results:** A chimeric periosteal flap was used in 12 of the 20 osteotomy sites. Periosteal flap osteotomies had a primary union rate of 100% (11/11) versus those without flaps at 28.6% (2/7) ($p = 0.0025$). Union occurred in the chimeric periosteal flaps at 8.5 months versus 16.75 months in the control group ($p = 0.023$). One case was excluded from primary analysis due to recurrent mycetoma. The number needed to treat = 2, indicating that 2 patients would

require a chimeric periosteal flap to avoid one non-union. Survival curves with a hazard ratio of 4.1 were observed, equating to a 4 times higher chance of union with periosteal flaps (log-rank $p = 0.0016$).

Conclusions: The chimeric fibula-periosteal flap may increase the consolidation rates in difficult cases of recalcitrant non-union. This elegant modification of the fibula flap uses periosteum that is normally discarded, and this adds to the accumulating data supporting the use of vascularised periosteal flaps in non-union.

Chronic Painless, Multiple Papulo-Nodular Skin Lesion at Foot Resembles Mycetoma Infection (Madura Foot): A Case Report.

Bahar Moni AS, Hoque MM.

Sept-2023

Int J Low Extrem Wounds.

<https://pubmed.ncbi.nlm.nih.gov/34223771/>

Madura foot is a chronic, progressively destructive bacterial or fungal infection of the subcutaneous tissues, which may affect skin, muscle, and bone. It is endemic in tropical and subtropical areas known as the "Mycetoma belt" between latitude 30°N and 15°S. Mycetoma is prevalent in the poor population living in remote areas of developing countries that lack proper reporting system and management. The World Health Organization recognized mycetoma as a neglected tropical disease back in 2016. Though the diagnosis is challenging, early detection and proper treatment can reduce morbidity and provide a promising outcome. We report a case of chronic painless, multiple papulo-nodular skin lesions at the foot that resembles mycetoma infection which was detected early and recovered with a satisfactory outcome with proper treatment.

Pian

Rapid Serologic Test for Diagnosis of Yaws in Patients with Suspicious Skin Ulcers.

Suñer C, John LN, Houinei W, Ubals M, Ouchi D, Alemany A, Galván-Casas C, Marks M, Mitjà O, Vall-Mayans M, Beiras CG.

Aug-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37486318/>

The Chembio DPP (Dual Path Platform) Syphilis Screen & Confirm kit (<https://chembio.com>) is a rapid serologic test that can be used to diagnose yaws. We evaluated its capacity to detect patients with ulcers that tested PCR positive for *Treponema pallidum* subsp. *pertenue*. DPP detected 84% of ulcers that were positive by PCR.

Rage

Cat rabies in Brazil: a growing One Health concern.

de Lima JS, Mori E, Kmetiuk LB, Biondo LM, Brandão PE, Biondo AW, Maiorka PC.

19-07-2023

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37538269/>

This review of human and cat rabies from 1986 to 2022 has shown mostly AgV3 variant in human cases with 29/45 (64.4%) reports including 23 from bats, four from cats, and two from unknown species, followed by 8/45 (17.8%) of AgV2 variant (all from dogs), 4/45 from marmoset variant (all from *Callithrix jacchus*), 2/45 samples compatible with wild canid variant (both from *Cerdocyon thous*), and one/45 of AgV1 variant from a domestic dog. Only one sample of human rabies was not typified, related to bat aggression. In addition, surveillance conducted in the state of São Paulo confirmed the presence of rabies in 7/23,839 cats (0.031%) and 3/106,637 dogs (0.003%) between 2003 and 2013, with a 10:1 overall cat-to-dog positivity ratio. This 10-fold higher infection rate for cat rabies may be explained by cats' hunting habits and predation. In addition, after 28 years of rabies-free status, a new cat rabies case was reported in the city of São Paulo in 2011. The rabid cat lived, along with other pets, in a household located near the largest downtown city park, whose owners presented animal hoarding behavior. Thus, animal hoarders and rescuers, public health agents, animal health professionals, and the general population with contact need to be aware of the risk of bat-borne rabies followed by spillover from cats to humans. In conclusion, cat rabies cases are becoming increasingly important in Brazil. This poses a One Health concern, given the overlapping of human, bat and cat populations within the same predisposed environment.

Evidence of insufficient genetic data and lack of regular genetic research on rabies virus in the Russian Federation: a study of the recent epizootic situation.

Gnezdilova LA, Laga VY, Marzanova SN, Pozyabin SV, Yarygina EI, Giordano CO.

03-08-2023

Arch Virol.

<https://pubmed.ncbi.nlm.nih.gov/37537312/>

Editorial: Rabies, a long-standing One Health example - progress, challenges, lessons and visions on the way to 2030.

Fahrion AS, Freuling CM, Léchenne M, Müller T, Recuenco S, Vigilato MAN, Busch F, Heitz-Tokpa K, Mauti S, Muturi M, Dürr S.

18-07-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37533452/>

Inventory management practices: implications on the pharmaceuticals expenditure of rabies vaccine in public health facilities, Namibia.

Shibabaw AD, Nakambale HN, Bangalee V.

02-08-2023

BMC Health Serv Res.

<https://pubmed.ncbi.nlm.nih.gov/37533090/>

The Many Hosts of Mycobacteria 9 (MHM9): A conference report.

Kleiver AM, Alexander KA, Almeida D, Anderson MZ, Ball RL, Beamer G, Boggiatto P, Buikstra JE, Chandler B, Claeys TA, Concha AE, Converse PJ, Derbyshire KM, Dobos KM, Dupnik KM, Endsley JJ, Endsley MA, Fennelly K, Franco-Paredes C, Hagge DA, Hall-Stoodley L, Hayes D Jr, Hirschfeld K, Hofman CA, Honda JR, Hull NM, Kramnik I, Lacourciere K, Lahiri R, Lamont EA, Larsen MH, Lemaire T, Lesellier S, Lee NR, Lowry CA, Mahfooz NS, McMichael TM, Merling MR, Miller MA, Nagajyothi JF, Nelson E, Nuermberger EL, Pena MT, Perea C, Podell BK, Pyle CJ, Quinn FD, Rajaram MVS, Mejia OR, Rothoff M, Sago SA, Salvador LCM, Simonson AW, Spencer JS, Sreevatsan S, Subbian S, Sunstrum J, Tobin DM, Vijayan KKV, Wright CTO, Robinson RT.

23-07-2023

Tuberculosis (Edinb).

<https://pubmed.ncbi.nlm.nih.gov/37531864/>

Tissue optical clearing and 3D imaging of virus infections.

Ushakov DS, Finke S.

2023

Adv Virus Res.

<https://pubmed.ncbi.nlm.nih.gov/37524483/>

Imaging pathogens within 3D environment of biological tissues provides spatial information about their localization and interactions with the host. Technological advances in fluorescence microscopy and 3D image analysis now permit visualization and quantification of pathogens directly in large tissue volumes and in great detail. In recent years large volume imaging became an important tool in virology research helping to understand the properties of viruses and the host response to infection. In this chapter we give a review of fluorescence microscopy modalities and tissue optical clearing methods used for large volume tissue imaging. A summary of recent applications for virus research is provided with particular emphasis on studies using light sheet fluorescence microscopy. We describe the challenges and approaches for volumetric image analysis. Practical examples of volumetric imaging implemented in virology laboratories and addressing specialized research questions, such as virus tropism and immune host response are described. We conclude with an overview of the emerging technologies and their potential for virus research.

Spatial resolution of virus replication: RSV and cytoplasmic inclusion bodies.

Risso-Ballester J, Rameix-Welti MA.

2023

Adv Virus Res.

<https://pubmed.ncbi.nlm.nih.gov/37524479/>

Sex differences in afferents and efferents of vasopressin neurons of the bed nucleus of the stria terminalis and medial amygdala in mice.

Rigney N, de Vries GJ, Petrulis A.

29-07-2023

Horm Behav.

<https://pubmed.ncbi.nlm.nih.gov/37523807/>

Steroid-sensitive vasopressin (AVP) neurons in the bed nucleus of the stria terminalis (BNST) and medial amygdala (MeA) have been implicated in the control of social behavior, but the connective architecture of these cells is not well understood. Here we used a modified rabies virus (RV) approach to identify cells that provide monosynaptic input to BNST and MeA AVP cells, and an adeno-associated viral (AAV) anterograde tracer strategy to map the outputs of these cells. Although the location of in- and outputs of these cells generally overlap, we observed several sex differences with differences in density of outputs typically favoring males, but the direction of sex differences in inputs vary based on their location. Moreover, the AVP cells located in both the BNST and MeA are in direct contact with each other suggesting that AVP cells in these two regions act in a coordinated manner, and possibly differently by sex. This study represents the first comprehensive mapping of the sexually dimorphic and steroid-sensitive AVP neurons in the mouse brain.

Special Issue "Advances in Rabies Research".

Nadin-Davis SA.

16-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515243/>

Hyperimmune Globulins for the Management of Infectious Diseases.

Pati I, Cruciani M, Candura F, Massari MS, Piccinini V, Masiello F, Profili S, De Fulvio L, Pupella S, De Angelis V.

13-07-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37515229/>

Comparative Neutralization Activity of Commercial Rabies Immunoglobulin against Diverse Lyssaviruses.

Coertse J, Viljoen N, Weyer J, Markotter W.

18-07-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37515070/>

Novel lyssaviruses, the causative agents of rabies, continue to be described mostly due to increased surveillance in bat hosts. Biologicals for the prevention of rabies in humans have, however, remained largely unchanged for decades. This study aimed to determine if commercial rabies immunoglobulin (RIG) could neutralize diverse lyssaviruses. Two commercial preparations, of human or equine origin, were evaluated against a panel consisting of 13 lyssavirus species. Reduced neutralization was observed for the majority of lyssaviruses compared to rabies virus and was more evident for lyssaviruses outside of phylogroup I. Neutralization of more diverse lyssaviruses only occurred at very high doses, except for

Ikoma lyssavirus, which could not be neutralized by the RIG evaluated in this study. The use of RIG is a crucial component of rabies post-exposure prophylaxis and the data generated here indicate that RIG, in its current form, will not protect against all lyssaviruses. In addition, higher doses of RIG may be required for neutralization as the genetic distance from vaccine strains increases. Given the limitations of current RIG preparations, alternative passive immunization options should be investigated.

Tick-Borne Encephalitis Virus and *Borrelia burgdorferi* Seroprevalence in Balkan Tick-Infested Individuals: A Two-Centre Study.

Jakimovski D, Mateska S, Dimitrova E, Bosilkovski M, Mijatović D, Simin V, Bogdan I, Grujić J, Budakov-Obradović Z, Meletis E, Kostoulas P, Cabezas-Cruz A, Banović P.
09-07-2023
Pathogens.
<https://pubmed.ncbi.nlm.nih.gov/37513769/>

You Are Not Welcome! A Media Analysis of Risk Factors, Prevalence and Management of Free-Roaming Dogs in Iran.

Amiraslani F.
18-07-2023
Animals (Basel).
<https://pubmed.ncbi.nlm.nih.gov/37508123/>

Antiviral activities of two nucleos(t)ide analogs against vaccinia, mpox, and cowpox viruses in primary human fibroblasts.

Dsouza L, Pant A, Offei S, Priyamvada L, Pope B, Satheshkumar PS, Wang Z, Yang Z.
Août-2023
Antiviral Res.
<https://pubmed.ncbi.nlm.nih.gov/37270160/>

Schistosomiasis

Prevalence and Determinants of *Schistosoma mansoni* Infection among Pre-School Age Children in Southern Ethiopia.

Tadele T, Astatkie A, Abay SM, Tadesse BT, Makonnen E, Aklillu E.
21-06-2023
Pathogens.
<https://pubmed.ncbi.nlm.nih.gov/37513705/>

School-based deworming program is implemented to control and eliminate *Schistosoma mansoni* infection in many endemic countries, including Ethiopia. However, pre-school-age children (pre-SAC) are not targeted to receive preventive chemotherapy against *S. mansoni* infection, partly due to a lack of information on the disease burden. We assessed the prevalence and correlates of *S. mansoni* infection among pre-SAC in Southern Ethiopia. A

S. mansoni infection among pre-SAC in Southern Ethiopia. A total of 1683 pre-SAC aged 4 to 7 years were screened for *S. mansoni* infection. A multilevel binary logistic regression was fitted to detect the significant determinants of *S. mansoni* infection. Adjusted odds ratios (AORs) with a 95% confidence interval (CI) were used to identify determinants of *S. mansoni* infection. The overall prevalence of *S. mansoni* infection was 14.3% (95% CI: 12.6, 16.0%). *S. mansoni* infection was significantly higher among 6-year-old (AOR = 2.58, 95% CI: 1.55, 4.27) and 7-year-old children (AOR = 4.63, 95% CI: 2.82, 7.62). Accompanying others to water sources sometimes (AOR = 2.60, 95% CI: 1.12, 6.01) and all the time (AOR = 5.91, 95% CI: 2.51, 13.90), and residing in less than one kilometer from the infested water source (AOR = 3.17, 95% CI: 1.47, 6.83) increased the odds of *S. mansoni* infection. In conclusion, the prevalence of *S. mansoni* infection among pre-SAC in the study area was moderate. The study highlights the urgent need to include pre-SAC aged 4 to 7 years in annual preventive chemotherapy campaigns to reduce the risk of possible sources of infection and enhance the achievement of the elimination target.

Detection of male genital schistosomiasis (MGS) by real-time TaqMan® PCR analysis of semen from fishermen along the southern shoreline of Lake Malawi.

Kayuni SA, Alharbi MH, Shaw A, Fawcett J, Makaula P, Lampiao F, Juziwele L, LaCourse EJ, Verweij JJ, Stothard JR.
21-06-2023
Heliyon.
<https://pubmed.ncbi.nlm.nih.gov/37539175/>

Background: Male genital schistosomiasis (MGS) is an underappreciated complication of schistosomiasis, first described in 1911. However, its epidemiology, diagnostic testing and case management are not well understood in sub-Saharan Africa. To shed new light on MGS prevalence in Malawi, a longitudinal cohort study was conducted among adult fishermen along the southern shoreline of Lake Malawi using detection of schistosome DNA in participants' semen by real-time TaqMan® PCR analyses.

Methods: Upon recruitment of 376 participants, 210 submitted urine samples and 114 semen samples for parasitological tests. Thereafter, the available semen samples were subsequently analysed by real-time TaqMan® PCR. Praziquantel (PZQ) treatment was provided to all participants with follow-ups attempted at 1, 3, 6 and 12-months' intervals.

Results: At baseline, real-time PCR detected a higher MGS cohort prevalence of 26.6% (n = 64, Ct-value range: 18.9-37.4), compared to 10.4% by semen microscopy. In total, 21.9% of participants (n = 114) were detected with MGS either by semen microscopy and/or by real-time PCR. Subsequent analyses at 1-, 3-, 6- and 12-month follow-ups indicated variable detection dynamics.

Conclusions: This first application of a molecular method, to detect MGS in sub-Saharan Africa, highlights the need for development of such molecular diagnostic tests which should be affordable and locally accessible. Our

investigation also notes the persistence of MGS over a calendar year despite praziquantel treatment.

Establishing a single-sex controlled human *Schistosoma mansoni* infection model for Uganda: protocol for safety and dose-finding trial.

Abaasa A, Egesa M, Driciru E, Koopman JPR, Kiyemba R, Sanya RE, Nassuuna J, Ssali A, Kimbugwe G, Wajja A, van Dam GJ, Corstjens PLAM, Cose S, Seeley J, Kamuya D, Webb EL, Yazdanbakhsh M, Kaleebu P, Siddiqui AA, Kabatereine N, Tukahebwa E, Roestenberg M, Elliott AM.

20-07-2023

Immunother Adv.

<https://pubmed.ncbi.nlm.nih.gov/37538934/>

Control of schistosomiasis depends on a single drug, praziquantel, with variable cure rates, high reinfection rates, and risk of drug resistance. A vaccine could transform schistosomiasis control. Preclinical data show that vaccine development is possible, but conventional vaccine efficacy trials require high incidence, long-term follow-up, and large sample size. Controlled human infection studies (CHI) can provide early efficacy data, allowing the selection of optimal candidates for further trials. A *Schistosoma* CHI has been established in the Netherlands but responses to infection and vaccines differ in target populations in endemic countries. We aim to develop a CHI for *Schistosoma mansoni* in Uganda to test candidate vaccines in an endemic setting. This is an open-label, dose-escalation trial in two populations: minimal, or intense, prior *Schistosoma* exposure. In each population, participants will be enrolled in sequential dose-escalating groups. Initially, three volunteers will be exposed to 10 cercariae. If all show infection, seven more will be exposed to the same dose. If not, three volunteers in subsequent groups will be exposed to higher doses (20 or 30 cercariae) following the same algorithm, until all 10 volunteers receiving a particular dose become infected, at which point the study will be stopped for that population. Volunteers will be followed weekly after infection until CAA positivity or to 12 weeks. Once positive, they will be treated with praziquantel and followed for one year. The trial registry number is ISRCTN14033813 and all approvals have been obtained. The trial will be subjected to monitoring, inspection, and/or audits.

Divide, conquer and reconstruct: How to solve the 3D structure of recalcitrant Micro-Exon Gene (MEG) protein from *Schistosoma mansoni*.

Nedvedova S, Guillière F, Miele AE, Cantrelle FX, Dvorak J, Walker O, Hologne M.

03-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37535563/>

Targeted insertion and reporter transgene activity at a gene safe harbor of the human blood fluke, *Schistosoma mansoni*.

Ittiprasert W, Moescheid MF, Chaparro C, Mann VH, Quack T, Rodpai R, Miller A, Wisitpongpan P, Buakaew W, Mentink-Kane M, Schmid S, Popratiloff A, Grevelding CG, Grunau C, Brindley PJ.

24-07-2023

Cell Rep Methods.

<https://pubmed.ncbi.nlm.nih.gov/37533651/>

The identification and characterization of genomic safe harbor sites (GSHs) can facilitate consistent transgene activity with minimal disruption to the host cell genome. We combined computational genome annotation and chromatin structure analysis to predict the location of four GSHs in the human blood fluke, *Schistosoma mansoni*, a major infectious pathogen of the tropics. A transgene was introduced via CRISPR-Cas-assisted homology-directed repair into one of the GSHs in the egg of the parasite. Gene editing efficiencies of 24% and transgene-encoded fluorescence of 75% of gene-edited schistosome eggs were observed. The approach advances functional genomics for schistosomes by providing a tractable path for generating transgenics using homology-directed, repair-catalyzed transgene insertion. We also suggest that this work will serve as a roadmap for the development of similar approaches in helminths more broadly.

Unexpected rapid symptom response after praziquantel to intestinal *Schistosoma mansoni* symptoms: A case report from Rwanda.

Sibomana JP, Getaneh FB, Graham B, Giraneza R.

31-07-2023

SAGE Open Med Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37533487/>

Natural regulatory T cells increase significantly in pediatric patients with parasitic infections: Flow cytometry study.

Kizilbash N, Suhail N, Alzahrani AK, Basha WJ, Soliman M.

Juil-Sept 2023

Indian J Pathol Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37530338/>

Epidemiology of malaria, schistosomiasis, and geohelminthiasis amongst children 3-15 years of age during the dry season in Northern Cameroon.

Nkemngo FN, W G Raissa L, Nebangwa DN, Nkeng AM, Kengne A, Mugenzi LMJ, Fotso-Toguem YG, Wondji MJ, Shey RA, Nguiffo-Nguete D, Fru-Cho J, Ndo C, Njiokou F, Webster JP, Wanji S, Wondji CS.

31-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37523402/>

Background: The double burden of malaria and helminthiasis in children poses an obvious public health challenge, particularly in terms of anemia morbidity. While both diseases frequently geographically overlap, most

studies focus on mono-infection and general prevalence surveys without molecular analysis. The current study investigated the epidemiological determinants of malaria, schistosomiasis, and geohelminthiasis transmission among children in the North Region of Cameroon.

Methodology: School and pre-school children aged 3-15 year-of-age were enrolled from three communities in March 2021 using a community cross-sectional design. Capillary-blood samples were obtained, and each was examined for malaria parasites using rapid-diagnostic-test (RDT), microscopy, and PCR while hemoglobin level was measured using a hemoglobinometer. Stool samples were analyzed for *Schistosoma mansoni*, *S. guineensis*, and soil-transmitted-helminthiasis (STH) infections using the Kato Katz method, and urine samples were assessed for the presence of *S. haematobium* eggs (including hybrids) using the standard urine filtration technique. **Result:** A malaria prevalence of 56% (277/495) was recorded by PCR as opposed to 31.5% (156/495) by microscopy and 37.8% (186/495) by RDT. Similarly, schistosomiasis was observed at prevalence levels of up to 13.3% (66/495) overall [*S. haematobium* (8.7%); *S. mansoni* (3.8%); mixed Sh/Sm (0.6%); mixed Sh/Sm/Sg (0.2%)]. Both infections were higher in males and the 3-9 year-of-age groups. A high frequency of PCR reported *P. falciparum* mono-infection of 81.9% (227/277) and mixed *P. falciparum*/*P. malariae* infection of 17.3% (48/277) was observed. Malaria-helminths co-infections were observed at 13.1% (65/495) with marked variation between *P. falciparum*/*S. haematobium* (50.8%, 33/65); *P. falciparum*/*S. mansoni* (16.9%, 11/65) and *P. falciparum*/*Ascaris* (9.2%, 6/65) ($\chi^2 = 17.5$, $p = 0.00003$). Anemia prevalence was 32.9% (163/495), categorically associated with *P. falciparum* (45.8%, 104/227), Pf/Sh (11.5%, 26/227), and Pf/Sm (3.9%, 9/227) polyparasitism. **Conclusion:** Polyparasitism with malaria and helminth infections is common in school-aged children despite periodic long-lasting insecticide-treated nets (LLINs) distribution and regular school-based praziquantel (for schistosomiasis) and albendazole (for STH) campaigns. Co-existence of *Plasmodium* parasites and helminths infections notably *Schistosoma* species among children may concurrently lead to an increase in *Plasmodium* infection with an enhanced risk of anemia, highlighting the necessity of an integrated approach for disease control interventions.

Epidemiology of bovine schistosomiasis and associated risk factors in Ethiopia: A systematic review with meta-analysis of published articles, 2008-2018.

Dagnaw M, Wodajnew B, Fentie T, Solomon A, Abuhay F, Bizu N, Abi A.

31-07-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37523370/>

Schistosomiasis is a tropical and subtropical parasitic infection that affects both animals and humans. It's caused by the *Schistosoma* genus and spreads via snails as an intermediate host. *Schistosoma bovis* is widely spread in Ethiopia's Northern, Eastern, Southwestern, and Central regions. It is an economically significant cattle disease with global health implications. Despite numerous prevalence

studies of bovine schistosomiasis in different regions of the country, no systematic review and meta-analysis of the disease has ever been undertaken. As a reason, the purpose of this research was to provide information that can be used in the planning and design of *Schistosoma* interventions in Ethiopia, as the world aims to eliminate schistosomiasis as a public health problem by 2030. The PRISMA statement guideline was used to check the eligibilities of the included studies. Electronic bibliographic databases such as PubMed, Google Scholar, HINARI, and Web of science, reference lists from retrieved articles, books, libraries, magazines and existing reviews manually were employed for literature searches. The pooled prevalence of bovine schistosomiasis and heterogeneity among included studies was estimated by employing random effect models and the inverse variance index, respectively. To investigate the source of heterogeneity across and within studies, subgroup analysis was undertaken based on sample size, study years, and study regions. To assess publication bias and small study effects, funnel plots and Egger's regression test were used. The pooled prevalence was calculated with a 95% confidence interval using STATA 17 software. To identify the various risk variables related to the prevalence of bovine schistosomiasis, a pooled odd ratio was used. Based on the inclusion criteria, a total of 20 studies were discovered and included in the meta-analysis. The prevalence of bovine schistosomiasis was found to range from 22 to 45.7%. In this meta-analysis, the estimated pooled prevalence of bovine schistosomiasis was 24% (95% CI: 17% to 31%). Substantial heterogeneity was observed across the included studies ($I^2 = 88.04\%$; $p < 0.001$). The results of the funnel plot and Egger's tests revealed no substantial publication bias (Egger's test; $p = 0.509$). The pooled odds ratio indicated that poor body condition was positively associated with the infection rate of bovine schistosomiasis (OR: 4.915, 95% CI: 2.675 to 9.030; $p < 0.001$), with poor body conditioned animals having 4.915 times higher likelihood to schistosomiasis infection. This review found that the overall prevalence of bovine schistosomiasis was high and the body condition of animals was identified risk factor for *Schistosoma* infection among the studied factors. Therefore, this review found that the occurrence of bovine schistosomiasis was strongly associated with the state of body condition of animals. Further, sufficient numbers of prospective studies should be conducted to address other potential risk factors of bovine schistosomiasis in Ethiopia.

Chemical modulation of *Schistosoma mansoni* lysine specific demethylase 1 (SmLSD1) induces wide-scale biological and epigenomic changes.

Padalino G, Celatka CA, Rienhoff HY Jr, Kalin JH, Cole PA, Lassalle D, Forde-Thomas J, Chalmers IW, Brancale A, Grunau C, Hoffmann KF.

30-03-2023

Wellcome Open Res.

<https://pubmed.ncbi.nlm.nih.gov/37520936/>

Editorial: "You shall not pass" or "Let's make a deal" - crosstalk between helminths and the host immune system.

Bąska P, Schabussova I, Zawistowska-Deniziak A.
14-07-2023
Front Cell Infect Microbiol.
<https://pubmed.ncbi.nlm.nih.gov/37520436/>

Effects of company and season on blood fluke (*Cardicola* spp.) infection in ranched Southern Bluefin Tuna: preliminary evidence infection has a negative effect on fish growth.

Power C, Carabott M, Widdicombe M, Coff L, Rough K, Nowak B, Bott NJ.
25-07-2023
PeerJ.
<https://pubmed.ncbi.nlm.nih.gov/37520261/>

Aporocotylid blood flukes *Cardicola forsteri* and *C. orientalis* are an ongoing health concern for Southern Bluefin Tuna (SBT), *Thunnus maccoyii*, ranched in Australia. Therapeutic application of praziquantel (PZQ) has reduced SBT mortalities, however PZQ is not a residual treatment therefore reinfection can occur after the single treatment application. This study documents the epidemiology of *Cardicola* spp. infection in ranched SBT post treatment over three ranching seasons (2018, 2019 and 2021). Infection prevalence (percentage of SBT affected) and intensity (parasite load) was determined by adult fluke counts from heart, egg counts from gill filaments and the use of specific quantitative polymerase chain reaction (qPCR) for detection of *C. forsteri* and *C. orientalis* ITS-2 DNA in SBT hearts and gills. SBT Condition Index decreased as intensity of *Cardicola* spp. DNA in SBT gills increased, suggesting blood fluke infection had a negative effect on SBT growth (Spearman's $r = -0.2426$, d.f. = 138, $p = 0.0041$). Prevalence and intensity of infection indicated PZQ remained highly effective at controlling *Cardicola* spp. infection in ranched SBT, 10 years after PZQ administration began in this industry. Company A had the highest prevalence and intensity of *Cardicola* spp. infection in 2018, and Company G had the highest in 2019. No consistent pattern was seen in 2021. Overall, intensity of infection did not increase as ranching duration increased post treatment. Results from this study improve our knowledge of the biology of blood flukes and helps the SBT industry to modify or design new blood fluke management strategies to reduce health risks and improve performance of SBT.

Ethnobotanical Survey and Cercaricidal Activity Screening of Medicinal Plants Used for Schistosomiasis Treatment in Atwima-Nwabiagya District, Ashanti Region, Ghana.

Asante-Kwatia E, Gyimah L, Forkuo AD, Anyan WK, Gbemu MA, Armah FA, Mensah AY.
19-07-2023
J Parasitol Res.
<https://pubmed.ncbi.nlm.nih.gov/37520159/>

This study focused on documenting and evaluating the cercaricidal activity of medicinal plants used for schistosomiasis treatment in an endemic area in Ghana. Through semistructured questionnaires, personal

interviews with herbalists in communities surrounding the Barekese dam in the Atwima-Nwabiagya district, where the disease is endemic, were carried out. Thirty medicinal plants distributed in 19 families were reported to be used for schistosomiasis treatment in the survey. Information on the plants, including scientific names, common names, families, and the used plant part were recorded. The families Apocynaceae and Euphorbiaceae recorded the highest number of plants (14% each), followed by Asteraceae (10%), Loranaceae (7%), and Rubiaceae (7%). *In vitro* cercaricidal activity of methanol extracts of nine out of the thirty plants was performed by exposing human *Schistosoma mansoni* cercariae obtained from *Biomphalaria pfeifferi* to various concentrations of extracts over a duration of 240 minutes. All the plants tested demonstrated time- and concentration-dependent cercaricidal activity. With lethality being set at <1000 µg/mL, the cercaricidal activity in order of decreasing potency was as follows: *Withania somnifera* ($LC_{50} = 1.29$) > *Balanites aegyptiaca* ($LC_{50} = 7.1$) > *Xylia evansii* ($LC_{50} = 11.14$) > *Jatropha multifida* ($LC_{50} = 12.9$) > *Justicia flava* ($LC_{50} = 22.9$) > *Anopyxis klaineana* ($LC_{50} = 182.81$) > *Ximenia americana* ($LC_{50} = 194.98$) > *Loranthus lecardii* ($LC_{50} = 223.87$) > *Bridelia tenuifolia* ($LC_{50} = 309.03$) > *Zanthoxylum zanthoxyloides* ($LC_{50} = 851.94$). Phytochemicals, including alkaloids, tannins, triterpenes, saponins, phytosterols, and flavonoids were identified in the plants. The result of this study gives scientific credence to the traditional use of these plants in the treatment of schistosomiasis and proves that the rich botanical knowledge of medicinal plants provides an incredible starting point for the discovery of new anti-schistosomal drugs for the local population.

The Establishment of a Tobramycin-Responsive Whole-Cell Micro-Biosensor Based on an Artificial Ribozyme Switch.

Wang Z, Cheng J, Dai G, Sun X, Yin X, Zhang Y.
13-07-2023
Life (Basel).
<https://pubmed.ncbi.nlm.nih.gov/37511928/>

Low Prevalence of *Schistosoma mekongi* Infection and High Prevalence of Other Helminth Infections among Domestic Animals in Southern Lao People's Democratic Republic.

Sayasone S, Khattignavong P, Keomalaphet S, Prasayasith P, Soundala P, Sannikone S, Kumagai T, Phomhaksu S, Inthavong P, Matsumoto-Takahashi ELA, Hongvanthong B, Brey PT, Kano S, Iwagami M.
18-07-2023
Trop Med Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37505668/>

The prevalence of *Schistosoma mekongi* in humans in the Lao People's Democratic Republic (Lao PDR) has been relatively well monitored and has decreased due to effective interventions such as preventative chemotherapy with mass drug administration of praziquantel and community awareness programs. However, the prevalence among potential domestic

reservoir animals remains broadly unclear, except for a few villages in the endemic area. Therefore, we conducted *S. mekongi* surveys for the domestic animals that had contact with Mekong River water. We conducted a cross-sectional study of the domestic animals in the seven sentinel villages in the Khong and Mounlapamok Districts of Champasak Province in southern Lao PDR in 2018 by random sampling with a statistically reliable sample size. Stool samples of the five predominant domestic animal species, cattle (n = 160), pig (n = 154), buffalo (n = 149), dog (n = 143), and goat (n = 85), were collected and examined using parasitological FECT method and the LAMP technique. The microscopic analysis did not detect any eggs of *S. mekongi* in the stool samples of any animal species. However, *S. mekongi* DNA was detected by the LAMP test in dog stool samples (0.7%; 1/143). On the other hand, the prevalence of other helminths was quite high and heterogeneous among animal species and sentinel sites by the microscopic analysis. These findings suggested that an intervention for *S. mekongi* infection should focus solely on human populations. However, periodic surveillance for *S. mekongi* infection among dogs should be conducted to monitor a possible resurgence of *S. mekongi* infection in the domestic animal population.

Advances in new target molecules against schistosomiasis: A comprehensive discussion of physiological structure and nutrient intake.

Zhu P, Wu K, Zhang C, Batool SS, Li A, Yu Z, Huang J.
27-07-2023
PLoS Pathog.
<https://pubmed.ncbi.nlm.nih.gov/37498810/>

TREM2 expression promotes liver and peritoneal M2 macrophage polarization in mice infected with *Schistosoma japonicum*.

Zhu D, Huang M, Shen P, Zhang B, Chen G, Chen J, Duan L, Duan Y.
Août-2023
J Cell Mol Med.
<https://pubmed.ncbi.nlm.nih.gov/37430471/>

Emerging biomedical tools for biomarkers detection and diagnostics in schistosomiasis.

Lima RRM, Lima JVA, Ribeiro JFF, Nascimento JB, Oliveira WF, Cabral Filho PE, Fontes A.
01-12-2023
Talanta.
<https://pubmed.ncbi.nlm.nih.gov/37423177/>

Molecular detection of *Fasciola*, *Schistosoma* and *Paramphistomum* species from freshwater snails occurring in Gauteng and Free State provinces, South Africa.

Molaba GG, Molefe-Nyembe NI, Taioe OM, Mofokeng LS, Thekiso OMM, Mtshali K.

Août-2023
Vet Parasitol.
<https://pubmed.ncbi.nlm.nih.gov/37364501/>

Trematodiasis are diseases caused by snail-borne trematode parasites that infect both animals and humans. Fascioliasis, schistosomiasis and paramphistomosis are some of these diseases and they affect millions of livestock, leading to significant economic losses. The aim of the study was to document freshwater snails occurring in selected study sites in the Free State and Gauteng provinces as well as identify and detect larval trematodes that they harbour. Samples were collected from a total of five study sites within two provinces of South Africa. Morphological features were used to identify snail species and were further confirmed genetically by polymerase chain reaction (PCR), sequencing and phylogenetic analysis. The larval trematodes were also detected by PCR, PCR-Restriction Length Fragment Polymorphism (PCR-RLFP), sequencing and phylogenetic analysis. A total of 887 freshwater snails were collected from Free State (n = 343) and Gauteng (n = 544). Five different genera of snails as well as species in the Succineidae family were documented. The snails in descending order of abundance were identified as: *Physa* (P.) spp. (51%), Succineidae spp. (20%), *Galba* (G.) *truncatula* (12%), *Pseudosuccinea* (Ps.) *columella* (10%), *Planorbella* (Pl.) *duryi* (6%) and *Bulinus* (B.) *truncatus* (1%). Approximately 272 DNA pools were created for genetic identification of snails and detection of trematode parasites. *Schistosoma* species were not detected from any of the snail species. A total prevalence of 46% was obtained for *Fasciola hepatica* in the identified snail species across all study sites. Overall, the highest prevalence of *F. hepatica* was obtained in *Physa* species (24%), whilst the lowest was observed in *B. truncatus* snails (1%). Forty three percent (43%) of the snail samples were PCR positive for *Paramphistomum* DNA. This is the first report of *P. mexicana* in South Africa. *Fasciola hepatica* was confirmed from all obtained snail species per study site. This is the first reported detection of *F. hepatica* in *Pl. duryi* and *P. mexicana* snails as well as the first confirmation of natural infection from *P. acuta* in South Africa.

Mapping schistosomiasis risk in Southeast Asia: a systematic review and geospatial analysis.

Luo C, Wang Y, Su Q, Zhu J, Tang S, Bergquist R, Zhang Z, Hu Y.
02-08-2023
Int J Epidemiol.
<https://pubmed.ncbi.nlm.nih.gov/36478466/>

Background: Schistosomiasis is a water-borne parasitic disease estimated to have infected >140 million people globally in 2019, mostly in sub-Saharan Africa. Within the goal of eliminating schistosomiasis as a public health problem by 2030 in the World Health Organization (WHO) Roadmap for neglected tropical diseases, other regions cannot be neglected. Empirical estimates of the disease burden in Southeast Asia largely remain unavailable.

Methods: We undertook a systematic review to identify empirical survey data on schistosomiasis prevalence in Southeast Asia using the Web of Science, ScienceDirect, PubMed and the Global Atlas of Helminth Infections, from inception to 5 February 2021. We then conducted advanced Bayesian geostatistical analysis to assess the geographical distribution of infection risk at a high spatial resolution (5 × 5 km) using the prevalence, number of infected individuals and doses needed for preventive chemotherapy. **Results:** We identified 494 *Schistosoma japonicum* surveys in the Philippines and Indonesia, and 285 in Cambodia and Laos for *S. mekongi*. The latest estimates suggest that 225 [95% credible interval (CrI): 168-285] thousand in the endemic areas of Southeast Asian population were infected in 2018. The highest prevalence of schistosomiasis was 3.86% (95% CrI: 3.40-4.31) in Laos whereas the lowest was 0.29% in Cambodia (95% CrI: 0.22-0.36). The estimated number of praziquantel doses needed per year was 1.99 million (95% CrI: 1.92-2.03 million) for the entire population in endemic areas of Southeast Asia. **Conclusions:** The burden of schistosomiasis remains far from the WHO goal and our estimates highlighted areas to target with strengthened interventions against schistosomiasis.

Trachome

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

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

20-07-2023

EClinicalMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37533412/>

Spatial and network mapping of comorbidity with trachoma and visual-impairing NCDs in a pastoralist community in Kenya: implications for SDGs and UHC.

Chweya RN, Onyango CA, Saigilu S, Mwangi C, Gachohi JM.

02-08-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37528750/>

Background: We explore the spatial distribution of comorbidity with trachoma and potentially visual-impairing non-communicable diseases (NCDs) and their risk factors among Kenyan pastoralists. **Methods:** Using a cross-sectional study design, we recruited and clinically examined 262 study participants for NCDs (hypertension or diabetes) and trachoma using the World Health Organization grading system. Network models estimated interactions and risks linked with trachoma and NCDs

while the Poisson point process determined their spatial distribution. **Results:** Of the 262 participants, 140 (53%) had trachoma, with >71% of these cases identified among females and those >60 y of age. A total of 36 trachoma cases co-occurred with hypertension (26%) and diabetes (0.01%). NCDs were frequent among those with recurring trachoma (21%) and trachomatous trichiasis (14.3%). Trachoma and NCDs clustered together in <1 km distances ($R=0.18$, $p=0.02$). In network analysis, age was strongly associated with trachoma and NCDs. Trachoma was linked with geographic location while diabetes was linked with water source distances. Education level became the central risk factor. **Conclusions:** We demonstrate a twin trachoma-NCD burden that is higher among elderly pastoralists in southern Kenya. Attenuating adverse population-level visual impairment, including integrating the trachoma SAFE strategy with NCD comprehensive care, amplifies the benefits from economies of scale, accelerating realization of Sustainable Development Goal 3 and universal health coverage in hard-to-reach areas.

Using model-based geostatistics for assessing the elimination of trachoma.

Sasanami M, Amoah B, Diori AN, Amza A, Souley ASY, Bakhtiari A, Kadri B, Szwarcwald CL, Ferreira Gomez DV, Almou I, Lopes MFC, Masika MP, Beidou N, Boyd S, Harding-Esch EM, Solomon AW, Giorgi E.

28-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37506060/>

Individual longitudinal compliance to neglected tropical disease mass drug administration programmes, a systematic review.

Maddren R, Phillips A, Rayment Gomez S, Forbes K, Collyer BS, Kura K, Anderson R.

17-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37459369/>

Synthesis and biological evaluation of sulfonylpyridine derivatives as potential anti-chlamydia agents.

Feng J, Janaína de Campos L, Seleem MA, Conda-Sheridan M.

15-08-2023

Bioorg Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37453189/>

Chlamydia trachomatis is the most prevalent sexually transmitted bacterial infection in the United States and the world. This pathogen can cause health problems ranging from trachoma (blindness) to damage of the fallopian tubes or ectopic pregnancy, which can be life-threatening if not treated properly. To this day, there is no chlamydia-specific drug on the market. Previously, we reported the activity and basic structure-activity relationships (SAR) of sulfonylpyridine molecules that possess antichlamydial action. Based on those results, we prepared a new series of derivatives. Our data indicate the new analogs can halt the growth of *C. trachomatis*. The

lead compound, 22, was more active than our previous molecules and did not affect the growth of *S. aureus* and *E. coli*, suggesting bacterial selectivity. We performed docking studies on the presumed target, the cylindrical protease of Chlamydia. The in-silico studies partially explained the in vitro biological result as well as predicted a possible binding pose in the binding pocket. The top compound displayed a good cytotoxicity profile towards mammalian cell lines and was stable in both serum and stimulated gastric fluid. The presented data suggests the sulfonylpyridines are promising and selective anti-chlamydial compounds that merit further structural optimization.

Prevalence of and factors associated with childhood anaemia in remote villages of the Peruvian Amazon: a cross-sectional study and geospatial analysis.

Morocho-Alburqueque N, Quincho-Lopez A, Neesemann JM, Cañari-Casaño JL, Elorreaga OA, Muñoz M, Talero S, Harding-Esch EM, Saboyá-Díaz MI, Honorio-Morales HA, Durand S, Carey-Angeles CA, Klausner JD, Keenan JD, Lescano AG.

03-08-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37039044/>

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

Comparison of Mini-FLOTAC, Flukefinder and sedimentation techniques for detection and quantification of *Fasciola hepatica* and *Calicophoron daubneyi* eggs using spiked and naturally infected bovine faecal samples.

Bosco A, Ciuca L, Maurelli MP, Vitiello P, Cringoli G, Prada JM, Rinaldi L.

02-08-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37533114/>

Background: Fasciolosis (*Fasciola hepatica*) and paramphistomosis (*Calicophoron daubneyi*) are two important infections of livestock. *Calicophoron daubneyi* is the predominant Paramphistomidae species in Europe, and its prevalence has increased in the last 10-15 years. In Italy, evidence suggests that the prevalence of *F. hepatica* in ruminants is low in the southern part, but *C. daubneyi* has been recently reported at high prevalence in the same area. Given the importance of reliable tools for liver and rumen fluke diagnosis in ruminants, this study evaluated the diagnostic performance of the Mini-FLOTAC (MF),

Flukefinder[®] (FF) and sedimentation (SED) techniques to detect and quantify *F. hepatica* and *C. daubneyi* eggs using spiked and naturally infected cattle faecal samples.

Methods: Briefly, negative bovine faecal samples were artificially spiked with either *F. hepatica* or *C. daubneyi* eggs to achieve different egg count levels: 10, 50 and 100 eggs per gram (EPG) of faeces. Moreover, ten naturally infected cattle farms from southern Italy with either *F. hepatica* and/or *C. daubneyi* were selected. For each farm, the samples were analysed individually only with MF technique and as pools using MF, FF and SED techniques. Bayesian latent class analysis (LCA) was used to estimate sensitivity and accuracy of the predicted intensity of infection as well as the infection rate in the naturally infected farms. **Results:** The outcome of this study showed that the highest number of eggs (*F. hepatica* and *C. daubneyi*) recovered was obtained with MF, followed by FF and SED in spiked infected samples at 50 and 100 EPG, while at lower infection levels of 10 EPG, FF gave the best results. Moreover, the sensitivity for all the techniques included in the study was estimated at > 90% at infection levels > 20 EPG for both *F. hepatica* and *C. daubneyi* eggs. However, MF was the most accurate of the three techniques evaluated to estimate fluke infection intensity. Nevertheless, all three techniques can potentially estimate infection rate at farm level accurately. **Conclusions:** Optimization and standardization of techniques are needed to improve the FEC of fluke eggs.

Novel recombinant proteins and peptides from *Clonorchis sinensis* and *Opisthorchis viverrini* for liver fluke exposure ELISA.

Mohan S, Natarajan M, Bruno JG.

18-06-2023

Biochem Biophys Res.

<https://pubmed.ncbi.nlm.nih.gov/37521374/>

Human serum samples from individuals living in Vietnam and Taiwan suspected of past *Clonorchis sinensis* or *Opisthorchis viverrini* infection were screened using several novel peptides and recombinant liver fluke proteins to determine if any consistent patterns could be discerned and used as the basis for future liver fluke ELISA development. Absorbance values at 405 nm were compared to those of pooled unexposed normal human serum and analyzed for statistical significance. The data exhibited some interesting patterns consistent with egg antigen sequestration in the gut possibly leading to lower serum antibody levels and potential regional exposure differences between Vietnamese and Taiwanese subjects. In particular, antibodies against Cathepsin B and B2 peptides, as well as a partial Catedrin Domain peptide may be elevated in some Taiwanese serum samples while antibodies against recombinant *Clonorchis* egg protein and Hepatocellular Carcinoma Peptide Antigen 59 may be elevated in some samples from both Taiwan and Vietnam. The data appear to suggest that some of the novel recombinant protein and peptide antigens selected and tested herein warrant further study with larger sample sizes as possible targets for detecting anti-liver fluke antibodies by ELISA from humans suspected of liver fluke infections.

Coprological and postmortem assessment and economic significance of bovine fasciolosis in cattle slaughtered at Tarcha Municipal Abattoir, Southern Ethiopia.

Mathewos M, Endale H, Kebamo M.

18-06-2023

Parasite Epidemiol Control.

<https://pubmed.ncbi.nlm.nih.gov/37521359/>

A systematic review and meta-analysis of the prevalence of parasitic infections in equids in Ethiopia.

Mesafint E, Dejene H, Maru M, Tarekegn ZS.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520199/>

Modified Hederagenin Derivatives Demonstrate Ex Vivo Anthelmintic Activity against *Fasciola hepatica*.

Chakroborty A, Pritchard DR, Bouillon ME, Cervi A, Kraehenbuehl R, Wild C, Fenn C, Holdsworth P, Capner C, Padalino G, Forde-Thomas JE, Payne J, Smith BG, Fisher M, Lahmann M, Baird MS, Hoffmann KF.

03-07-2023

Pharmaceutics.

<https://pubmed.ncbi.nlm.nih.gov/37514055/>

Infection with *Fasciola hepatica* (liver fluke) causes fasciolosis (or fascioliasis) and poses a considerable economic as well as welfare burden to both the agricultural and animal health sectors. Here, we explore the ex vivo anthelmintic potential of synthetic derivatives of hederagenin, isolated in bulk from *Hedera helix*. Thirty-six compounds were initially screened against *F. hepatica* newly excysted juveniles (NEJs) of the Italian strain. Eleven of these compounds were active against NEJs and were selected for further study, using adult *F. hepatica* derived from a local abattoir (provenance unknown). From these eleven compounds, six demonstrated activity and were further assessed against immature liver flukes of the Italian strain. Subsequently, the most active compounds ($n = 5$) were further evaluated in ex vivo dose response experiments against adult Italian strain liver flukes. Overall, MC042 was identified as the most active molecule and the EC_{50} obtained from immature and adult liver fluke assays (at 24 h post co-culture) are estimated as 1.07 μ M and 13.02 μ M, respectively. When compared to the in vitro cytotoxicity of MDBK bovine cell line, MC042 demonstrated the highest anthelmintic selectivity (44.37 for immature and 3.64 for adult flukes). These data indicate that modified hederagenins display properties suitable for further investigations as candidate flukicides.

Cystatins from the Human Liver Fluke *Opisthorchis viverrini*: Molecular Characterization and Functional Analysis.

Geadkaew-Krenc A, Grams R, Siricoon S, Kosa N, Krenc D, Phadungsil W, Martviset P.

18-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513796/>

Infectious Agents Induce Wnt/ β -Catenin Pathway Deregulation in Primary Liver Cancers.

Catalano T, Selvaggi F, Esposito DL, Cotellesse R, Aceto GM.

22-06-2023

Microorganisms.

<https://pubmed.ncbi.nlm.nih.gov/37512809/>

Interaction between infectious agents and liver tissue, as well as repeated and extreme biological events beyond adaptive capacities, may result in pathological conditions predisposing people to development of primary liver cancers (PLCs). In adults, PLCs mainly comprise hepatocellular carcinoma (HCC) and cholangiocarcinoma (CCA). Various infectious agents in the hepatic microenvironment can destabilize normal liver cell functions by modulating the Wnt/ β -catenin pathway components. Among them, hepatotropic viruses B, C, and D are involved in Wnt/ β -catenin signaling dysregulation. Other microbial agents, including oncogenic viruses such as Epstein-Barr virus (EBV) and human papilloma virus (HPV), bacteria, e.g., *Mycoplasma hyorhinis* and *Salmonella Typhi*, the protozoan parasite *Toxoplasma gondii*, the fungus *Aspergillus flavus*, and liver flukes such as *Clonorchis sinensis* or *Opisthorchis viverrini*, may induce malignant transformation in hepatocytes or in target cells of the biliary tract through aberrant Wnt signaling activation. This review focuses on new insights into infectious agents implicated in the deregulation of Wnt signaling and PLC development. Since the Wnt/ β -catenin pathway is a driver of cancer following viral and bacterial infections, molecules inhibiting the complex axis of Wnt signaling could represent novel therapeutic approaches in PLC treatment.

Antigens from the Helminth *Fasciola hepatica* Exert Antiviral Effects against SARS-CoV-2 In Vitro.

Serrat J, Francés-Gómez C, Becerro-Recio D, González-Miguel J, Geller R, Siles-Lucas M.

18-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37511355/>

Exudative pleural effusion caused by lung fluke infection: a practical diagnostic approach.

Wang H, Wang L, Yu D, Luo G, Yang S, Liu Y, Ren T, Wang M.

26-06-2023

Int J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37507085/>

Combination Vaccines of *Fasciola gigantica* Saposin-like Protein-2 and Leucine Aminopeptidase.

Changklungmoa N, Cheukamud W, Jaikua W, Meemon K, Sobhon P, Kueakhai P.

22-06-2023

Trop Med Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37505630/>

Saprosin-like protein-2 (SAP-2) and leucine aminopeptidase (LAP) are major proteins involved in the digestive process of *Fasciola gigantica* (Fg). Both SAP-2 and LAP are highly expressed in *F. gigantica*; therefore, they could be vaccine candidates for fasciolosis. The aims of this study are (1) to observe the tissue expression of *F. gigantica* SAP-2 (FgSAP-2) and *F. gigantica* LAP (FgLAP) in *F. gigantica* by indirect immunofluorescence technique under confocal microscopy and (2) to test the vaccine potentials of individual and combined recombinant (r) FgSAP-2 and rFgLAP against *F. gigantica* in Imprinting Control Region (ICR) mice (n = 10 per group). By indirect immunofluorescence-confocal microscopy, FgSAP-2 and FgLAP were localized in the caecal epithelium but at different sites: FgSAP-2 appeared in small granules that are distributed in the middle and lower parts of the cytoplasm of epithelial cells, while FgLAP appeared as a line or zone in the apical cytoplasm of caecal epithelial cells. For vaccine testing, the percent protection of combined rFgSAP-2 and rFgLAP vaccines against *F. gigantica* was at 80.7 to 81.4% when compared with aluminum hydroxide (alum) adjuvant and unimmunized controls, respectively. The levels of IgG1 and IgG2a in the sera were significantly increased in single and combine vaccinated groups compared with the control groups. Vaccinated mice showed reduced liver damage when compared with control groups. This study indicates that the combined rFgSAP-2 and rFgLAP vaccine had a higher vaccine potential than a single vaccine. These results support the further testing and application of this combined vaccine against *F. gigantica* infection in farmed livestock animals.

Study of the cross-talk between *Fasciola hepatica* juveniles and the intestinal epithelial cells of the host by transcriptomics in an in vitro model.

Becerro-Recio D, Serrat J, López-García M, Torres-Valle M, Colina F, Fernández IM, González-Miguel J, Siles-Lucas M.

AOÛT-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37450963/>

Fasciolosis is a globally widespread trematodiasis with a major economic and veterinary impact. Therefore, this disease is responsible for millions of dollars in losses to the livestock industry, and also constitutes an emerging human health problem in endemic areas. The ubiquitous nature of *Fasciola hepatica*, the main causative agent, is one of the key factors for the success of fasciolosis. Accordingly, this parasite is able to subsist in a wide variety of ecosystems and hosts, thanks to the development of a plethora of strategies for adaption and immune evasion. Fasciolosis comprises a growing concern due to its high prevalence rates, together with the emergence of strains of the parasite resistant to the treatment of choice (triclabendazole). These facts highlight the importance of

developing novel control measures which allow for an effective protection against the disease before *F. hepatica* settles in a niche inaccessible to the immune system. However, knowledge about the initial phases of the infection, including the migration mechanisms of the parasite and the early innate host response, is still scarce. Recently, our group developed an in vitro host-parasite interaction model that allowed the early events to be unveiled after the first contact between the both actors. This occurs shortly upon ingestion of *F. hepatica* metacercariae and the emergence of the newly excysted juveniles (FhNEJ) in the host duodenum. Here, we present a transcriptomic analysis of such model using an approach based on RNA sequencing (RNA-Seq), which reveals changes in gene expression related to proteolysis and uptake of metabolites in FhNEJ. Additionally, contact with the parasite triggered changes in host intestinal cells related to pseudogenes expression and host defence mechanisms, including immune response, among others. In sum, these results provide a better understanding of the early stages of fasciolosis at molecular level, and a pool of targets that could be used in future therapeutic strategies against the disease.

Molecular detection of *Fasciola*, *Schistosoma* and *Paramphistomum* species from freshwater snails occurring in Gauteng and Free State provinces, South Africa.

Molaba GG, Molefe-Nyembe NI, Taioe OM, Mofokeng LS, Thekiso OMM, Mtshali K.

AOÛT-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37364501/>

Trematodiasis are diseases caused by snail-borne trematode parasites that infect both animals and humans. Fascioliasis, schistosomiasis and paramphistomosis are some of these diseases and they affect millions of livestock, leading to significant economic losses. The aim of the study was to document freshwater snails occurring in selected study sites in the Free State and Gauteng provinces as well as identify and detect larval trematodes that they harbour. Samples were collected from a total of five study sites within two provinces of South Africa. Morphological features were used to identify snail species and were further confirmed genetically by polymerase chain reaction (PCR), sequencing and phylogenetic analysis. The larval trematodes were also detected by PCR, PCR-Restriction Length Fragment Polymorphism (PCR-RLFP), sequencing and phylogenetic analysis. A total of 887 freshwater snails were collected from Free State (n = 343) and Gauteng (n = 544). Five different genera of snails as well as species in the Succineidae family were documented. The snails in descending order of abundance were identified as: *Physa* (P.) spp. (51%), Succineidae spp. (20%), *Galba* (G.) *truncatula* (12%), *Pseudosuccinea* (Ps.) *columella* (10%), *Planorbella* (Pl.) *durys* (6%) and *Bulinus* (B.) *truncatus* (1%). Approximately 272 DNA pools were created for genetic identification of snails and detection of trematode parasites. *Schistosoma* species were not detected from any of the snail species. A total prevalence of 46% was obtained for *Fasciola hepatica* in the identified

snail species across all study sites. Overall, the highest prevalence of *F. hepatica* was obtained in *Physa* species (24%), whilst the lowest was observed in *B. truncatus* snails (1%). Forty three percent (43%) of the snail samples were PCR positive for *Paramphistomum* DNA. This is the first report of *P. mexicana* in South Africa. *Fasciola hepatica* was confirmed from all obtained snail species per study site. This is the first reported detection of *F. hepatica* in *Pl. duryi* and *P. mexicana* snails as well as the first confirmation of natural infection from *P. acuta* in South Africa.

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

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

Août-2023

Vet Parasitol.

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

Cloning and expression of *Fasciola hepatica* enolase gene and efficacy of recombinant protein in the serodiagnosis of sheep fasciolosis.

Celik F, Simsek S, Selcuk MA, Kesik HK, Gunyakti Kilinc S, Aslan Celik B.

Août-2023

Vet Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37290212/>

Trypanosomes (trypanosomiasis et maladie de Chagas)

Antimicrobial and in silico studies of the triterpenoids of *Dichapetalum albidum*.

Chama MA, Dziwornu GA, Popli E, Mas-Claret E, Egyir B, Ayine-Tora DM, Owusu KB, Reid DG, Osei-Safo D, Duer M, Mulholland D, Bender A.

14-07-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37539285/>

Here we report a new polyhydroxylated triterpene, 2 β ,6 β ,21 α -trihydroxyfriedelan-3-one (**4**) isolated from the root and stem bark of *Dichapetalum albidum* A. Chev (Dichapetalaceae), along with six known triterpenoids (**1-3**, **5**, **6**, **8**), sitosterol-3 β -O-D-glucopyranoside (**9**), a dipeptide (**7**), and a tyramine derivative of coumaric acid (**10**). Friedelan-3-one (**2**) showed an antimicrobial activity (IC₅₀) of 11.40 μ g/mL against *Bacillus cereus*, while friedelan-3 α -ol (**1**) gave an IC₅₀ of 13.07 μ g/mL against *Staphylococcus aureus* with ampicillin reference standard of 19.52 μ g/mL and 0.30 μ g/mL respectively. 3 β -Acetyl tormentic acid (**5**) showed an IC₅₀ of 12.50 μ g/mL against *Trypanosoma brucei brucei* and sitosterol-3 β -O-d-glucopyranoside (**9**) showed an IC₅₀ of 5.06 μ g/mL against *Leishmania donovani* with respective reference standards

of IC₅₀ 5.02 μ g/mL for suramin and IC₅₀ 0.27 μ g/mL for amphotericin B. Molecular docking of the isolated compounds on the enzyme glucose-6-phosphate dehydrogenase (G6PDH) suggested 3 β -acetyl tormentic acid (**5**) and sitosterol-3 β -O-D-glucopyranoside (**9**) as plausible inhibitors of the enzyme in accordance with the experimental biological results observed.

Digestive α -L-fucosidase activity in *Rhodnius prolixus* after blood feeding: effect of secretagogue and nutritional stimuli.

Gama MDVF, Alexandre YDN, Pereira da Silva JM, Castro DP, Genta FA.

19-07-2023

Front Physiol.

<https://pubmed.ncbi.nlm.nih.gov/37538373/>

Heterologous mRNA-protein vaccination with Tc24 induces a robust cellular immune response against *Trypanosoma cruzi*, characterized by an increased level of polyfunctional CD8⁺ T-cells.

Poveda C, Leão AC, Mancino C, Taraballi F, Chen YL, Adhikari R, Villar MJ, Kundu R, Nguyen DM, Versteeg L, Strych U, Hotez PJ, Bottazzi ME, Pollet J, Jones KM.

20-07-2023

Curr Res Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37534309/>

Nanostructured lipid carriers containing benzimidazole: physicochemical, biopharmaceutical and cellular in vitro studies.

Muraca G, Ruiz ME, Gambaro RC, Scioli-Montoto S, Sbaraglini ML, Padula G, Cisneros JS, Chain CY, Álvarez VA, Huck-Iriart C, Castro GR, Piñero MB, Marchetto MI, Alba Soto C, Islan GA, Talevi A.

28-07-2023

Beilstein J Nanotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37533841/>

Chagas disease is a neglected endemic disease prevalent in Latin American countries, affecting around 8 million people. The first-line treatment, benzimidazole (BNZ), is effective in the acute stage of the disease but has limited efficacy in the chronic stage, possibly because current treatment regimens do not eradicate transiently dormant *Trypanosoma cruzi* amastigotes. Nanostructured lipid carriers (NLC) appear to be a promising approach for delivering pharmaceutical active ingredients as they can have a positive impact on bioavailability by modifying the absorption, distribution, and elimination of the drug. In this study, BNZ was successfully loaded into nanocarriers composed of myristyl myristate/Crodamol oil/poloxamer 188 prepared by ultrasonication. A stable NLC formulation was obtained, with \approx 80% encapsulation efficiency (%EE) and a biphasic drug release profile with an initial burst release followed by a prolonged phase. The hydrodynamic average diameter and zeta potential of NLC obtained by

dynamic light scattering were approximately 150 nm and -13 mV, respectively, while spherical and well-distributed nanoparticles were observed by transmission electron microscopy. Fourier-transform infrared spectroscopy, differential scanning calorimetry, thermogravimetric analysis, and small-angle X-ray scattering analyses of the nanoparticles indicated that BNZ might be dispersed in the nanoparticle matrix in an amorphous state. The mean size, zeta potential, polydispersity index, and %EE of the formulation remained stable for at least six months. The hemolytic effect of the nanoparticles was insignificant compared to that of the positive lysis control. The nanoparticle formulation exhibited similar performance in vitro against *T. cruzi* compared to free BNZ. No formulation-related cytotoxic effects were observed on either Vero or CHO cells. Moreover, BNZ showed a 50% reduction in CHO cell viability at 125 µg/mL, whereas NLC-BNZ and non-loaded NLC did not exert a significant effect on cell viability at the same concentration. These results show potential for the development of new nanomedicines against *T. cruzi*.

FAZ assembly in bloodstream form *Trypanosoma brucei* requires kinesin KIN-E.

Albisetti AC, Douglas RL, Welch MD.

03-08-2023

Mol Biol Cell.

<https://pubmed.ncbi.nlm.nih.gov/37531263/>

Trypanosoma brucei, the causative agent of African sleeping sickness, uses its flagellum for movement, cell division, and signaling. The flagellum is anchored to the cell body membrane via the flagellum attachment zone (FAZ), a complex of proteins, filaments, and microtubules that spans two membranes with elements on both flagellum and cell body sides. How FAZ components are carried into place to form this complex is poorly understood. Here, we show that the trypanosome-specific kinesin KIN-E is required for building the FAZ in bloodstream-form parasites. KIN-E is localized along the flagellum with a concentration at its distal tip. Depletion of KIN-E by RNAi rapidly inhibits flagellum attachment and leads to cell death. A detailed analysis reveals that KIN-E depletion phenotypes include failure in cytokinesis completion, kinetoplast DNA missegregation, and transport vesicle accumulation. Together with previously published results in procyclic form parasites, these data suggest KIN-E plays a critical role in FAZ assembly in *T. brucei*.

Target product profile: diagnostic test for *Trypanosoma brucei gambiense*.

Priotto G, Franco JR, Lejon V, Büscher P, Matovu E, Ndung'u J, Biéler S, Mumba D, Van Reet N, Verlé P, Jamonneau V, Simarro PP, Ebeja AK, Sankara D, Dagne DA.

01-08-2023

Bull World Health Organ.

<https://pubmed.ncbi.nlm.nih.gov/37529027/>

Target product profile: *Trypanosoma brucei gambiense* test for low-prevalence settings.

Priotto G, Franco JR, Lejon V, Büscher P, Matovu E, Ndung'u J, Biéler S, Mumba D, Van Reet N, Verlé P, Jamonneau V, Simarro PP, Ebeja AK, Sankara D, Dagne DA.

01-08-2023

Bull World Health Organ.

<https://pubmed.ncbi.nlm.nih.gov/37529025/>

Having caused devastating epidemics during the 20th century, the incidence of life-threatening human African trypanosomiasis has fallen to historically low levels as a result of sustained and coordinated efforts over the past 20 years. Humans are the main reservoir of one of the two pathogenic trypanosome subspecies, *Trypanosoma brucei gambiense*, found in western and central Africa. The expected advent of a safe and easy-to-use treatment to be given to seropositive but microscopically unconfirmed individuals would lead to further depletion; in the meantime, the presence of *T. b. gambiense* infection in the community must be monitored to allow the control strategy to be adapted and the elimination status to be assessed. The World Health Organization has therefore developed a target product profile that describes the optimal and minimal characteristics of an individual laboratory-based test to assess *T. b. gambiense* infection in low-prevalence settings. Development of the target product profile involved the formation of a Neglected Tropical Diseases Diagnostics Technical Advisory Group and a subgroup on human African trypanosomiasis diagnostic innovation needs, and an analysis of the available products and development pipeline. According to the product profile, the test should ideally: (i) require a minimally invasive or non-invasive specimen, collectable at peripheral facilities by minimally trained health workers; (ii) demonstrate good sensitivity and high specificity; (iii) have a stability of samples allowing transfer to reference laboratories preferably without cold chain; (iv) be stable over a wide range of environmental conditions for more than 2 years; and (v) after marketing, be available at low cost for at least 7 years.

Target product profile: diagnostic test for *Trypanosoma brucei rhodesiense*.

Priotto G, Franco JR, Lejon V, Büscher P, Matovu E, Ndung'u J, Biéler S, Mumba D, Van Reet N, Verlé P, Jamonneau V, Simarro PP, Ebeja AK, Sankara D, Dagne DA.

01-08-2023

Bull World Health Organ.

<https://pubmed.ncbi.nlm.nih.gov/37529024/>

Rhodesiense human African trypanosomiasis is a lethal parasitic infection caused by *Trypanosoma brucei rhodesiense* and transmitted by tsetse flies in eastern and southern Africa. It accounts for around 5% of all cases of human African trypanosomiasis. Currently, there is no simple serological test for rhodesiense human African trypanosomiasis and diagnosis relies on microscopic confirmation of trypanosomes in samples of blood or other tissues. The availability of a simple and accurate

diagnostic test would aid the control, surveillance and treatment of the disease. A subcommittee of the World Health Organization's Neglected Tropical Diseases Diagnostics Technical Advisory Group has developed a target product profile for a diagnostic tool to identify *T. b. rhodesiense* infection. The optimum tool would have a sensitivity and specificity above 99% for detecting *T. b. rhodesiense*, but be simple enough for use by minimally trained health-care workers in unsophisticated peripheral health facilities or mobile teams in villages. The test should yield a qualitative result that can be easily observed and can be used to determine treatment. An antigen test would be preferable, with blood collected by finger-prick. Ideally, there should be no need for a cold chain, instrumentation or precision liquid handling. The test should be usable between 10 °C and 40 °C and between 10% and 88% relative humidity. Basic training should take under 2 hours and the test should involve fewer than five steps. The unit cost should be less than 1 United States dollar.

Target product profile: Trypanosoma brucei gambiense test to verify elimination.

Priotto G, Franco JR, Lejon V, Büscher P, Matovu E, Ndung'u J, Biéler S, Mumba D, Van Reet N, Verlé P, Jamonneau V, Simarro PP, Ebeja AK, Sankara D, Dagne DA.

01-08-2023

Bull World Health Organ.

<https://pubmed.ncbi.nlm.nih.gov/37529018/>

The Pampa del Indio project: sustainable vector control and long-term declines in the prevalence and abundance of Triatoma infestans infected with Trypanosoma cruzi in the Argentine Chaco.

Gürtler RE, Enriquez GF, Gaspe MS, Macchiaverna NP, Del Pilar Fernández M, Rodríguez-Planes LI, Provecho YM, Cardinal MV.

02-08-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37528423/>

Background: The Gran Chaco region is a major hotspot of Chagas disease. We implemented a 9-year program aimed at suppressing house infestation with *Triatoma infestans* and stopping vector-borne transmission to creole and indigenous (Qom) residents across Pampa del Indio municipality (Argentine Chaco). The aim of the present study was to assess the intervention effects on parasite-based transmission indices and the spatial distribution of the parasite, and test whether house-level variations in triatomine infection with *Trypanosoma cruzi* declined postintervention and were influenced by household ethnicity, persistent infestation linked to pyrethroid resistance and other determinants of bug infection.

Methods: This longitudinal study assessed house infestation and bug infection with *T. cruzi* before and after spraying houses with pyrethroids and implemented systematic surveillance-and-response measures across

four operational areas over the period 2007-2016. Live triatomines were individually examined for infection by optical microscopy or kinetoplast DNA (kDNA)-PCR and declared to be infected with *T. cruzi* when assessed positive by either method. **Results:** The prevalence of infection with *T. cruzi* was 19.4% among 6397 *T. infestans* examined. Infection ranged widely among the study areas (12.5-26.0%), household ethnicity (15.3-26.9%), bug ecotopes (1.8-27.2%) and developmental stages (5.9-27.6%), and decreased from 24.1% (baseline) to 0.9% (endpoint). Using random-intercept multiple logistic regression, the relative odds of bug infection strongly decreased as the intervention period progressed, and increased with baseline domestic infestation and bug stage and in Qom households. The abundance of infected bugs and the proportion of houses with ≥ 1 infected bug remained depressed postintervention and were more informative of area-wide risk status than the prevalence of bug infection. Global spatial analysis revealed sharp changes in the aggregation of bug infection after the attack phase. Baseline domestic infestation and baseline bug infection strongly predicted the future occurrence of bug infection, as did persistent domestic infestation in the area with multiple pyrethroid-resistant foci. Only 19% of houses had a baseline domestic infestation and 56% had ever had ≥ 1 infected bug. **Conclusions:** Persistent bug infection postintervention was closely associated with persistent foci generated by pyrethroid resistance. Postintervention parasite-based indices closely agreed with human serosurveys at the study endpoint, suggesting transmission blockage. The program identified households and population subgroups for targeted interventions and opened new opportunities for risk prioritization and sustainable vector control and disease prevention.

[Towards elimination of human African trypanosomiasis].

Solano P, Courtin F, Kaba D, Camara, Kagbadouno M, Rayaisse JB, Jamonneau V, Bucheton B, Bart JM, Thevenon S, Lejon V.

10-02-2023

Med Trop Sante Int.

<https://pubmed.ncbi.nlm.nih.gov/37525637/>

Decoding the impact of nuclear organization on antigenic variation in parasites.

Barcons-Simon A, Carrington M, Siegel TN.

Août-2023

Nat Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37524976/>

Towards the sustainable elimination of gambiense human African trypanosomiasis in Côte d'Ivoire using an integrated approach.

Kaba D, Koffi M, Kouakou L, N'Gouan EK, Djohan V, Courtin F, N'Djetchi MK, Coulibaly B, Adingra GP, Berté D, Ta BTD, Koné M, Traoré BM, Sutherland SA, Crump RE, Huang CI, Madan J, Bessell PR, Barreaux A, Solano P, Crowley EH, Rock KS, Jamonneau V.

31-07-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37523361/>

Discovery of a Hidden Trypanosoma cruzi Spermidine Synthase Binding Site and Inhibitors through In Silico, In Vitro, and X-ray Crystallography.

Yoshino R, Yasuo N, Hagiwara Y, Ishida T, Inaoka DK, Amano Y, Tateishi Y, Ohno K, Namatame I, Niimi T, Orita M, Kita K, Akiyama Y, Sekijima M.

12-07-2023

ACS Omega.

<https://pubmed.ncbi.nlm.nih.gov/37521650/>

In drug discovery research, the selection of promising binding sites and understanding the binding mode of compounds are crucial fundamental studies. The current understanding of the proteins-ligand binding model extends beyond the simple lock and key model to include the induced-fit model, which alters the conformation to match the shape of the ligand, and the pre-existing equilibrium model, selectively binding structures with high binding affinity from a diverse ensemble of proteins. Although methods for detecting target protein binding sites and virtual screening techniques using docking simulation are well-established, with numerous studies reported, they only consider a very limited number of structures in the diverse ensemble of proteins, as these methods are applied to a single structure. Molecular dynamics (MD) simulation is a method for predicting protein dynamics and can detect potential ensembles of protein binding sites and hidden sites unobservable in a single-point structure. In this study, to demonstrate the utility of virtual screening with protein dynamics, MD simulations were performed on *Trypanosoma cruzi* spermidine synthase to obtain an ensemble of dominant binding sites with a high probability of existence. The structure of the binding site obtained through MD simulation revealed pockets in addition to the active site that was present in the initial structure. Using the obtained binding site structures, virtual screening of 4.8 million compounds by docking simulation, *in vitro* assays, and X-ray analysis was conducted, successfully identifying two hit compounds.

A systematic review and meta-analysis of the prevalence of parasitic infections in equids in Ethiopia.

Mesafint E, Dejene H, Maru M, Tarekegn ZS.

Sept-2023

J Parasit Dis.

<https://pubmed.ncbi.nlm.nih.gov/37520199/>

Two sticky traps baited with synthetic host odors to capture Triatoma infestans, an important vector of Chagas disease.

Ibarra Bouzada LME, Martinez Beningaza A, Cecere MC, Babino L, Guerenstein PG.

27-07-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37516421/>

Recent advances in genome editing of bloodstream forms of Trypanosoma congolense using CRISPR-Cas9 ribonucleoproteins: Proof of concept.

Minet C, Chantal I, Berthier D.

28-07-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37516291/>

African Animal Trypanosomosis (AAT or Nagana) is a vector-borne disease caused by Trypanosomatidae, genus Trypanosoma. The disease is transmitted by the bite of infected hematophagous insects, mainly tsetse flies but also other blood-sucking insects including stomoxes and tabanids. Although many trypanosome species infect animals, the main agents responsible for this disease with a strong socio-economic and veterinary health impact are Trypanosoma congolense (T. congolense or Tc), Trypanosoma vivax (T.vivax), and to a lesser extent, Trypanosoma brucei brucei (T.brucei brucei or Tbb). These parasites mainly infect livestock, including cattle, in sub-Saharan Africa, with major repercussions in terms of animal productivity and poverty for populations which are often already very poor. As there is currently no vaccine, the fight against the disease is primarily based on diagnosis, treatment and vector control. To develop new tools (particularly therapeutic tools) to fight against the disease, we need to know both the biology and the genes involved in the pathogenicity and virulence of the parasites. To date, unlike for Trypanosoma brucei (T.brucei) or Trypanosoma cruzi (T.cruzi), genome editing tools has been relatively little used to study T. congolense. We present an efficient, reproducible and stable CRISPR-Cas9 genome editing system for use in Tc bloodstream forms (Tc-BSF). This plasmid-free system is based on transient expression of Cas9 protein and the use of a ribonucleoprotein formed by the Cas9 and sgRNA complex. This is the first proof of concept of genome editing using CRISPR-Cas9 ribonucleoproteins on Tc-BSF. This adapted protocol enriches the "toolbox" for the functional study of genes of interest in blood forms of the Trypanosoma congolense. This proof of concept is an important step for the scientific community working on the study of trypanosomes and opens up new perspectives for the control of and fight against animal trypanosomosis.

Novel Lipophilic Hydroxamates Based on Spirocarbocyclic Hydantoin Scaffolds with Potent Antiviral and Trypanocidal Activity.

Pardali V, Giannakopoulou E, Mpekoulis G, Tsopela V, Panos G, Taylor MC, Kelly JM, Vassilaki N, Zoidis G.

24-07-2023

Pharmaceuticals (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37513957/>

Flaviviridae infections, such as those caused by hepatitis C (HCV) and dengue viruses (DENVs), represent global health risks. Infected people are in danger of developing chronic liver failure or hemorrhagic fever, both of which can be fatal if not treated. The tropical parasites *Trypanosoma*

brucei and *Trypanosoma cruzi* cause enormous socioeconomic burdens in Sub-Saharan Africa and Latin America. Anti-HCV chemotherapy has severe adverse effects and is expensive, whereas dengue has no clinically authorized treatment. Antiparasitic medicines are often toxic and difficult to administer, and treatment failures are widely reported. There is an urgent need for new chemotherapies. Based on our previous research, we have undertaken structural modification of lead compound **V** with the goal of producing derivatives with both antiviral and trypanocidal activity. The novel spirocarbocyclic-substituted hydantoin analogs were designed, synthesized, and tested for antiviral activity against three HCV genotypes (1b, 3a, 4a), DENV, yellow fever virus (YFV), and two trypanosome species (*T. brucei*, *T. cruzi*). The optimization was successful and led to compounds with significant antiviral and trypanocidal activity and exceptional selectivity. Several modifications were made to further investigate the structure-activity relationships (SARs) and confirm the critical role of lipophilicity and conformational degrees of freedom.

Occurrence, Prevalence, and Distribution of Haemoparasites of Poultry in Sub-Saharan Africa: A Scoping Review.

Tembe D, Malatji MP, Mukaratirwa S.

17-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513792/>

Neglected Zoonotic Diseases: Advances in the Development of Cell-Penetrating and Antimicrobial Peptides against Leishmaniosis and Chagas Disease.

Robledo SM, Pérez-Silanes S, Fernández-Rubio C, Poveda A, Monzote L, González VM, Alonso-Collado P, Carrión J.

15-07-2023

Pathogens.

<https://pubmed.ncbi.nlm.nih.gov/37513786/>

Synthesis of Benzocycloalkanone-Based Michael Acceptors and Biological Activities as Antimalarial and Antitrypanosomal Agents.

Mijoba A, Fernandez-Moreira E, Parra-Giménez N, Espinosa-Tapia S, Blanco Z, Ramírez H, Charris JE.

21-07-2023

Molecules.

<https://pubmed.ncbi.nlm.nih.gov/37513441/>

In Silico Identification and Analysis of Proteins Containing the Phox Homology Phosphoinositide-Binding Domain in Kinetoplastea Protists: Evolutionary Conservation and Uniqueness of Phox-Homology-Domain-Containing Protein Architectures.

Petsana M, Roumia AF, Bagos PG, Boleti H, Braliou GG.

15-07-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37511280/>

Kinetoplastea are free living and parasitic protists with unique features among Eukaryota. Pathogenic Kinetoplastea parasites (i.e., *Trypanosoma* and *Leishmania* spp.) undergo several developmental transitions essential for survival in their hosts. These transitions require membrane and cytoskeleton reorganizations that involve phosphoinositides (PIs). Phospholipids like PIs are key regulators of vital functions in all eukaryotes including signal transduction, protein transport and sorting, membrane trafficking, and cytoskeleton and membrane remodeling. A large repertoire of PI-metabolizing enzymes and PI-binding proteins/effectors carrying distinct PI-binding modules like the PX (phox homology) module could play significant roles in the life and virulence of pathogenic Kinetoplastea. The aim of this study was to retrieve the entire spectrum of Kinetoplastea protein sequences containing the PX module (PX-proteins), predict their structures, and identify in them evolutionary conserved and unique traits. Using a large array of bioinformatics tools, protein IDs from two searches (based on Pfam's pHMM for PX domain (PF00787)) were combined, aligned, and utilized for the construction of a new Kinetoplastea_PX pHMM. This three-step search retrieved 170 PX-protein sequences. Structural domain configuration analysis identified PX, Pkinase, Lipocalin_5, and Vps5/BAR3-WASP domains and clustered them into five distinct subfamilies. Phylogenetic tree and domain architecture analysis showed that some domain architectures exist in proteomes of all Kinetoplastea spp., while others are genus-specific. Finally, amino acid conservation logos of the Kinetoplastea spp. and *Homo sapiens* PX domains revealed high evolutionary conservation in residues forming the critical structural motifs for *PtdIns3P* recognition. This study highlights the PX-Pkinase domain architecture as unique within *Trypanosoma* spp. and forms the basis for a targeted functional analysis of Kinetoplastea PX-proteins as putative targets for a rational design of anti-parasitic drugs.

In Vitro Antioxidant and Antitrypanosomal Activities of Extract and Fractions of Terminalia catappa.

Araújo SA, Lima ADS, Rocha CQD, Previtali-Silva H, Hardoim DJ, Taniwaki NN, Calabrese KDS, Almeida-Souza F, Abreu-Silva AL.

22-06-2023

Biology (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37508328/>

Chagas disease is a severe infectious and parasitic disease caused by the protozoan *Trypanosoma cruzi* and considered a public health problem. Chemotherapeutics are still the main means of control and treatment of the disease, however with some limitations. As an alternative treatment, plants have been pointed out due to their proven pharmacological properties. Many studies carried out with *Terminalia catappa* have shown several biological activities, but its effect against *T. cruzi* is still unknown. The objective of this work is to evaluate the therapeutic

potential of extracts and fractions obtained from *T. catappa* on the parasite *T. cruzi*, in addition to analyzing its antioxidant activity. *T. catappa* ethyl acetate fraction were produced and submitted the chemical characterization by Liquid Chromatography Coupled to Mass Spectrometry (LC-MS). From all *T. catappa* extracts and fractions evaluated, the ethyl acetate and the aqueous fraction displayed the best antioxidant activity by the 2,2-diphenyl-1-picryl-hydrazyl (DPPH) radical scavenging method (IC₅₀ of 7.77 ± 1.61 and 5.26 ± 1.26 µg/mL respectively), and by ferric ion reducing (FRAP) method (687.61 ± 0.26 and 1009.32 ± 0.13 µM of Trolox equivalent/mg extract, respectively). The ethyl acetate fraction showed remarkable *T. cruzi* inhibitory activity with IC₅₀ of 8.86 ± 1.13 , 24.91 ± 1.15 and 85.01 ± 1.21 µg/mL against epimastigotes, trypomastigotes and intracellular amastigotes, respectively, and showed no cytotoxicity for Vero cells (CC₅₀ > 1000 µg/mL). The treatment of epimastigotes with the ethyl acetate fraction led to drastic ultrastructural changes such as the loss of cytoplasm organelles, cell disorganization, nucleus damage and the loss of integrity of the parasite. This effect could be due to secondary compounds present in this extract, such as luteolin, kaempferol, quercetin, ellagic acid and derivatives. The ethyl acetate fraction obtained from *T. catappa* leaves can be an effective alternative in the treatment and control of Chagas disease, and material for further investigations.

Structure-Guided Design and Synthesis of a Pyridazinone Series of Trypanosoma cruzi Proteasome Inhibitors.

Thomas MG, McGonagle K, Rowland P, Robinson DA, Dodd PG, Camino-Díaz I, Campbell L, Cantizani J, Castañeda P, Conn D, Craggs PD, Edwards D, Ferguson L, Fosberry A, Frame L, Goswami P, Hu X, Korczynska J, MacLean L, Martin J, Mutter N, Osuna-Cabello M, Paterson C, Peña I, Pinto EG, Pont C, Riley J, Shishikura Y, Simeons FRC, Stojanovski L, Thomas J, Wrobel K, Young RJ, Zmuda F, Zuccotto F, Read KD, Gilbert IH, Marco M, Miles TJ, Manzano P, De Rycker M.
28-07-2023
J Med Chem.
<https://pubmed.ncbi.nlm.nih.gov/37506194/>

Space-environment relationship in the identification of potential areas of expansion of Trypanosoma cruzi infection in Didelphis aurita in the Atlantic Rainforest.

Testai R, Ferreira de Siqueira M, Rocha DSB, Roque ALR, Jansen AM, Xavier SCDC.
28-07-2023
PLoS One.
<https://pubmed.ncbi.nlm.nih.gov/37506103/>

Ecological Niche Modeling is widely used for animals, but rarely for understanding the parasite ecology. *Trypanosoma cruzi* is a heterogeneous and widely dispersed multi-host parasite. *Didelphis aurita* is a generalist species, both in terms of diet and environments. We modeled the *D. aurita* niche and *T. cruzi* infection in

the Brazilian Atlantic Rainforest, using the models of two common vector species (*Triatoma vitticeps* and *Panstrongylus megistus*) as biotic variables, predicting their occurrence. Records of *T. cruzi* infected and non-infected *D. aurita* were analyzed through climate and landscape approaches by the Ecoland method. Models for each triatomine species and infected and noninfected *D. aurita* were produced considering climate and landscape: resolution of ~1km² selected by Pearson's correlation [$-0.7 \leq \alpha \leq 0.7$]. For modeling, seven algorithms available in ModleR package were used. True Skill Statistic was used to evaluate the models' performance (≥ 0.7). *T. vitticeps* indicates that there is a spatial dependence with warm areas in the southeastern region while *P. megistus* presented a distribution with high environmental suitability concentrated in the Southeast. High values of climatic suitability, landscape and potential presence of *T. vitticeps* and *P. megistus* were considered necessary, but not sufficient for the presence of *D. aurita* infected by *T. cruzi*. Climate models showed an ecological niche with suitability variations homogeneous, and landscape models showed a distribution of habitat conditions along the biome, with a fragmented profile and heterogeneous between locations. Ecoland demonstrated that *D. aurita* has different degrees of impact on its role in the enzootic cycle in different locations of the Atlantic Rainforest. Associating the models with the Ecoland method allowed the recognition of areas where *D. aurita* are important *T. cruzi* reservoirs. Areas of high suitability for the presence of marsupials are a necessary, but not sufficient for *D. aurita* to act as a reservoir for *T. cruzi*.

What Do You Need to Know before Studying Chagas Disease? A Beginner's Guide.

De Fuentes-Vicente JA, Santos-Hernández NG, Ruiz-Castillejos C, Espinoza-Medinilla EE, Flores-Villegas AL, de Alba-Alvarado M, Cabrera-Bravo M, Moreno-Rodríguez A, Vidal-López DG.
10-07-2023
Trop Med Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37505656/>

Theracurmin Modulates Cardiac Inflammation in Experimental Model of Trypanosoma cruzi Infection.

Louise V, Machado BAA, Pontes WM, Menezes TP, Dias FCR, Ervilhas LOG, Pinto KMC, Talvani A.
28-06-2023
Trop Med Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37505639/>

Theracurmin is a nanoparticle formulation derived from curcumin, a bioactive compound known for its antioxidant and anti-inflammatory properties. *Trypanosoma cruzi*, the etiological agent of Chagas disease, triggers an intense inflammatory response in mammals and also causes severe tissue damage. To evaluate the immunomodulatory and antiparasitic effects of Theracurmin, Swiss mice were experimentally infected with 10³ trypomastigote forms of the Colombian strain of *T. cruzi* and submitted to daily therapy with 30 mg/kg of

Theracurmin. In addition, daily benznidazole therapy (100 mg/kg) was performed as a positive control. We evaluated the systemic and tissue parasitism, the survival and the body mass rate, the release of inflammatory mediators (TNF, IL-6, IL-15, CCL2 and creatine kinase) and the tissue inflammation at day 30 post-infection. Theracurmin therapy reduced the parasitemia curve without altering the animals' survival rate, and it protected mice from losing body mass. Theracurmin also reduced CCL2 in cardiac tissue, IL-15 in cardiac and skeletal tissue, and plasma CK. Even without effects on TNF and IL-6 production and tissue amastigote nests, Theracurmin reduced the leukocyte infiltrate in both evaluated tissues, even in the case of more effective results observed to the benznidazole treatment. Our data suggest Theracurmin has an immunomodulatory (CCL2, IL-15, CK and tissue leukocyte infiltration) and a trypanocidal effect (on circulating parasites) during experimental infection triggered by the Colombian strain of *T. cruzi*. Further investigations are necessary to comprehend the Theracurmin role performed in combination with benznidazole or other potential anti-*T. cruzi* chemical compounds.

Genotyping of *Trypanosoma brucei evansi* in Egyptian camels: detection of a different non-RoTat 1.2 *Trypanosoma brucei evansi* in Egyptian camels.

Behour TS, Abd El Fattah EM.

28-06-2023

Trop Anim Health Prod.

<https://pubmed.ncbi.nlm.nih.gov/37505344/>

Trypanosoma brucei evansi (*T. b. evansi*) is an enzootic organism found in Egyptian camels, which genetically classified into types A and B. To detect the parasite genotype circulating in Egyptian camels, we collected 94 blood samples from three distant districts and subjected them to different PCR assays; *T. brucei* repeat (TBR), internal transcribed spacer-1 (ITS-1), and variable surface glycoproteins (VSG) (RoTat 1. 2, JN 2118Hu) and EVAB PCRs. The highest prevalence was obtained with TBR (80/91; 87.9%), followed by ITS-1 (52/91; 57.1%), VSG JN 2118Hu (42/91; 46.2%), and VSG RoTat 1. 2 (34/91; 37.4%). We reported a different non-RoTat 1. 2 *T. b. evansi* for the first time in Egyptian camels. Results showed that 47 (58.7%) out of 80 samples were classified as *T. b. evansi*. Of these, 14 (29.8%) were RoTat 1. 2 type, 13 (27.6%) were non-RoTat 1. 2 type, and 20 (42.6%) samples were from mixed infection with both types. All samples were tested negative with EVAB PCR. RoTat 1. 2 *T. b. evansi* was the most prevalent in Giza and El Nubariyah, whereas, in Aswan, the only type detected was non-RoTat 1. 2 *T. b. evansi*. The nucleotide sequences of the VSG RoTat 1.2 and JN 2118Hu PCR products were submitted to DNA Data Bank of Japan (DDBJ) and GenBank under the accession numbers LC738852, and (OP800400-OP800403). Further research is required to increase the sample size and verify the new sequences to corroborate the prevalence of a new variant of non-RoTat 1.2 *T. b. evansi* in Egypt.

Epitopes and Mimotopes Identification Using Phage Display for Vaccine Development against Infectious Pathogens.

Palma M.

29-06-2023

Vaccines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37514992/>

Ulcère de Buruli

Evaluation of In2Care mosquito stations for suppression of the Australian backyard mosquito, *Aedes notoscriptus* (Diptera: Culicidae).

Paris V, Bell N, Schmidt TL, Endersby-Harshman NM, Hoffmann AA.

03-08-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37535973/>

Aedes notoscriptus (Skuse) is a container-inhabiting mosquito endemic to Australia that vectors arboviruses and is suspected to transmit *Mycobacterium ulcerans*, the cause of Buruli ulcer. We evaluated the effectiveness of the In2Care station, which suppresses mosquito populations via the entomopathogenic fungus, *Beauveria bassiana*, and the insect growth regulator pyriproxyfen, the latter of which is autodisseminated among larval habitats by contaminated mosquitoes. A field trial was conducted using 110 In2Care stations in a 50,000 m² area and results were compared to 4 control areas that did not receive the treatment. Efficacy was evaluated by comparing egg counts and measuring larvicidal impact in surrounding breeding sites. Laboratory experiments validated the effect of *B. bassiana* on adult survival. Results of this field trial indicate that, 6 wk after the In2Care stations were deployed, treatment site ovitraps contained 43% fewer eggs than control site ovitraps, and 33% fewer eggs after 10 wk, suggesting that the In2Care station was able to reduce the egg density of *Ae. notoscriptus*. Population reduction remained evident for up to 3 wk after In2Care stations were removed. Treatment site ovitraps had significantly fewer *Ae. notoscriptus* eclosing than control site ovitraps, confirming the pyriproxyfen autodissemination feature of the stations. An average reduction of 50% in adult eclosion was achieved. Exposure to *B. bassiana* resulted in four-times higher mortality among adult mosquitoes. Additionally, using fresh In2Care nettings led to an 88% decrease in average survival compared to 4-wk-old nettings. The use of In2Care stations has potential for suppressing *Ae. notoscriptus* egg density.

Behavioral interplay between mosquito and mycolactone produced by *Mycobacterium ulcerans* and bacterial gene expression induced by mosquito proximity.

Kim D, Crippen TL, Dhungel L, Delclos PJ, Tomberlin JK, Jordan HR.

03-08-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37535670/>

The Many Hosts of Mycobacteria 9 (MHM9): A conference report.

Klever AM, Alexander KA, Almeida D, Anderson MZ, Ball RL, Beamer G, Boggiatto P, Buikstra JE, Chandler B, Claey's TA, Concha AE, Converse PJ, Derbyshire KM, Dobos KM, Dupnik KM, Endsley JJ, Endsley MA, Fennelly K, Franco-Paredes C, Hagge DA, Hall-Stoodley L, Hayes D Jr, Hirschfeld K, Hofman CA, Honda JR, Hull NM, Kramnik I, Lacourciere K, Lahiri R, Lamont EA, Larsen MH, Lemaire T, Lesellier S, Lee NR, Lowry CA, Mahfooz NS, McMichael TM, Merling MR, Miller MA, Nagajyothi JF, Nelson E, Nuermberger EL, Pena MT, Perea C, Podell BK, Pyle CJ, Quinn FD, Rajaram MVS, Mejia OR, Rothoff M, Sago SA, Salvador LCM, Simonson AW, Spencer JS, Sreevatsan S, Subbian S, Sunstrum J, Tobin DM, Vijayan KKV, Wright CTO, Robinson RT.

23-07-2023

Tuberculosis (Edinb).

<https://pubmed.ncbi.nlm.nih.gov/37531864/>

The Many Hosts of Mycobacteria (MHM) meeting series brings together basic scientists, clinicians and veterinarians to promote robust discussion and dissemination of recent advances in our knowledge of numerous mycobacterial diseases, including human and bovine tuberculosis (TB), nontuberculous mycobacteria (NTM) infection, Hansen's disease (leprosy), Buruli ulcer and Johne's disease. The 9th MHM conference (MHM9) was held in July 2022 at The Ohio State University (OSU) and centered around the theme of "Confounders of Mycobacterial Disease." Confounders can and often do drive the transmission of mycobacterial diseases, as well as impact surveillance and treatment outcomes. Various confounders were presented and discussed at MHM9 including those that originate from the host (comorbidities and coinfections) as well as those arising from the environment (e.g., zoonotic exposures), economic inequality (e.g. healthcare disparities), stigma (a confounder of leprosy and TB for millennia), and historical neglect (a confounder in Native American Nations). This conference report summarizes select talks given at MHM9 highlighting recent research advances, as well as talks regarding the historic and ongoing impact of TB and other infectious diseases on Native American Nations, including those in Southwestern Alaska where the regional TB incidence rate is among the highest in the Western hemisphere.

Health-Seeking Behavior Regarding Coughs in Urban Slums in Lagos, Nigeria.

Adepoju VA, Oladimeji O, Sokoya OD.

26-07-2023

Medicines (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37505059/>

Background: TB is a major cause of morbidity and mortality, with slum residents being disproportionately affected. This study aimed to assess health-seeking

behavior among adult residents of slum communities presenting with coughs in Lagos, Nigeria. **Methods:** A community-based, cross-sectional study was conducted across six urban slums in Nigeria as part of community outreaches to mark World TB Day. A structured, pretested questionnaire was used to capture relevant sociodemographic details and questions regarding symptoms of coughs and related symptoms as well as care-seeking behavior. Data were explored, analyzed, and presented using descriptive statistics. **Results:** A total of 632 respondents participated in this study. The majority were 25-34 years old (24.7%), male (65.8%), Christian (55.7%), married (73.7%), with secondary education (37.8%), with 3-4 persons per household (41%) and with 1-2 persons per room (44.5%). In total, 26.6% had had a cough for two weeks or more and were considered as presumptive TB patients. Overall, 37.2% of respondents with a cough visited patent proprietary medicine vendors (PPMVs) as the first port of call. Good health-seeking behavior was exhibited by only 36.2% of respondents. In total, 38.9% delayed seeking care from a health facility (government or private) more than one month after the onset of symptoms. None of the factors included in the multivariate analysis showed a significant association with good health-seeking behavior (i.e., visiting government or private hospitals/clinics). **Conclusions:** The poor health-seeking behavior, delay in seeking TB care and preference for PPMVs emphasizes the need for National tuberculosis programs (NTPs) to further engage these informal providers in TB prevention, diagnosis and treatment services in urban slum communities.

Alternative boronic acids in the detection of Mycolactone A/B using the thin layer chromatography (f-TLC) method for diagnosis of Buruli ulcer.

Akolgo GA, Partridge BM, D Craggs T, Amewu RK.

27-07-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37501134/>