



Veille scientifique

Maladies tropicales négligées

Semaine 37
11 au 17 septembre 2023

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Dengue, chikungunya et maladie à virus Zika

Larvicidal proficiency of volatile compounds present in *Commiphora wightii* gum extract against *Aedes aegypti* (Linnaeus, 1762).

Patel K, Akbari D, Pandya RV, Trivedi J, Mevada V, Wanale SG, Patel R, Yadav VK, Tank JG, Sahoo DK, Patel A.

30-08-2023

Front Plant Sci.

<https://pubmed.ncbi.nlm.nih.gov/37711311/>

Aedes mosquitoes are the major cause of several vector-borne diseases in tropical and subtropical regions. Synthetic pesticides against these mosquitoes have certain limitations; hence, natural, eco-friendly, and safe larvicides obtained from plant resources are used to overcome these. In the present study, the larvicidal efficiency of *Commiphora wightii* against the fourth instar stage of the dengue fever mosquito *Aedes aegypti* (Linnaeus, 1762) was studied. The gum resin of *C. wightii* was collected using the borehole tapping method, and hexane extracts in different concentrations were prepared. The fourth-instar larvae were exposed to the extracts, and percent mortality, as well as LC₂₀, LC₅₀, and LC₉₀, was calculated. Volatile compounds of the hexane gum extract were analyzed by Headspace GC/MS, and the sequence of the acetylcholine, Gamma-aminobutyric acid (GABA) receptor, and octopamine receptor subunit of *A. aegypti* was obtained. It was found that the hexane gum extract was toxic and lethal for larvae at different concentrations. Minimum mortality was observed at 164 µg mL⁻¹ (10%/h), while maximum mortality was at 276 µg mL⁻¹ (50%/h). The lethal concentrations LC₂₀, LC₅₀, and LC₉₀ were 197.38 µg mL⁻¹, 294.13 µg mL⁻¹, and 540.15 µg mL⁻¹, respectively. The GC/MS analysis confirmed the presence of diterpenes, monoterpenes, monoterpene alcohol, and sesquiterpenes in the gum samples, which are lethal for larvae due to their inhibitory activity on the acetylcholinesterase enzyme, GABA receptor, and octopamine receptor subunit. The use of commonly occurring plant gum for the control of mosquitoes was explored, and it was found that the gum of *C. wightii* had larvicidal activities and could be potentially insecticidal.

The 2013 Chikungunya outbreak in the Caribbean was structured by the network of cultural relationships among islands.

Dommar CJ, López L, Paul R, Rodó X.

13-09-2023

R Soc Open Sci.

<https://pubmed.ncbi.nlm.nih.gov/37711149/>

In 2013, the Caribbean underwent an unprecedented epidemic of Chikungunya that affected 29 islands and mainland territories throughout the Caribbean in the first six months. Analysing the spread of the epidemic among the Caribbean islands, we show that the initial patterns of the epidemic can be explained by a network model based on the flight connections among islands. The network does

not follow a random graph model and its topology is likely the product of geo-political relationships that generate increased connectedness among locations sharing the same language. Therefore, the infection propagated preferentially among islands that belong to the same cultural domain, irrespective of their human and vector population densities. Importantly, the flight network topology was also a more important determinant of the disease dynamics than the actual volume of traffic. Finally, the severity of the epidemic was found to depend, in the first instance, on which island was initially infected. This investigation shows how a simple epidemic model coupled with an appropriate human mobility model can reproduce the observed epidemiological dynamics. Also, it sheds light on the design of interventions in the face of the emergence of infections in similar settings of naive subpopulations loosely interconnected by host movement. This study delves into the feasibility of developing models to anticipate the emergence of vector-borne infections, showing the importance of network topology, bringing valuable methods for public health officials when planning control policies. Significance statement: The study shows how a simple epidemic model associated with an appropriate human mobility model can reproduce the observed epidemiological dynamics of the 2014 Chikungunya epidemic in the Caribbean region. This model sheds light on the design of interventions in the face of the emergence of infections in similar settings of naive subpopulations loosely interconnected by the host.

A Unique Case of Dark Brown Plasma: Why Colour Variation should be Reported.

Afzal N.

Janv-2023

J Coll Physicians Surg Pak.

<https://pubmed.ncbi.nlm.nih.gov/37710942/>

Qdenga® - Schutz vor Dengue-Fieber.

Wedekind S.

Sept-2023

MMW Fortschr Med.

<https://pubmed.ncbi.nlm.nih.gov/37710130/>

Dynamics analysis of a nonlocal diffusion dengue model.

Chang K, Zhang Z, Liang G.

14-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37709860/>

Due to the unrestricted movement of humans over a wide area, it is important to understand how individuals move between non-adjacent locations in space. In this research, we introduce a nonlocal diffusion model for dengue, which is driven by integral operators. First, we use the semigroup theory and continuously Fréchet differentiable to demonstrate the existence, uniqueness, positivity and boundedness of the solution. Next, the global stability and uniform persistence of the system are proved by analyzing the eigenvalue problem of the nonlocal diffusion term. To achieve this, the Lyapunov function is derived and the

comparison principle is applied. Finally, numerical simulations are carried out to validate the results of the theorem, and it is revealed that controlling the disease's spread can be achieved by implementing measures to reduce the transmission of the virus through infected humans and mosquitoes.

Provider Perceptions of Facilitators of and Barriers to Implementation of the Zika Contraception Access Network: A Qualitative Evaluation.

Acosta-Pérez E, Lathrop E, Vega S, Zapata LB, Mendoza Z, Huertas-Pagán X, Hurst S, Powell R, Romero L.
Sept-2023

P R Health Sci J.

<https://pubmed.ncbi.nlm.nih.gov/37709681/>

Reporting delays of chikungunya cases during the 2017 outbreak in Lazio region, Italy.

Manica M, Marini G, Solimini A, Guzzetta G, Poletti P, Scognamiglio P, Virgillito C, Della Torre A, Merler S, Rosà R, Vairo F, Caputo B.
14-09-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37708121/>

Preliminary results on an autochthonous dengue outbreak in Lombardy Region, Italy, August 2023.

Cassaniti I, Ferrari G, Senatore S, Rossetti E, Defilippo F, Maffeo M, Vezzosi L, Campanini G, Sarasini A, Paolucci S, Piralla A, Lelli D, Moreno A, Bonini M, Tirani M, Cerutti L, Paglia S, Regazzetti A, Farioli M, Lavazza A, Faccini M, Rovida F, Cereda D, Baldanti F; Lombardy Dengue network; Lombardy Dengue Network.
Sept-2023

Euro Surveill.

<https://pubmed.ncbi.nlm.nih.gov/37707980/>

In August 2023, six locally acquired dengue virus 1 infections were detected in Lodi province, Lombardy Region, in northern Italy, where the vector *Aedes albopictus* is present. Four cases were hospitalised, none died. The viruses clustered with Peruvian and Brazilian strains collected between 2021 and 2023. This preliminary report highlights the importance of continued integrated surveillance of imported vector-borne virus infections and the potential for tropical disease outbreaks in highly populated regions of northern Italy where competent vectors are present.

ZIKV induction of tristetraprolin in endothelial and Sertoli cells post-transcriptionally inhibits IFN β / λ expression and promotes ZIKV persistence.

Schutt WR, Conde JN, Mladinich MC, Himmler GE, Mackow ER.
14-09-2023

mBio.

<https://pubmed.ncbi.nlm.nih.gov/37707056/>

Zika virus (ZIKV) is a mosquito-borne *Flavivirus* that persistently infects patients; enters protected brain, placental, and testicular compartments; is sexually transmitted; and causes fetal microcephaly *in utero*. ZIKV persistently infects human brain microvascular endothelial cells (hBMECs) that form the blood-brain barrier and Sertoli cells that form testicular barriers, establishing reservoirs that enable viral dissemination. ZIKV persistence requires inhibiting interferon (IFN) responses that direct viral clearance. We found that ZIKV induces IFN β and IFN λ in hBMECs but post-transcriptionally inhibits IFN β /IFN λ expression. IFN β /IFN λ mRNAs contain AU-rich elements (AREs) in their 3' untranslated regions which regulate protein expression through interactions with ARE-binding proteins (ARE-BPs). We found that ZIKV infection of primary hBMECs induces the expression of the ARE-BP tristetraprolin (TTP) and that TTP is a novel regulator of endothelial IFN secretion. In hBMECs, TTP knockout (KO) increased IFN β /IFN λ mRNA abundance and IFN β /IFN λ secretion in response to ZIKV infection and inhibited viral persistence. In contrast, TTP expression dramatically reduced IFN β /IFN λ secretion in hBMECs. IFN β /IFN λ mRNA stability was not significantly altered by TTP and is consistent with TTP inhibition of IFN β /IFN λ translation. TTP is similarly induced by ZIKV infection of Sertoli cells, and like hBMECs, TTP expression or KO inhibited or enhanced IFN β /IFN λ mRNA levels, respectively. These findings reveal a mechanism for ZIKV-induced TTP to promote viral persistence in hBMECs and Sertoli cells by post-transcriptionally regulating IFN β /IFN λ secretion. Our results demonstrate a novel role for virally induced TTP in regulating IFN secretion in barrier cells that normally restrict viral persistence and spread to protected compartments. **IMPORTANCE** Our findings define a novel role for ZIKV-induced TTP expression in regulating IFN β /IFN λ production in primary hBMECs and Sertoli cells. These cells comprise key physiological barriers subverted by ZIKV to access brain and testicular compartments and serve as reservoirs for persistent replication and dissemination. We demonstrate for the first time that the ARE-binding protein TTP is virally induced and post-transcriptionally regulates IFN β /IFN λ secretion. In ZIKV-infected hBMEC and Sertoli cells, TTP knockout increased IFN β /IFN λ secretion, while TTP expression blocked IFN β /IFN λ secretion. The TTP-directed blockade of IFN secretion permits ZIKV spread and persistence in hBMECs and Sertoli cells and may similarly augment ZIKV spread across IFN λ -protected placental barriers. Our work highlights the importance of post-transcriptional ZIKV regulation of IFN expression and secretion in cells that regulate viral access to protected compartments and defines a novel mechanism of ZIKV-regulated IFN responses which may facilitate neurovirulence and sexual transmission.

Molecular Evidence of Wolbachia Species in Wild-Caught *Aedes albopictus* and *Aedes aegypti* Mosquitoes in Four States of Northeast India.

Vinayagam S, Nirmolia T, Chetry S, Kumar NP, Saini P, Bhattacharyya DR, Bhowmick IP, Sattu K, Patgiri SJ.
05-09-2023

J Trop Med.

<https://pubmed.ncbi.nlm.nih.gov/37706052/>

Wolbachia, a Gram-negative intracellular bacterium, naturally infects many arthropods, including mosquito vectors responsible for the spread of arboviral diseases such as Zika, chikungunya, and dengue fever. Certain *Wolbachia* strains are involved in inhibiting arbovirus replication in mosquitoes, and this phenomenon is currently being studied to combat disease vectors. A study was conducted in four states in north-eastern India to investigate the presence of natural *Wolbachia* infection in wild-caught *Aedes albopictus* and *Aedes aegypti* mosquitoes, the established vectors of dengue. The detection of a *Wolbachia* infection was confirmed by nested PCR and sequencing in the two mosquito species *Ae. aegypti* and *Ae. albopictus*. Positivity rates observed in *Ae. aegypti* and *Ae. albopictus* pools were 38% (44 of 115) and 85% (41 of 48), respectively, and the difference was significant (chi-square = 28.3174, $p = 0.00000010$). Sequencing revealed that all detected *Wolbachia* strains belonged to supergroup B. Although *Wolbachia* infection in *Ae. aegypti* has been previously reported from India, no such reports are available from north-eastern India. Data on naturally occurring *Wolbachia* strains are essential for selecting the optimal strain for the development of *Wolbachia*-based control measures. This information will be helpful for the future application of *Wolbachia*-based vector control measures in this part of the country.

Identification of immunodominant T cell epitopes induced by natural Zika virus infection.

Eickhoff CS, Meza KA, Terry FE, Colbert CG, Blazevic A, Gutiérrez AH, Stone ET, Brien JD, Pinto AK, El Sahly HM, Mulligan MJ, Rouphael N, Alcaide ML, Tomashek KM, Focht C, Martin WD, Moise L, De Groot AS, Hoft DF.

29-08-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37705976/>

Evaluation and monitoring of eye findings in children exposed to Zika virus during gestation: 3 years of follow-up.

Dos Santos MLB, Lima LCSS, Zin AA, Moreira MEL, De Vasconcelos ZFM, Neves LMA, Pereira MB, Vianna RAO, Velarde LGC, De Oliveira SA, Riley LW, Cardoso CAA.

07-09-2023

J Trop Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37705261/>

Introduction: Congenital Zika syndrome (CZS) is a recently described disease. Our main objective was to evaluate and monitor, over 3 years, the ophthalmoscopic findings in children exposed to Zika virus (ZIKV) during gestation.

Methods: This prospective observational study was conducted in Rio de Janeiro, Brazil, between April 2016 and May 2019. We evaluated two groups with exanthema serving as a proxy for viremia: (i) children whose mothers had exanthema during pregnancy and (ii) children who had microcephaly without maternal exanthema during pregnancy. We performed indirect ophthalmoscopy at recruitment and every 6 months thereafter. We also

tested the association between ocular findings with maternal exanthema, microcephaly, CZS and maternal infection confirmed by reverse transcriptase quantitative polymerase chain reaction and gender. **Results:** Of the 72 children included, 16 (22.2%) had optic nerve and/or retinal lesions. All 16 had CZS and 15 (93.7%) had microcephaly (14 at birth and 1 postnatally). The child with postnatally acquired microcephaly was born to a mother without exanthema during pregnancy. Fifty-six (77.8%) of the 72 children were followed for a median time of 24 months and none exhibited differences between admission and follow-up examinations. After logistic regression, only microcephaly at birth was associated with eye abnormalities (odds ratio, 77.015; 95% confidence interval, 8.85-670.38; $p < 0.001$). **Conclusion:** We observed that there was no progression of the lesions over the follow-up period. We also showed that the eye findings were associated only with microcephaly at birth. Attention should be paid to all children born during a ZIKV epidemic, regardless of maternal exanthema and/or microcephaly at birth.

The dynamics of deltamethrin resistance evolution in *Aedes albopictus* has an impact on fitness and dengue virus type-2 vectorial capacity.

Guo Y, Hu K, Zhou J, Xie Z, Zhao Y, Zhao S, Gu J, Zhou X, Yan G, James AA, Chen XG.

13-09-2023

BMC Biol.

<https://pubmed.ncbi.nlm.nih.gov/37704988/>

Alzheimer's Disease as A Viral Infectious Disease: Revisiting the Infectious Hypothesis.

Bruno F, Abondio P, Bruno R, Ceraudo L, Pararazzo E, Citrigno L, Luiselli D, Bruni AC, Passarino G, Colao R, Maletta R, Montesanto A.

11-09-2023

Ageing Res Rev.

<https://pubmed.ncbi.nlm.nih.gov/37704050/>

Characterization of pH-induced conformational changes in recombinant DENV NS2B-NS3pro.

Hisamuddin M, Rizvi I, Malik A, Nabi F, Hassan MN, Ali SM, Khan JM, Khan TH, Khan RH.

11-09-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37703975/>

The increasing frequency of Dengue is a cause of severe epidemics and therefore demands strategies for effective prevention, diagnosis, and treatment. DENV-protease is being investigated as a potential therapeutic target. However, due to the flat and highly charged active site of the DENV-protease, designing orthosteric medicines is very difficult. In this study, we have done a thorough analysis of pH-dependent conformational changes in recombinantly expressed DENV protease using various spectroscopic techniques. Our spectroscopic study of DENV protease (NS2B-NS3pro) at different pH conditions

gives important insights into the dynamicity of structural conformation. At physiological pH, the DENV-protease exists in a random-coiled state. Lowering the pH promotes the formation of alpha-helical and beta-sheet structures i.e. gain of secondary structure as shown by Far-UV CD. The light scattering and Thioflavin T (ThT)-binding assay proved the aggregation-prone tendency of DENV-protease at pH 4.0. Further, the confocal microscopy image intensity showed the amorphous aggregate formation of DENV protease at pH 4.0. Thus, the DENV protease acquires different conformations with changes in pH conditions. Together, these results have the potential to facilitate the design of a conformation destabilizer-based therapeutic strategy for dengue fever.

Dengue 1 outbreak in Rosso, northern Senegal, October 2021: entomologic investigations.

Diouf B, Gaye A, Dieng I, Diagne CT, Ndiaye EH, Mhamadi M, Gueye A, Ndiaye O, Sene NM, Sy FA, Faye O, Dia I, Weaver SC, Diallo M, Diallo D.

13-09-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37703355/>

Senegal has experienced periodic epidemics of dengue in urban areas with increased incidence in recent years. However, few data are available on the local ecology of the epidemic vectors. In October 2021, a dengue outbreak was reported in northern Senegal to the Institute Pasteur de Dakar. Entomologic investigations then were undertaken to identify the areas at risk of transmission and to identify the vector(s). Adult mosquitoes were collected indoors and outdoors at selected households, while containers with water were inspected for mosquito larvae. All the *Aedes aegypti* (L.) collected were tested for dengue virus NS1 protein using a rapid diagnostic test (RDT), and positive samples were confirmed by real-time RT-PCR. The qRT-PCR positive samples were subjected to whole genome sequencing using Nanopore technology. The majority of the larvae-positive containers (83.1%) were used for water storage. The Breteau and Container indices exceeded the WHO-recommended thresholds for the risk of dengue virus transmission except at 2 localities. *Ae. aegypti*, the only reputed dengue vector, was collected resting indoors as well as outdoors and biting during the day and night. The NS1 protein was detected in 22 mosquito pools, including one pool of females emerging from field-collected larvae. All NS1-positive results were confirmed by RT-PCR. Virus serotyping showed that the outbreak was caused by DENV-1. This study demonstrates the need for continuous control of adult and aquatic stages of *Ae. aegypti* to prevent future dengue epidemics in Senegal. RDTs appear to be a promising tool for dengue diagnostics and surveillance.

Influence of host genetic polymorphisms involved in immune response and their role in the development of Chikungunya disease: a review.

Gotay WJP, Rodrigues RO, Yaochite JNU.

08-09-2023

Braz J Med Biol Res.

<https://pubmed.ncbi.nlm.nih.gov/37703107/>

Chikungunya virus (CHIKV) is transmitted by the bite of infected mosquitoes and can cause significant pathogenicity in humans. Moreover, its importance has increased in the Americas since 2013. The primary vectors for viral delivery are the mosquito species *Aedes aegypti* and *Aedes albopictus*. Several factors, including host genetic variations and immune response against CHIKV, influence the outcomes of Chikungunya disease. This work aimed to gather information about different single nucleotide polymorphisms (SNPs) in genes that influence the host immune response during an infection by CHIKV. The viral characteristics, disease epidemiology, clinical manifestations, and immune response against CHIKV are also addressed. The main immune molecules related to this arboviral disease elucidated in this review are TLR3/7/8, DC-SIGN, HLA-DRB1/HLA-DQB1, TNF, IL1RN, OAS2/3, and CRP. Advances in knowledge about the genetic basis of the immune response during CHIKV infection are essential for expanding the understanding of disease pathophysiology, providing new genetic markers for prognosis, and identifying molecular targets for the development of new drug treatments.

Dengue virus NS1 secretion is regulated via importin-subunit $\beta 1$ controlling expression of the chaperone GRp78 and targeted by the clinical drug ivermectin.

Denolly S, Guo H, Martens M, Płaszczycza A, Scaturro P, Prasad V, Kongmanas K, Punyadee N, Songjaeng A, Mairiang D, Pichlmair A, Avirutnan P, Bartenschlager R.

13-09-2023

mBio.

<https://pubmed.ncbi.nlm.nih.gov/37702492/>

Prevalence of acute kidney injury among dengue cases: a systematic review and meta-analysis.

Bushi G, Shabil M, Padhi BK, Ahmed M, Pandey P, Satapathy P, Rustagi S, Pradhan KB, Al-Qaim ZH, Sah R.

13-09-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37702193/>

A strategy for entomo-virological surveillance of yellow fever, dengue, zika, and chikungunya viruses in field-collected mosquitoes.

Calderón-Peláez MA, Mantilla-Granados JS, Velandia-Romero ML, Calvo E, Castellanos JE, Olano VA.

01-09-2023

MethodsX.

<https://pubmed.ncbi.nlm.nih.gov/37701736/>

Arboviruses transmitted by Culicidae insects are significant threats to human health, presenting dynamic transmission cycles and involving different vectors and hosts. The surveillance and characterization of the vectors involved in these cycles are crucial for understanding and preventing potential outbreaks. Therefore, we propose a strategy that

we used for entomological surveillance of urban, rural, and sylvatic mosquitoes and to characterize natural infection by four major arboviruses. •Immature and adult mosquitoes were collected intra, peri and extradomicilie of urban and rural households, using different collection methodologies. •Mosquitoes were pooled or separated in head-thorax and abdomen, according to the species. •A multiplex nested RT-PCR (Reverse transcription polymerase chain reaction) method was used for the simultaneous detection of dengue virus (DENV), zika virus (ZIKV), chikungunya virus (CHIKV), and yellow fever virus (YFV). Overall, this strategy proved helpful for vectors surveillance at different ecosystems, as well as for implementing a low-cost molecular surveillance system that allows the early detection of potential outbreaks, and identify other potential vectors involved in viral transmission.

MICROVASCULAR ENDOTHELIAL ACTIVATION/DYSFUNCTION AND DYSREGULATION OF THE ANGIOPOIETIN-TIE₂ SYSTEM IN THE PATHOGENESIS OF LIFE-THREATENING INFECTIONS.

Liles WC.

2023

Trans Am Clin Climatol Assoc.

<https://pubmed.ncbi.nlm.nih.gov/37701588/>

Developing brain under renewed attack: viral infection during pregnancy.

Recaioglu H, Kolk SM.

28-08-2023

Front Neurosci.

<https://pubmed.ncbi.nlm.nih.gov/37700750/>

Octadecadienoate derivatives from *Michelia champaca* seed extract as potential larvicide and pupicide against Dengue vector *Aedes albopictus*.

Dutta M, Chandra G.

12-09-2023

BMC Res Notes.

Development of a plastic waste treatment process by combining deep eutectic solvent (DES) pretreatment and bioaugmentation with a plastic-degrading bacterial consortium.

Krainara S, Mistry AN, Malee C, Chavananikul C, Pinyakong O, Assavalapsakul W, Jitraphai SM, Kachenchart B, Luepromchai E.

07-09-2023

J Hazard Mater.

<https://pubmed.ncbi.nlm.nih.gov/37699265/>

Polyethylene terephthalate (PET), a petroleum-based plastic, and polylactic acid (PLA), a biobased plastic, have a similar visual appearance thus they usually end up in municipal waste treatment facilities. The objective of this project was to develop an effective PET and PLA waste

treatment process that involves pretreatment with deep eutectic solvent (DES) followed by biodegradation with a plastic-degrading bacterial consortium in a composting system. The DES used was a mixture of choline chloride and glycerol, while the bacterial strains (*Chitinophaga jiangningensis* EA02, *Nocardioides zeae* EA12, *Stenotrophomonas pavanii* EA33, *Gordonia desulfuricans* EA63, *Achromobacter xylosoxidans* A9 and *Mycolicibacterium parafortuitum* J101) used to prepare the bacterial consortium were selected based on their ability to biodegrade PET, PLA, and plasticizer. The plastic samples (a PET bottle, PLA cup, and PLA film) were pretreated with DES through a dip-coating method. The DES-coated plastic samples exhibited higher surface wettability and biofilm formation, indicating that DES increases the hydrophilicity of the plastic and facilitates bacterial attachment to the plastic surface. The combined action of DES pretreatment and bioaugmentation with a plastic-degrading bacterial consortium led to improved degradation of PET and PLA samples in various environments, including aqueous media at ambient temperature, lab-scale traditional composting, and pilot-scale composting.

Quantifying the impact of *Wolbachia* releases on dengue infection in Townsville, Australia.

Ogunlade ST, Adekunle AI, Meehan MT, McBryde ES.

11-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37696983/>

Clinical, Virological, and Immunological Features in Cosmopolitan Genotype DENV-2-Infected Patients during a Large Dengue Outbreak in Sri Lanka in 2017.

Nwe KM, Ngwe Tun MM, Muthugala R, Nabeshima T, Balingit JC, Rajamanthri L, Jayawardana D, Attanayake S, Inoue S, Takamatsu Y, Urano T, Morita K.

11-09-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37696512/>

Prenatal Zika virus exposure is associated with lateral geniculate nucleus abnormalities in juvenile rhesus macaques.

Ball EE, Bennett JL, Keesler RI, Van Rompay KKA, Coffey LL, Bliss-Moreau E.

11-09-2023

Neuroreport.

<https://pubmed.ncbi.nlm.nih.gov/37695589/>

The effects of the COVID-19 pandemic on dengue cases in Malaysia.

Md Iderus NH, Singh SSL, Ghazali SM, Zulkifli AA, Ghazali NAM, Lim MC, Ahmad LCRQ, Md Nadzri MN, Tan CV, Md Zamri ASS, Lai CH, Nordin NS, Kamarudin MK, Wan MK, Mokhtar N, Jelip J, Gill BS, Ahmad NAR.

24-08-2023

Background: Globally, the COVID-19 pandemic has affected the transmission dynamics and distribution of dengue. Therefore, this study aims to describe the impact of the COVID-19 pandemic on the geographic and demographic distribution of dengue incidence in Malaysia.

Methods: This study analyzed dengue cases from January 2014 to December 2021 and COVID-19 confirmed cases from January 2020 to December 2021 which was divided into the pre (2014 to 2019) and during COVID-19 pandemic (2020 to 2021) phases. The average annual dengue case incidence for geographical and demographic subgroups were calculated and compared between the pre and during the COVID-19 pandemic phases. In addition, Spearman rank correlation was performed to determine the correlation between weekly dengue and COVID-19 cases during the COVID-19 pandemic phase.

Results: Dengue trends in Malaysia showed a 4-year cyclical trend with dengue case incidence peaking in 2015 and 2019 and subsequently decreasing in the following years. Reductions of 44.0% in average dengue cases during the COVID-19 pandemic compared to the pre-pandemic phase was observed at the national level. Higher dengue cases were reported among males, individuals aged 20-34 years, and Malaysians across both phases. Weekly dengue cases were significantly correlated ($p = -0.901$) with COVID-19 cases during the COVID-19 pandemic.

Conclusion: There was a reduction in dengue incidence during the COVID-19 pandemic compared to the pre-pandemic phase. Significant reductions were observed across all demographic groups except for the older population (>75 years) across the two phases.

The Role of Car Tyres in the Ecology of *Aedes aegypti* Mosquitoes in Ghana.

Abdulai A, Owusu-Asenso CM, Haizel C, Mensah SKE, Sr IK, Mohammed AR, Akuamoah-Boateng Y, Forson AO, Afrane YA.

28-08-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37693506/>

Prior water availability modifies the effect of heavy rainfall on dengue transmission: a time series analysis of passive surveillance data from southern China.

Cheng Q, Jing Q, Collender PA, Head JR, Li Q, Yu H, Li Z, Ju Y, Chen T, Wang P, Cleary E, Lai S.

31-08-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37693392/>

Background Given the rapid geographic spread of dengue and the growing frequency and intensity of heavy rainfall events, it is imperative to understand the relationship between these phenomena in order to propose effective interventions. However, studies exploring the association between heavy rainfall and dengue infection risk have reached conflicting conclusions. **Methods** In this study, we use a distributed lag non-linear model to examine the

association between dengue infection risk and heavy rainfall in Guangzhou, a dengue transmission hotspot in southern China, stratified by prior water availability. **Results** Our findings suggest that the effects of heavy rainfall are likely to be modified by prior water availability. A 24-55 day lagged impact of heavy rainfall was associated with an increase in dengue risk when prior water availability was low, with the greatest incidence rate ratio (IRR) of 1.37 (95% credible interval (CI): 1.02-1.83) occurring at a lag of 27 days. In contrast, a heavy rainfall lag of 7-121 days decreased dengue risk when prior water availability was high, with the lowest IRR of 0.59 (95% CI: 0.43-0.79), occurring at a lag of 45 days. **Conclusions** These findings may help to reconcile the inconsistent conclusions reached by previous studies and improve our understanding of the complex relationship between heavy rainfall and dengue infection risk.

Genomic characterization of dengue virus serotype 2 during dengue outbreak and endemics in Hangzhou, Zhejiang (2017-2019).

Sun H, Yao W, Siddique A, He F, Yue M.

25-08-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37692383/>

Introduction: Dengue fever (DF) is a mosquito-borne viral disease caused by the dengue virus (DENV). In recent years, Hangzhou has undergone a DF epidemic, particularly in 2017, with an outbreak of 1,128 patients. The study aimed to investigate the genetic diversity and molecular evolution among the DF clinical isolates during and after the outbreak to aid in mapping its spread.

Methods: To understand the genetic diversity, 74 DENV-2 strains were isolated from DF epidemic cases between 2017 and 2019. Combining whole genome sequencing (WGS) technology, additional phylogenetic, haplotype, amino acid (AA) substitution, and recombination analyses were performed. **Results:** The results revealed that strains from 2017 were closely related to those from Singapore, Malaysia, and Thailand, indicating an imported international transmission. Local strains from 2018 were clustered with those recovered from 2019 and were closely associated with Guangzhou isolates, suggesting a within-country transmission after the significant outbreak in 2017. Compared to DENV-2 virus P14337 (Thailand/0168/1979), a total of 20 AA substitutions were detected. Notably, V431I, T288I, and K3291T mutations only occurred in indigenous cases from 2017, and A1402T, V1457I, Q2777E, R3189K, and Q3310R mutations were exclusively found in imported cases from 2018 to 2019. The recombination analysis indicated that a total of 14 recombination events were observed. **Conclusion:** This study may improve our understanding of DENV transmission in Hangzhou and provide further insight into DENV-2 transmission and the local vaccine choice.

Blood components requirement in Brazilian dengue outbreaks: A retrospective analysis between 2008 to 2019.

Oliveira DS, Britto DG, de Sá GF, Lima ACNR, Silva JVA, de Araújo AVB, Rebelo RC, Sales LCV, de Abreu MFT, de Meneses ER.

28-08-2023

Hematol Transfus Cell Ther.

<https://pubmed.ncbi.nlm.nih.gov/37690978/>

Chikungunya virus virus-like particle vaccine is well tolerated and immunogenic in chikungunya seropositive individuals.

McCarty JM, Bedell L, Mendy J, Coates EE, Chen GL, Ledgerwood JE, Tredo SR, Warfield KL, Richardson JS.

08-09-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37690874/>

Mathematical model estimation of dengue fever transmission risk from Southeast and South Asia into Japan between 2016 and 2018.

Sakamoto K, Yamauchi T, Kokaze A.

2023

Environ Health Prev Med.

<https://pubmed.ncbi.nlm.nih.gov/37690835/>

Background: Dengue fever is a viral infection transmitted to humans through the bite of a mosquito infected with the dengue virus. Dengue is one of the most common infectious diseases in the world, and its incidence is rapidly increasing. We estimated the risk of dengue importation from endemic countries to Japan and the transmission risk within Japan using data collected between 2016 and 2018.

Methods: We conducted simulations that included the number of reported dengue infections and travelers per month in ten countries in Southeast and South Asia.

Results: The estimated importation risks for Japanese returnees and international travelers from each of the ten endemic countries was approximately 1.0 every month from 2016 to 2018. The autochthonous transmission risk in Japan from any target country was 1.0 from June to September yearly. The estimated number of Japanese dengue cases returning to Japan is approximately 25 times higher than that of imported cases reported in Japan.

Conclusions: The risk of dengue importation into Japan can be sufficiently high. Attention should be paid to autochthonous transmission spread between June and September when mosquitoes are active in Japan. Estimates of seasonal risk variation from each dengue virus-endemic country can be used to inform preventive and control measures for dengue in Japan.

[Four undescribed triterpenes from the aerial parts of *Verbena officinalis*.](#)

Yang JY, Guo CS, Su L, Xu CX, Li RT, Zhong JD.

09-09-2023

Fitoterapia.

Label-free genosensing of dengue serotypes with an electrodeposited

reduced graphene oxide-tris(bipyridine)ruthenium(II).

Kanagavalli P, Andrew C, Anand Babu K, Jayakumar M, Veerapandian M.

07-09-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37689295/>

Constructing a label-free electrochemical transducer platform without compromising inherent biocompatibility against specific bioreceptor remains challenging, particularly probing nucleic acid hybridization at electrode interface without external redox-mediator. Here, we show that electrochemically reduced graphene oxide-tris(bipyridine)ruthenium(II) (ErGO-TBR) nanosheets electrodeposited on carbon screen printed electrode can quantify hybridization of clinically important target sequences specific to serotypes of dengue virus (DENV) non-structural 1 (NS1) protein. Different variables including deposition potential, time, and electrolytic composition were optimized for fabrication of label-free transducer platform. Structural and electrochemical properties of ErGO-TBR/SPE were comprehensively elucidated using microscopic and spectroscopic techniques. Electrochemical quartz crystal microbalance (EQCM) analysis reveals the growth of electrodeposited redox-active species on the electrode interface. Surface functional group investigations suggested that TBR deposited on the basal and edges of ErGO substrate via electrostatic and π - π interactions. Functionalization of bio-affinity layer (B) on ErGO-TBR/SPE enables better loading of probe DNA (PDNA) toward specific detection of DENV target DNA (TDNA) with an ultralow detection limit promising for clinical diagnosis. Scalable chronoamperometry-based redox-active surface growth, customizable bioactivation strategy and external mediator-less probing of nucleic acid hybridization make the present system suitable for other translational application in healthcare diagnosis.

Virucidal activity of trehalose 6-monolaurate against dengue virus in vitro.

Lu JW, Huang CK, Chen YC, Lee GC, Ho YJ.

09-09-2023

Drug Dev Res.

<https://pubmed.ncbi.nlm.nih.gov/37688413/>

Two Sides of The Same Coin: Normal and Tumoral Stem Cells, The Relevance of In Vitro Models and Therapeutic Approaches: The Experience with Zika Virus in Nervous System Development and Glioblastoma Treatment.

Tinnirello R, Chinnici CM, Miceli V, Busà R, Bulati M, Gallo A, Zito G, Conaldi PG, Iannolo G.

31-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37686355/>

Multiple Factors Involved in Bone Damage Caused by Chikungunya Virus Infection.

Avila-Trejo AM, Rodríguez-Páez LI, Alcántara-Farfán V, Aguilar-Faisal JL.

23-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37685893/>

Chronic cases of chikungunya fever represent a public health problem in countries where the virus circulates. The disease is prolonged, in some cases, for years, resulting in disabling pain and bone erosion among other bone and joint problems. As time progresses, tissue damage is persistent, although the virus has not been found in blood or joints. The pathogenesis of these conditions has not been fully explained. Additionally, it has been considered that there are multiple factors that might intervene in the viral pathogenesis of the different conditions that develop. Other mechanisms involved in osteoarthritic diseases of non-viral origin could help explain how damage is produced in chronic conditions. The aim of this review is to analyze the molecular and cellular factors that could be involved in the tissue damage generated by different infectious conditions of the chikungunya virus.

Genetic diversity of *Aedes aegypti* and *Aedes albopictus* from cohabiting fields in Hainan Island and the Leizhou Peninsula, China.

Zhao M, Ran X, Bai Y, Ma Z, Gao J, Xing D, Li C, Guo X, Jian X, Liu W, Liao Y, Chen K, Zhang H, Zhao T.

08-09-2032

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37684698/>

Background: *Aedes aegypti* and *Ae. albopictus* are important human arbovirus vectors that can spread arboviral diseases such as yellow fever, dengue, chikungunya and Zika. These two mosquito species coexist on Hainan Island and the Leizhou Peninsula in China. Over the past 40 years, the distribution of *Ae. albopictus* in these areas has gradually expanded, while *Ae. aegypti* has declined sharply. Monitoring their genetic diversity and diffusion could help to explain the genetic influence behind this phenomenon and became key to controlling the epidemic of arboviruses. **Methods:** To better understand the genetic diversity and differentiation of these two mosquitoes, the possible cohabiting areas on Hainan Island and the Leizhou Peninsula were searched between July and October 2021, and five populations were collected. Respectively nine and 11 microsatellite loci were used for population genetic analysis of *Ae. aegypti* and *Ae. albopictus*. In addition, the mitochondrial *cox1* gene was also selected for analysis of both mosquito species. **Results:** The results showed that the mean diversity index (PIC and SI values) of *Ae. albopictus* (mean PIC = 0.754 and SI = 1.698) was higher than that of *Ae. aegypti* (mean PIC = 0.624 and SI = 1.264). The same results were also observed for the *cox1* gene: the genetic diversity of all populations of *Ae. albopictus* was higher than that of *Ae. aegypti* (total H = 45 and Hd = 0.89958 vs. total H = 23 and Hd = 0.76495, respectively). UPGMA

dendrogram, DAPC and STRUCTURE analyses showed that *Ae. aegypti* populations were divided into three clusters and *Ae. albopictus* populations into two. The Mantel test indicated a significant positive correlation between genetic distance and geographic distance for the *Ae. aegypti* populations ($R^2 = 0.0611$, $P = 0.001$), but the correlation was not significant for *Ae. albopictus* populations ($R^2 = 0.0011$, $P = 0.250$). **Conclusions:** The population genetic diversity of *Ae. albopictus* in Hainan Island and the Leizhou Peninsula was higher than that of *Ae. aegypti*. In terms of future vector control, the most important and effective measure was to control the spread of *Ae. albopictus* and monitor the population genetic dynamics of *Ae. aegypti* on Hainan Island and the Leizhou Peninsula, which could theoretically support the further elimination of *Ae. aegypti* in China.

Zika virus targets human trophoblast stem cells and prevents syncytialization in placental trophoblast organoids.

Wu H, Huang XY, Sun MX, Wang Y, Zhou HY, Tian Y, He B, Li K, Li DY, Wu AP, Wang H, Qin CF.

08-09-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37684223/>

Hepatic damage caused by flaviviruses: A systematic review.

Pinheiro BSS, Rodrigues JG, Dias FCR, de Oliveira Gomes A, de Lucca Moreira Gomes M.

06-09-2023

Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/37683724/>

Flaviviruses infect arthropods and mammals and their pathologies are a considerable global health problem, affecting about 400 million people per year. The symptoms of these flaviviruses range from mild manifestations such as nausea, vomiting, and headache to more serious cases such as hemorrhage, meningitis, microcephaly, kidney, and liver failure. This review aims to compile the morphological changes that occur due to infections caused by dengue, yellow fever, and Zika viruses, as well as to describe possible mechanisms of action of such flaviviruses in the liver. PRISMA guidelines were used to search for studies associating flavivirus with liver disorders. Two independent reviewers selected the studies on PubMed/Medline, Web of Science, and Scopus search platforms. The SYRCL software was used for the evaluation of the study's quality. Eighteen experimental articles were included. The experimental animals often used in experiments were monkeys (5 %), hamsters (10 %), chicken embryos (10 %), and mice (75 %). It is evident that there is a strong hepatic interaction with flaviviruses, and the main hepatic alterations found were steatosis, apoptosis, necrosis, hemorrhage, elevation of ALT and AST levels, and total bilirubin. Flavivirus infection, in general, trigger an upregulation of pro-inflammatory cytokines, leading to structural changes in mitochondria that activate cascades of cellular death and promote insulin resistance. The majority of the studies primarily focus on dengue and yellow fever viruses, while the findings related to Zika virus

exposure are still relatively limited and require further investigation.

Broad-Spectrum Antiviral Effect of Cannabidiol Against Enveloped and Nonenveloped Viruses.

Marquez AB, Vicente J, Castro E, Vota D, Rodríguez-Varela MS, Lanza Castronuovo PA, Fuentes GM, Parise AR, Romorini L, Alvarez DE, Bueno CA, Ramirez CL, Alaimo A, García CC.

08-09-2023

Cannabis Cannabinoid Res.

<https://pubmed.ncbi.nlm.nih.gov/37682578/>

Unhealthy Dietary Patterns and Their Associations with Sociodemographic Factors as Predictors among Underweight and Overweight Adolescents in Southern Thailand.

Kunset P, Punsawad C, Petsirasan R, Suwanbamrung C, Shohaimi S, Narkkul U, Noonil N.

01-09-2023

Int J Environ Res Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37681843/>

Synthesis of copaiba (*Copaifera officinalis*) oil nanoemulsion and the potential against Zika virus: An in vitro study.

Carvalho T, Landim MG, Lima MLD, Bittar C, Faria BCAO, Rahal P, de Lima MCF, Junior VFDV, Joanitti GA, Calmon MF.

07-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37676868/>

Zika virus (ZIKV) has spread all over the world since its major outbreak in 2015. This infection has been recognized as a major global health issue due to the neurological complications related to ZIKV infection, such as Guillain-Barré Syndrome and Zika virus Congenital Syndrome. Currently, there are no vaccines or specific treatments for ZIKV infection, which makes the development of specific therapies for its treatment very important. Several studies have been developed to analyze the potential of compounds against ZIKV, with the aim of finding new promising treatments. Herein, we evaluate the ability of a copaiba (*Copaifera officinalis*) oil nanoemulsion (CNE) to inhibit ZIKV. First, the highest non-cytotoxic concentration of 180 µg/mL was chosen since this concentration maintains 80% cell viability up to 96h after treatment with CNE in VERO cells resulted from MTT assay. The intracellular uptake assay was performed, and confirmed the internalization of the nanoemulsion in cells at all times analyzed. VERO cells were infected with ZIKV and simultaneously treated with CNE and the nanoformulation without oil (ENE) at the highest non-toxic concentration. The results evaluated by plaque assay revealed a viral inhibition of 80% for CNE and 70% for ENE. A dose-dependence assay revealed that the CNE treatment demonstrated a dose-dependent response in the viral RNA levels, whereas all ENE tested concentrations

exhibited a similar degree of reduction. Taken together, our results suggest CNE as a promising nano-sized platform to be further studied for antiviral treatments.

Secondary vectors of Zika Virus, a systematic review of laboratory vector competence studies.

Bisia M, Montenegro-Quinoñez CA, Dambach P, Deckert A, Horstick O, Kolimenakis A, Louis VR, Manrique-Saide P, Michaelakis A, Runge-Ranzinger S, Morrison AC.

31-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37651473/>

Designing Quantum Capacitive Peptide Interfaces for Electroanalytical Applications.

Brandão STR, Dos Santos A, Bueno PR, Cilli EM.

12-09-2023

Anal Chem.

<https://pubmed.ncbi.nlm.nih.gov/37647515/>

DENV-specific IgA contributes protective and non-pathologic function during antibody-dependent enhancement of DENV infection.

Wegman AD, Waldran MJ, Bahr LE, Lu JQ, Baxter KE, Thomas SJ, Waickman AT.

28-08-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37639455/>

Dengue represents a growing public health burden worldwide, accounting for approximately 100 million symptomatic cases and tens of thousands of fatalities yearly. Prior infection with one serotype of dengue virus (DENV) is the greatest known risk factor for severe disease upon secondary infection with a heterologous serotype, a risk which increases as serotypes co-circulate in endemic regions. This disease risk is thought to be mediated by IgG-isotype antibodies raised during a primary infection, which poorly neutralize heterologous DENV serotypes and instead opsonize virions for uptake by FcγR-bearing cells. This antibody-dependent enhancement (ADE) of infection leads to a larger proportion of susceptible cells infected, higher viremia and greater immunopathology. We have previously characterized the induction of a serum IgA response, along with the typical IgM and IgG responses, during dengue infection, and have shown that DENV-reactive IgA can neutralize DENV and competitively antagonize IgG-mediated ADE. Here, we evaluate the potential for IgA itself to cause ADE. We show that IgG, but not IgA, mediated ADE of infection in cells expressing both FcαR and FcγRs. IgG-mediated ADE stimulated significantly higher pro-inflammatory cytokine production by primary human macrophages, while IgA did not affect, or slightly suppressed, this production. Mechanistically, we show that DENV/IgG immune complexes bind susceptible cells significantly more efficiently than DENV/IgA complexes or virus alone. Finally, we show that over the course of primary dengue infection, the expression of FcγRI (CD64) increases during the period of acute viremia, while FcγRIIa

(CD32) and FcαR (CD89) expression decreases, thereby further limiting the ability of IgA to facilitate ADE in the presence of DENV. Overall, these data illustrate the distinct protective role of IgA during ADE of dengue infection and highlight the potential therapeutic and prognostic value of DENV-specific IgA.

Actomyosin-dependent cell contractility orchestrates Zika virus infection.

Huang X, Xing Y, Cui Y, Ji B, Ding B, Zhong J, Jiu Y.

01-09-2023

J Cell Sci.

<https://pubmed.ncbi.nlm.nih.gov/37622381/>

Recombinant protein based on domain III and capsid regions of zika virus induces humoral and cellular immune response in immunocompetent BALB/c mice.

Valdes I, Gil L, Lazo L, Cobas K, Romero Y, Bruno A, Suzarte E, Pérez Y, Cabrales A, Ramos Y, Hermida L, Guillén G.

15-09-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37599141/>

Zika virus infection continues to be a global concern for human health due to the high-risk association of the disease with neurological disorders and microcephaly in newborn. Nowadays, no vaccine or specific antiviral treatment is available, and the development of safe and effective vaccines is yet a challenge. In this study, we obtained a novel subunit vaccine that combines two regions of zika genome, domain III of the envelope and the capsid, in a chimeric protein in *E. coli* bacteria. The recombinant protein was characterized with polyclonal anti-ZIKV and anti-DENV antibodies that corroborate the specificity of the molecule. In addition, the PBMC from zika-immune donors stimulated with the ZEC recombinant antigen showed the capacity to recall the memory T cell response previously generated by the natural infection. The chimeric protein ZEC was able to self-assemble after combination with an immunomodulatory specific oligonucleotide to form aggregates. The inoculation of BALB/c mice with ZEC aggregated and not aggregated form of the protein showed a similar humoral immune response, although the aggregated variant induced more cell-mediated immunity evaluated by *in vitro* IFNγ secretion. In this study, we propose a novel vaccine candidate against the zika disease based on a recombinant protein that can stimulate both arms of the immune system.

Dengue overview: An updated systemic review.

Khan MB, Yang ZS, Lin CY, Hsu MC, Urbina AN, Assavalapsakul W, Wang WH, Chen YH, Wang SF.

Oct-2023

J Infect Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37595484/>

Dengue is caused by the dengue virus (DENVs) infection and clinical manifestations include dengue fever (DF), dengue hemorrhagic fever (DHF), or dengue shock syndrome (DSS). Due to a lack of antiviral drugs and effective vaccines, several therapeutic and control strategies have been proposed. A systemic literature review was conducted according to PRISMA guidelines to select proper references to give an overview of DENV infection. Results indicate that understanding the virus characteristics and epidemiology are essential to gain the basic and clinical knowledge as well as dengue disseminated pattern and status. Different factors and mechanisms are thought to be involved in the presentation of DHF and DSS, including antibody-dependent enhancement, immune dysregulation, viral virulence, host genetic susceptibility, and preexisting dengue antibodies. This study suggests that dissecting pathogenesis and risk factors as well as developing different types of therapeutic and control strategies against DENV infection are urgently needed.

Tropism and immune response of chikungunya and zika viruses: An overview.

Ravindran S, Lahon A.

Oct-2023

Cytokine.

<https://pubmed.ncbi.nlm.nih.gov/37579710/>

Craniofacial and dental features in children aged 3-5 years with congenital Zika syndrome.

Díaz C, Aragón N, Lopez-Medina E, Arango MC, Dávalos D, Contreras-Rengifo A.

Sept-2023

Clin Oral Investig.

<https://pubmed.ncbi.nlm.nih.gov/37578656/>

Objective: Zika virus infection has been associated to congenital zika syndrome (CZS) in newborns and is characterized by microcephaly, central/axial motor and sensory dysfunction, dysphagia among other previously described severe health complications. CZS is usually diagnosed postpartum by evident/apparent neural development problems. Although there are some reports of craniofacial/dentition development in CZS, several clinical oral aspects are still unknown. This study describes some structural and functional characteristics of facial and cranial growth and deciduous dentition in CZS-affected children. **Material and methods:** Some cranial, facial and dental characteristics were determined in 14 children with CZS aged 3-5 years and compared them against 12 apparently healthy children paired by age and gender. **Results:** Fourteen CZS cases presented microcephaly, maxillary prognathism, altered facial thirds, asymmetric pupillary line, bruxism ($p = 0.006$), deep and anterior open bite and distal step deciduous molar relationship ($p = 0.031$). CZS children cannot feed by themselves and most cannot walk and have not develop coordinated and intelligible language according to their chronological age. In contrast, controls presented normal skull features, have autonomous locomotion skills, speak intelligible language,

feed by themselves, presented a harmonic intermaxillary relationship and have symmetrical facial thirds.

Conclusion: Microcephaly, dysphagia, bruxism, mandibular retrognathia, altered facial proportions and malocclusion are the main craniofacial and oral features at CZS. **Clinical relevance:** The complications of CZS including those related with the face and the oral cavity are still being identified. This study revealed some cranial, facial and oral features in children affected by CSZ. Interdisciplinary rehabilitation protocols must address these syndromic features that could improve children and parents living conditions.

Associating biological context with protein-protein interactions through text mining at PubMed scale.

Sosa DN, Hintzen R, Xiong B, de Giorgio A, Fauqueur J, Davies M, Lever J, Altman RB.

Sept-2023

J Biomed Inform.

<https://pubmed.ncbi.nlm.nih.gov/37572825/>

Inferring knowledge from known relationships between drugs, proteins, genes, and diseases has great potential for clinical impact, such as predicting which existing drugs could be repurposed to treat rare diseases. Incorporating key biological context such as cell type or tissue of action into representations of extracted biomedical knowledge is essential for principled pharmacological discovery. Existing global, literature-derived knowledge graphs of interactions between drugs, proteins, genes, and diseases lack this essential information. In this study, we frame the task of associating biological context with protein-protein interactions extracted from text as a classification task using syntactic, semantic, and novel meta-discourse features. We introduce the Insider corpora, which are automatically generated PubMed-scale corpora for training classifiers for the context association task. These corpora are created by searching for precise syntactic cues of cell type and tissue relevancy to extracted regulatory relations. We report F1 scores of 0.955 and 0.862 for identifying relevant cell types and tissues, respectively, for our identified relations. By classifying with this framework, we demonstrate that the problem of context association can be addressed using intuitive, interpretable features. We demonstrate the potential of this approach to enrich text-derived knowledge bases with biological detail by incorporating cell type context into a protein-protein network for dengue fever.

Northeast Regional Center for Excellence in Vector-Borne Diseases' Master of Science training program: a curriculum to support future capacity in public health entomology.

Harrington LC, Mader EM.

12-09-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37531091/>

A major lack of expertise in vector biology, surveillance, and control for public health professionals has been acknowledged over the past several decades, especially in

light of the introduction of West Nile and Zika viruses to the United States. To address this growing need, the Northeast Regional Center for Excellence in Vector-Borne Diseases (NEVBD) designed a unique educational program to cross-train students in the fundamentals of vector biology and public health. Here, we summarize the formation, evaluation, and outcomes of NEVBD's Master of Science in Entomology: Vector-Borne Disease Biology program and provide details on core competencies to enable adoption and adaptation of the program to other institutions and contexts. A discussion of major barriers to filling the nation's need for public health personnel with medical entomology training, such as financial barriers and recruitment of underrepresented students, is presented. We conclude with considerations for administering these training programs.

The Viral Protein K7 Inhibits Biochemical Activities and Condensate Formation by the DEAD-box Helicase DDX3X.

Venus S, Tandjigora K, Jankowsky E.

01-10-2023

J Mol Biol.

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

Importation of a novel Indian Ocean lineage carrying E1-K211E and E2-V264A of Chikungunya Virus in Zhejiang Province, China, in 2019.

Su L, Lou X, Yan H, Yang Z, Mao H, Yao W, Sun Y, Pan J, Zhang Y.

Oc-2023

Virus Genes.

<https://pubmed.ncbi.nlm.nih.gov/37468826/>

Neurodevelopmental outcomes in congenital and perinatal infections.

Fortin O, Mulkey SB.

01-10-2023

Curr Opin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37466092/>

Purpose of review: Congenital infections are a major cause of childhood multidomain neurodevelopmental disabilities. They contribute to a range of structural brain abnormalities that can cause severe neurodevelopmental impairment, cerebral palsy, epilepsy, and neurosensory impairments. New congenital infections and global viral pandemics have emerged, with some affecting the developing brain and causing neurodevelopmental concerns. This review aims to provide current understanding of fetal infections and their impact on neurodevelopment. **Recent findings:** There are a growing list of congenital infections causing neurodevelopmental issues, including cytomegalovirus, Zika virus, syphilis, rubella, lymphocytic choriomeningitis virus, and toxoplasmosis. Fetal exposure to maternal SARS-CoV-2 may also pose risk to the developing brain and impact neurodevelopmental outcomes, although studies have conflicting results. As Zika virus was a recently identified congenital infection, there are several new reports on

child neurodevelopment in the Caribbean and Central and South America. For many congenital infections, children with in-utero exposure, even if asymptomatic at birth, may have neurodevelopmental concerns manifest over time. **Summary:** Congenital infections should be considered in the differential diagnosis of a child with neurodevelopmental impairments. Detailed pregnancy history, exposure risk, and testing should guide diagnosis and multidisciplinary evaluation. Children with congenital infections should have long-term follow-up to assess for neurodevelopmental delays and other neurosensory impairments. Children with confirmed delays or high-risk should be referred for rehabilitation therapies.

African ZIKV lineage fails to sustain infectivity in an in vitro mimetic urban cycle.

Molina BF, Marques NN, Bittar C, Batista MN, Rahal P.
Sept-2023

Braz J Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37458982/>

Zika virus (ZIKV) is an arbovirus maintained in nature in two distinct cycles of transmission: urban and sylvatic. Each cycle includes specific vertebrate and invertebrate hosts, and through alternate infections, a conserved consensus sequence is maintained that might vary depending on the cycle. The current study aimed to investigate the ability of ZIKV^{AF} and ZIKV^{BR} to maintain an infectious cycle by alternating passages in cells mimicking the urban (UC) and semi-sylvatic (SC) cycles. The complete genome of the original inoculum and the last passages for each cycle were sequenced by Sanger. Ten passages were performed, as planned, for ZIKV^{BR} UC, ZIKV^{AF} SC, and ZIKV^{BR} SC. ZIKV^{BR} SC showed significant variation in viral titers along the passages, suggesting that the virus is not well adapted to the non-human primate host. ZIKV^{AF} passage in UC was abrogated in the third passage, showing the inability of the African lineage to sustain cycles in human cells, suggesting a low capacity to establish an urban cycle. Several mutations were found in both strains along the passages, but not occurring at equivalent positions. Further studies are needed to elucidate whether any of these specific mutations affect viral fitness. ZIKV strains behave differently in artificial transmission cycles in vitro: Brazilian ZIKV was able to establish urban and semi-sylvatic cycles in vitro. African ZIKV proved unable to cycle among human and mosquito cells and is compatible only with the semi-sylvatic cycle. The main mutations arose in the NS2A region after artificial transmission cycles for both ZIKV strains but not at equivalent positions.

Seroprevalence of Dengue, Chikungunya, and Zika viruses antibodies in a cohort of asymptomatic pregnant women in a low-income region of Minas Gerais, Brazil, 2018-2019.

Santos JD, Garcia BCC, Rocha KLS, Silva TJ, da Silva Lage SL, de Souza Macedo M, Teixeira RA, Rocha-Vieira E, de Oliveira DB.

Sept-2023

Braz J Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37454038/>

New human in vitro co-culture model of keratinocytes and sensory neurons like cells releasing substance P with an evaluation of the expression of ZIKV entry receptors: A potent opportunity to test Zika virus entry and to study Zika virus' infection in neurons?

Bocciarelli C, Cordel N, Leschiera R, Talagas M, Le Gall-ianotto C, Hu W, Marcorelles P, Bellemere G, Bredif S, Fluhr J, Misery L, Lebonvallet N.

Sept-2023

Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37395585/>

During the course of acute ZIKV infection, pruritus is a cardinal symptom widely documented in the literature. Its frequent association with dysesthesia and several dysautonomic manifestations, suggests a pathophysiological mechanism involving the peripheral nervous system. The aim of this study was to develop a functional human model to potentially able to be infected by ZIKV: by demonstrating the functionality on a new human model of co-culture of keratinocyte and sensory neuron derived from induced pluripotent stem cells using a classical method of capsaicin induction and SP release, and verify the presence of ZIKV entry receptor in these cells. Depending of cellular type, receptors of the TAMs family, TIMs (TIM1, TIM3 and TIM4) and DC-SIGN and RIG1 were present/detected. The cells incubations with capsaicin resulted in an increase of the substance P. Hence, this study demonstrated the possibility to obtain co-cultures of human keratinocytes and human sensory neurons that release substance P in the same way than previously published in animal models which can be used as a model of neurogenic skin inflammation. The demonstration of the expression of ZIKV entry receptors in these cells allows to considerate the potent possibility that ZIKV is able to infect cells.

Zika virus infection induces expression of NRF2 and antioxidant systems in trophoblast cells.

Cervantes MAV, Martinez JAV, García LDG, Ortega OL, Romero HA, Estrada AM, Castillo MM, Pliego AF, Reyes GL, Repetto ACH, Cordero JG, Juárez ML.

Oct-2023

Virus Genes.

<https://pubmed.ncbi.nlm.nih.gov/37326824/>

Role of N-acetylcysteine in liver injury due to dengue fever.

Gupta M, Gupta S, Sood D, Gupta A, Jesrani G.

Oct-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37312532/>

Dengue fever (DF) is a common mosquito-borne viral infection which is endemic in Southeast Asia. Liver involvement may vary from asymptomatic elevation of liver enzymes to fulminant hepatitis. Although the

valuable effects of N-acetylcysteine (NAC) in paracetamol toxicity and non-paracetamol liver failure have been extensively studied, its use in DF-associated hepatitis remains unclear. We made a literature search in an online format from libraries such as PubMed, Google Scholar, and EMBASE, and selected 33 articles including original research articles, case reports, and systemic analyses. The majority of the articles reviewed had a positive outcome but treatment strategies involved NAC together with supportive care. Hence, data on sole use of NAC from large randomised control trials remain unclear.

Uncovering the mosaic of emerging infections: The threat of Japanese encephalitis virus in Pakistan.

Manan MR, Nawaz I, Zafar F.

Oct-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37278007/>

Infectious Causes of Acute Encephalitis Syndrome in India - Decadal Change and the Way Forward.

Tandale BV, Narang R, Vijay Kumar G, Jain M, Tomar SJ, Deshmukh PS.

15-09-2023

Indian Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37260063/>

Genetic differences of dengue virus 2 in patients with distinct clinical outcome.

de Carvalho Marques B, Sacchetto L, Banho CA, Estofolete CF, Dourado FS, da Silva Cândido D, Dutra KR, da Silva Salles FC, de Jesus JG, Sabino EC, Faria NR, Nogueira ML.

Sept-2023

Braz J Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37178262/>

The genetic diversity of the dengue virus is characterized by four circulating serotypes, several genotypes, and an increasing number of existing lineages that may have differences in the potential to cause epidemics and disease severity. Accurate identification of the genetic variability of the virus is essential to identify lineages responsible for an epidemic and understanding the processes of virus spread and virulence. Here, we characterize, using portable nanopore genomic sequencing, different lineages of dengue virus 2 (DENV-2) detected in 22 serum samples from patients with and without dengue warning signs attended at Hospital de Base of São José do Rio Preto (SJRP) in 2019, during a DENV-2 outbreak. Demographic, epidemiological, and clinical data were also analyzed. The phylogenetic reconstruction and the clinical data showed that two lineages belonging to the American/Asian genotype of DENV-2-BR3 and BR4 (BR4L1 and BR4L2)-were co-circulating in SJRP. Although preliminary, these results indicate no specific association between clinical form and phylogenetic clustering at the virus consensus sequence level. Studies with larger sample sizes and which explore single nucleotide variants are needed. Therefore, we

showed that portable nanopore genome sequencing could generate quick and reliable sequences for genomic surveillance to monitor viral diversity and its association with disease severity as an epidemic unfolds.

Building an Infectious Disease Diversity, Equity, and Antiracism (ID2EA) Curriculum: A Single Center's Experience and Reflections.

Gleeson SE, Zapata H, Bathgate ME, Emu B, Frederick J, Friedland G, Golden MP, Meyer JP, Radin J, Sideleau R, Shaw A, Sheno SV, Trubin PA, Virata M, Barakat LA, Desruisseaux MS.

11-09-2023

Clin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37078888/>

Dracunculose

Implementation of water hyacinth (*Eichhornia crassipes*) and water lettuce (*Pistia stratiotes*) in the re-treatment of conventionally treated pharmaceutical wastewater: a case study of Radiant Pharmaceuticals Limited, Dhaka, Bangladesh.

Das EJ, Bhuiyan MAR, Hasan MM.

14-09-2023

Environ Monit Assess.

<https://pubmed.ncbi.nlm.nih.gov/37707630/>

Evaluation and phenotypic plasticity of taro [*Colocasia esculenta* (L.) Schott.] genotypes for nutrient and anti-nutrient composition.

Donkor EF, Nyadanu D, Akromah R, Osei K, Odoom DA.

PLoS One. 2023 Sep 13;

<https://pubmed.ncbi.nlm.nih.gov/37703222/>

The study was carried out to determine the nutritional and anti-nutritional composition of taro genotypes and also determine the phenotypic plasticity of the genotypes in two agro ecological zones in Ghana. The towns and zones were Bunso in the semi deciduous forest (an upland) and Tano Dumasi in the forest savannah transition agro-ecological (a waterlogged area) zone in the Eastern and Ashanti regions respectively. Two (2) freshly harvested corms of each genotype from each location were assessed for their nutritional (moisture, protein, carbohydrate, ash and fat) and anti-nutritional (phytate, oxalate and tannin) composition. Data collected were subjected to analysis of variance and AMMI analysis using GenStat 12 edition to assess the effect of genotype, environment and their interaction on the traits studied. Phenotypic plasticity for the genotypes and the traits studied was also calculated. Pearson correlation was also conducted to assess the relationship between the traits studied. There were significant differences among the genotypes for nutrient and anti-nutrient composition except for percentage fat, indicating enough genetic variability among the genotypes, giving room for good selection progress for

development of taro varieties. A higher magnitude of the environment over genotype and genotype by environment interaction observed indicates the influence of environment in the expression of the nutritional and anti-nutritional traits. Observed varied phenotypic plasticity among the genotypes for the nutrient and anti-nutrients composition also indicates varied adaptation of the genotypes to the environment. Genotypes BL/SM/115, CE/MAL/32 and CE/IND/16 and hybrids KAO19 × CE/MAL/32 and CE/IND/16 × KAO19, CE/IND/16 × BL/SM/10, and CE/IND/16 × BL/SM/115 which recorded high nutrients and low anti-nutrients content and were stable across the environments can be released to farmers for cultivation. They could also be included in breeding programs for the development of enhanced nutritional quality of taro in Ghana.

Potential of Predatory Bacteria to Colonize the Duckweed Microbiome and Change Its Structure: A Model Study Using the Obligate Predatory Bacterium, *Bacteriovorax* sp. HI3.

Inoue D, Nakamura S, Sugiyama T, Ike M.

2023

Microbes Environ.

<https://pubmed.ncbi.nlm.nih.gov/37690850/>

Chromosome level genome assembly of colored calla lily (*Zantedeschia elliottiana*).

Wang Y, Yang T, Wang D, Gou R, Jiang Y, Zhang G, Zheng Y, Gao D, Chen L, Zhang X, Wei Z.

09-09-2023

Sci Data.

<https://pubmed.ncbi.nlm.nih.gov/37689767/>

Extract of *Artemisia dracunculus* L. Modulates Osteoblast Proliferation and Mineralization.

Scott MC, Bourgeois A, Yu Y, Burk DH, Smith BJ, Floyd ZE.

30-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37686232/>

Thiazolidinediones (TZD) significantly improve insulin sensitivity via action on adipocytes. Unfortunately, TZDs also degrade bone by inhibiting osteoblasts. An extract of *Artemisia dracunculus* L., termed PMI5011, improves blood glucose and insulin sensitivity via skeletal muscle, rather than fat, and may therefore spare bone. Here, we examine the effects of PMI5011 and an identified active compound within PMI5011 (2',4'-dihydroxy-4-methoxydihydrochalcone, DMC-2) on pre-osteoblasts. We hypothesized that PMI5011 and DMC-2 will not inhibit osteogenesis. To test our hypothesis, MC3T3-E1 cells were induced in osteogenic media with and without PMI5011 or DMC-2. Cell lysates were probed for osteogenic gene expression and protein content and were stained for osteogenic endpoints. Neither compound had an effect on early stain outcomes for alkaline phosphatase or collagen. Contrary to our hypothesis, PMI5011 at 30 µg/mL significantly increases osteogenic gene expression as early

as day 1. Further, osteogenic proteins and cell culture mineralization trend higher for PMI5011-treated wells. Treatment with DMC-2 at 1 µg/mL similarly increased osteogenic gene expression and significantly increased mineralization, although protein content did not trend higher. Our data suggest that PMI5011 and DMC-2 have the potential to promote bone health via improved osteoblast maturation and activity.

Anti-Inflammatory Effects of *Spirodela polyrhiza* (L.) SCHLEID. Extract on Contact Dermatitis in Mice-Its Active Compounds and Molecular Targets.

Kim K, Lee D, Kim HY, Kim S, Lyu JH, Park S, Park YC, Kim H.

26-08-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37686078/>

Spirodela polyrhiza (L.) SCHLEID. has been used to treat epidemic fever, dysuria, and various skin ailments, such as measles eruptions, eczema, and pruritus, in China, Japan, and Korea. In this study, the active compounds in *S. polyrhiza* and their target genes were identified by network-based analysis. Moreover, the study evaluated the effects of a 70% ethanolic extract of *S. polyrhiza* (EESP) on skin lesions, histopathological changes, inflammatory cytokines, and chemokines in mice with contact dermatitis (CD) induced by 1-fluoro-2,4-dinitrobenzene (DNFB), and examined the inhibitory effects of EESP on mitogen-activated protein kinase (MAPK) signalling pathways. In our results, 14 active compounds and 29 CD-related target genes were identified. Among them, tumour necrosis factor (TNF) and interleukin 6 (IL-6) were identified as hub genes, and luteolin and apigenin showed a strong binding affinity with TNF (<-8 kcal/mol) and IL-6 (<-6 kcal/mol). Our in vivo studies showed that topical EESP ameliorated DNFB-induced skin lesions and histopathological abnormalities, and reduced the levels of TNF-α, interferon (IFN)-γ, IL-6, and monocyte chemotactic protein (MCP)-1 in inflamed tissues. In conclusion, our findings suggest the potential for dermatological applications of *S. polyrhiza* and suggest that its anti-dermatitis action is related to the inhibition of TNF and IL-6 by luteolin and luteolin glycosides.

Ethnobotanical study on medicinal plants used by Bulang people in Yunnan, China.

Zhou H, Zhang J, Kirbis BS, Mula Z, Zhang W, Kuang Y, Huang Q, Yin L.

07-09-2023

J Ethnobiol Ethnomed.

<https://pubmed.ncbi.nlm.nih.gov/37679773/>

Pharmaceutical-contaminated irrigation water: implications for ornamental plant production and phytoremediation using enrofloxacin-accumulating species.

Rocha CS, Kochi LY, Brito JCM, Kitamura RSA, Carneiro DM, Dos Reis MV, Gomes MP.

Sept-2023

Drop impact dynamics on the hydrophobic leaf surface of an aquatic plant: a case study of *Pistia stratiotes*.

Papierowska E, Beczek M, Mazur R, Szatyłowicz J, Szewińska J, Polakowski C, Ryżak M, Stańczyk T, Sochan A, Frankowska-Łukawska J, Bieganski A.

13-09-2023

J Exp Bot.

<https://pubmed.ncbi.nlm.nih.gov/37249250/>

Pistia stratiotes is an aquatic plant with a complex structure that allows it to stay afloat. It grows quickly, and in large numbers becomes an undesirable plant as an invasive species. Describing the dynamics of a water drop splash on *P. stratiotes* leaves can contribute to increasing knowledge of its behavior and finding alternative methods for eradicating it or using it for the benefit of the environment. The non-wettable surface of *P. stratiotes* presents a complex structure-simple uniseriate trichomes and also ridges and veins. We analyzed the drop impact on a leaf placed on the water surface and recorded it by high-speed cameras. Based on the recordings, quantitative and qualitative analyses were performed. After impacting the leaf, the water drop spread until it reached its maximum surface area accompanied by the ejection of early droplets in the initial stage. Thereafter, three scenarios of water behavior were observed: (i) drop receding and stabilization; (ii) drop receding and ejection of late droplets formed in the later stage as an effect of elastic deformation of the leaf; and (iii) drop breaking apart and ejection of late droplets. The results indicated that the increasing kinetic energy of the impacting drops expressed by the Weber number and the complex leaf surface have an effect on the course of the splash. The simple uniseriate trichomes of the *P. stratiotes* leaf and the high energy of the falling drops were responsible for the formation and characteristics of the early droplets. The presence of ridges and veins and the leaf's mechanical response had an impact on the occurrence of late droplets.

Echinococcosis

Cardiac hydatid disease; a systematic review.

Banisehid E, Baghernezhad K, Beheshti R, Hamzehzadeh S, Nemati S, Samadifar Z, Owaysee Osque H, Javanshir E, Naseri A.

13-09-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37705012/>

microRNA silencing in a whole worm cestode model provides insight into miR-71 function.

Grecco A, Macchiaroli N, Pérez M, Casulli A, Cucher M, Cecilia Rosenzvit M.

10-09-2023

Int J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37699506/>

Parasites belonging to the class Cestoda include zoonotic species such as *Echinococcus* spp. and *Taenia* spp. that cause morbidity and mortality in endemic areas, mainly affecting pastoral and rural communities in low income countries but also upper middle income countries. Cestodes show remarkable developmental plasticity, implying tight regulation of gene expression throughout their complex life cycles. Despite the recent availability of genomic data for cestodes, little progress was made on postgenomic functional studies. MicroRNAs (miRNAs) are key components of gene regulatory systems that guide diverse developmental processes in multicellular organisms. miR-71 is a highly expressed miRNA in cestodes, which is absent in vertebrates and targets essential parasite genes, representing a potential key player in understanding the role of miRNA in cestodes biology. Here we used transfection with antisense oligonucleotides to perform whole worm miRNA knockdown in tetrathyridia of *Mesocestoides vogae*, a laboratory model of cestodes. We believe this is the first report of miRNA knockdown at the organism level in these parasites. Our results showed that *M. vogae* miR-71 is involved in the control of strobilation in vitro and the establishment of murine infection. In addition, we identified miR-71 targets in *M. vogae*, several of them being de-repressed upon miR-71 knockdown. This study provides new knowledge on gene expression regulation in cestodes and suggests that miRNAs could be evaluated as new selective therapeutic targets for treating Neglected Tropical Diseases prioritised by the World Health Organization.

Echinococcus granulosus cyst fluid inhibits inflammatory responses through inducing histone demethylase KDM5B in macrophages.

Wang X, Lin R, Fu C, Yang C, Dong D, Wu X, Chen X, Wang L, Hou J.

09-09-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37689671/>

Background: *Echinococcus granulosus* cyst fluid (EgCF) weakens macrophage inflammatory responses, thereby enabling the parasite to evade the immune system. However, the role of histone modification in this process remains to be explored. **Methods:** The levels of IL-6, TNF- α , IL-10, H3K4me3, and KDM5B were detected using quantitative real-time PCR, ELISA, and Western blotting. The enrichment of H3K4me3 and KDM5B at the promoter of inflammatory factors was detected by chromatin immunoprecipitation. **Results:** Based on EgCF-stimulated macrophage models, we found that EgCF significantly inhibited mRNA expression and protein secretion of IL-6 and TNF- α and upregulated mRNA expression of IL-10 under the influence of TLR4. EgCF lowered the level of H3K4me3 and promoted the transcription and protein stability of histone demethylase KDM5B. Chromatin immunoprecipitation analysis revealed that EgCF suppressed the enrichment of H3K4me3 modification at the promoters of TNF- α and IL-6 and downregulated their expression in macrophages. Additionally, the inhibition of KDM5B activity by CPI-455 weakened the anti-

inflammatory effect of EgCF. **Conclusions:** Our findings demonstrate a novel mechanism through which EgCF promotes KDM5B expression and inhibits the enrichment of H3K4me3 at the promoters of inflammatory cytokines to suppress the inflammatory response.

Modeling and analysis of the transmission dynamics of cystic echinococcosis: Effects of increasing the number of sheep.

He Y, Cui Q, Hu Z.

05-07-2023

Math Biosci Eng.

<https://pubmed.ncbi.nlm.nih.gov/37679150/>

Watch-and-wait approach for inactive echinococcal cysts: scoping review update since the issue of the WHO-IWGE Expert Consensus and current perspectives.

Brunetti E, Tamarozzi F.

01-10-2023

Curr Opin Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37466115/>

Purpose of review: This work aims to provide an update of knowledge on the evolution of inactive cystic echinococcosis (CE) cysts (CE4-CE5) managed by 'watch-and-wait', by means of a scoping review of the literature published after the publication of the WHO-IWGE (Informal Working Group on Echinococcosis) Expert Consensus document in 2010. **Recent findings:** A total of 31 articles were included. Population ultrasound-based studies showed that spontaneously inactivated CE cysts represent 50.2% (95% confidence interval 38.7-61.8) of all detected untreated CE cysts, and that the prevalence of CE4-CE5 cysts tends to increase with age. Four longitudinal population-based studies showed that CE cysts naturally tend to evolve towards inactivation and that spontaneously inactivated cysts reactivate in a minority of cases. This was confirmed by four hospital-based studies, showing that spontaneously inactivated cysts reactivate rarely, while rate of reactivation is higher if inactivity was obtained posttreatment. It was not possible to draw conclusions on any difference in the clinical course of infection in immunocompromised or pregnant patients.

Summary: CE cysts tend to evolve spontaneously to inactivation over time. The published literature supports the safety of the watch-and-wait approach for inactive cysts, sparing treatment to a substantial proportion of asymptomatic patients. A regular follow-up with ultrasound of all inactive cysts is required to detect reactivations.

Filariose lymphatique

Coverage of preventive measures and surveillance for neglected tropical diseases in hard-to-reach communities in Ghana.

Forson AO, Awuah RB, Mohammed AR, Owusu-Asenso CM, Akosah-Brempong G, Abdulai A, Sraku IK, Dhikrullahi SB, Atakora SB, Attah SK, Afrane YA.

14-09-2023

BMC Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37710219/>

Integrated Prevalence Assessment of Wuchereria bancrofti and Onchocerca volvulus in Three Co-Endemic Districts of Gambella Region, Ethiopia.

Hassen M, Mohammed A, Endeshaw T, Seid T, Samuel F, Asmare T, Birhanu H, Bekele F, Yayeh A, Seife F, Tamiru M, Meribo K, Tadesse Z, Griswold E, Katabarwa M, Richards F, Noland GS.

11-09-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37696513/>

Lymphatic filariasis (LF) and onchocerciasis (OV) are among the neglected tropical diseases (NTD) targeted for elimination in Ethiopia. We used a transmission assessment survey (TAS-1) to evaluate the serological status of OV in three co-endemic districts in Gambella simultaneously. During May and June 2019, blood samples were collected from 6- to 7-year-old children who were randomly selected through standard community-based TAS methodology. Children were tested for both circulating filarial antigen (CFA) for LF via filariasis test strip and for *Onchocerca volvulus* 16 (Ov16) antibody for OV via laboratory-based ELISA. A total of 3,377 children from 150 villages in the three districts were tested; 1,823 (54.0%) were male. All three districts had CFA results below the critical threshold for stopping LF mass drug administration (MDA). In contrast, 40 children (1.2%) were positive for Ov16 antibody, well above the WHO's OV stop MDA threshold of 0.1%. The integrated assessment indicated two programmatic decisions: stop MDA for LF and continue MDA for OV. Accordingly, albendazole MDA was discontinued in the districts but ivermectin MDA continued. This integrated assessment showed that a random sample for TAS can give important information about OV transmission status in co-endemic areas.

Coverage evaluation of mass drug administration with triple drug regimen in an evaluation unit in Nagpur district of Maharashtra, India.

Dinesh RJ, Srividya A, Subramanian S, Krishnamoorthy K, Sabesan S, Raghorte MC, Kumar A, Jambulingam P.

07-09-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37676897/>

Background: Triple drug regimen (IDA; Ivermectin, Diethylcarbamazine, Albendazole) recommended for accelerating elimination of lymphatic filariasis was launched in India in December 2018. Nagpur district in Maharashtra was one of the first five districts where this strategy was introduced. The National Vector Borne Disease Control Programme (NVBDCP) at the district reported ~85.0% treatment coverage in the first round of mass drug administration (MDA) with IDA implemented in

EU-2 in Nagpur district in January 2019. As per the national guideline, a coverage evaluation survey was carried out and both quantitative and qualitative data were collected to assess the treatment coverage, the level of community preparation and identify the gaps, if any, for improvement.

Methodology: A Coverage Evaluation Survey (CES) following the WHO recommended protocol was conducted in one of the two evaluation units (EU-2) in Nagpur district in March 2019. Coverage Sample Builder (CSB) V2.9 tool was used to calculate the sample size, select sites and estimate drug coverage. The CSB tool followed a two-stage cluster sampling procedure to select 30 primary sampling units (ward/village as a cluster) and a list of random numbers for selecting households (HHs) in each cluster. The results were analyzed for operational indicators. Stata ver. 14.0 software was used to construct the 95% confidence limits accounting for clustering.

Results: A total of 1601 individuals aged 5-85 years of both gender from 328 HHs were surveyed from the 30 randomly selected clusters in EU-2. The mean age was 33.8±17.6 years. Among the surveyed population, 78.0% received the drugs (programme reach) and 66.1% consumed the drugs (survey coverage). Survey coverage was significantly higher in rural (82.6%) than in urban (59.4%) and peri-urban (58.6%) areas ($P<0.001$). Directly observed treatment (DOT) among the surveyed population was 51.6%. Adverse events were reported among 6.9% respondents who reported to have consumed the drugs. **Conclusion:** The IDA based MDA strategy could achieve just the required level of treatment coverage (~65%) in EU-2, Nagpur district, which had previously undergone several rounds of DA-MDAs (Diethylcarbamazine, Albendazole). Having achieved an effective treatment coverage of >80% in rural areas, the coverage in urban and peri-urban areas need to be improved in order to attain the impact of IDA-MDA. It is imperative to strengthen drug delivery and community preparation activities along with improved DOT especially in urban and peri-urban areas to achieve the required level of treatment coverage. Addition of ivermectin did not have any additional perceived adverse events.

Scabies prevalence after ivermectin-based mass drug administration for lymphatic filariasis, Samoa 2018-2019.

Willis GA, Kearns T, Mayfield HJ, Sheridan S, Thomsen R, Naseri T, David MC, Engelman D, Steer AC, Graves PM, Lau CL.

22-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37607196/>

Gale

Cloth sharing with a scabies case considerably explains human scabies among children in a low socioeconomic rural community of Ethiopia.

Melese F, Malede A, Sisay T, Geremew A, Gebrehiwot M, Woretaw L, Atanaw G, Azanaw J, Melese M, Feleke H.

15-09-2023

Trop Med Health.

<https://pubmed.ncbi.nlm.nih.gov/37710350/>

Background: In 2020, scabies were integrated into the WHO roadmap for neglected tropical diseases, aimed at ending the negligence to realize the SDGs. Ethiopia has also introduced scabies as a notifiable disease in drought-prone localities since 2015. Many of the previous studies employed study designs that might be subject to bias. Moreover, there is no scientific evidence about scabies in this area. Hence, this study aimed to determine the prevalence and associated factors of scabies among children aged below 15 years in rural Ethiopia. **Methods:** A community-based cross-sectional study was carried out among 942 children in rural kebeles of Lay Gayent District from March through May 15, 2021. A two-stage sampling technique was applied. Data on sociodemographics, housing, water supply and sanitation, children's personal hygiene, and caregivers' knowledge about scabies were collected by a structured questionnaire. Data quality was maintained through pretesting, training of data collectors and supervisors, and supervision. An adjusted binary logistic regression was modelled to identify factors associated with scabies. The Hosmer-Lemeshow goodness-of-fit test was run to check the model fitness.

Results: The prevalence of scabies was 21.5% (95% CI 19.0-24.3). Maternal illiteracy (adjusted odds ratio (AOR) = 1.61; 95% CI 1.07-2.43); low household wealth (AOR = 2.04; 95% CI 1.25-3.33); unimproved water source (AOR = 1.58; 95% CI 1.05-2.40); not cleaning a house daily (AOR = 2.43; 95% CI 1.63-3.62); not trimming nails (AOR = 2.21; 95% CI 1.50-3.25); cloth sharing with a scabies case (AOR = 11.77; 95% CI 6.94-19.97); and low caregiver knowledge about scabies (AOR = 2.44; 95% CI 1.64-3.63) were factors associated with scabies. **Conclusions:** Scabies remains a significant public health issue among children aged below 15 years in the district. Maternal illiteracy, low household wealth, unimproved water source, not cleaning a house daily, not trimming nails, cloth sharing with a scabies case, and low caregiver knowledge about scabies were factors associated with scabies. Community-wide interventions with prime emphasis on improving maternal education and caregivers' knowledge about scabies, upgrading household wealth, ensuring a safe water supply, providing healthy housing, and ensuring adequate personal hygiene are warranted.

Worldwide Differences in Clinical Management Practices of Scabies: a Survey Using Clinical Vignettes.

Paucard L, Chosidow O, Bernigaud C, Walker SL, Marks M.

13-09-2023

J Eur Acad Dermatol Venereol.

<https://pubmed.ncbi.nlm.nih.gov/37703134/>

Infantile scabies misdiagnosed and treated as Langerhans cell histiocytosis: a case report.

Yuan M, Pan H, Cui B, Pan J, Ruan Z, Chen Y, Yu H, Liu R, Lu T.

13-09-2023

J Eur Acad Dermatol Venereol.
<https://pubmed.ncbi.nlm.nih.gov/37703133/>

Using ultraviolet dermoscopy in diagnosing scabies.

Yürekli A, Muslu İ, Pektaş SD, Alataş ET, Aydoğdu CT, Daşgin D.
13-09-2023
Exp Dermatol.
<https://pubmed.ncbi.nlm.nih.gov/37702268/>

The latest generation ultraviolet (UV) dermatoscopes, which emit UV light at a wavelength of 365 nm and enlarge lesions, are practical devices that can facilitate the diagnosis and follow-up of some dermatological diseases with fluorescence that can be observed in skin lesions. In 305 patients, 468 tunnels were evaluated: first in polarized mode and later in UV mode. The recorded samples were compared one-to-one by the same dermatologist. Due to the study's design, images were examined in three stages: tunnel borders, tunnel content and mite appearance. In UV mode, the entire body of mites gives a bright reflex along with an oval-shaped diagnostic clue well beyond the delta sign. The borders of the tunnel reflect brightly in UV mode, with borders that are more sharply visible than in polarized mode. Although the tunnel content cannot be clearly distinguished in polarized mode, especially in people with hyperkeratotic palms, or 'working hands' (e.g. farmers, mechanics and construction workers), with the bright reflex, the tunnel borders in UV mode give a bright reflection and provide a clear view of tunnels. Tunnel content gives a bright reflection in UV mode. Our results show that UV dermatoscopes provide more effective and clearer images than polarized dermatoscopes in the diagnosis of scabies.

Characterization of a novel galectin in *Sarcoptes scabiei* and its role in regulating macrophage functions.

He R, Zhang Q, Xu L, Guo M, Gu X, Xie Y, Xu J, Shen Z.
24-08-2032
Front Microbiol.
<https://pubmed.ncbi.nlm.nih.gov/37692380/>

Hailey-Hailey disease exacerbated by scabies: the role of dermoscopy in preventing misdiagnosis.

Żychowska M, Kołt-Kamińska M, Kijowski R, Reich A.
Août-2023
Postepy Dermatol Alergol.
<https://pubmed.ncbi.nlm.nih.gov/37692273/>

Comment on "Permethrin-unresponsive scabies in London, United Kingdom - a wake up call".

Potestio L, Scalvenzi M, Martora F, Costanzo L, Gallo L.
08-09-2023
Clin Exp Dermatol.
<https://pubmed.ncbi.nlm.nih.gov/37683073/>

Scabies prevalence after ivermectin-based mass drug administration for lymphatic filariasis, Samoa 2018-2019.

Willis GA, Kearns T, Mayfield HJ, Sheridan S, Thomsen R, Naseri T, David MC, Engelman D, Steer AC, Graves PM, Lau CL.
22-08-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37607196/>

Background: Scabies is a common skin infestation caused by the *Sarcoptes scabiei* mite. Ivermectin, one of three drugs used in mass drug administration (MDA) for lymphatic filariasis, is also effective for treating scabies. Ivermectin-based MDA was first conducted in Samoa in August 2018, with ivermectin being offered to those aged ≥ 5 years. Here, we report scabies prevalence in Samoa after MDA. **Methods:** We conducted household surveys 1.5-3.5 months (Survey 1) and 6-8 months (Survey 2) after the 2018 MDA in 35 primary sampling units. We conducted clinical examination for scabies-like rash and used International Alliance for the Control of Scabies classification criteria. We estimated scabies prevalence by age, gender and region. Multivariable logistic regression was used to assess factors associated with prevalence. **Results:** We surveyed 2868 people (499 households) and 2796 people (544 households) aged 0-75 years in Surveys 1 and 2, respectively. Scabies prevalence increased from 2.4% (95% CI 2.1-2.7%) to 4.4% (95% CI 4.0-4.9%) between surveys. Scabies was associated with younger age (0-4 years: aOR 3.5 [2.9-4.2]; 5-15 years: aOR 1.6 [1.4-1.8] compared to ≥ 16 years), female gender (aOR 1.2 [95% CI 1.1-1.4]; region (aOR range from 1.4 [1.1-1.7] to 2.5 [2.1-3.1] between regions), large households (aOR 2.6 [2.0-3.4] households ≥ 13), and not taking MDA in 2018 (aOR 1.3 [95% CI 1.1-1.6]). **Conclusions:** We found moderate prevalence of scabies in two population-representative surveys conducted within 8 months of the 2018 MDA for lymphatic filariasis. Prevalence appeared to increase between the surveys, and ongoing surveillance is recommended, particularly in young children.

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

Prevalence of soil-transmitted helminths and associated risk factors among primary school children in Kandahar, Afghanistan: A cross-sectional analytical study.

Rahimi BA, Rafiqi N, Tareen Z, Kakar KA, Wafa MH, Stanikzai MH, Beg MA, Dost AK, Taylor WR.
11-09-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37695763/>

Background: Soil-transmitted helminth (STH) infections are global health problem, especially in low-income

countries. Main objectives of this study were to estimate the prevalence and intensity of STH and its risk factors among school children in Kandahar city of Afghanistan. **Methodology/principal findings:** This was a school-based cross-sectional analytical study, with data collected during eight-month-period (May-December, 2022) from 6- and 12-years old school children in Kandahar city, Afghanistan. All the stool samples were examined by saline wet mount method and Kato-Katz technique. Data were analyzed by using descriptive statistics, Chi square test, and multivariate logistic regression. A total of 1275 children from eight schools of Kandahar city were included in this study. Mean age of these children was 8.3 years with 53.3% boys. The overall prevalence of any intestinal parasitic infection was 68.4%. The overall prevalence of STH infection was 39.1%, with *Ascaris lumbricoides* (29.4%) as the most prevalent STH species. Mean intensity of overall STH infection was 97.8. Multivariate logistic regression revealed playing barefoot (AOR 1.6, 95% CI 1.1-2.2), not washing hands after defecating and before eating (AOR 1.3, 95% CI 1.0-1.7), having untrimmed nails (AOR 1.4, 95% CI 1.1-1.8), and belonging to poor families (AOR 1.3, 95% CI 1.0-1.7) as the risk factors associated with the predisposition of school children for getting STH in Kandahar city of Afghanistan. **Conclusions/significance:** There is high prevalence of STH among school children of Kandahar city in Afghanistan. Most of the risk factors are related to poverty, decreased sanitation, and improper hygiene. Improvement of socioeconomic status, sanitation, and health education to promote public awareness about health and hygiene together with periodic mass deworming programs are better strategies for the control of STH infections in Afghanistan.

Leishmaniose

Antimalarial drug efficacy and resistance in malaria-endemic countries in HANMAT-PIAM_net countries of the Eastern Mediterranean Region 2016-2020: Clinical and genetic studies.

Adam M, Nahzat S, Kakar Q, Assada M, Witkowski B, Tag Eldin Elshafie A, Abuobaida D, Safi N, Khan MA, Nagi M, Mustafa SA, Kohestani K, Muhammad J, Khim N, Al-Hadi M, Elfaki TM, Habib MN, Khairy AKA, Hamid H, Uddin Z, Amer Y, Hassan AH, Elhag MS, Sediqi AW, Kakar I, Abdul-Ghani R, Amran JGH, Abdallahrahim TA, Tamim MS, Aljasari A, Rasmussen C, Azkoul L, Warsame M.

13-09-2023

Trop Med Int Health.

<https://pubmed.ncbi.nlm.nih.gov/37705047/>

Increased copy number of the target gene squalene monooxygenase as the main resistance mechanism to terbinafine in *Leishmania infantum*.

Potvin JÉ, Fani F, Queffeuilou M, Gazanion É, Leprohon P, Ouellette M.

09-09-2023

Int J Parasitol Drugs Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37703646/>

We use here two genomic screens in an attempt to understand the mode of action and resistance mechanism of terbinafine, an antifungal contemplated as a potential drug against the parasite *Leishmania*. One screen consisted in in vitro drug evolution where 5 independent mutants were selected step-by-step for terbinafine resistance. Sequencing of the genome of the 5 mutants revealed no single nucleotide polymorphisms related to the resistance phenotype. However, the ERG1 gene was found amplified as part of a linear amplicon, and transfection of ERG1 fully recapitulated the terbinafine resistance phenotype of the mutants. The second screen, Cos-seq, consisted in selecting a gene overexpression library with terbinafine followed by the sequencing of the enriched cosmid. This screen identified two cosmids derived from loci on chromosomes 13 and 29 encoding the squalene monooxygenase (ERG1) and the C8 sterol isomerase (ERG2), respectively. Transfection of the ERG1-cosmid, but not the ERG2-cosmid, produced resistance to terbinafine. Our screens suggest that ERG1 is the main, if not only, target for terbinafine in *Leishmania* and amplification of its gene is the main resistance mechanism.

Phlebotomine sand flies (Psychodidae: Phlebotominae) in an area of canine infection caused by *Leishmania infantum* in the state of Amapá, eastern Amazon.

Pessoa LMB, Pinto EHC, Chaves TES, Rabelo GDS, Brito AL, Zanini VM, Nunes MCL, Viana LA.

08-09-2023

Rev Bras Parasitol Vet.

<https://pubmed.ncbi.nlm.nih.gov/37703122/>

In 2017, the Brazilian State of Amapá registered the first occurrence of visceral leishmaniasis (VL) in 17 dogs in the outskirts of the capital, Macapá. Given the lack of knowledge on phlebotomines in that area, this study aimed to survey the fauna of these Diptera. Sampling was performed using CDC light traps placed at ten sampling sites. The specimens captured were *Evandromyia walkeri* (n=237), *Nyssomyia antunesi* (n=65) and *Bichromomyia flaviscutellata* (n=6). The phlebotomine species composition resulted in low species diversity, and none of the main vectors of the etiological agent of VL were identified in the study area.

Factors associated with mucosal involvement in tegumentary leishmaniasis: a nation-based study using surveillance data from Brazil.

Monachesi CF, Gomes-Silva A, Carvalho-Costa FA.

08-09-2023

Rev Inst Med Trop Sao Paulo.

<https://pubmed.ncbi.nlm.nih.gov/37703118/>

Detection of *Leishmania* DNA in Phlebotomine Sand Flies in Tsatee, a Community in the Volta Region, Ghana.

Addo SO, Amoako EK, Bentil RE, Agbodji B, Mosore MT, Yeboah C, Attram N, Larbi JA, Kwakye-Nuako G, de Souza DK, Wilson MD, Boakye DA.

04-09-2023

Biomed Res Int.

<https://pubmed.ncbi.nlm.nih.gov/37700879/>

Leishmania parasites, which are spread by infected female sand flies, are the cause of the disease leishmaniasis. Although cutaneous leishmaniasis has been found to occur in the Volta Region, there is limited data on vector species and reservoirs. This study focused on the Tsatee community, in the South Dayi District of the Volta Region, and is aimed at identifying the sand fly fauna and detecting the presence of *Leishmania* DNA by the use of primers that target the conserved region of *Leishmania* spp. minicircle DNA of the parasite kinetoplast. The miniature light traps and hand aspirators provided by the Centers for Disease Control and Prevention (CDC) were used to collect outdoor and indoor sand flies for five months in a guinea woodland and semideciduous forest area. From the collections, 4,580 phlebotomine sand flies were obtained and identified, and females were examined for *Leishmania* DNA using PCR. The male flies were 1,202 (26.24%), non-blood-fed females were 3,321 (72.51%), and 57 (1.25%) were blood-fed females. It was observed that *Sergentomyia* species constituted 99.91% of the total collected sand flies with *S. africana* (76.77%) as the predominant species. *Phlebotomus rodhaini* (0.09%) was the only *Phlebotomus* species identified from the study area. From 283 non-blood-fed sand fly pools and 57 individual blood-fed species screened, *Leishmania* DNA was detected in 12 (4.24%) pools and 8 (14.04%) individuals, respectively. It was observed that *Leishmania* DNA was detected in all the sand fly species identified except *S. collarti*. This study reports the first detection of *Leishmania* DNA in *P. rodhaini* in Ghana, with an infection rate of 33.33% (95% CI, 1.23-88.32). The findings suggest that the role of *Phlebotomus* in disease transmission in the study area cannot be discounted. Future studies should include continuous surveillance, blood meal preferences, and vector competence of the various infected phlebotomine sand flies to create effective control measures.

Computational evaluation of phytochemicals targeting DNA topoisomerase I in *Leishmania donovani*: molecular docking and molecular dynamics simulation studies.

Arya PK, Mandal P, Barik K, Singh DV, Kumar A.

11-09-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37697722/>

Diversity of RNA viruses in the cosmopolitan monoxenous trypanosomatid *Leptomonas pyrrhocoris*.

Macedo DH, Grybchuk D, Režnarová J, Votýpka J, Kloczek D, Yurchenko T, Ševčík J, Magri A, Dolinská MU, Záhonová K, Lukeš J, Serviené E, Jászayová A, Serva S, Malysheva MN, Frolov AO, Yurchenko V, Kostygov AY.

12-09-2023

BMC Biol.

<https://pubmed.ncbi.nlm.nih.gov/37697369/>

Biting rhythms and infection rates of anthropophilic sand fly species (Diptera: Phlebotominae) in sites with different land use in southern Mexico.

de Oca-Aguilar ACM, Pavón-Mendez MI, López-Ávila KB, Sosa-Bibiano EI, Rebollar-Téllez EA, Palacio-Vargas JA, Fernández-Figueroa EA, Loria-Cervera EN.

09-09-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37696485/>

Could tropical forest conversion shape sand fly (Diptera: Phlebotominae) biting rhythms and *Leishmania* infection rates? Using a Shannon trap, we estimated the bite rate and infection prevalence among anthropophilic sand flies at sites with different land use in southern Mexico. We estimated the expected monthly infection rate of the *Leishmania* parasite along the gradient and generated information on the biting rhythm of sand flies in a poorly characterized cutaneous leishmaniasis endemic region. We used generalized mixed linear and mixed additives models to evaluate differences in the biting rate, nocturnal activity, and inoculation rate of female sand flies, as well as their relationship with the loss of forest cover and environmental disparities recorded throughout the study area. Our results show that the loss of forest cover influences the biting rhythm of sand fly species and the potential number of infectious bites with *Leishmania*, but the greatest entomological and potential epidemiological risk continues to be associated with sylvatic areas (amplification events). Despite this, we detected that the effect of forest cover (%) on the entomological exposure seems to be also dependent on the sand fly species, and that, albeit to a lesser extent, *Leishmania* parasite is circulating in disturbed landscapes through generalist and competent sand fly vector species. We also found that land use change did not affect the nocturnal activity, however we detected that important vector species were active most of the time. Contrary to our expectation, temperature and humidity did not shape the biting rhythm of sand fly species. We discuss the limitations and epidemiological implications of our findings regarding the risk of contracting leishmaniasis in southern Mexico.

Antimalarial Dibenzoannulated Medium-Ring Keto Lactams.

Ren R, Wang X, Leas DA, Scheurer C, Hoevel S, Cal M, Chen G, Zhong L, Katneni K, Pham T, Patil R, Sil D, Walters MJ, Schulze TT, Neville AJ, Dong Y, Wittlin S, Kaiser M, Davis PH, Charman SA, Vennerstrom JL.

11-09-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37695781/>

CXCR5 and TIM-3 expressions define distinct exhausted T cell subsets in experimental cutaneous infection with *Leishmania mexicana*.

Diupotex M, Zamora-Chimal J, Gajón JA, Bonifaz LC, Becker I.

25-08-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37691941/>

T-cell exhaustion is a key stage in chronic infections since it limits immunopathology, but also hinders the elimination of pathogens. Exhausted T (Tex) cells encompass dynamic subsets, including progenitor cells that sustain long-term immunity through their memory/stem like properties, and terminally-differentiated cells, resembling the so-called Tex cells. The presence of Tex cells in chronic leishmaniasis has been reported in humans and murine models, yet their heterogeneity remains unexplored. Using flow cytometry, we identified Tex cells subtypes based on PD-1, CXCR5 and TIM-3 expressions in draining lymph nodes (dLNs) and lesion sites of C57BL/6 mice infected with *L. mexicana* at 30-, 60- and 90-days post-infection. We showed that infected mice developed a chronic infection characterized by non-healing lesions with a high parasite load and impaired Th1/Th2 cytokine production. Throughout the infection, PD-1⁺ cells were observed in dLNs, in addition to an enhanced expression of PD-1 in both CD4⁺ and CD8⁺ T lymphocytes. We demonstrated that CD4⁺ and CD8⁺ T cells were subdivided into PD-1⁺CXCR5⁺TIM-3⁻ (CXCR5⁺), PD-1⁺CXCR5⁺TIM-3⁺ (CXCR5⁺TIM-3⁺), and PD-1⁺CXCR5⁻TIM-3⁺ (TIM-3⁺) subsets. CXCR5⁺ Tex cells were detected in dLNs during the whole course of the infection, whereas TIM-3⁺ cells were predominantly localized in the infection sites at day 90. CXCR5⁺TIM-3⁺ cells only increased at 30 and 60 days of infection in dLNs, whereas no increase was observed in the lesions. Phenotypic analysis revealed that CXCR5⁺ cells expressed significantly higher levels of CCR7 and lower levels of CX3CR1, PD-1, TIM-3, and CD39 compared to the TIM-3⁺ subset. CXCR5⁺TIM-3⁺ cells expressed the highest levels of all exhaustion-associated markers and of CX3CR1. In agreement with a less exhausted phenotype, the frequency of proliferating Ki-67 and IFN- γ expressing cells was significantly higher in the CXCR5⁺ subset within both CD4⁺ and CD8⁺ T cells compared to their respective TIM-3⁺ subsets, whereas CD8⁺CXCR5⁺TIM-3⁺ and CD8⁺TIM-3⁺ subsets showed an enhanced frequency of degranulating CD107a⁺ cells. In summary, we identified a novel, less-differentiated CXCR5⁺ Tex subset in experimental cutaneous leishmaniasis caused by *L. mexicana*. Targeting these cells through immune checkpoint inhibitors such as anti-PD-1 or anti PD-L1 might improve the current treatment for patients with the chronic forms of leishmaniasis.

Rodents as vehicle for delivery of transgenic bacteria to make paratransgenic sand fly vectors of cutaneous leishmaniasis in field condition.

Ghassemi M, Akhavan AA, Zahraei-Ramazani A, Yakhchali B, Arandian MH, Jafari R, Akhlaghi M, Shirani-Bidabadi L, Azam K, Koosha M, Oshaghi MA.

09-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37689736/>

Vector-borne diseases, among them leishmaniasis, cause more than 700,000 deaths annually. The lack of an

effective vaccination and the increasing resistance of sand flies to insecticides require the urgent development of innovative approaches to contain the disease. The use of engineered bacteria that express anti-parasite molecules (paratransgenesis) shows much promise. However, a challenge for implementation of this strategy is to devise means to introduce modified bacteria into sand flies in the field. In this study, we use rodent food bait as a delivery strategy to introduce two mCherry-fluorescent bacteria, *Serratia* AS1 and *Enterobacter cloacae*, into adult sand flies in field settings. Bacteria-infected food was provided to *Rhombomys opimus* rodents. These bacteria transiently pass through the rodent alimentary tract and are delivered to larval habitats with the rodent feces. The feces are ingested by sand fly larvae and, in the case of *Serratia* AS1, are trans-stadially transmitted to adults. This is the first report of targeting delivery of *Serratia* AS1 in a paratransgenic system to control transmission of leishmaniasis under field condition. This novel strategy shows promise for delivering transgenic bacteria to *Leishmania* vectors in the field.

Healing effects of autologous platelet gel and growth factors on cutaneous leishmaniasis wounds in addition to antimony; a self-controlled clinical trial with randomized lesion assignment.

Shadmand E, Solhjoo K, Taghipour A, Tayer AH, Sadeghi F, Meshkin A.

09-09-2023

BMC Res Notes.

<https://pubmed.ncbi.nlm.nih.gov/37689656/>

Reactive oxygen species trigger inflammasome activation after intracellular microbial interaction.

Rosa CP, Belo TCA, Santos NCM, Silva EN, Gasparotto J, Corsetti PP, de Almeida LA.

06-09-2023

Life Sci.

<https://pubmed.ncbi.nlm.nih.gov/37683723/>

Antileishmanial potentials of azacitidine and along with meglumine antimoniate on *Leishmania major*: In silico prediction and in vitro analysis.

Derakhshani A, Sharifi I, Salarkia E, Keyhani A, Agha Kuchak Afshari S, Iranmanesh B, Lashkarizadeh M, Nejad Biglari H, Lari Najafi M, Bamorovat M.

08-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37682979/>

This study aimed to investigate the in vitro and in silico antileishmanial activity of azacitidine (AZA) on *Leishmania major* promastigotes and amastigotes. The in silico method was used to evaluate the possibility of the interaction of AZA into the binding pocket of inducible nitric oxide synthase (iNOS), a leading defensive oxidative metabolite. Following that, in vitro anti-promastigote, and anti-amastigote activity of AZA was determined using an MTT assay and a macrophage model, respectively.

Cytotoxic effects of AZA and meglumine antimoniate (MA) were also assessed by MTT assay on murine macrophages. All experiments were performed in triplicate. The results showed that AZA interacted with Ser133, Gln134, and Lys13 amino acids of iNOS, and the molecular docking score was obtained at -241.053 kcal/mol. AZA in combination with MA significantly ($P < 0.001$) inhibited the growth rate of nonclinical promastigote (IC_{50} 247.6 ± 7.3 μ M) and 8.5-fold higher of clinical intramacrophage amastigote stage (29.8 ± 5.3 μ M), compared to the untreated group. A significant upsurge of Th1 subsets and transcription genes and a meaningful decline in Th2 cytokines subclasses at the equivalent concentrations of AZA and MA was observed ($P < 0.001$). The apoptosis effect of AZA along with MA was significantly induced on L. major in a dose-dependent manner ($P < 0.001$). The present study demonstrated that AZA possesses antileishmanial activity in in vitro and in silico models. However, AZA combined with MA was more effective than AZA alone in inhibiting the growth rate of promastigotes and amastigotes of L. major. This study indicates that AZA in combination with MA demonstrated a potent antileishmanial mechanism, promoting immune response and enhancing an immunomodulatory role toward the Th1 pathway. This experimental study is a basic study for applying more knowledge about the mechanisms of AZA along with MA in animal models in the future.

In silico and in vitro potentials of crocin and amphotericin B on Leishmania major: Multiple synergistic mechanisms of actions.

Salarkia E, Sharifi I, Keyhani A, Tavakoli Oliaee R, Khosravi A, Sharifi F, Bamorovat M, Babaei Z.

08-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37682934/>

A significant barrier to optimal antileishmanial treatment is low efficacy and the emergence of drug resistance. Multiple approaches were used to monitor and assess crocin (a central component of saffron) mixed with amphotericin B (AmpB) potential in silico and in vitro consequences. The binding behavior of crocin and iNOS was the purpose of molecular docking. The results showed that crocin coupled with AmpB demonstrated a safe combination, extremely antileishmanial, suppressed Leishmania arginase absorption, and increased parasite death. This natural flower component is a robust antioxidant, significantly promoting the expression of the Th1-connected cytokines (IL12p40, IFN- γ , and TNF- α), iNOS, and transcription factors (Elk-1, c-Fos, and STAT-1). In comparison, the expression of the Th2-associated phenotypes (IL-10, IL-4, and TGF- β) was significantly reduced. The leishmanicidal effect of this combination was also mediated through programmed cell death (PCD), as confirmed by the manifestation of phosphatidylserine and cell cycle detention at the sub-G0/G1 phase. In conclusion, crocin with AmpB synergistically exerted in vitro antileishmanial action, generated nitric oxide and reactive oxygen species, modulated Th1, and Th2 phenotypes and transfer factors, enhanced PCD profile and arrested the cell cycle of Leishmania major promastigotes. The main action of crocin and AmpB

involved wide-ranging mechanistic insights for conducting other clinical settings as promising drug candidates for cutaneous leishmaniasis. Therefore, this combination could be esteemed as a basis for a potential bioactive component and a logical source for leishmanicidal drug development against CL in future advanced clinical settings.

Dual-scRNA-seq analysis reveals rare and uncommon parasitized cell populations in chronic L. donovani infection.

Karagiannis K, Gannavaram S, Verma C, Pacheco-Fernandez T, Bhattacharya P, Nakhasi HL, Satoskar AR.

07-09-2023

Cell Rep.

<https://pubmed.ncbi.nlm.nih.gov/37682713/>

Nucleoside-Derived Metallohydrogel Induces Cell Death in Leishmania Parasites.

Bhattacharya S, Bhattacharyya T, Khanra S, Banerjee R, Dash J.

08-09-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37606735/>

A byproduct from the Valles Calchaquies vineyards (Argentina) rich in phenolic compounds: a tool against endemic Leishmania dissemination.

Salazar PB, Fanzone M, Zabala BA, Rodriguez Vaquero MJ, Cilli E, Barroso PA, Minahk C, Acuña L.

Sept-2023

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/37592068/>

Vineyard-derived pomace is a byproduct of the wine industry that can have a negative impact on the environment if it is only disposed of or used as a fertilizer. Owing to its polyphenol content, grape pomace is an alternative to biocontrol undesirable microorganisms. In the present study, we characterized the phenolic composition of red and white grape pomace from Valles Calchaquies, Argentina, and explored its activity against Leishmania (Leishmania) amazonensis, an etiological agent of American tegumentary leishmaniasis, a neglected endemic disease in northern Argentina. Red and white pomace extracts similarly reduced Leishmania viability after a 48-h treatment, with the fractions containing a higher proportion of phenolic compounds being more active. Both extracts stimulated ATPase activity on the parasite plasma membranes, with white grape pomace having a stronger effect than red grape pomace. In addition, the extracts displayed fairly good anticholinesterase activity, which may have contributed to their anti-Leishmania activity. These results reinforce the potential applicability of grape pomace as an antimicrobial agent for the development of biopesticides.

A Difficult-To-Diagnose Case of American Tegumentary Leishmaniasis.

Khoury F, Campos JE.

10-09-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37701165/>

The emerging role of miRNA-122 in infectious diseases: Mechanisms and potential biomarkers.

Mirzaei R, Karampoor S, Korotkova NL.

Sept-2023

Pathol Res Pract.

<https://pubmed.ncbi.nlm.nih.gov/37544130/>

microRNAs (miRNAs) are small, non-coding RNA molecules that play crucial regulatory roles in numerous cellular processes. Recent investigations have highlighted the significant involvement of miRNA-122 (miR-122) in the pathogenesis of infectious diseases caused by diverse pathogens, encompassing viral, bacterial, and parasitic infections. In the context of viral infections, miR-122 exerts regulatory control over viral replication by binding to the viral genome and modulating the host's antiviral response. For instance, in hepatitis B virus (HBV) infection, miR-122 restricts viral replication, while HBV, in turn, suppresses miR-122 expression. Conversely, miR-122 interacts with the hepatitis C virus (HCV) genome, facilitating viral replication. Regarding bacterial infections, miR-122 has been found to regulate host immune responses by influencing inflammatory cytokine production and phagocytosis. In *Vibrio anguillarum* infections, there is a significant reduction in miR-122 expression, contributing to the pathophysiology of bacterial infections. Toll-like receptor 14 (TLR14) has been identified as a novel target gene of miR-122, affecting inflammatory and immune responses. In the context of parasitic infections, miR-122 plays a crucial role in regulating host lipid metabolism and immune responses. For example, during *Leishmania* infection, miR-122-containing extracellular vesicles from liver cells are unable to enter infected macrophages, leading to a suppression of the inflammatory response. Furthermore, miR-122 exhibits promise as a potential biomarker for various infectious diseases. Its expression level in body fluids, particularly in serum and plasma, correlates with disease severity and treatment response in patients affected by HCV, HBV, and tuberculosis. This paper also discusses the potential of miR-122 as a biomarker in infectious diseases. In summary, this review provides a comprehensive and insightful overview of the emerging role of miR-122 in infectious diseases, detailing its mechanism of action and potential implications for the development of novel therapeutic strategies.

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.

25-10-2023

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.

Evolution of RNA viruses in trypanosomatids: new insights from the analysis of *Sauroleishmania*.

Klocek D, Grybchuk D, Tichá L, Votýpka J, Volf P, Kostygov AY, Yurchenko V.

Oct-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37490143/>

Unusual transformation of *Leishmania* spp. amastigotes to promastigotes in a bone marrow sample from a Greyhound dog.

Rodríguez-Cariño C, López Loarte J, Marí-Martorell D, Pantchev N, Hernandez Martinez L.

Sept-2023

Vet Clin Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37408304/>

The objective of the study was to confirm the presence of different morphological forms of *Leishmania infantum* promastigotes on bone marrow aspirates from a Spanish Greyhound with canine leishmaniosis.

2-Aroyl quinazolinone: Synthesis and in vitro anti-parasitic activity.

Setshedi KJ, Beteck RM, Jesumoroti OJ, Ilbeigi K, Mabille D, Caljon G, Van der Kooy F, Legoabe LJ.

Oct-2023

Chem Biol Drug Des.

<https://pubmed.ncbi.nlm.nih.gov/37353860/>

Trypanosomes and *Leishmania* are parasitic protozoans that affect millions of people globally. Herein we report the synthesis of 2-aroyl quinazolinones and their antiprotozoal efficacy against *Trypanosoma brucei*, *Trypanosoma brucei rhodesiense*, *Trypanosoma cruzi*, and *Leishmania infantum*. These compounds were counter-screened against a human cell line for cytotoxicity.

Thirteen of the twenty target compounds in this study inhibited the growth of these parasites, with compounds KJ1, and KJ10 exhibiting IC₅₀ values of 4.7 µM (*T. b. brucei*) and 1.1 µM (*T. b. rhodesiense*), respectively.

Population dynamics of *Nyssomyia whitmani* (Diptera: Psychodidae) in domestic and peridomestic environments in Northeast Argentina, a tegumentary leishmaniasis outbreak area.

Manteca-Acosta M, Cueto GR, Poullain M, Santini MS, Salomón OD.

12-09-2023

J Med Entomol.

<https://pubmed.ncbi.nlm.nih.gov/37313956/>

Lèpre

Leprosy Reactions: Experience in the Puerto Rico Hansen's Disease Population.

Rodriguez-Rivera DV, Pelet-Del Toro NM, Quintero-Noriega AL.

Sept-2023

P R Health Sci J.

<https://pubmed.ncbi.nlm.nih.gov/37709675/>

Objective: Hansen's disease (HD) is a chronic granulomatous infection endemic in the tropics. Its main clinical manifestations involve the cutaneous, nervous, and musculoskeletal systems. Leprosy reactions (LR) are systemic inflammatory and immune-mediated complications of HD. These include reversal reactions (RR), erythema nodosum leprosum (ENL), and Lucio phenomenon. These reactions significantly increase disease-related morbidity and disability. We aimed to determine the number and type of LR, their association to hosts' immune responses (Ridley Jopling classification), timing of development, and treatment of HD patients in Puerto Rico. **Methods:** A retrospective medical record review was performed on 291 HD patients containing LR status data available from the Dermatology Service at the Hispanic Alliance for Clinical & Translational Research.

Results: Our data revealed that 83 (29%) patients developed LR, of which 31% had RR and 69% had ENL. Most LR were observed in patients in the lepromatous border (97%): Borderline lepromatous leprosy (BL) and Lepromatous Leprosy (LL). Most patients with RR and ENL had a single episode (83% and 62%, respectively), and those that received multi-drug therapy (MDT) had a reaction onset occurring most frequently within the first year of MDT and after the first year of MDT, respectively. Prednisone was the first line treatment used to manage both types of LR. **Conclusion:** Most lepromatous reactions occur within the lepromatous border. ENL was the most common LR. Prompt recognition and management of these immunologic reactions is essential to prevent long term nerve function impairment.

Challenges in engaging the private sector for tuberculosis prevention and care in Nigeria: a mixed methods study.

Chijioko-Akaniro O, Onyemaechi S, Kuye J, Ubachioma E, Omoniyi A, Urhioke O, Lawanson A, Ombeka VO, Hassan A, Asuke S, Anyaie C, Merle CS.

13-09-2023

BMJ Open.

<https://pubmed.ncbi.nlm.nih.gov/37709312/>

The Gabrin Sign's Potential for Identifying High-Risk Patients for COVID-19 with Androgenic Alopecia.

Mohta A, Pareek S, Prasad V, Mohta A, Nyati A.

14-09-2023

J Eur Acad Dermatol Venereol.

<https://pubmed.ncbi.nlm.nih.gov/37708567/>

A Psittacine bite and subcutaneous basidiobolomycosis: A case with a therapeutic challenge.

Choubey S, Khadanga S, Asati DP, Garg R, Maurya AK, Bhadade A, Tadepalli K.

14-05-2023

Med Mycol Case Rep.

Basidiobolus ranarum is a saprophyte that can be found in soil, rotting vegetables, and frogs' digestive tracts. Clinically, basidiobolomycosis presents as a persistent infection of subcutaneous tissue affecting the trunk and extremities in an immunocompetent host. We describe a case of subcutaneous basidiobolomycosis in a 56-year-old immunocompetent woman farmer by occupation residing at remote part of central India. This study highlights the traumatic implantation and zoonotic potential of fungal species. Clinical suspicion of fungal etiology and timely mycology laboratory diagnostic support is key to address such cases. This case is documented to emphasize the problems of compliance to treatment specially in remote and poor patients challenging the treatment with complete cure. 2012 Elsevier Ltd. All rights reserved.

Assessment of minimally invasive file systems on resistance to fracture using traditional and contracted access cavity designs in the maxillary first and second molars.

Kapadia KH, Patni PM, Jain P, Raghuvanshi S, Pandey SH, Singhal RR.

Juil-Août 2023

J Conserv Dent.

<https://pubmed.ncbi.nlm.nih.gov/37705550/>

Objective: The objective of the study was to evaluate the effect of access cavity design on fracture resistance of the extracted maxillary first and second molars prepared with three minimally invasive files. **Materials and methods:** One hundred and twelve extracted human maxillary molars were selected for the study and divided randomly into three groups according to different minimally invasive files used (self-adjusting files [SAF], XP-endo Shaper [XP], and 4 V-Taper 2H [VT]) and one control group (CG). All

experimental groups were subdivided into two subgroups, i.e., conservative access cavity (CAC) and traditional access cavity (TAC). All the canals in different experimental groups were enlarged up to apical size 30. The data were analyzed using the analysis of variance and *Post hoc* Tukey tests ($P < 0.05$). **Results:** The highest mean fracture resistance of teeth with CAC was of the CG (1399.957), followed by teeth with CAC instrumented by SAF (1378.314) and XP-endo Shaper (1202.929). The least value was of the V-Taper file system (937.157). Furthermore, the highest mean fracture resistance value of teeth with TAC was of the CG (1143.171), followed by teeth with TAC instrumented by SAF (1150.607) and then XP-endo Shaper (998.150). The least value was of the V-Taper file system (757.050). **Conclusion:** Conservative endodontic access (CAC) in the maxillary molars had shown significantly increased fracture resistance over TAC. SAF showed the maximum fracture resistance, while V-Taper files showed the least fracture resistance among the experimental groups compared.

Nail Whispers Revealing Dermatological and Systemic Secrets: An Analysis of Nail Disorders Associated With Diverse Dermatological and Systemic Conditions.

Satasia M, Sutaria AH.

11-09-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37701161/>

Background and objective Nail disorders encompass a wide spectrum of conditions, spanning congenital, developmental, infectious, neoplastic, degenerative, dermatological, and systemic diseases. A comprehensive exploration of their clinical manifestations, incidence, and associations is crucial for precise diagnosis and effective management. Methods This observational cross-sectional study conducted at B.J. Medical College and Civil Hospital, Ahmedabad involved 300 consecutive patients with nail changes from July 2017 to June 2019 reporting diverse dermatological and systemic conditions. The inclusion criteria involved patients of both genders and all age groups displaying nail changes associated with dermatological and systemic diseases. Data collection entailed a comprehensive clinical history, systemic and dermatological examinations, nail assessment using Dermoscope (DermLite 3, 10x), and supplementary tests. Analyses were performed on Microsoft Excel 2007 software. The study was approved by the Institute Ethics Committee. Results Among the 300 cases, females had a higher prevalence of nail involvement (57%), with a female-to-male ratio of 1.3:1. The most affected age group was 21-40 years, with 6-10 nails typically affected. Notably, housewives showed a higher prevalence. The most frequent nail condition was onychomycosis (24.33%) followed by psoriatic nail changes (20%). Less frequent nail changes involved eczema (5.7%), paronychia (5%), drug-induced (4.3%), lichen planus (3.7%), trauma-induced (3%), twenty nail dystrophy (2.33%), Darier's disease (2%), pemphigus vulgaris (2%), alopecia areata (1.67%), median Heller dystrophy (1.33%), atopic dermatitis (1%), epidermolysis bullosa (1%), racquet nail (1%), leprosy

(1%), pityriasis rubra pilaris (0.67%), vitiligo (0.67%), secondary syphilis (0.67%), pachyonychia congenita (0.67%), as well as a case each of total leukonychia, subungual warts, Koenen tumor, and periungual fibroma (0.33%). Systemic autoimmune connective tissue disorders (CTD) accounted for 9%; the most common nail finding observed was nail fold erythema (48.1%) followed by nail fold telangiectasis (44.4%). In systemic sclerosis (SS), the most common finding was nail fold telangiectasia, and in systemic lupus erythematosus (SLE), the most common was nail fold erythema. Scleroderma capillary pattern on nail fold capillaroscopy was found in seven patients with SS, two patients with dermatomyositis, and only one patient with SLE. Nail changes observed in systemic diseases include onychomycosis in diabetes mellitus and chronic renal failure patients, splinter hemorrhages in ischemic heart disease and hypertension, longitudinal melanonychia in HIV, and koilonychia and platynychia in iron deficiency anemia. Other systemic diseases, such as Addison's disease and renal failure, also exhibited various nail changes. Conclusions Beyond their cosmetic importance, nails hold a vital pathologic role. Proficiency in nail terminology and classification is key for skillful evaluation. Understanding normal and abnormal nail variants, along with their disease associations, benefits diagnosis and tailored management. Nails, often overlooked but accessible, serve as a window into patients' general health and should be an integral part of thorough examinations. This study highlights an intricate clinical panorama of nail disorders, highlighting their significant role in both dermatological and systemic contexts.

Artificial intelligence and digital health in improving primary health care service delivery in LMICs: A systematic review.

Saif-Ur-Rahman KM, Islam MS, Alaboson J, Ola O, Hasan I, Islam N, Mainali S, Martina T, Silenga E, Muyangana M, Joarder T.

10-09-2023

J Evid Based Med.

<https://pubmed.ncbi.nlm.nih.gov/37691394/>

A qualitative exploration of tuberculosis patients who were lost to follow-up in Malaysia.

Tok PSK, Wong LP, Liew SM, Razali A, Mahmood MI, Chinnayah T, Kawatsu L, Toha HR, Mohd Yusof K, Abd Rahman R, Che Mat Din SNA, Loganathan T.

07-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37676902/>

Effects of Intravenous Dexmedetomidine on Hemodynamic Responses to Pneumoperitoneum During Laparoscopic Cholecystectomy.

Shakya R, Maharjan SK.

01-06-2023

Asian J Anesthesiol.

<https://pubmed.ncbi.nlm.nih.gov/37553724/>

Background: Dexmedetomidine is a potent α_2 agonist which has been used for blunting the stress responses during critical events such as laryngoscopy, endotracheal intubation, pneumoperitoneum creation, and extubation. The purpose of this study was to see the efficacy of intravenously administered dexmedetomidine at a dose of 0.5 mcg/kg in attenuating the hemodynamic responses due to pneumoperitoneum during laparoscopic cholecystectomy under general anesthesia. **Methods:** Sixty patients, ASA-PS class I (American Society of Anesthesiologist physical status class I), aged between 18 and 60 years, of either sex with weight ranging from 50 to 80 kg, scheduled for laparoscopic cholecystectomy were randomized into two groups (groups A and B) in a double-blinded fashion. Both groups were pre-medicated with an injection glycopyrrolate. Group A received 100 mL normal saline (NS) over 10 minutes while group B received dexmedetomidine 0.5 mcg/kg diluted in 100 mL NS over 10 minutes before induction of general anesthesia. Heart rate, systolic, diastolic, and mean arterial pressures were noted. **Results:** Following pneumoperitoneum, there was no statistically significant difference in the hemodynamic parameters between the two groups ($P > 0.05$). **Conclusion:** Administration of dexmedetomidine at a dose of 0.5 mcg/kg before induction did not blunt the hemodynamic responses to pneumoperitoneum during laparoscopic cholecystectomy.

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.

Sept-2023

Tuberculosis (Edinb).

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

Triaging cases of fever with vesicular rash relevant to the monkeypox epidemic.

Sardana K, Sachdeva S, Narula S, Gogate S.

Oct-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37403493/>

Histoid leprosy complicated by erythema nodosum leprosum mimicking connective tissue disease.

Pal D.

Oct-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37401254/>

Erythema nodosum leprosum (ENL) is an immunological complication of leprosy seen in 50% of lepromatous and 10% of borderline lepromatous leprosy. It usually presents as a multisystem disease with papulo-nodular skin lesions and fever. Arthralgia or arthritis is a common initial presentation of erythema nodosum leprosum. Pure rheumatologic presentation of lepromatous leprosy complicated by erythema nodosum leprosum is extremely rare, mimics connective tissue disease and is treated with steroids.

Leprosy: The age-old companion of humans - Re-evaluation and comparative analysis of Avar-period cases with Hansen's disease from the Danube-Tisza Interfluve, Hungary.

Spekker O, Tihanyi B, Kis L, Madai Á, Pálfi G, Csuvár-Andrási R, Wicker E, Szalontai C, Samu L, Koncz I, Marcsik A, Molnár E.

Sept-2023

Tuberculosis (Edinb).

<https://pubmed.ncbi.nlm.nih.gov/37684080/>

In recent years, our knowledge of leprosy in the past has substantially been enriched. Nonetheless, much still remains to be discovered, especially in regions and periods from where no written sources are available. To fill in some research gaps, we provide the comparative analysis of eight Avar-period leprosy cases from the Danube-Tisza Interfluve (Hungary). In every case, to reconstruct the biological consequences of leprosy, the detected bony changes were linked with palaeopathological and modern medical information. To reconstruct the social consequences of being affected by leprosy, conceptualisation of the examined individuals' treatment in death was conducted. In every case, the disease resulted in deformation and disfigurement of the involved anatomical areas (rhinomaxillary region, feet, and/or hands) with difficulties in conducting certain physical activities. These would have been disadvantageous for the examined individuals and limited or changed their possibilities to participate in social situations. The most severe cases would have required continuous support from others to survive. Our findings indicate that, despite their very visible disease and associated debility, the examined communities did not segregate leprosy sufferers but provided and cared for them, and maintained a strong enough social network that made their survival possible even after becoming incapable of self-sufficiency.

Morsures de serpent

Comments on systematic review and meta-analysis of global prevalence of neurotoxic and hemotoxic snakebite envenomation, paper published in EMHJ Vol. 28 No. 12.

Mullins M.

31-08-2023

East Mediterr Health J.

<https://pubmed.ncbi.nlm.nih.gov/37698223/>

Cortical Blindness and Thrombotic Microangiopathy Following a Hemotoxic Snake Envenomation: An Unusual Presentation.

Ramkumar A, Tvsp M, Elanjeran R, Chaitanya YV, Harika K.

08-08-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37692596/>

Snake envenomation leads to significant morbidity and mortality with local, hematological, renal, and neurological complications. Hemotoxic envenomation activates a hemorrhagic cascade, leading to many manifestations ranging from skin bleeds to major organ bleeds and fatal intracranial hemorrhage. Although rare, ischemic manifestations are possible following a hemotoxic envenomation, and they may present as cortical blindness, an unusual ocular symptom. Snake envenomation is also known to cause multifactorial acute kidney injury (AKI), precipitated by hemodynamic disturbances secondary to rhabdomyolysis, hemoglobinuria, direct tubular toxicity, and thrombotic microangiopathy. Thrombotic microangiopathy (TMA) is often overlooked in snake bites, as the hematological manifestations are often conveniently attributed to venom-induced consumptive coagulopathy (VICC). The distinct clinical entity of thrombotic microangiopathy should factor into one's differential diagnosis in patients presenting with microangiopathic hemolytic anemia, thrombocytopenia, and acute kidney injury following a snake bite. We report a patient who developed cortical blindness and thrombotic microangiopathy following snake envenomation, which are uncommon sequelae.

Partial segmental thrombosis of the corpus cavernosum following Russell's viper bite.

Senthilkumaran S, Sampath S, Miller SW, Almeida JR, Williams J, Williams HF, Thirumalaikolundusubramanian P, Patel K, Vaiyapuri S.

07-09-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37683700/>

Investigating the Clinical Value of Novel Kidney Injury Inflammatory Biomarkers in Snakebite Victims.

Chen N, Wang S, Ye J, Zhang L, Wang H, Ye S, Lu Y, Zhong G, Qian W.

Aug-2023

Arch Esp Urol.

<https://pubmed.ncbi.nlm.nih.gov/37681339/>

Analysis of News Media-Reported Snakebite Envenoming in Nepal during 2010-2022.

Pandey DP, Thapa NB.

28-08-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37639403/>

Background: Snakebite envenoming is a well-known medical emergency in the Terai of Nepal in particular. However, there is an epidemiological knowledge gap. The news media data available online provide substantial information on envenomings. Assessing this information can be a pristine approach for understanding snakebite epidemiology and conducting knowledge-based interventions. We firstly analyzed news media-reported quantitative information on conditions under which bites occur, treatment-seeking behavior of victims, and outcomes of snakebite envenomings in Nepal.

Methodology/principal findings: We analyzed 308 Nepalese snakebite envenomed cases reported in 199 news media articles published between 2010 and 2022 using descriptive statistics, Wilcoxon, and Chi-square tests to know why and how victims were bitten, their treatment-seeking behavior, and the outcomes. These envenomed cases known with substantial information represented 48 districts (mostly located in the Terai region) of Nepal. These envenomings mostly occurred in residential areas affecting children. Generally, envenomings among males and females were not significantly different. But, in residential areas, females were more envenomed than males. Further, victims' extremities were often exposed to venomous snakebites while their active status and these episodes often occurred at night while victims were passive during snakebites indoors and immediate surroundings of houses. Snakebite deaths were less among referred than non-referred cases, males than females, and while active than passive conditions of victims. **Conclusion/significance:**

The most of reported envenomed patients were children, and most envenomings were due to cobra bites. Consultation with traditional healers complicated snakebite management. In most cases, deaths that occur without medical interventions are a severe snakebite consequence in Nepal. Further, several deaths in urban areas and mountains and higher hills of Nepal suggest immediate need of snakebite management interventions in the most affected districts. Therefore, there is an urgent need to immediately admit Nepalese snakebite victims to nearby snakebite treatment centers without adopting non-recommended prehospital interventions. The strategies for preventing snakebite and controlling venom effects should also include hilly and mountain districts where snakebite-associated deaths are reported.

Risk factors and outcome of acute kidney injury in children with snake envenomation.

Das K, Das S, Mohakud NK, Pradhan SK, Sahu SK.

Oct-2023

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/37545383/>

Bothrops atrox venom: Biochemical properties and cellular phenotypes of three highly toxic classes of toxins.

Lopes-de-Souza L, Costal-Oliveira F, Rodrigues CR, Stransky S, de Assis TCS, Liberato C, Vivas-Ruiz D, Chocas AY, Guerra-Duarte C, Braga VMM, Chávez-Olortegui C. 01-11-2023

Biochim Biophys Acta Proteins Proteom.

<https://pubmed.ncbi.nlm.nih.gov/37442518/>

Risk of stroke following antivenom use after venomous snakebite: correspondence.

Chen CC, Yang PJ, Wang PH, Chen SC.

12-09-2023

QJM.

<https://pubmed.ncbi.nlm.nih.gov/37099702/>

Mycétome

A Rare Case of Oral Cavity Eumycetoma.

Wadde KR, Khaire SD, Joy T, Sardar MA, Kri M, Venkatakrishnan L.

Jan-Juin 2023

Ann Maxillofac Surg.

<https://pubmed.ncbi.nlm.nih.gov/37545383/>

Rationale: Mycetoma is a chronic granulomatous infection that involves the skin and subcutaneous tissue which presents as an abscess with multiple draining sinuses. It is common in the tropical and subtropical regions where the conditions favour the growth of the soil saprophytes - fungi and bacteria. **Patient concerns:** We report the rare case of a 62-year-old patient who presented with a soft-tissue overgrowth in the mandibular posterior ridge area for eight months. **Diagnosis:** The patient was diagnosed with eumycetoma, with foreign-body reaction based on clinical and histopathological examination which revealed characteristic brown-coloured amorphous grains. **Treatment:** The lesion was surgically excised under local anaesthesia. **Outcomes:** On the seventh day post-operative follow-up, the patient was relieved of pre-operative symptoms and the surgical site had healed well. **Take-away lessons:** This particular case of eumycetoma had an unusual site and appearance, making the clinical diagnosis confusing with other reactionary lesions of the oral cavity.

Improving mycetoma case detection through the training of community health workers in Northern Uganda: protocol for a stepped-wedge cluster-randomized trial.

Kibone W, Semulimi AW, Kwizera R, Bongomin F.

08-09-2023

Ther Adv Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37693860/>

Introduction: The World Health Organization acknowledges the need for countries to incorporate neglected tropical disease care into their routine health care system. However, low detection rates and late presentation of mycetoma to health facilities have been observed in endemic countries, including Uganda.

Objective: To empower community health workers (CHWs) in Northern Uganda to recognize and refer suspects of mycetoma to health facilities. **Design:** This will be a stepped-wedge cluster-randomized trial based in Gulu and Pader districts over a period of 9 months with sequential crossover from intervention phase to the control phase at different time points until both districts are exposed to the intervention. **Methods and analysis:** The study will leverage on the ongoing partnership between Northern Uganda Medical Mission and the Uganda Ministry of Health that has trained over 300 CHWs in Gulu and Pader. The study evaluation will be done using the RE-AIM (Reach, Effectiveness, Adoption, Implementation, and Maintenance) framework. The expected outcome of the study is increased detection and referral of suspects of mycetoma. Data will be analyzed using STATA 17.0 and Friedman statistics or Analysis of Variance to determine increase in case identifications and referrals. **Ethics and registration:** The study was approved by Mulago Hospital Research and Ethics Committee (MHREC 2406) and registered with Pan African Clinical Trial Registry (PACTR202301534749787). **Dissemination:** The results from this trial will be published in a peer-reviewed journal. In addition, the findings will be shared at conferences, with funders, and at other research meetings.

Epidemiology and etiology of brain cancer in Africa: A systematic review.

Uwishema O, Frederiksen KS, Badri R, Pradhan AU, Shariff S, Adanur I, Dost B, Esene I, Rosseau G.

Sept-2023

Brain Behav.

<https://pubmed.ncbi.nlm.nih.gov/37312649/>

Onchocercose

Integrated Prevalence Assessment of Wuchereria bancrofti and Onchocerca volvulus in Three Co-Endemic Districts of Gambella Region, Ethiopia.

Hassen M, Mohammed A, Endeshaw T, Seid T, Samuel F, Asmare T, Birhanu H, Bekele F, Yayeh A, Seife F, Tamiru M, Meribo K, Tadesse Z, Griswold E, Katarbarwa M, Richards F, Noland GS.

11-09-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37696513/>

Pian

In vitro evaluation of the effect of yogurt acid whey fractions on iron bioavailability.

Stefos GC, Dalaka E, Papoutsis G, Palamidi I, Andreou V, Katsaros G, Bossis I, Politis I, Theodorou G.

12-09-2023

J Dairy Sci.

<https://pubmed.ncbi.nlm.nih.gov/37709016/>

A side effect of the raised consumption of Greek yogurt is the generation of massive amounts of yogurt acid whey (YAW). The dairy industry has tried several methods for handling these quantities which constitute an environmental problem. Although the protein content of YAW is relatively low, given the huge amounts of produced YAW, the final protein content of the produced YAW should not be underestimated. Taking into consideration the increased interest for bioactive peptides and the increased demand for dietary proteins, combined with YAW's protein and peptides content, efforts should be made toward reintroducing the latter in the food supply chain. In this context and in view of the prevalent dietary iron deficiency problem, the objective of the present study was the investigation of YAW fractions' effect on Fe bioavailability. With this purpose, an in vitro digest approach, following the INFOGEST protocol, was coupled with the Caco2 cell model. To evaluate whether YAW digest fractions exert positive, negative or neutral effect on Fe bioavailability, they were compared with the ones derived from milk, a well-studied food in this context. YAW and milk showed the same effectiveness on both Fe bioavailability and the expression of relative genes (DCYTB, DMT1, FPN1 and HEPH). Focusing further on YAW's fractions, by comparison with their blank digest control counterparts, it resulted that YAW 3-10 kDa digests fraction had a superior effect over the 0-3 kDa fraction on Fe-uptake, which was accompanied by a similar effect on the expression of Fe metabolism-related genes (DCYTB, FPN1 and HEPH). Finally, although the 3-10 kDa fraction of bovine YAW digests resulted in a statistically non-significant increased Fe uptake, compared with the ovine and caprine YAWs, the expression of DCYTB and FPN1 genes underlined this difference by showing a similar pattern with statistically significant higher expression of bovine compared with ovine and bovine compared with both ovine and caprine, respectively. The present study deals with the novel concept that YAW may contain factors affecting Fe bioavailability. The results show that it does not exercise any negative effect and support the extensive investigation for specific peptides with positive effect as well as that YAW proteins should be further assessed on the prospect that they can be used in human nutrition.

How to find a forgotten disease like yaws: Lessons from the Philippine experience.

Dofitas BL.

14-09-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37708120/>

The genomes of the yaws bacterium, *Treponema pallidum* subsp. *pertenue*, of nonhuman primate and human origin are not genomically distinct.

Janečková K, Roos C, Fedrová P, Tom N, Čejková D, Lueert S, Keyyu JD, Chuma IS, Knauf S, Šmajš D.

13-09-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37703251/>

Background: *Treponema pallidum* subsp. *pertenue* (TPE) is the causative agent of human yaws. Yaws is currently reported in 13 endemic countries in Africa, southern Asia, and the Pacific region. During the mid-20th century, a first yaws eradication effort resulted in a global 95% drop in yaws prevalence. The lack of continued surveillance has led to the resurgence of yaws. The disease was believed to have no animal reservoirs, which supported the development of a currently ongoing second yaws eradication campaign. Concomitantly, genetic evidence started to show that TPE strains naturally infect nonhuman primates (NHPs) in sub-Saharan Africa. In our current study we tested hypothesis that NHP- and human-infecting TPE strains differ in the previously unknown parts of the genomes. **Methodology/principal findings:** In this study, we determined complete (finished) genomes of ten TPE isolates that originated from NHPs and compared them to TPE whole-genome sequences from human yaws patients. We performed an in-depth analysis of TPE genomes to determine if any consistent genomic differences are present between TPE genomes of human and NHP origin. We were able to resolve previously undetermined TPE chromosomal regions (sequencing gaps) that prevented us from making a conclusion regarding the sequence identity of TPE genomes from NHPs and humans. The comparison among finished genome sequences revealed no consistent differences between human and NHP TPE genomes. **Conclusion/significance:** Our data show that NHPs are infected with strains that are not only similar to the strains infecting humans but are genomically indistinguishable from them. Although interspecies transmission in NHPs is a rare event and evidence for current spillover events is missing, the existence of the yaws bacterium in NHPs is demonstrated. While the low risk of spillover supports the current yaws treatment campaign, it is of importance to continue yaws surveillance in areas where NHPs are naturally infected with TPE even if yaws is successfully eliminated in humans.

Rage

"Dying alone and being eaten": dog scavenging on the remains of an elderly animal hoarder-a case report.

Kmetiuk LB, Maiorka PC, Beck AM, Biondo AW.

29-08-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37706076/>

A Retrospective Observational Study of Facial Dog Bite Injuries and Its Management in a Tertiary Care Center.

Sreeramajulu V, Babu VS, Sharma MK, Jha MK, Bhattacharya S.

04-08-2023

Indian J Plast Surg.

<https://pubmed.ncbi.nlm.nih.gov/37705817/>

Background : Facial dog bite injuries result in significant emotional, psychological, and physical trauma to the

victims involved and should be considered a significant health issue. The purpose of this study is to share our experience in the management and to add to the existing medical literature regarding the epidemiological patterns of facial dog bite injuries. **Materials and Methods** : This is a single-center retrospective observational study conducted at Dr. RML Hospital, New Delhi, from January 2021 to January 2022. A total of 105 patients were included. The wounds were managed according to the recommendations made by the national rabies control program and surgical intervention was performed in the form of primary suturing or flap cover. **Results** : Children of age group 0 to 10 years are most commonly affected. Pet dogs are the cause in 61% of cases and 57.1% of bites were provoked. Midface is most commonly affected and modified Lackmann's class 3A and 3B are the most common wounds. **Conclusion** : In view of raising incidence of dog bites with pet dogs, the general public needs to be educated regarding the practices to prevent these injuries. Postexposure prophylaxis should be given to all affected individuals irrespective of the vaccination status of the dog. Immediate surgical intervention gives better results.

A Pediatric Level III Trauma Center Experience With Dog Bite Injuries.

Mattice T, Schnaith A, Ortega HW, Segura B, Kaila R, Amoni I, Shanley R, Louie JP.

13-09-2023

Clin Pediatr (Phila).

<https://pubmed.ncbi.nlm.nih.gov/37705176/>

Potential applicability of the importation risk index for predicting the risk of rarely imported infectious diseases.

Min KD, Kim SY, Cho YY, Kim S, Yeom JS.

12-09-2023

BMC Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37700251/>

Molecular mechanism of de novo replication by the Ebola virus polymerase.

Peng Q, Yuan B, Cheng J, Wang M, Gao S, Bai S, Zhao X, Qi J, Gao GF, Shi Y.

12-09-2023

Nature.

<https://pubmed.ncbi.nlm.nih.gov/37699521/>

Risk mapping and risk factors analysis of rabies in livestock in Bangladesh using national-level passive surveillance data.

Lu T, Cao JMD, Rahman AKMA, Islam SS, Sufian MA, Martínez-López B.

29-08-2023

Prev Vet Med.

<https://pubmed.ncbi.nlm.nih.gov/37696207/>

Rabies is a major zoonotic disease around the world, causing significant mortality to both humans and animals, especially in low- and middle-income countries. In Bangladesh, rabies is transmitted mostly by the bite of

infected dogs and jackals to humans and domestic livestock, causing severe economic losses and public health hazards. Our study analyzed national passive surveillance data of veterinary hospital-reported rabies cases in cattle, buffalo, sheep, and goats from 2015 to 2017 in all 64 districts of Bangladesh. We used a zero-inflated negative binomial regression model to identify the main environmental and socio-economic risk factors associated with rabies occurrence in livestock, and we used model results to generate risk maps. Our study revealed that monsoon precipitation ($RR=1.28$, $p\text{-value}=0.043$) was positively associated with rabies cases in livestock, and the percentage of adults who have completed university education was also a significant predictor ($RR=0.58$, $p\text{-value}<0.001$) likely suggesting that districts with higher education levels tended to have a lower reporting of rabies cases in livestock. The standardized incidence ratio maps and predicted relative risk maps revealed a high risk of rabies cases in southeast areas in Bangladesh. We recommend implementing risk-based vaccination strategies in dogs and jackals in those high-risk areas before monsoon to reduce the burden of rabies cases in domestic ruminants and humans in Bangladesh.

Rabies infection recognized as a psychosis: A misleading psychiatric presentation.

Ferdaouss Q, Boujraf S, Ismail C, Rim EA, Amine B, Chadya A, Rachid A.

Juil-Sept 2023

J Neurosci Rural Pract.

<https://pubmed.ncbi.nlm.nih.gov/37692826/>

Hydrogel-based 3D human iPSC-derived neuronal culture for the study of rabies virus infection.

Muangsanit P, Chailangkarn T, Tanwattana N, Wongwanakul R, Lekcharoensuk P, Kaewborisuth C.

25-08-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37692167/>

Hydrophobia (Fear of Fluids) in Septic Shock Does Not Pay!

Nguyen HB.

Sept-2023

Chest.

<https://pubmed.ncbi.nlm.nih.gov/37689470/>

Immune Response of Inactivated Rabies Vaccine Inoculated via Intraperitoneal, Intramuscular, Subcutaneous and Needle-Free Injection Technology-Based Intradermal Routes in Mice.

Zhao H, Li P, Bian L, Zhang W, Jiang C, Chen Y, Kong W, Zhang Y.

02-09-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37686393/>

Inoculation routes may significantly affect vaccine performance due to the local microenvironment, antigen localization and presentation, and, therefore, final immune responses. In this study, we conducted a head-to-head comparison of immune response and safety of inactivated rabies vaccine inoculated via intraperitoneal (IP), intramuscular (IM), subcutaneous (SC) and needle-free injection technology-based intradermal (ID) routes in ICR mice. Immune response was assessed in terms of antigen-specific antibodies, antibody subtypes and neutralizing antibodies for up to 28 weeks. A live rabies virus challenge was also carried out to evaluate vaccine potency. The dynamics of inflammatory cell infiltration at the skin and muscle levels were determined via histopathological examination. The kinetics and distribution of a model antigen were also determined by using in vivo fluorescence imaging. Evidence is presented that the vaccine inoculated via the ID route resulted in the highest antigen-specific antibody and neutralizing antibody titers among all administration routes, while IP and IM routes were comparable, followed by the SC route. Antibody subtype analysis shows that the IP route elicited a Th1-biased immune response, while SC and IM administration elicited a prominent Th2-type immune response. Unexpectedly, the ID route leads to a balanced Th1 and Th2 immune response. In addition, the ID route conferred effective protection against lethal challenge with 40 LD50 of the rabies CVS strain, which was followed by IP and IM routes. Moreover, a one-third dose of the vaccine inoculated via the ID route provided comparable or higher efficacy to a full dose of the vaccine via the other three routes. The superior performance of ID inoculation over other routes is related to longer local retention at injection sites and higher lymphatic drainage. Histopathology examination reveals a transient inflammatory cell infiltration at ID and IM injection sites which peaked at 48 h and 24 h, respectively, after immunization, with all side effects disappearing within one week. These results suggest that needle-free injection technology-based ID inoculation is a promising strategy for rabies vaccination in regard to safety and efficacy.

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, 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.

Sept-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.

Schistosomiasis

Ovarian schistosomiasis: challenges of a neglected ectopic involvement of blood flukes. Case report and review of literature.

Elias E, Silvestri V, Mushi V, Mandarano M.

Aug-2023

Pathologica.

<https://pubmed.ncbi.nlm.nih.gov/37711041/>

Co-infection of Plasmodium falciparum and Schistosoma mansoni is associated with anaemia.

Dassah SD, Nyaah KE, Senoo DKJ, Ziem JB, Aniweh Y, Amenga-Etego L, Awandare GA, Abugri J.

14-09-2023

Malar J.

<https://pubmed.ncbi.nlm.nih.gov/37710279/>

Construction and characterization of microsatellite markers for the Schistosoma japonicum isolate from a hilly area of China based on whole genome sequencing.

Sun M, Cheng Y, Gao C, Peng H, Wang N, Gu W, Lu D.

15-09-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37710024/>

Schistosoma japonicum had once caused the greatest disease burden in China and has still been transmitted in some hilly areas, for example, in Shitai of Anhui province,

where rodents are projected to be the main reservoir. This may lead to a critical need of molecular tools with high efficiency in monitoring the dynamic of the rodent-associated *S. japonicum*, as an appropriate amount of schistosome input can re-establish its life cycle in a place with snails and then result in the re-emergence of schistosomiasis. Therefore, the goal of this study was to develop high polymorphic microsatellites from the whole genome of rodent-associated *S. japonicum* strain to monitor its transmission dynamic. We sampled the hilly schistosome isolate from Shitai of Anhui in China and sequenced the parasite with the next-generation sequencing technology. The whole genome was assembled with four different approaches. We then developed 71 microsatellite markers at a genome-wide scale throughout two best assembled genomes. Based on their chromosome mapping and the expected length of targeted sequences, we selected 24 markers for the development of multiplex reactions. Two multiplexes composed of 10 loci were finally developed, and their potential was revealed by their successful application on and capturing the genetic diversity of three schistosome populations. The selected 10 markers, each with clear chromosome location and characteristics, will be greatly useful in tracing the dispersal pathways or/and dynamics of the rodent-associated *S. japonicum* or others in the hilly area of China or elsewhere.

Clinicopathological characteristics and its association with digestive system tumors of 1111 patients with Schistosomiasis japonica.

Yang Y, Wang XY, Duan C, Wang ZJ, Sheng HY, Xu XL, Wang WJ, Yang JH.

13-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37704736/>

Schistosomiasis japonicum can cause different degrees of organ damage and complex human immune pathological reactions, which often invade the intestine and liver. The purpose of this study was to explore the pathological types and pathological changes of Schistosomiasis and their correlation with some digestive system tumors. Hematoxylin eosin staining was performed on the diseased tissues of 1111 Schistosomiasis cases. We counted the deposition sites of *Schistosoma* eggs, analyzed the pathological characteristics, and compared the clinicopathological characteristics of Schistosomiasis associated digestive system tumors and non-Schistosomiasis digestive system tumors. We found that *Schistosoma japonicum* can cause multi organ and multi system damage, with 469 cases of inflammation, 47 cases of adenoma, and 519 cases of adenocarcinoma. Other types include cysts, stromal tumors, malignant lymphomas, and neuroendocrine tumors. Schistosomiasis associated tumors, including gastric cancer, liver cancer, colon cancer and rectal cancer, were compared with non-Schistosomiasis tumors. There were significant differences in age, gender and tumor differentiation between the two groups. Our study shows Schistosomiasis is a systemic disease, causing multiple organ and system damage in the human body. Its clinicopathological types are diverse, and

there may be a pathological change process of "Inflammation-adenoma-carcinoma". Schistosomiasis associated digestive system tumors differ from non-Schistosomiasis tumors in some clinicopathological features.

Temperature affects predation of schistosome-competent snails by a novel invader, the marbled crayfish *Procambarus virginalis*.

Faiad SM, Williams MA, Goodman M, Sokolow S, Olden JD, Mitchell K, Andrianthosa R, Gordon Jones JP, Andriamaro L, Ravoniarimbina P, Rasamy J, Ravelomanana T, Ravelotafita S, Ravo R, Rabinowitz P, De Leo GA, Wood CL.

13-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37703262/>

The human burden of environmentally transmitted infectious diseases can depend strongly on ecological factors, including the presence or absence of natural enemies. The marbled crayfish (*Procambarus virginalis*) is a novel invasive species that can tolerate a wide range of ecological conditions and colonize diverse habitats. Marbled crayfish first appeared in Madagascar in 2005 and quickly spread across the country, overlapping with the distribution of freshwater snails that serve as the intermediate host of schistosomiasis—a parasitic disease of poverty with human prevalence ranging up to 94% in Madagascar. It has been hypothesized that the marbled crayfish may serve as a predator of schistosome-competent snails in areas where native predators cannot and yet no systematic study to date has been conducted to estimate its predation rate on snails. Here, we experimentally assessed marbled crayfish consumption of uninfected and infected schistosome-competent snails (*Biomphalaria glabrata* and *Bulinus truncatus*) across a range of temperatures, reflective of the habitat range of the marbled crayfish in Madagascar. We found that the relationship between crayfish consumption and temperature is unimodal with a peak at ~27.5°C. Per-capita consumption increased with body size and was not affected either by snail species or their infectious status. We detected a possible satiation effect, i.e., a small but significant reduction in per-capita consumption rate over the 72-hour duration of the predation experiment. Our results suggest that ecological parameters, such as temperature and crayfish weight, influence rates of consumption and, in turn, the potential impact of the marbled crayfish invasion on snail host populations.

Schistosoma mansoni-induced oxidative stress triggers hepatocellular proliferation.

von Bülow V, Schneider M, Dreizler D, Russ L, Baier A, Buss N, Lichtenberger J, Härle L, Müller H, Tschuschner A, Schramm G, Pons-Kühnemann J, Greveling CG, Roeb E, Roderfeld M.

09-09-2023

Cell Mol Gastroenterol Hepatol.

<https://pubmed.ncbi.nlm.nih.gov/37696392/>

Inhibition of carbonic anhydrase using aspirin is a novel method to block schistosomiasis infection of the parasitic trematode, *Schistosoma mansoni*, in the intermediate snail host, *Biomphalaria glabrata*.

Parn S, Lewis G, Knight M.

09-09-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37696327/>

Schistosomiasis is a major public health concern worldwide. Although praziquantel is currently available as the only treatment option for schistosomiasis, the absence of reliable diagnostic and prognostic tools highlights the need for the identification and characterization of new drug targets. Recently, we identified the *B. glabrata* homolog (accession number XP_013075832.1) of human CAXIV, showing 37% amino acid sequence identity, from a BLAST search in NCBI (National Center for Biotechnology Information). Carbonic Anhydrases (CAs) are metalloenzymes that catalyze the reversible hydration/dehydration of CO_2/HCO_3 . These enzymes are associated with many physiological processes, and their role in tumorigenesis has been widely implicated. CAs create an acidic extracellular environment that facilitates the survival, metastasis, and growth of cancer cells. In this study, we investigated the role of CA inhibition in *B. glabrata* snails exposed to *S. mansoni* miracidia. We analyzed the expression of the *B. glabrata* CA encoding transcript in juvenile susceptible and resistant snails, with and without exposure to *S. mansoni*. Our results showed that the expression of the CA mRNA encoding transcript was upregulated during early and prolonged infection in susceptible snails (BBO2), but not in the resistant BS-90 stock. Notably, sodium salicylate, a form of aspirin, inhibited the expression of CA, post-exposure, to the parasite. Increasing research between parasites and cancer has shown that schistosomes and cancer cells share similarities in their capacity to proliferate, survive, and evade host immune mechanisms. Here, we show that this model system is a potential new avenue for understanding the role of CA in the metastasis and proliferation of cancer cells. Further studies are needed to explore the potential of CA as a biomarker for infection in other schistosomiasis-causing parasites, including *S. japonicum* and *S. haematobium*.

Prevalence and factors associated with ongoing transmission of *Schistosoma haematobium* after 12 rounds of Praziquantel Mass Drug Administration among school age children in Southern Tanzania.

Malibiche D, Mushi V, Justine NC, Silvestri V, Mhamilawa LE, Tarimo D.

01-09-2023

Parasite Epidemiol Control.

<https://pubmed.ncbi.nlm.nih.gov/37692460/>

Severity of *Schistosoma haematobium* co-infection with malaria in school-

children is potentially modulated by host CD14 gene variants.

Oboh-Imafidon MA, Torbit SM, Jacob S, Schroeter MN, Tucker AR, Ojurongbe O, Thomas BN.

08-09-2023

BMC Res Notes.

<https://pubmed.ncbi.nlm.nih.gov/37684680/>

Performance evaluation of the AiDx multi-diagnostic automated microscope for the detection of schistosomiasis in Abuja, Nigeria.

Makau-Barasa L, Assefa L, Aderogba M, Bell D, Solomon J, Urude RO, Nebe OJ, A-Enegela J, Damen JG, Popoola S, Diehl JC, Vdovine G, Agbana T.

08-09-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37684541/>

In this research, we report on the performance of automated optical digital detection and quantification of *Schistosoma haematobium* provided by AiDx NTDx multi-diagnostic Assist microscope. Our study was community-based, and a convenient sampling method was used in 17 communities in Abuja Nigeria, based on the disease prevalence information extracted from the baseline database on schistosomiasis, NTD Division, of the Federal Ministry of Health. At baseline, samples from 869 participants were evaluated of which 358 (34.1%) tested *S. haematobium* positive by the reference diagnostic standard. Registered images from the fully automated (autofocusing, scanning, image registration and processing, AI image analysis and automatic parasite count) AiDx assist microscope were analyzed. The Semi automated (autofocusing, scanning, image registration & processing and manual parasite count) and the fully automated AiDx Assist showed comparable sensitivities and specificities of [90.3%, 98%] and [89%, 99%] respectively. Overall, estimated egg counts of the semi-automated & fully automated AiDx Assist correlated significantly with the egg counts of conventional microscopy ($r = 0.93$, $p \leq 0.001$ and $r = 0.89$, $p \leq 0.001$ respectively). The AiDx Assist device performance is consistent with requirement of the World Health Organization diagnostic target product profile for monitoring, evaluation, and surveillance of Schistosomiasis elimination Programs.

Epidemiology and aetiology of moderate to severe diarrhoea in hospitalised patients ≥ 5 years old living with HIV in South Africa, 2018-2021: A case-control analysis.

Johnstone SL, Erasmus L, Thomas J, Groome MJ, du Plessis NM, Avenant T, de Villiers M, Page NA.

08-09-2023

PLOS Glob Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37682831/>

Identification and characterization of microRNAs in *Biomphalaria tenagophila*

and comparative analysis of their expression in *Schistosoma mansoni*-resistant and -susceptible snail populations.

Alves TC, Queiroz FR, de Melo Neto AB, da Rocha Fernandes G, Pais FS, de Jesus Jeremias W, Babá EH, de Moraes Mourão M, Morais ER, Cabral FJ, do Amaral LR, Caldeira RL, Zech Coelho PM, de Souza Gomes M.

30-10-2023

Gene.

<https://pubmed.ncbi.nlm.nih.gov/37634882/>

Background: Schistosomiasis is a neglected tropical disease caused by *Schistosoma* and affects over 240 million people worldwide. One of the most prominent causative agents is *Schistosoma mansoni*, which develops inside the intermediate host. *Biomphalaria tenagophila* is the second most important vector of schistosomiasis in Brazil and the Taim population is completely resistant to infection by *S. mansoni*. **Objective:** This study aims to identify and characterize *B. tenagophila* microRNAs (miRNAs) and evaluate their differential expression in *S. mansoni*-susceptible and -resistant populations of *B. tenagophila*. **Methods:** Two populations of *B. tenagophila* snails, susceptible and resistant to *S. mansoni* infection, were used to investigate the small RNA response of these snails after being infected with the parasite. Small RNA sequencing and quantitative real-time PCR were employed to identify and validate differentially expressed miRNAs. Bioinformatics analysis were performed to identify miRNA precursors and mature and evaluate their differential expression. **Findings:** The study predicted 173 mature miRNAs and 123 precursors. Among them were six Lophotrochozoa-specific miRNAs, three mollusk-specific miRNAs, and six pre-miRNAs in a cluster. The small RNA sequencing and RT-PCR of *B. tenagophila* samples allowed assessing the expression patterns of miRNAs. **Main conclusions:** The results obtained may support future studies in *Biomphalaria* spp., generating a global impact on disease control.

Bisphenol A effects on the host *Biomphalaria alexandrina* and its parasite *Schistosoma mansoni*.

Habib MR, Mohamed AH, Nassar AHA, Sheir SK.

Sept-2023

Environ Sci Pollut Res Int.

<https://pubmed.ncbi.nlm.nih.gov/37597145/>

Bisphenol A (BPA) is one of the most potent endocrine-disrupting chemicals (EDCs) that adversely affect aquatic organisms. The present investigation explored the effects of exposure to BPA at 0.1 and 1 mgL⁻¹ concentrations on the fecundity of *Biomphalaria alexandrina*, snail's infection with *Schistosoma mansoni*, and histology of the ovotestis and topographical structure of *S. mansoni* cercariae emerged from exposed snails. The 24 h LC₅₀ and LC₉₀ values of BPA against *B. alexandrina* were 8.31 and 10.88 mgL⁻¹ BPA, respectively. The exposure of snails to 0.1 or 1 mgL⁻¹ BPA did not affect the snail's survival. However, these concentrations caused an increase in the reproductive rate (R₀) of infected snails. A slight decrease in egg production was observed in snails exposed to 0.1

mgL⁻¹ BPA after being infected (infected then exposed). However, a significant increase in egg production was noted in snails exposed to 1 mgL⁻¹ BPA after infection with *S. mansoni*. Histopathological investigations indicated a clear alteration in the ovotestis tissue structure of exposed and infected-exposed groups compared to the control snails. Chronic exposure to BPA caused pathological alterations in the gametogenic cells. SEM preparations of *S. mansoni* cercariae emerged from infected-exposed snails showed obvious body malformations. From a public health perspective, BPA pollution may negatively impact schistosomiasis transmission, as indicated by the disturbance in cercarial production and morphology. However, it has adverse effects on the reproduction and architecture of reproductive organs of exposed snails, indicating that *B. alexandrina* snails are sensitive to sublethal BPA exposure.

Praziquantel meets Niclosamide: A dual-drug Antiparasitic Cocrystal.

D'Abbrunzo I, Bianco E, Gigli L, Demitri N, Birolo R, Chierotti MR, Škorić I, Keiser J, Häberli C, Voinovich D, Hasa D, Perissutti B.

25-09-2023

Int J Pharm.

<https://pubmed.ncbi.nlm.nih.gov/37579827/>

In this paper we report a successful example of combining drugs through cocrystallization. Specifically, the novel solid is formed by two anthelmintic drugs, namely praziquantel (PZQ) and niclosamide (NCM) in a 1:3 molar ratio, and it can be obtained through a sustainable one-step mechanochemical process in the presence of micromolar amounts of methanol. The novel solid phase crystallizes in the monoclinic space group of P2₁/c, showing one PZQ and three NCM molecules linked through homo- and heteromolecular hydrogen bonds in the asymmetric unit, as also attested by SSNMR and FT-IR results. A plate-like habitus is evident from scanning electron microscopy analysis with a melting point of 202.89 °C, which is intermediate to those of the parent compounds. The supramolecular interactions confer favorable properties to the cocrystal, preventing NCM transformation into the insoluble monohydrate both in the solid state and in aqueous solution. Remarkably, the PZQ - NCM cocrystal exhibits higher anthelmintic activity against in vitro *S. mansoni* models than corresponding physical mixture of the APIs. Finally, due to in vitro promising results, in vivo preliminary tests on mice were also performed through the administration of minicapsules size M.

MicroRNA-1 targets ribosomal protein genes to regulate the growth, development and reproduction of *Schistosoma japonicum*.

Sun C, Luo F, You Y, Gu M, Yang W, Yi C, Zhang W, Feng Z, Wang J, Hu W.

Oct-2023

Int J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37355197/>

Praziquantel efficacy, urinary and intestinal schistosomiasis reinfection - a systematic review.

Aboagye IF, Addison YAA.

Oct-2023

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36394218/>

Trématodoses d'origine alimentaire (clonorchiose, opisthorchiase, fasciolase et paragonimose

Coprovalence, seroprevalence, and geographic distribution of *Fasciola* spp. infection in beef and dairy cattle in Pak Chong highland, Nakhon-Ratchasima Province, Northeast Thailand.

Martviset P, Geadkaew-Krenc A, Piyatadsananon P, Jirojwong R, Chantree P, Phadungsil W, Wangboon C, Jamklang M, Chumkiew S, Poomkhokrak R, Taylor A, Kosa N, Grams R.

11-09-2023

Parasitol Int.

<https://pubmed.ncbi.nlm.nih.gov/37704000/>

Elevated circulating TLR4+ monocytes in patients with liver fluke *Opisthorchis viverrini* is associated with advanced periductal fibrosis.

Salao K, Thapphan C, Thai TD, Faksri K, Suttiprapa S, Tangkawattana S, Sripa B B, Edwards SW.

31-08-2023

J Infect Dev Ctries.

<https://pubmed.ncbi.nlm.nih.gov/37699102/>

Introduction: *Opisthorchis viverrini* (Ov) infection can lead to several disease manifestations of the bile duct including advanced periductal fibrosis (APF) and the most severe complication, cholangiocarcinoma (CCA). Monocytes migrate to the infection site and differentiate into tissue macrophages to express and release molecules such as cytokines, reactive oxygen species, and growth factors. TLR4+ monocytes are classified as having a pro-tumor phenotype and secrete tumor-promoting factors. The aim of this study is to investigate the role of monocytes in the pathogenesis of opisthorchiasis. **Methodology:** We used flow cytometry to measure the number of TLR4+ monocytes in the circulating blood of Ov infected patients with or without APF compared to healthy, non-Ov-infected controls. **Results:** We found, for the first time, that patients with APF have elevated numbers of circulating TLR4+ monocytes when compared to patients without fibrosis and healthy individuals. Intriguingly, when we measured ROS from these monocytes, we found increased ROS

production in patients with APF. **Conclusions:** We propose that excessive production of ROS from these TLR4+ monocytes may lead to excessive injury of surrounding tissue and hence contribute to the pathological processes that lead to the development of advanced periductal fibrosis.

Multinomial logistic regression based on neural networks reveals inherent differences among dairy farms depending on the differential exposure to *Fasciola hepatica* and *Ostertagia ostertagi*.

Oehm AW, Leinmueller M, Zablotzki Y, Campe A, Hoedemaker M, Springer A, Jordan D, Strube C, Knubben-Schweizer G.

Oct-2023

Int J Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37355196/>

A common presentation of uncommon disease - Biliary *Fasciola Hepatica*.

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

Oct-2023

Trop Doct.

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

Trypanosomes (trypanosomiasis et maladie de Chagas)

A ribosome-bound tRNA half stimulates mitochondrial translation during stress recovery in *Trypanosoma brucei*.

Brogli R, Cristodero M, Schneider A, Polacek N.

12-09-2023

Cell Rep.

<https://pubmed.ncbi.nlm.nih.gov/37703180/>

The protozoan parasite *Trypanosoma brucei* and its disease-causing relatives are among the few organisms that barely regulate the transcription of protein-coding genes. Yet, alterations in its gene expression are essential to survive in different host environments. Recently, tRNA-derived RNAs have been implicated as regulators of many cellular processes within and beyond translation. Previously, we identified the tRNA^{Thr}-3'-half (AGU) as a ribosome-associated non-coding RNA able to enhance global translation. Here we report that the tRNA^{Thr}-3'-half is generated upon starvation inside the mitochondria. The tRNA^{Thr}-3'-half associates with mitochondrial ribosomes and stimulates translation during stress recovery, positively affecting mitochondrial activity and, consequently, cellular energy production capacity. Our results describe an organelle ribosome-associated ncRNA involved in translation regulation to boost the central hub of energy metabolism as an immediate stress recovery response.

Multitask learning-driven identification of novel antitrypanosomal compounds.

Lemos JM, Brito da Silva MF, Dos Santos Carvalho AM, Vicente Gil HP, Fiaia Costa VA, Andrade CH, Braga RC, Grellier P, Muratov EN, Charneau S, Moreira-Filho JT, Dourado Bastos IM, Neves BJ.

13-09-2023

Future Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37701989/>

Clinical Characteristics and Outcomes of Chagas Disease in the United States: A Multicenter Retrospective Analysis.

Henao-Martínez AF, Olivo-Freites C, Higueta NIA, Ferraz C, Franco-Paredes C, Tuells J, Woc-Colburn L, Villalpando-Carrión S, Chastain DB, Rassi A

11-09-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37696508>

Chagas disease affects approximately 300,000 patients in the United States. We evaluated a multicenter U.S.-based network to obtain clinical characteristics and outcomes of chronic Chagas disease by disease forms. This was a U.S.-based, multicenter, population-based, retrospective cohort study. We queried TriNetX, a global research network, to identify patients with dual-positive IgG serology for *Trypanosoma cruzi*. We captured outcomes of interest for up to 5 years. We found 429 patients with evidence of dual-positive *T. cruzi* IgG out of 19,831 patients with an available test result from 31 U.S. medical centers. The positive proportion for those tested was 2.2%, up to 4.6% among Hispanics. We found a prevalence of a positive Chagas serology of 0.02% among Hispanics. Cardiomyopathy risk reached an annual rate of 1.3% during the initial 5 years of follow-up among patients with the indeterminate form. We found no new events for pulmonary embolism, sudden death, or left ventricular aneurysms at 5 years. Annual risks for arrhythmias and stroke for chronic Chagas cardiomyopathy (CCC) were 1.6% and 0.8%, respectively. The yearly mortality and hospitalization rates for CCC were 2.7% and 17.1%, respectively. Only 13 patients had a documented antitrypanosomal therapy course within 6 months after diagnosis. Of those receiving treatment, 10 patients received benznidazole and three nifurtimox. Chagas disease screening in patients from endemic areas living in the United States remains crucial. Chronic Chagas cardiomyopathy carries a considerable disease burden, translating into increased morbidity and mortality and an enlarging medical health service utilization.

Structural basis for evolutionarily conserved interactions between TFIIS and Paf1C.

Gao J, Jishage M, Wang Y, Wang R, Chen M, Zhu Z, Zhang J, Diwu Y, Xu C, Liao S, Roeder RG, Tu X.

09-09-2023

Int J Biol Macromol.

<https://pubmed.ncbi.nlm.nih.gov/37696373/>

First Report of *Eratyrus cuspidatus* (Hemiptera: Reduviidae) Infected with *Trypanosoma cruzi* in Peridomestic Environment in Chiapas, Mexico.

Velázquez-Ramírez DD, De Fuentes-Vicente JA, Debboun M, Pérez de León AA, Irecta-Nájera C, Cruz-Méndez L, Espinoza-Medinilla EE, Ochoa-Díaz-López H.

11-09-2023

Vector Borne Zoonotic Dis.

Background: Triatomine bugs are natural vectors of *Trypanosoma cruzi*, which causes Chagas disease or American trypanosomiasis. The role of sylvatic triatomine species as vectors of *T. cruzi* in Mexico remains to be fully understood. Our research on the epidemiology of Chagas disease in Southeastern Mexico involved sampling triatomines in rural settings. **Materials and Methods:** A triatomine was collected in a peridomestic environment of a rural dwelling in the state of Chiapas. The triatomine was identified morphologically as an adult female *Eratyrus cuspidatus* Stal. **Results:** Microscopic analysis revealed flagellate forms of *T. cruzi* in the feces of the *E. cuspidatus* collected. This was confirmed by quantitative polymerase chain reaction. Amplification of the mini-exon gene showed that the *T. cruzi* infecting *E. cuspidatus* corresponded to lineage I. **Conclusions:** This is the first report from Mexico of *E. cuspidatus* found infected in a human dwelling, which represents an important adaptation process to inhabit human environments.

Antimalarial Dibenzannulated Medium-Ring Keto Lactams.

Ren R, Wang X, Leas DA, Scheurer C, Hoevel S, Cal M, Chen G, Zhong L, Katneni K, Pham T, Patil R, Sil D, Walters MJ, Schulze TT, Neville AJ, Dong Y, Wittlin S, Kaiser M, Davis PH, Charman SA, Vennerstrom JL.

11-09-2023

ACS Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37695781/>

Correction to: *Trypanosoma rangeli* Tejera, 1920, in chronic Chagas' disease patients under ambulatory care at the Evandro Chagas Clinical Research Institute (IPEC-Fiocruz, Brazil).

de Sousa MA, da Silva Fonseca T, Dos Santos BN, Dos Santos Pereira SM, Carvalhal C, Hasslocher-Moreno AM.

09-09-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37688592/>

Prevalence and Diversity of Blood Parasites (*Plasmodium*, *Leucocytozoon* and *Trypanosoma*) in Backyard Chickens (*Gallus gallus domesticus*) Raised in Southern Thailand.

Boonchuay K, Thomrongsuwannakij T, Chagas CRF, Pornpanom P.

03-09-2023

Animals (Basel).

Avian malaria and leucocytozoonosis can cause fatal diseases, whereas avian trypanosomiasis is reported to be harmless in chickens. Backyard chickens can be infected by several pathogens, including blood parasites, that may shed to industrial poultry production, with a consequently higher economic impact. This study aimed to investigate the presence of several blood parasites (*Plasmodium*, *Leucocytozoon* and *Trypanosoma*) in backyard chickens raised in Southern Thailand, using PCR-based detection and microscopic methods. From June 2021 to June 2022, 57 backyard chickens were sampled. Fresh thin blood smears were prepared from 11 individuals, and buffy coat smears were prepared from 55 of them. Both thin blood smears and buffy coat smears were used for microscopic analysis. Two nested PCR protocols that amplify a fragment of cytochrome *b* (*cytb*) and small subunit rRNA (*SSU rRNA*) genes were used to identify Haemosporida and *Trypanosoma* parasites, respectively. The number of positive samples was higher with the application of nested PCR than when buffy coat smears were used. Three new *Plasmodium* lineages (GALLUS47-49) and thirteen *Leucocytozoon* lineages (GALLUS50-62) were found. Trophozoites, meronts and gametocytes of *Plasmodium gallinaceum* (GALLUS01) were present in one thin blood smear. All thin blood smears revealed *Leucocytozoon* infections, but only three samples were a single infection. These three samples revealed the presence of fusiform host cell-parasite complexes, of which the morphological features resembled those of *Leucocytozoon macleani* (possible synonym is *Leucocytozoon sabrazesi*), while the *cytb* showed that this parasite is closely related to the lineage GALLUS06-07, described as *Leucocytozoon schouteni*. The *Trypanosoma* prevalence was 33.33%; it was present in only one of the thin blood smears, and it resembles *Trypanosoma calmettei*. This study showed the prevalence of a high diversity of *Plasmodium* (64.91%) and *Leucocytozoon* (89.47%) in Thai chickens. Both nested-PCR and buffy coat smear can be used as the diagnostic tool for the testing of *Plasmodium*, *Leucocytozoon* and *Trypanosoma* for parasitic control in backyard chickens and poultry farms. The information on the parasite species that can be found in chickens raised in Southern Thailand was also considered as the baseline information for further study.

Use of sera cell free DNA (cfDNA) and exovesicle-DNA for the molecular diagnosis of chronic Chagas disease.

Lozano N, Samblas MG, Calabuig E, Giménez Martí MJ, Gómez Ruiz MD, Arce JMS, Sequera-Arquelladas S, Moreno JMM, Trelis M, Osuna A.

08-09-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37682970/>

Ulcère de Buruli

A Bibliometric Study on Buruli Ulcer Based on the Web of Science Database.

Alkan S, Şahinoğlu MS.

13-09-2023

Int J Low Extrem Wounds.

<https://pubmed.ncbi.nlm.nih.gov/37700690/>

Implementing patient-public engagement for improved health: Lessons from three Ghanaian community-based programmes.

Ankomah SE, Fusheini A, Derrett S.

11-09-2023

Health Expect.

<https://pubmed.ncbi.nlm.nih.gov/37694501/>

Background: Community-based health interventions have been implemented as a key strategy for achieving improved health outcomes in Ghana. Effectiveness, however, largely depends on the successful implementation of patient-public engagement (PPE). Although several PPE studies have been conducted in Ghana, little research has been done to understand the specific role of PPE in the context of implementing community-based health programmes. This paper, therefore, examines the extent of PPE implementation in three selected community-based health programmes (Community-based Health Planning and Service [CHPS], Community-based Maternal and Child Health and Buruli Ulcer) to understand their specific effects on health outcomes. **Methods:** Three focus groups, involving 26 participants, were held in three districts of the Ashanti region of Ghana. Participants were mainly health service users involving community health committee members/volunteers, residents and health professionals. They were invited to participate based on their roles in the design and implementation of the programmes. Participants focused on each of Rifkin's spider-gram components. Data were transcribed and analysed descriptively using NVIVO 12 Plus. **Results:** PPE implementation was found to be extensive across the three programmes in specific areas such as organisation and resource mobilisation. PPE was more restricted in relation to community needs assessment, leadership and management, particularly for the CHPS and Buruli Ulcer programmes. **Conclusion:** Findings suggest that benefits from community-based health interventions are likely to be greater if PPE can be widely implemented across all dimensions of the spider-gram framework.

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.

12-09-2023

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.

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, 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.

Sept-2023

Tuberculosis (Edinb).

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