



Veille scientifique

Maladies tropicales négligées

Semaine 16
17 au 23 avril 2023

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Cysticercose

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

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

19-04-2023

Trans R Soc Trop Med Hyg.

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

Tapeworm infections in humans are considered to be a significant public health menace. Despite its public health importance, the data on tapeworm infection remains fragmented and underutilised. The present study reviews the overall burden and distribution of taeniasis and cysticercosis caused by *Taenia solium* and *Taenia saginata* in India by conducting a systematic review of the scientific literature based on Preferred Reporting Items for Systematic reviews and Meta-Analyses guidelines. Data from 19 eligible articles were analysed and the prevalence of *T. solium*-associated taeniasis/cysticercosis was found to be 11.06% (95% confidence interval [CI] 6.856 to 16.119) and the prevalence of *T. saginata*-associated taeniasis was found to be 4.7% (95% CI 3.301 to 6.301). This systematic review and meta-analysis provides a comprehensive analysis of the available literature on tapeworm infections and assesses the burden of *Taenia* infection from India, identifying areas of high prevalence requiring active surveillance and public health interventions.

Dystonic head tremor secondary to neurocysticercosis.

Puig I, Gea M, Núñez F, Ispuerto L, Grau-López L, Roure S, Lozano M, Lucente G, Vilas D.

Apr-2023

Neurologia (Engl Ed).

<https://pubmed.ncbi.nlm.nih.gov/37059575/>

Lower lip cysticercosis: An unusual case report.

Sagar M, Rawat S, Singh A, Anuragini.

Feb-2023

J Oral Maxillofac Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37082280/>

Cysticercosis is a disease that occurs when humans are infected with *Taenia solium* larvae. The parasitic illness cysticercosis, which is common in impoverished nations, hardly ever affects the mouth. Oral cysticercosis is rare that might be challenging to diagnose clinically. This rare case report documents an oral cysticercosis case in a 38-year-old male patient who had an asymptomatic lesion in the buccal mucosa of his lower lip. A *T. solium* larva was identified on histopathological examination in a cystic cavity after an excisional biopsy.

Dengue, chikungunya et maladie à virus Zika

Discovery and structural characterization of monkeypox virus methyltransferase VP39 inhibitors reveal similarities to SARS-CoV-2 nsp14 methyltransferase.

Silhan J, Klima M, Otava T, Skvara P, Chalupska D, Chalupsky K, Kozic J, Nencka R, Boura E.

20-04-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37080993/>

An optimized messenger RNA vaccine candidate protects non-human primates from Zika virus infection.

Bollman B, Nunna N, Bahl K, Hsiao CJ, Bennett H, Butler S, Foreman B, Burgomaster KE, Aleshnick M, Kong WP, Fisher BE, Ruckwardt TJ, Morabito KM, Graham BS, Dowd KA, Pierson TC, Carfi A.

20-04-2023

NPJ Vaccines.

<https://pubmed.ncbi.nlm.nih.gov/37080988/>

Zika virus (ZIKV), an arbovirus transmitted by mosquitoes, was identified as a cause of congenital disease during a major outbreak in the Americas in 2016. Vaccine design strategies relied on limited available isolate sequence information due to the rapid response necessary. The first-generation ZIKV mRNA vaccine, mRNA-1325, was initially generated and, as additional strain sequences became available, a second mRNA vaccine, mRNA-1893, was developed. Herein, we compared the immune responses following mRNA-1325 and mRNA-1893 vaccination and reported that mRNA-1893 generated comparable neutralizing antibody titers to mRNA-1325 at 1/20th of the dose and provided complete protection from ZIKV challenge in non-human primates. In-depth characterization of these vaccines indicated that the observed immunologic differences could be attributed to a single amino acid residue difference that compromised mRNA-1325 virus-like particle formation.

Phylogenetic Analysis of Transmission Dynamics of Dengue in Large and Small Population Centers, Northern Ecuador.

Márquez S, Lee G, Gutiérrez B, Bennett S, Coloma J, Eisenberg JNS, Trueba G.

May-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37080979/>

Deforestation impacts on dengue incidence in the Brazilian Amazon.

da Silva CFA, Dos Santos AM, do Bonfim CV, da Silva Melo JL, Sato SS, Barreto EP.

20-04-2023

Environ Monit Assess.

<https://pubmed.ncbi.nlm.nih.gov/37079116/>

The objective of the study is to perform the spatial analysis of the conditioning factors for the increase in the incidence rate of dengue cases in municipalities located in the Amazon biome, in the period from 2016 to 2021. Three statistical approaches were applied: Moran's index, ordinary least squares regression, and geographically weighted regression. The results revealed that the incidence rates of dengue cases cluster in two areas, both located in the south of the Amazon biome, which is associated with the Arc of Deforestation. The variable deforestation influences the increase in dengue incidence rates revealed by the OLS and GWR model. The adjusted R^2 of the GWR model was 0.70, that is, the model explains about 70% of the total case variation of dengue incidence rates in the Amazon biome. The results of the study evidence the need for public policies aimed at the prevention and combat of deforestation in the Amazon region.

An in silico approach for prediction of B cell and T cell epitope candidates against Chikungunya virus.

Venkatesan A, Chouhan U, Suryawanshi SK, Choudhari JK.

20-04-2023

Immunol Med.

<https://pubmed.ncbi.nlm.nih.gov/37078425/>

Association of 410L, 1016I and 1534C kdr mutations with pyrethroid resistance in *Aedes aegypti* from Ouagadougou, Burkina Faso, and development of a one-step multiplex PCR method for the simultaneous detection of 1534C and 1016I kdr mutations.

Sombié A, Ouédraogo WM, Oté M, Saiki E, Sakurai T, Yaméogo F, Sanon A, McCall PJ, Kanuka H, Weetman D, Badolo A.

Mar-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37076920/>

Background: Since 2000, Burkina Faso has experienced regular dengue cases and outbreaks, making dengue an increasingly important health concern for the country. Previous studies in Burkina Faso reported that resistance of *Aedes aegypti* to pyrethroid insecticides was associated with the F1534C and V1016I kdr mutations. The current study reports high resistance of *Ae. aegypti* populations to pyrethroid insecticides, likely supported by mutations in the voltage-gated sodium channel, here evidenced by genotyping the kdr SNPs V410L, V1016I and F1534C. We also describe a new multiplex PCR-based diagnostic of F1534C and V1016I kdr SNPs. **Methods:** Larvae of *Ae. aegypti* were collected from three health districts of Ouagadougou in 2018. The resistance status of *Ae. aegypti* to permethrin (15 µg/ml) and deltamethrin (10 µg/ml) was tested using bottles and to malathion (5%) using WHO tube tests. All bioassays used 1-h exposure and mortality recorded 24 h post-exposure. Bioassay results were interpreted according to WHO thresholds for resistance

diagnosis. The kdr mutations were screened using AS-PCR and TaqMan methods in exposed and non-exposed *Aedes* mosquitoes. **Results:** Females from all health districts were resistant to permethrin and deltamethrin (< 20% mortality) but were fully susceptible to 5% malathion. The F1534C and V1016I kdr mutations were successfully detected using a newly developed multiplex PCR in perfect agreement with TaqMan method. The 1534C/1016I/410L haplotype was correlated with permethrin resistance but not with deltamethrin resistance; however, the test power was limited by a low frequency of dead individuals in deltamethrin exposure.

Conclusions: Resistance to pyrethroid insecticides is associated with kdr mutant haplotypes, while the absence of substantial resistance to malathion suggests that it remains a viable option for dengue vector control in Ouagadougou.

Burden of mosquito-borne diseases across rural versus urban areas in Cameroon between 2002 and 2021: prospective for community-oriented vector management approaches.

Alenou LD, Nwane P, Mbakop LR, Pameu M, Ekoko W, Mandeng S, Bikoy EN, Toto JC, Onguina H, Etang J.

19-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37076896/>

Background: Over the past two decades, Cameroon has recorded one of the highest rates of urban population growth in sub-Saharan Africa. It is estimated that more than 67% of Cameroon's urban population lives in slums, and the situation is far from improving as these neighbourhoods are growing at an annual rate of 5.5%. However, it is not known how this rapid and uncontrolled urbanization affects vector populations and disease transmission in urban versus rural areas. In this study, we analyse data from studies conducted on mosquito-borne diseases in Cameroon between 2002 and 2021 to determine the distribution of mosquito species and the prevalence of diseases they transmit with regards to urban areas versus rural areas. **Methods:** A search of various online databases, such as PubMed, Hinari, Google and Google Scholar, was conducted for relevant articles. A total of 85 publications/reports were identified and reviewed for entomological and epidemiological data from the ten regions of Cameroon. **Results:** Analysis of the findings from the reviewed articles revealed 10 diseases transmitted by mosquitoes to humans across the study regions. Most of these diseases were recorded in the Northwest Region, followed by the North, Far North and Eastern Regions. Data were collected from 37 urban and 28 rural sites. In the urban areas, dengue prevalence increased from 14.55% (95% confidence interval [CI] 5.2-23.9%) in 2002-2011 to 29.84% (95% CI 21-38.7%) in 2012-2021. In rural areas, diseases such as Lymphatic filariasis and Rift valley fever, which were not present in 2002-2011, appeared in 2012-2021, with a prevalence of 0.4% (95% CI 0.0- 2.4%) and 10% (95% CI 0.6-19.4%), respectively. Malaria prevalence remained the same in urban areas (67%; 95% CI 55.6-78.4%) between the two periods, while it significantly decreased in rural areas from

45.87% (95% CI 31.1-60.6%) in 2002-2011 to 39% (95% CI 23.7-54.3%) in the 2012-2021 period (*P = 0.04). Seventeen species of mosquitoes were identified as involved in the transmission of these diseases, of which 11 were involved in the transmission of malaria, five in the transmission of arboviruses and one in the transmission of malaria and lymphatic filariasis. The diversity of mosquito species was greater in rural areas than in urban areas during both periods. Of the articles reviewed for the 2012-2021 period, 56% reported the presence of *Anopheles gambiae* sensu lato in urban areas compared to 42% reported in 2002-2011. The presence of *Aedes aegypti* increased in urban areas in 2012-2021 but this species was absent in rural areas. Ownership of long-lasting insecticidal nets varied greatly from one setting to another. **Conclusions:** The current findings suggest that, in addition to malaria control strategies, vector-borne disease control approaches in Cameroon should include strategies against lymphatic filariasis and Rift Valley fever in rural areas, and against dengue and Zika viruses in urban areas.

Effects of Glutathionylation on Guanylyltransferase Activity of NS5 N-terminal Capping Domain from Dengue, Japanese Encephalitis, and Zika Viruses.

Saisawang C, Reamtong O, Nachampa I, Petcharat P, Priewkhiew S, Sakdee S, Wongsantichon J, J Ketterman A.

18-04-2023

Protein Pept Lett.

<https://pubmed.ncbi.nlm.nih.gov/37076471/>

A Case Report of Cefixime, Paracetamol, and Nimesulide Induced Toxic Epidermal Necrolysis in a Woman with Dengue Infection without any Other Associated Comorbidities.

Munshi R, Maurya M.

18-04-2023

Curr Drug Saf.

<https://pubmed.ncbi.nlm.nih.gov/37076467/>

Background: Toxic Epidermal Necrolysis (TEN) is a rare, acute, and life-threatening mucocutaneous disease that occurs after the administration of certain drugs, resulting in extensive keratinocyte cell death, skin involvement at the dermal-epidermal junction, and extensive bullous skin eruptions and sloughing. Many published case reports have observed the presence of fever with a viral infection, drug, and/or genetic association as a possible trigger for TEN but associated with other comorbidities. Physicians still struggle to predict which individuals could be predisposed to TEN. The case report that we present had a history of multiple drug intake and fever due to dengue virus infection but was not associated with any other comorbidity. **Case presentation:** We present an unusual case of a 32-year-old woman of Western Indian origin who had developed dengue infection and suffered toxic epidermal necrolysis following a five-day course of a third-generation cephalosporin antibiotic, cefixime and a three-day course of 2 analgesic drugs, paracetamol

(acetaminophen), and nimesulide, with the adverse event occurring on the fifth day of the dengue infection. The offending drugs were stopped, and patient survived with supportive management and hydration. **Conclusion:** The presence of comorbidities may not always be the triggering factor for TEN, though it can affect patient outcomes. Rational drug use is always recommended for patient care. Further research is required to understand the pathomechanism behind the viral-drug-gene interaction.

Rapid diagnostic tests for dengue would reduce hospitalizations, healthcare costs and antibiotic prescriptions in Spain: A cost-effectiveness analysis.

Camprubí-Ferrer D, Ramponi F, Balerdi-Sarasola L, Godoy A, Sicuri E, Muñoz J.

17-04-2023

Enferm Infecc Microbiol Clin (Engl Ed).

<https://pubmed.ncbi.nlm.nih.gov/37076328/>

Background: Current gold standard diagnostic techniques for dengue are expensive and time-consuming. Rapid diagnostic tests (RDTs) have been proposed as alternatives, although data about their potential impact in non-endemic areas is scarce. **Methods:** We performed a cost-effectiveness analysis comparing the costs of dengue RDTs to the current standard of care for the management of febrile returning travelers in Spain. Effectiveness was measured in terms of potential averted hospital admissions and reduction of empirical antibiotics, based on 2015-2020 dengue admissions at Hospital Clinic Barcelona (Spain). **Results:** Dengue RDTs were associated with 53.6% (95% CI: 33.9-72.5) reduction of hospital admissions and were estimated to save 289.08-389.31€ per traveler tested. Moreover, RDTs would have avoided the use of antibiotics in 46.4% (95% CI: 27.5-66.1) of dengue patients. **Discussion:** Implementation of dengue RDTs for the management of febrile travelers is a cost-saving strategy that would lead to a reduction of half of dengue admissions and a reduction of inappropriate antibiotics in Spain.

Antibody and memory B cell responses to the dengue virus NS1 antigen in individuals with varying severity of past infection.

Ramu ST, Dissanayake M, Jeewandara C, Bary F, Harvie M, Gomes L, Wijesinghe A, Ariyaratne D, Ogg GS, Malavige GN.

19-04-2023

Immunology.

<https://pubmed.ncbi.nlm.nih.gov/37075785/>

To further understand the role of NS1-specific antibodies (Abs) in disease pathogenesis, we compared neutralizing antibody levels (Nabs), NS1-Ab levels, IgG antibody subclass profiles and NS1-specific memory B-cell responses (Bmems) in individuals, with varying severity of past dengue. Nabs (Neut50 titres) were assessed using the Foci Reduction Neutralization Test (FRNT) and in-house ELISAs were used to assess NS1-Abs and NS1-Ab subclasses for all four DENV serotypes in individuals with

past DF (n = 22), those with past DHF (n = 14) and seronegative (SN) individuals (n = 7). B-cell ELISpot assays were used to assess NS1-specific Bmem responses. 15/22 (68.18%) individuals with past DF and 9/14 (64.29%) individuals with past DHF had heterotypic infections. Neut50 titres were found to be significantly higher for DENV1 than DENV2 (p = 0.0006) and DENV4 (p = 0.0127), in those with past DHF, whereas there was no significant difference seen in titres for different DENV serotypes in those with past DF. Overall NS1-Ab to all serotypes and NS1-specific IgG1 responses for DENV1, 2 and 4 serotypes were significantly higher in those with past DHF than individuals with past DF. Those with past DHF also had higher IgG1 than IgG3 for DENV1 and DENV3, whereas no differences were seen in those with past DF. Over 50% of those with past DF or DHF had NS1-specific Bmem responses to >2 DENV serotypes. There was no difference in the frequency of Bmem responses to any of the DENV serotypes between individuals with past DF and DHF. Although the frequency of Bmem responses to DENV1 correlated with DENV1-specific NS1-Abs levels (Spearman r = 0.35, p = 0.02), there was no correlation with other DENV serotypes. We found that those with past DF had broadly cross-reactive Nabs, while those with past DHF had higher NS1-Ab responses possibly with a different functionality profile than those with past DF. Therefore, it would be important to further evaluate the functionality of NS1-specific antibody and Bmem responses to find out the type of antibody repertoire that is associated with protection against severe disease.

Cellular uptake of metal oxide-based nanocomposites and targeting of chikungunya virus replication protein nsP3.

Bhatia P, Singh VA, Rani R, Nath M, Tomar S.

12-04-2023

J Trace Elem Med Biol.

<https://pubmed.ncbi.nlm.nih.gov/37075567/>

Relationship between microcephaly and indicators of social inequality in the state of Paraíba, Brazil.

Bezerra ACD, Vasconcelos ML, Lima Filho LMA, Cunha DAD, Alves GÂDS, Pernambuco L.

17-04-2023

Einstein (Sao Paulo).

<https://pubmed.ncbi.nlm.nih.gov/37075460/>

Objective: • Seventy-four (33.18%) municipalities in the state of Paraíba registered live births with microcephaly. • The highest proportion of cases (23.03%) was concentrated in the capital, João Pessoa. • Number of inhabitants, number of cases of Zika virus, water supply, and average household income were associated with a higher proportion of new cases. To analyze the relationship between microcephaly and social inequality indicators in the state of Paraíba during the biennium January 2015 and December 2016. **Methods:** Ecological study with data from newborn microcephaly records and municipal socioeconomic, environmental, and demographic indicators was conducted using two health

information systems from the Brazilian Ministry of Health (SINASC and SINAN) and the Brazilian Institute of Geography and Statistics. A Poisson multiple regression model was applied with a significance level of 5%. **Results:** Among 223 municipalities in Paraíba, 74 registered new cases of microcephaly. The number of Zika virus cases, number of inhabitants, number of households without adequate water supply, and household income were predictor variables of the number of new cases of microcephaly in Paraíba. **Conclusion:** Microcephaly is associated with indicators of social inequality in Paraíba. Zika virus cases, water supply, and family income are the indicators that best explain the increase in microcephaly cases. Therefore, these variables must be monitored by health professionals and authorities.

Burden and distribution of dengue infection in Pakistan (2000-19): a review.

Khattak A, Khan S, Ali I, Gul A, Khabir MN, Javed B, Ayesha, Adnan M, Khan SN, Attaullah S.

14-04-2023

Braz J Biol.

<https://pubmed.ncbi.nlm.nih.gov/37075435/>

Hydroxychloroquine for the management of chronic chikungunya arthritis.

Nogueira IA, Cordeiro RA, Henn GAL, Oliveira JL.

14-04-2023

Rev Inst Med Trop Sao Paulo.

<https://pubmed.ncbi.nlm.nih.gov/37075333/>

CMPK2 restricts Zika virus replication by inhibiting viral translation.

Pawlak JB, Hsu JC, Xia H, Han P, Suh HW, Grove TL, Morrison J, Shi PY, Cresswell P, Laurent-Rolle M.

19-04-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37075076/>

Flaviviruses continue to emerge as global health threats. There are currently no Food and Drug Administration (FDA) approved antiviral treatments for flaviviral infections. Therefore, there is a pressing need to identify host and viral factors that can be targeted for effective therapeutic intervention. Type I interferon (IFN-I) production in response to microbial products is one of the host's first line of defense against invading pathogens. Cytidine/uridine monophosphate kinase 2 (CMPK2) is a type I interferon-stimulated gene (ISG) that exerts antiviral effects. However, the molecular mechanism by which CMPK2 inhibits viral replication is unclear. Here, we report that CMPK2 expression restricts Zika virus (ZIKV) replication by specifically inhibiting viral translation and that IFN-I induced CMPK2 contributes significantly to the overall antiviral response against ZIKV. We demonstrate that expression of CMPK2 results in a significant decrease in the replication of other pathogenic flaviviruses including dengue virus (DENV-2), Kunjin virus (KUNV) and yellow fever virus (YFV). Importantly, we determine that the N-terminal domain (NTD) of CMPK2, which lacks kinase

activity, is sufficient to restrict viral translation. Thus, its kinase function is not required for CMPK2's antiviral activity. Furthermore, we identify seven conserved cysteine residues within the NTD as critical for CMPK2 antiviral activity. Thus, these residues may form an unknown functional site in the NTD of CMPK2 contributing to its antiviral function. Finally, we show that mitochondrial localization of CMPK2 is required for its antiviral effects. Given its broad antiviral activity against flaviviruses, CMPK2 is a promising potential pan-flavivirus inhibitor.

Exploration of limonoids for their broad spectrum antiviral potential *via* DFT, molecular docking and molecular dynamics simulation approach.

Rochlani S, Bhatia M, Rathod S, Choudhari P, Dhavale R.
19-04-2023

Nat Prod Res.

<https://pubmed.ncbi.nlm.nih.gov/37074699/>

Dengue and zika seropositivity, burden, endemicity, and cocirculation antibodies in Nigeria.

Asaga Mac P, Tadele M, Airiohuodion PE, Nisansala T, Zubair S, Aigohbahi J, Anyaike C, Velayudha R, Kroeger A, Panning M.

Dec-2023

Ann Med.

<https://pubmed.ncbi.nlm.nih.gov/37074313/>

Molecular and expression characterization of insulin-like signaling in development and metabolism of *Aedes albopictus*.

Dai Y, Li X, Ding J, Liang Z, Guo R, Yi T, Zhu Y, Chen S, Liang S, Liu W.

18-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37072796/>

Background: Insulin-like signaling (IS) in insects is a conserved pathway that regulates development, reproduction and longevity. Insulin-like peptides (ILPs) activate the IS pathway by binding to the insulin receptor (InR) and trigger the ERK and AKT cascades. A varying number of ILPs were identified in *Aedes aegypti* mosquito and other insects. *Aedes albopictus* is an invasive mosquito which transmits dengue and Zika viruses worldwide. Until now, the molecular and expression characteristics of IS pathway in *Ae. albopictus* have not been investigated. **Methods:** The orthologues of ILP in *Ae. albopictus* genome assembly was analyzed by using sequence blast. Phylogenetic analysis and molecular characterization were performed to identify the functional domains of ILPs. Quantitative analysis was performed to determine the expression characteristics of ILPs, InR as well as ERK and AKT in mosquito development and different tissues of female adults after blood-feeding. In addition, the knockdown of InR was achieved by feeding larvae with *Escherichia coli*-producing dsRNA to

investigate the impact of IS pathway on mosquito development. **Results:** We identified seven putative ILP genes in *Ae. albopictus* genome assembly, based on nucleotide similarity to the ILPs of *Ae. aegypti* and other insects. Bioinformatics and molecular analyses suggested that the ILPs contain the structural motif which is conserved in the insulin superfamily. Expression levels of ILPs, InR as well as ERK and AKT varied in *Ae. albopictus* development stages and between male and female adults. Quantitative analyses revealed that expression of ILP6, the putative orthologue of the insulin growth factor peptides, was highest in the midgut of female adults after blood-feeding. Knockdown of *Ae. albopictus* InR induces a significant decrease in the phosphorylation levels of ERK and AKT proteins and results in developmental delays and smaller body sizes. **Conclusions:** The IS pathway of *Ae. albopictus* mosquito contains ILP1-7, InR and ERK/AKT cascades, which exhibited different developmental and tissue expression characteristics. Feeding *Ae. albopictus* larvae with *E. coli*-producing InR dsRNA blocks the ERK and AKT cascades and interferes with the development of mosquito. Our data suggest that IS pathway plays an important role in the metabolism and developmental process and could represent a potential target for controlling mosquito-borne diseases.

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

Kibenge FSB.

Apr2023

J Am Vet Med Assoc.

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

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

events in humans and other species are the subjects of the companion Currents in One Health by Kibenge, AJVR, June 2023.

Transcription factor Dmrt1 triggers the SPRY1-NF- κ B pathway to maintain testicular immune homeostasis and male fertility.

Zhang MF, Wan SC, Chen WB, Yang DH, Liu WQ, Li BL, Aierken A, Du XM, Li YX, Wu WP, Yang XC, Wei YD, Li N, Peng S, Li XL, Li GP, Hua JL.

18-05-2023

Zool Res.

<https://pubmed.ncbi.nlm.nih.gov/37070575/>

The role of viruses in human acute appendicitis: a systematic literature review.

Soltani S, Kesheh MM, Siri G, Faramarzi S, Shahbahrami R, Didehdar M, Erfani Y, Farahani A.

18-04-2023

Int J Colorectal Dis.

<https://pubmed.ncbi.nlm.nih.gov/37069433/>

Tissue-specific expansion of Zika virus isogenic variants drive disease pathogenesis.

Chan KWK, Bifani AM, Watanabe S, Choy MM, Ooi EE, Vasudevan SG.

15-04-2023

EBioMedicine.

<https://pubmed.ncbi.nlm.nih.gov/37068347/>

Background: The Asian lineage Zika virus (ZIKV) emerged as a public health emergency in 2016 causing severe neurological pathologies with no apparent historical correlate to the mild, disease-causing innocuous member of the mosquito-borne flavivirus genus that was discovered in Africa in 1947. Replication error rate of RNA viruses combined with viral protein/RNA structural plasticity can lead to evolution of virus-induced pathogenicity that is critical to identify and validate.

Methods: Infection studies in cells and A129 interferon alpha/beta receptor deficient mice with ZIKV French Polynesian H/PF/2013 clinical isolate, plaque-purified isogenic clone derivatives as well as infectious cDNA clone derived wild-type and site-specific mutant viruses, were employed together with Next-Generation Sequencing (NGS) to pin-point the contributions of specific viral variants in neurovirulence recapitulated in our ZIKV mouse model. **Findings:** NGS analysis of the low-passage inoculum virus as well as mouse serum, brain and testis derived virus, revealed specific enrichment in the mouse brain that were not found in the other tissues. Specifically, non-structural (NS) protein 2A variant at position 117 along with changes in NS1 and NS4B were uniquely associated with the mouse brain isolate. Mutational analysis of these variants in cDNA infectious clones identified the NS2A A117V as the lethal pathogenic determinant with potential epistatic contribution of NS1 and NS4B variants in ZIKV brain penetrance. **Interpretation:** Our findings confirm that viral subpopulations drive ZIKV neuropathogenicity and

identify specific sequence variants that expand in the mouse brain that associates with this phenotype which can serve as predictors of severe epidemics. **Funding:** Duke-NUS Khoo Post-doctoral Fellowship Award 2020 (KWK) and National Medical Research Council of Singapore grants MOH-000524 (OFIRG) (SW) and MOH-OFIRG20nov-0002 (SGV).

Associated risk factors of severe dengue in Reunion Island: A prospective cohort study.

Carras M, Maillard O, Cousty J, Gérardin P, Boukerrou M, Raffray L, Mavingui P, Poubeau P, Cabie A, Bertolotti A.

17-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37068115/>

Community perceptions on challenges and solutions to implement an Aedes aegypti control project in Ponce, Puerto Rico (USA).

Pérez-Guerra CL, Rosado-Santiago C, Ramos SA, Marrero KM, González-Zeno G, Miranda-Bermúdez J, Ortíz-Ortiz M, Rivera-Amill V, Waterman S, Paz-Bailey G, Sánchez-González L.

17-04-02023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37068074/>

This study characterizes community perceptions on a large-scale project seeking to reduce the population of Aedes aegypti mosquitoes and prevent arboviral disease transmission in Ponce, Puerto Rico; and to leverage on these perceptions to make modifications to ensure effective project implementation. In 2017-2018 the team conducted informal interviews, focus groups, and in-depth interviews with leaders and residents of the communities, focusing on challenges and potential solutions to the project implementation. Possible challenges to the project implementation included the lack of geographic consistency between clusters defined by researchers and the participants' description of the communities' geographic boundaries. Few children living in the communities could affect the ability of the project to adequately measure arboviral disease incidence. Also, population attrition due to out-migration, and lack of community leaders and communication channels after Hurricane Maria could affect participation in project activities. Lack of trust on strangers was an important challenge due to criminal activity involving violence and drug use in some community areas. Solutions to the identified challenges included identifying emerging leaders and implementing community meetings to promote project activities. The information that community members provided helped us to understand the natural disasters' impact on population attrition in these communities with a disproportionate impact in younger groups, resulting in an aging population. We identified lack of community organization and leadership and increasing number of abandoned houses that could turn into Aedes aegypti breeding sites. The formative work helped to better define the geographic areas that the

study would cover, evaluate the acceptability of innovative vector control methods, and identify communication methods used by residents. With this information, challenges and potential solutions in recruiting participants were anticipated, and the community engagement and communications plans were developed. We recommend selecting clusters before research, because opinions towards mosquito control technologies could vary in added clusters.

Interferon ϵ restricts Zika virus infection in the female reproductive tract.

Xu C, Wang A, Ebrahim L, Sullivan L, Tasker C, Pizutelli V, Couret J, Hernandez C, Deb PQ, Fritzky L, Subbian S, Gao N, Lo Y, Salvatore M, Rivera A, Lemenze A, Fitzgerald-Bocarsly P, Tyagi S, Lu W, Beaulieu A, Chang TL.

07-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37066223/>

Insulin-like peptides regulate oogenesis by stimulating ovarian ecdysteroid production in the Indian malaria mosquito *Anopheles stephensi*.

Phipps BL, Brown MR, Strand MR.

08-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37066167/>

Look Out for Fever: Clinical Profile of Dengue in Young Adults in a Tertiary Care Center in North India.

Kaur G, Kumar V, Puri S, Tyagi R, Singh A, Kaur H.

17-08-2022

J Lab Physicians.

<https://pubmed.ncbi.nlm.nih.gov/37064990/>

Background Dengue fever (DF) is a common viral disease, clinical manifestations of which vary from influenza-like illness (DF) to life-threatening dengue hemorrhagic fever (DHF)/dengue shock syndrome (DSS). The aim of this article was to study the clinical profile of DF in young adults. **Material and Methods** This was an observational study conducted in the department of medicine over a period of 2 years (January 1, 2013-December 31, 2014). Patients aged between 18 and 30 years with serology proven (nonstructural protein 1 [NS1]/dengue immunoglobulin M [IgM]) DF were included in this study. The clinical and laboratory data was recorded and analyzed. **Results** Out of 418 cases, the incidence of DF, DHF, and DSS was 87.32, 7.66, and 5.02%, respectively. The most common presentations were fever (99.76%) followed by vomiting (29.43%), pain abdomen (17.94%), myalgias (13.16%), petechial rash (12.92%), and bleeding (10.29%). Dengue NS1 and IgM antibodies were positive in 87.3% and 88.12% of the patients, respectively. Ascites, splenomegaly, hepatomegaly, pleural effusion, gall bladder wall edema, and pericardial effusion were present in 8.13, 6.94, 6.70, 5.98, 2.63, and 0.72% of the patients, respectively. Complications included bleeding (10.29%), acute respiratory distress syndrome (1.67%), myocarditis

(1.44%), seizures (1.44%), hemarthrosis (0.24%), and encephalopathy (0.24%). The mortality rate was 3.35% with death of 14 patients. Shock, bleeding, and elevated serum glutamic oxaloacetic transaminase (SGOT) and serum glutamic pyruvic transaminase levels predicted adverse outcome. **Conclusion** DF can present with a plethora of clinical manifestations in endemic areas. Adverse outcome is more likely if patients have elevated SGOT levels, shock, and bleeding. Continuous seroepidemiological surveillance is essential to control outbreak and minimize morbidity and mortality.

Epidemiology of dengue reported in the World Health Organization's Western Pacific Region, 2013-2019.

Togami E, Chiew M, Lowbridge C, Biaukula V, Bell L, Yajima A, Eshofonie A, Saulo D, Hien DTH, Otsu S, Dai TC, Ngon MS, Lee CK, Tsuyuoka R, Tuseo L, Khalakdina A, Kab V, Abeyasinghe RR, Yadav RP, Esguerra P, Casey S, Soo CP, Fukusumi M, Matsui T, Olowokure B.

22-03-2023

Western Pac Surveill Response J.

<https://pubmed.ncbi.nlm.nih.gov/37064541/>

Recent outbreak of dengue in Bangladesh: A threat to public health.

Bhowmik KK, Ferdous J, Baral PK, Islam MS.

11-04-2023

Health Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37064322/>

EVALUATION OF TENOTOMY IN THE HIP SUBLUXATION TREATMENT OF CHILDREN WITH ZIKA SYNDROME.

de Almeida TDR, Carvalho PRC, Cavalcanti BS, Cordeiro GG, Siqueira CCB, Aires VGB, Rolim EL.

17-04-2023

Acta Ortop Bras.

<https://pubmed.ncbi.nlm.nih.gov/37082154/>

Objectives: Evaluate the efficacy and effects of releasing the muscles of subluxated hips of patients with SCZ. **Methods:** This is a retrospective study with 29 patients with subluxation of the hip, corresponding to 55 hips operated in a public hospital in Recife, Brazil. Preoperative femoral head migration (PM) percentages were evaluated and compared with 6- and 12-month postoperative results. **Results:** Twenty-nine patients were eligible, representing 55 hips evaluated. 19 were female (65.5%), with a mean age of 31.45 months (ranging from 23 to 42 years). 19 patients were GMFCS level V (65.5%), 34.5% were level IV, and 20 of the 29 patients (69%) had no complications. The PM had an absolute reduction of 11.6% (GMFCS IV) and 13.31% (GMFCS V) in the first six months. After 12 months, there was a regression of MP of 7.14% (GMFCS V) and 11.25% (GMFCS IV) compared to preoperative values, with no significant statistical difference among MP values presented between 6 and 12 months after surgery. **Conclusions:** The surgery was effective in PM regression during the analyzed period and presented a low complication rate. **Level of Evidence III; Comparative retrospective study.**

Is new dengue vaccine efficacy data a relief or cause for concern?

Thomas SJ.

15-04-2023

NPJ Vaccines.

<https://pubmed.ncbi.nlm.nih.gov/37061527/>

Impact of proactive and reactive vaccination strategies for health-care workers against MERS-CoV: a mathematical modelling study.

Laydon DJ, Cauchemez S, Hinsley WR, Bhatt S, Ferguson NM.

May-2023

Lancet Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37061313/>

Human brain microphysiological systems in the study of neuroinfectious disorders.

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

13-04-2023

Exp Neurol.

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

Microphysiological systems (MPS) are 2D or 3D multicellular constructs able to mimic tissue microenvironments. The latest models encompass a range of techniques, including co-culturing of various cell types, utilization of scaffolds and extracellular matrix materials, perfusion systems, 3D culture methods, 3D bioprinting, organ-on-a-chip technology, and examination of tissue structures. Several human brain 3D cultures or brain MPS (BMPS) have emerged in the last decade. These organoids or spheroids are 3D culture systems derived from induced pluripotent cells or embryonic stem cells that contain neuronal and glial populations and recapitulate structural and physiological aspects of the human brain. BMPS have been introduced recently in the study and modeling of neuroinfectious diseases and have proven to be useful in establishing neurotropism of viral infections, cell-pathogen interactions needed for infection, assessing cytopathological effects, genomic and proteomic profiles, and screening therapeutic compounds. Here we review the different methodologies of organoids used in neuroinfectious diseases including spheroids, guided and unguided protocols as well as microglia and blood-brain barrier containing models, their specific applications, and limitations. The review provides an overview of the models existing for specific infections including Zika, Dengue, JC virus, Japanese encephalitis, measles, herpes, SARS-CoV2, and influenza viruses among others, and provide useful concepts in the modeling of disease and antiviral agent screening.

A cellular screening platform, stably expressing DENV2 NS5, defines a novel anti-DENV mechanism of action of Apigenin based on STAT2 activation.

Accchioni C, Accchioni M, Mancini F, Amendola A, Marsili G, Tirelli V, Gwee CP, Chan KW, Sandini S, Bisbocci M,

Mysara M, ElHefnawi M, Sanchez M, Venturi G, Barreca ML, Manfroni G, Bresciani A, Vasudevan SG, Sgarbanti M.

05-04-2023

Virology.

<https://pubmed.ncbi.nlm.nih.gov/37060797/>

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

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

15-04-2023

Emerg Microbes Infect.

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

Abstract SARS-CoV-2 has caused a global pandemic with significant humanity and economic loss since 2020. Currently, only limited options are available to treat SARS-CoV-2 infections for vulnerable populations. In this study, we report a universal fluorescence polarization (FP)-based high throughput screening (HTS) assay for SAM-dependent viral methyltransferases (MTases), using a fluorescent SAM-analog, FL-NAH. We performed the assay against a reference MTase, NSP14, an essential enzyme for SARS-CoV-2 to methylate the N7 position of viral 5'-RNA guanine cap. The assay is universal and suitable for any SAM-dependent viral MTases such as the SARS-CoV-2 NSP16/NSP10 MTase complex and the NS5 MTase of Zika virus (ZIKV). Pilot screening demonstrated that the HTS assay was very robust and identified two candidate inhibitors, NSC 111552 and 288387. The two compounds inhibited the FL-NAH binding to the NSP14 MTase with low micromolar IC₅₀. We used three functional MTase assays to unambiguously verified the inhibitory potency of these molecules for the NSP14 N7-MTase function. Binding studies indicated that these molecules are bound directly to the NSP14 MTase with similar low micromolar affinity. Moreover, we further demonstrated that these molecules significantly inhibited the SARS-CoV-2 replication in cell-based assays at concentrations not causing cytotoxicity. Furthermore, NSC111552 significantly synergized with known SARS-CoV-2 drugs including nirmatrelvir and remdesivir. Finally, docking suggested that these molecules bind specifically to the SAM-binding site on the NSP14 MTase. Overall, these molecules represent novel and promising candidates to further develop broad-spectrum inhibitors for the management of viral infections.

Indoor resting behavior of *Aedes aegypti* (Diptera: Culicidae) in northeastern Thailand.

Seang-Arwut C, Hanboonsong Y, Muenworn V, Rocklöv J, Haque U, Ekalaksananan T, Paul RE, Overgaard HJ.

14-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37060087/>

Characterizing the Wolbachia infection in field-collected Culicidae mosquitoes from Hainan Province, China.

Li Y, Sun Y, Zou J, Zhong D, Liu R, Zhu C, Li W, Zhou Y, Cui L, Zhou G, Lu G, Li T.

14-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37060070/>

Background: Mosquitoes are vectors of many pathogens, such as malaria, dengue virus, yellow fever virus, filaria and Japanese encephalitis virus. Wolbachia are capable of inducing a wide range of reproductive abnormalities in their hosts, such as cytoplasmic incompatibility. Wolbachia has been proposed as a tool to modify mosquitoes that are resistant to pathogen infection as an alternative vector control strategy. This study aimed to determine natural Wolbachia infections in different mosquito species across Hainan Province, China. **Methods:** Adult mosquitoes were collected using light traps, human landing catches and aspirators in five areas in Hainan Province from May 2020 to November 2021. Species were identified based on morphological characteristics, species-specific PCR and DNA barcoding of cox1 assays. Molecular classification of species and phylogenetic analyses of Wolbachia infections were conducted based on the sequences from PCR products of cox1, wsp, 16S rRNA and FtsZ gene segments. **Results:** A total of 413 female adult mosquitoes representing 15 species were identified molecularly and analyzed. Four mosquito species (*Aedes albopictus*, *Culex quinquefasciatus*, *Armigeres subalbatus* and *Culex gelidus*) were positive for Wolbachia infection. The overall Wolbachia infection rate for all mosquitoes tested in this study was 36.1% but varied among species. Wolbachia types A, B and mixed infections of A × B were detected in *Ae. albopictus* mosquitoes. A total of five wsp haplotypes, six FtsZ haplotypes and six 16S rRNA haplotypes were detected from Wolbachia infections. Phylogenetic tree analysis of wsp sequences classified them into three groups (type A, B and C) of Wolbachia strains compared to two groups each for FtsZ and 16S rRNA sequences. A novel type C Wolbachia strain was detected in *Cx. gelidus* by both single locus wsp gene and the combination of three genes. **Conclusion:** Our study revealed the prevalence and distribution of Wolbachia in mosquitoes from Hainan Province, China. Knowledge of the prevalence and diversity of Wolbachia strains in local mosquito populations will provide part of the baseline information required for current and future Wolbachia-based vector control approaches to be conducted in Hainan Province.

Developing African arbovirus networks and capacity strengthening in arbovirus surveillance and response: findings from a virtual workshop.

Braack L, Wulandhari SA, Chanda E, Fouque F, Merle CS, Nwangwu U, Velayudhan R, Venter M, Yahouedo AG, Lines J, Aung PP, Chan K, Abeku TA, Tibenderana J, Clarke SE.

14-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37059998/>

This meeting report presents the key findings and discussion points of a 3-h virtual workshop, held on 21 September 2022, and organized by the "Resilience Against Future Threats through Vector Control (RAFT)" research consortium. The workshop aimed to identify priorities for advancing arbovirus research, network and capacity strengthening in Africa. Due to increasing human population growth, urbanization and global movement (trade, tourism, travel), mosquito-borne arboviral diseases, such as dengue, Chikungunya and Zika, are increasing globally in their distribution and prevalence. This report summarizes the presentations that reviewed the current status of arboviruses in Africa, including: (i) key findings from the recent WHO/Special Programme for Research & Training in Tropical Diseases (WHO/TDR) survey in 47 African countries that revealed deep and widespread shortfalls in the capacity to cope with arbovirus outbreak preparedness, surveillance and control; (ii) the value of networking in this context, with examples of African countries regarding arbovirus surveillance; and (iii) the main priorities identified by the breakout groups on "research gaps", "networks" and "capacity strengthening".

Massive mosquito factory in Brazil aims to halt dengue.

Lenharo M.

14-04-2023

Nature.

<https://pubmed.ncbi.nlm.nih.gov/37059855/>

Flaviviruses & the Traveler: Around the World and to Your Stage.

Hale GL.

12-04-2023

Mod Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37059228/>

Mimotope discovery as a tool to design a vaccine against Zika and dengue viruses.

Cuevas-Juárez E, Liñan-Torres A, Hernández C, Kopylov M, Potter CS, Carragher B, Ramírez OT, Palomares LA.

14-04-2023

Biotechnol Bioeng.

<https://pubmed.ncbi.nlm.nih.gov/37058415/>

Predictors of Mortality in Patients With Dengue Fever: Insights From a Comparative Analysis.

Mahmood A, Haq AU, Amin S, Rahim F, Noor M, Gul H, Zafar S, Ahmed Qureshi S, Batul K, Haq M.

13-03-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37056528/>

Objective To determine the clinical and biochemical predictors of mortality in patients with dengue fever. **Methods** This was an analytical, cross-sectional study conducted at Hayatabad Medical Complex, Peshawar, Pakistan. The study participants were patients admitted to

the hospital for the management of dengue fever. Clinical parameters (age, gender, duration of hospital stay, and the presence of complications) and biochemical parameters [white blood cells count (WBC), platelet count, serum c-reactive protein (CRP) level, serum alanine aminotransferase (ALT) level, and serum creatinine] were recorded. These parameters were compared between the survivors and non-survivors of dengue fever. Results Out of 115 patients, the majority (n=82, 71.3%) were up to 45 years and the mean age was 38.40 ± 18.1 years. Most of the patients (n=105, 91.3%) survived. On univariate logistic regression analysis, age more than 45 years [odds ratio (OR) 0.141, 95% confidence interval (CI) 0.034 - 0.585, $p = 0.007$], leukocytosis ($> 11,000/\text{mCL}$) (OR 0.187, 95% CI 0.049 - 0.719, $p = 0.015$), and acute kidney injury (creatinine $> 1.5 \text{ mg/dL}$) (OR 0.124, 95% CI 0.029 - 0.531, $p = 0.005$)] at the time of admission reduced the likelihood to survive. Leukocytosis and acute kidney injury remained significant independent predictors of mortality on multivariate logistic regression analysis. [(OR 0.201, 95% CI 0.042 - 0.960, $p = 0.044$) and (OR 0.148, 95% CI 0.026 - 0.857, $p = 0.033$) for survival, respectively]. Gender, duration of inpatient stay, thrombocytopenia (platelets $< 30,000/\text{mCL}$), and acute liver injury (ALT $> 200 \text{ IU/L}$) were not associated with mortality from dengue fever. Conclusion Age over 45 years, leukocytosis, and acute kidney injury at presentation increased the likelihood of mortality from dengue fever in this study. Gender, duration of hospital stay, thrombocytopenia, and acute liver injury did not affect the odds of mortality.

Integrated systems immunology approach identifies impaired effector T cell memory responses as a feature of progression to severe dengue fever.

Ioannidis LJ, Studniberg SI, Eriksson EM, Suwanto S, Denis D, Liao Y, Shi W, Garnham AL, Sasmono RT, Hansen DS.

13-04-2023

J Biomed Sci.

<https://pubmed.ncbi.nlm.nih.gov/37055751/>

Background: Typical symptoms of uncomplicated dengue fever (DF) include headache, muscle pains, rash, cough, and vomiting. A proportion of cases progress to severe dengue hemorrhagic fever (DHF), associated with increased vascular permeability, thrombocytopenia, and hemorrhages. Progression to severe dengue is difficult to diagnose at the onset of fever, which complicates patient triage, posing a socio-economic burden on health systems.

Methods: To identify parameters associated with protection and susceptibility to DHF, we pursued a systems immunology approach integrating plasma chemokine profiling, high-dimensional mass cytometry and peripheral blood mononuclear cell (PBMC) transcriptomic analysis at the onset of fever in a prospective study conducted in Indonesia. **Results:** After a secondary infection, progression to uncomplicated dengue featured transcriptional profiles associated with increased cell proliferation and metabolism, and an expansion of ICOS⁺CD4⁺ and CD8⁺ effector memory T cells. These responses were virtually absent in cases progressing to severe DHF, that instead mounted an innate-like

response, characterised by inflammatory transcriptional profiles, high circulating levels of inflammatory chemokines and with high frequencies of CD4^{low} non-classical monocytes predicting increased odds of severe disease. **Conclusions:** Our results suggests that effector memory T cell activation might play an important role ameliorating severe disease symptoms during a secondary dengue infection, and in the absence of that response, a strong innate inflammatory response is required to control viral replication. Our research also identified discrete cell populations predicting increased odds of severe disease, with potential diagnostic value.

SIR-SI model with a Gaussian transmission rate: Understanding the dynamics of dengue outbreaks in Lima, Peru.

Ramírez-Soto MC, Machuca JVB, Stalder DH, Champin D, Martínez-Fernández MG, Schaerer CE.

13-04-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37053225/>

Circulation of West Nile virus in mosquitoes approximate to the migratory bird stopover in West Coast Malaysia.

Natasha JA, Yasmin AR, Sharma RSK, Nur-Fazila SH, Nur-Mahiza MI, Arshad SS, Mohammed HO, Kumar K, Loong SK, Ahmad Khusaini MKS.

06-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37023172/>

Being a tropical country with a conducive environment for mosquitoes, mosquito-borne illnesses such as dengue, chikungunya, lymphatic filariasis, malaria, and Japanese encephalitis are prevalent in Malaysia. Recent studies reported asymptomatic infection of West Nile virus (WNV) in animals and humans, but none of the studies included mosquitoes, except for one report made half a century ago. Considering the scarcity of information, our study sampled mosquitoes near migratory bird stopover wetland areas of West Coast Malaysia located in the Kuala Gula Bird Sanctuary and Kapar Energy Venture, during the southward migration period in October 2017 and September 2018. Our previous publication reported that migratory birds were positive for WNV antibody and RNA. Using a nested RT-PCR analysis, WNV RNA was detected in 35 (12.8%) out of 285 mosquito pools consisting of 2,635 mosquitoes, most of which were *Culex* spp. (species). Sanger sequencing and phylogenetic analysis revealed that the sequences grouped within lineage 2 and shared 90.12%-97.01% similarity with sequences found locally as well as those from Africa, Germany, Romania, Italy, and Israel. Evidence of WNV in the mosquitoes substantiates the need for continued surveillance of WNV in Malaysia.

The E2 glycoprotein holds key residues for Mayaro virus adaptation to the urban *Aedes aegypti* mosquito.

Cereghino C, Roesch F, Carrau L, Hardy A, Ribeiro-Filho HV, Henrion-Lacritick A, Koh C, Marano JM, Bates TA, Rai P, Chuong C, Akter S, Vallet T, Blanc H, Elliott TJ, Brown AM, Michalak P, LeRoith T, Bloom JD, Marques RE, Saleh MC, Vignuzzi M, Weger-Lucarelli J.

05-04-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37018377/>

A cryopreservation method to recover laboratory- and field-derived bacterial communities from mosquito larval habitats.

Zhao SY, Hughes GL, Coon KL.

05-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37018374/>

Mosquitoes develop in a wide range of aquatic habitats containing highly diverse and variable bacterial communities that shape both larval and adult traits, including the capacity of adult females of some mosquito species to transmit disease-causing organisms to humans. However, while most mosquito studies control for host genotype and environmental conditions, the impact of microbiota variation on phenotypic outcomes of mosquitoes is often unaccounted for. The inability to conduct reproducible intra- and inter-laboratory studies of mosquito-microbiota interactions has also greatly limited our ability to identify microbial targets for mosquito-borne disease control. Here, we developed an approach to isolate and cryopreserve bacterial communities derived from lab and field-based larval rearing environments of the yellow fever mosquito *Aedes aegypti*-a primary vector of dengue, Zika, and chikungunya viruses. We then validated the use of our approach to generate experimental microcosms colonized by standardized lab- and field-derived bacterial communities. Our results overall reveal minimal effects of cryopreservation on the recovery of both lab- and field-derived bacteria when directly compared with isolation from non-cryopreserved fresh material. Our results also reveal improved reproducibility of bacterial communities in replicate microcosms generated using cryopreserved stocks over fresh material. Communities in replicate microcosms further captured the majority of total bacterial diversity present in both lab- and field-based larval environments, although the relative richness of recovered taxa as compared to non-recovered taxa was substantially lower in microcosms containing field-derived bacteria. Altogether, these results provide a critical next step toward the standardization of mosquito studies to include larval rearing environments colonized by defined microbial communities. They also lay the foundation for long-term studies of mosquito-microbe interactions and the identification and manipulation of taxa with potential to reduce mosquito vectorial capacity.

Mathematical modeling of plus-strand RNA virus replication to identify broad-spectrum antiviral treatment strategies.

Zitzmann C, Dächert C, Schmid B, van der Schaar H, van Hemert M, Perelson AS, van Kuppeveld FJM, Bartenschlager R, Binder M, Kaderali L.

04-04-2023

PLoS Comput Biol.

<https://pubmed.ncbi.nlm.nih.gov/37014904/>

Plus-strand RNA viruses are the largest group of viruses. Many are human pathogens that inflict a socio-economic burden. Interestingly, plus-strand RNA viruses share remarkable similarities in their replication. A hallmark of plus-strand RNA viruses is the remodeling of intracellular membranes to establish replication organelles (so-called "replication factories"), which provide a protected environment for the replicase complex, consisting of the viral genome and proteins necessary for viral RNA synthesis. In the current study, we investigate pan-viral similarities and virus-specific differences in the life cycle of this highly relevant group of viruses. We first measured the kinetics of viral RNA, viral protein, and infectious virus particle production of hepatitis C virus (HCV), dengue virus (DENV), and coxsackievirus B3 (CVB3) in the immunocompromised Huh7 cell line and thus without perturbations by an intrinsic immune response. Based on these measurements, we developed a detailed mathematical model of the replication of HCV, DENV, and CVB3 and showed that only small virus-specific changes in the model were necessary to describe the in vitro dynamics of the different viruses. Our model correctly predicted virus-specific mechanisms such as host cell translation shut off and different kinetics of replication organelles. Further, our model suggests that the ability to suppress or shut down host cell mRNA translation may be a key factor for in vitro replication efficiency, which may determine acute self-limited or chronic infection. We further analyzed potential broad-spectrum antiviral treatment options in silico and found that targeting viral RNA translation, such as polyprotein cleavage and viral RNA synthesis, may be the most promising drug targets for all plus-strand RNA viruses. Moreover, we found that targeting only the formation of replicase complexes did not stop the in vitro viral replication early in infection, while inhibiting intracellular trafficking processes may even lead to amplified viral growth.

Evolutionary dynamics of dengue virus in India.

Jagtap S, Pattabiraman C, Sankaradoss A, Krishna S, Roy R.

03-04-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37011104/>

Challenges of acute febrile illness diagnosis in a national infectious diseases center in Rio de Janeiro: 16-year experience of syndromic surveillance.

Bressan CDS, Teixeira MLB, Gouvêa MIFDS, de Pina-Costa A, Santos HFP, Calvet GA, Lupi O, Siqueira AM, Valls-de-Souza R, Valim C, Brasil P.

03-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37011087/>

Introduction: Acute febrile illnesses (AFI) are a frequent chief complaint in outpatients. Because the capacity to investigate the causative pathogen of AFIs is limited in low- and middle-income countries, patient management may be suboptimal. Understanding the distribution of causes of AFI can improve patient outcomes. This study aims to describe the most common etiologies diagnosed over a 16-years period in a national reference center for tropical diseases in a large urban center in Rio de Janeiro, Brazil.

Methods: From August 2004-December 2019, 3591 patients > 12 years old, with AFI and/or rash were eligible. Complementary exams for etiological investigation were requested using syndromic classification as a decision guide. Results. Among the 3591 patients included, endemic arboviruses such as chikungunya (21%), dengue (15%) and zika (6%) were the most common laboratory-confirmed diagnosis, together with travel-related malaria (11%). Clinical presumptive diagnosis lacked sensitivity for emerging diseases such as zika (31%). Rickettsia disease and leptospirosis were rarely investigated and an infrequent finding when based purely on clinical features. Respiratory symptoms increased the odds for the diagnostic remaining inconclusive. **Conclusions:** Numerous patients did not have a conclusive etiologic diagnosis. Since syndromic classification used for standardization of etiological investigation and presumptive clinical diagnosis had moderate accuracy, it is necessary to incorporate new diagnostic technologies to improve diagnostic accuracy and surveillance capacity.

Development of NS2B-NS3 protease inhibitor that impairs Zika virus replication.

Lin WW, Huang YJ, Wang YT, Lin YS, Mazibuko N, Chen CS, Cheng TL, Chang CS, Leu YL, Chen CY, Chuang CH.

May-2023

Virus Res.

<https://pubmed.ncbi.nlm.nih.gov/36965673/>

Chimeric protection to dengue.

Taglialegna A.

May-2023

Nat Rev Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36949283/>

Predicting 3D structures and stabilities for complex RNA pseudoknots in ion solutions.

Wang X, Tan YL, Yu S, Shi YZ, Tan ZJ.

18-04-2023

Biophys J.

<https://pubmed.ncbi.nlm.nih.gov/36924021/>

RNA pseudoknots are a kind of important tertiary motif, and the structures and stabilities of pseudoknots are generally critical to the biological functions of RNAs with the motifs. In this work, we have carefully refined our previously developed coarse-grained model with salt effect through involving a new coarse-grained force field and a replica-exchange Monte Carlo algorithm, and

employed the model to predict structures and stabilities of complex RNA pseudoknots in ion solutions beyond minimal H-type pseudoknots. Compared with available experimental data, the newly refined model can successfully predict 3D structures from sequences for the complex RNA pseudoknots including SARS-CoV-2 programming-1 ribosomal frameshifting element and Zika virus xrRNA, and can reliably predict the thermal stabilities of RNA pseudoknots with various sequences and lengths over broad ranges of monovalent/divalent salts. In addition, for complex pseudoknots including SARS-CoV-2 frameshifting element, our analyses show that their thermally unfolding pathways are mainly dependent on the relative stabilities of unfolded intermediate states, in analogy to those of minimal H-type pseudoknots.

Pharmacological Elevation of Cellular Dihydrosphingomyelin Provides a Novel Antiviral Strategy against West Nile Virus Infection.

Jiménez de Oya N, San-Félix A, Casasampere M, Blázquez AB, Mingo-Casas P, Escribano-Romero E, Calvo-Pinilla E, Poderoso T, Casas J, Saiz JC, Pérez-Pérez MJ, Martín-Acebes MA.

18-04-2023

Antimicrob Agents Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36920206/>

The flavivirus life cycle is strictly dependent on cellular lipid metabolism. Polyphenols like gallic acid and its derivatives are promising lead compounds for new therapeutic agents as they can exert multiple pharmacological activities, including the alteration of lipid metabolism. The evaluation of our collection of polyphenols against West Nile virus (WNV), a representative medically relevant flavivirus, led to the identification of *N,N'*-(dodecane-1,12-diyl)bis(3,4,5-trihydroxybenzamide) and its 2,3,4-trihydroxybenzamide regioisomer as selective antivirals with low cytotoxicity and high antiviral activity (half-maximal effective concentrations [EC₅₀s] of 2.2 and 0.24 μM, respectively, in Vero cells; EC₅₀s of 2.2 and 1.9 μM, respectively, in SH-SY5Y cells). These polyphenols also inhibited the multiplication of other flaviviruses, namely, Usutu, dengue, and Zika viruses, exhibiting lower antiviral or negligible antiviral activity against other RNA viruses. The mechanism underlying their antiviral activity against WNV involved the alteration of sphingolipid metabolism. These compounds inhibited ceramide desaturase (Des1), promoting the accumulation of dihydrosphingomyelin (dhSM), a minor component of cellular sphingolipids with important roles in membrane properties. The addition of exogenous dhSM or Des1 blockage by using the reference inhibitor GT-11 {*N*-[(1*R*,2*S*)-2-hydroxy-1-hydroxymethyl-2-(2-tridecyl-1-cyclopropenyl)ethyl]octanamide} confirmed the involvement of this pathway in WNV infection. These results unveil the potential of novel antiviral strategies based on the modulation of the cellular levels of dhSM and Des1 activity for the control of flavivirus infection.

Climate change and the displaced person: how vectors and climate are changing the landscape of infectious

diseases among displaced and migrant populations.

Choi SH, Beer J, Charrow A.

May-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36912708/>

Lymphopenia with Altered T Cell Subsets in Hospitalized COVID-19 Patients in Pune, India.

Suryawanshi P, Takbhate B, Athavale P, Jali P, Memane N, Mirza S, Karandikar M, Kakrani AL, Kanitkar S, Gandham N, Barthwal MS, Dole S, Chaturvedi S, Pawale S, Tripathy A, Bhawalkar JS, Tripathy S.

Apr-2023

Viral Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36897333/>

Beauty and the beast: host microRNA-155 versus SARS-CoV-2.

Papadopoulos KI, Papadopoulou A, Aw TC.

May-2023

Hum Cell.

<https://pubmed.ncbi.nlm.nih.gov/36847920/>

Severe acute respiratory coronavirus 2 (SARS-CoV-2) infection in the young and healthy usually results in an asymptomatic or mild viral syndrome, possibly through an erythropoietin (EPO)-dependent, protective evolutionary landscape. In the old and in the presence of co-morbidities, however, a potentially lethal coronavirus disease 2019 (COVID-19) cytokine storm, through unrestrained renin-angiotensin aldosterone system (RAAS) hyperactivity, has been described. Multifunctional microRNA-155 (miR-155) elevation in malaria, dengue virus (DENV), the thalassemias, and SARS-CoV-1/2, plays critical antiviral and cardiovascular roles through its targeted translational repression of over 140 genes. In the present review, we propose a plausible miR-155-dependent mechanism whereby the translational repression of AGRT1, Arginase-2 and Ets-1, reshapes RAAS towards Angiotensin II (Ang II) type 2 (AT2R)-mediated balanced, tolerable, and SARS-CoV-2-protective cardiovascular phenotypes. In addition, it enhances EPO secretion and endothelial nitric oxide synthase activation and substrate availability, and negates proinflammatory Ang II effects. Disrupted miR-155 repression of AT1R + 1166C-allele, significantly associated with adverse cardiovascular and COVID-19 outcomes, manifests its decisive role in RAAS modulation. BACH1 and SOCS1 repression creates an anti-inflammatory and cytoprotective milieu, robustly inducing antiviral interferons. MiR-155 dysregulation in the elderly, and in comorbidities, allows unimpeded RAAS hyperactivity to progress towards a particularly aggressive COVID-19 course. Elevated miR-155 in thalassemia plausibly engenders a favorable cardiovascular profile and protection against malaria, DENV, and SARS-CoV-2. MiR-155 modulating pharmaceutical approaches could offer novel therapeutic options in COVID-19.

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

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

Apr-2023

Viral Immunol.

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

Development and validation of LC-MS/MS methods for the simultaneous quantification of sofosbuvir and its major metabolite (GS-331007) in blood plasma and cerebrospinal and seminal fluid: Application to a pilot clinical trial with a focus on Zika.

Vilhena LS, de Azevedo da Silva AC, Dias da Silva DM, Pinto DP, Coelho EF, de Araújo JFGM, da Silveira GPE, Pereira HM, da Silva LSFV, Estrela Marins RCE, Bortolini RG, Souza TML, Dos Santos VGV, de Assis Nascimento V, Amendoeira FC, da Fonseca LB.

May-2023

Biomed Chromatogr.

<https://pubmed.ncbi.nlm.nih.gov/36797051/>

Targeting first trimester trophoblast cell metabolism modulates its susceptibility to Zika virus infection.

Kafer D, Marquez A, Merech F, Hauk V, Paparini D, Ramhorst R, Leirós CP, García C, Vota D.

Apr-2023

J Cell Physiol.

<https://pubmed.ncbi.nlm.nih.gov/36790938/>

In the last 15 years Zika virus (ZIKV) caused several outbreaks of increasing scale in Micronesia, South Pacific islands, and more recently in the Caribbean and South America. The severity of the clinical presentation in neonates from pregnant women infected with ZIKV during the last outbreak supports the relevance of unraveling the mechanism of infection and viral persistence in the placenta with local viral isolates. Here, we investigated the relevance of trophoblast metabolic rewiring for viral multiplication and the role of the vasoactive intestinal peptide (VIP) as an endogenous factor associated with placental restriction to ZIKV infection at early pregnancy. Our in vitro model demonstrated that ZIKV triggers metabolic rewiring in first trimester cytotrophoblast-derived cells by increasing glucose utilization as fuel to sustain its replication, decreasing long-chain polyunsaturated fatty acid uptake, and promoting lipid droplets accumulation to favor its multiplication. Of note, variations in nutrient availability modulated viral spread in trophoblast cultures. The presence of VIP during trophoblast infection impaired ZIKV infective particle production and viral replication, restoring cell migration and metabolism. Moreover, the blockade of endogenous VIP signaling increased viral particle production and the viral entry receptor AXL expression. These results highlight the potential role of VIP as an endogenous antiviral factor related to trophoblast cell permissiveness to ZIKV infection at early pregnancy.

The Genetic Variant TNFA (rs361525) Is Associated with Increased Susceptibility to Developing Dengue Symptoms.

Villanueva-Aguilar ME, Rizo-de-la-Torre LDC, Granados-Muñiz MDP, Montoya-Fuentes A, Montoya-Fuentes H.
Apr-2023

Viral Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36730734/>

Dengue virus (DENV) is the causal agent of dengue fever. The symptoms and signs of dengue vary from febrile illness to hemorrhagic syndrome. *IFITM3* and *TNFA* are genes of the innate immune system. Variants *IFITM3* (rs12252 T>C) and *TNFA* (rs1800629 G > A and rs361525 G>A) might alter gene expression and change the course of the disease. Our first objective was to determine whether these variants were associated with the susceptibility and severity of dengue. The second was to assess the association of these variants with each symptom. We studied 272 cases with suspected dengue infection, of which 102 were confirmed dengue cases (DENV+) and 170 were dengue-like cases without DENV infection (DENV-). Samples of 201 individuals from the general population of Mexico were included as a reference. Genotyping was performed by the polymerase chain reaction-restriction fragment length polymorphism technique. Odds ratios and confidence intervals were calculated using Pearson's chi-square test and later adjusted for age and sex with a binary logistic regression model. Haldane correction is applied when necessary. We found a significantly higher frequency of the A allele of *TNFA* rs361525 in both the DENV+ and DENV- groups compared with the general population. Focusing on DENV+ and DENV-, the frequency of the A allele of *TNFA* rs361525 was higher in the DENV+ group. A broad spectrum of symptoms was related to the A allele of both *TNFA* variants. We conclude that *TNFA* rs361525 increases the susceptibility to symptomatic dengue but can also be associated with susceptibility to other dengue-like symptoms from unknown causes.

[Transmission routes of neuropathogenic pathogens-Possible mechanisms of neuroinvasion].

Craemer EM.

Apr-2023

Nervenarzt.

<https://pubmed.ncbi.nlm.nih.gov/36690702/>

Educational intervention for the control of Aedes aegypti with Wolbachia in Yucatan, Mexico.

Martinez-Cruz C, Arenas-Monreal L, Gomez-Dantes H, Villegas-Chim J, Barrera-Fuentes Gloria A, Toledo-Romani Maria E, Pavia-Ruz N, Che-Mendoza A, Manrique-Saide P.

Apr-2023

Eval Program Plann.

<https://pubmed.ncbi.nlm.nih.gov/36580820/>

A spectrum of viral diseases in Odisha state, eastern India: An evidence-based analysis from 2010-2017.

Sabat J, Subhadra S, Ho LM, Dwibedi B.

Apr-Jun 2023

J Postgrad Med.

<https://pubmed.ncbi.nlm.nih.gov/36571329/>

The 2019-2020 Dengue Fever Epidemic: Genomic Markers Indicating Severity in Dominican Republic Children.

Simpson BN, Mejía Sang ME, Collado Puello Y, Díaz Brockmans EJ, Díaz Soto MF, Rivera Defilló SM, Taveras Cruz KM, Santiago Pérez JO, Husami A, Day ME, Pilipenko V, Mena R, Mota C, Hostetter MK, Muglia LJ, Schlaudecker E, Gonzalez Del Rey J, Martin LJ, Prada CE.
18-04-2023

J Pediatric Infect Dis Soc.

<https://pubmed.ncbi.nlm.nih.gov/36537278/>

We performed an observational cohort study to assess associations between genetic factors of dengue fever (DF) severity in children in the Dominican Republic. A total of 488 participants had serologically confirmed DF. We replicated the association between the *IFIH1* gene (rs1990760) and severe DF ($n = 80/488$, $p = 0.006$) and identified novel associations needing further investigation.

Extract from Opuntia ficus-indica cladode delays the Aedes aegypti larval development by inducing an axenic midgut environment.

Nova ICV, de Almeida WA, Procópio TF, Godoy RSM, Miranda FR, Barbosa RC, Nascimento JDS, Paiva PMG, Ferreira MRA, Soares LAL, Pimenta PFP, Martins GF, Navarro DMDAF, Napoleão TH, Pontual EV.

May-2023

Arch Insect Biochem Physiol.

<https://pubmed.ncbi.nlm.nih.gov/35112391/>

This study evaluated the effects of acute exposure of *Aedes aegypti* third instar (L_3) larvae to the saline extract of *Opuntia ficus-indica* cladodes on the biological cycle and fertility of the emerging adults. For this, larvae were treated for 24 h with the extract at $\frac{1}{4}$ LC_{50} (lethal concentration to kill 50% of larvae), $\frac{1}{2}$ LC_{50} or LC_{50} ; the development and reproduction of the emerged adults were evaluated after a recovery period of 9 days. The resistance of proteins in the extract to hydrolysis by L_3 digestive enzymes and histomorphological alterations in the larval midgut were also investigated. The extract contained lectin, flavonoids, cinnamic derivatives, terpenes, steroids, and reducing sugars. It showed a LC_{50} of 3.71% for 48 h. The data indicated mean survival times similar in control and extract treatments. It was observed development delay in extract-treated groups, with a lower number of adults than in control. However, the females that emerged laid similar number of eggs in control and treatments. Histological evaluation revealed absence of bacterial and fungal microorganisms in the food content in midguts from larvae treated with cladode extract. Electrophoresis revealed that three polypeptides in the extract resisted to hydrolysis by L_3 digestive proteases for 90 min. The lectin activity was not altered even after 24-h incubation with the enzymes. In conclusion, the extract from *O. ficus-indica* can delay the development of *Ae.*

aegypti larvae, which may be linked to induction of an axenic environment at larval midgut and permanence of lectin activity even after proteolysis.

Dengue-Related Information Needs and Information-Seeking Behavior in Pakistan.

Ahmad M, Malik A, Mahmood K.

May-2023

Health Commun.

<https://pubmed.ncbi.nlm.nih.gov/34747288/>

Echinococcosis

Past and Present of Diagnosis of Echinococcosis: A Review (1999-2021).

Alvi MA, Ali RMA, Khan S, Saqib M, Qamar W, Li L, Fu BQ, Yan HB, Jia WZ.

18-04-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37080264/>

The larval forms of taeniid cestodes belonging to the genus *Echinococcus* are the source of the zoonotic infection known as echinococcosis. Alveolar and cystic echinococcosis are caused by *Echinococcus multilocularis* and *Echinococcus granulosus* (s. s) respectively. It is endemic in several regions of the world. In this systematic review, we describe diagnosis, and the species (human, canids, livestock, and small rodents) affected by cystic (CE) and alveolar echinococcosis (AE). From 1999 to 2021, we searched the online directory through PubMed, SCOPUS, Web of Science, and google scholar. Among the 37,700 records found in the online databases, 187 publications met our eligibility requirements. The majority of investigations employed a range of diagnostic methods, such as ELISA, imaging, copro-PCR, necropsy or arecoline hydrobromide purgation, morphological cestode confirmation, and fecal sieving/flotation to detect and confirm *Echinococcus* infection. ELISA was the most commonly used method followed by PCR, and imaging. The research team retrieved data describing the incidence or assessment of the diagnostic test for *E. multilocularis* in humans (N = 99), canids (N = 63), small ruminants (N = 13), large ruminants (N= 3), camel (N= 2), pigs (N=2) and small mammals (N= 5). This study was conducted to explore the diagnostic tools applied to detect echinococcosis in humans as well as animals in prevalent countries, and to report the characteristic of new diagnostic tests for disease surveillance. This systematic review revealed that ELISA (alone or in combination) was the most common method used for disease diagnosis and diagnostic efficacy and prevalence rate increased when recombinant antigens were used. It is highly recommended to use combination protocols such as serological with molecular and imaging technique to diagnose disease. Our study identified scarcity of data of reporting echinococcosis in humans/ animals in low-income or developing countries particularly central Asian countries. Study reports in small rodents indicate their role in disease dissemination but real situation in these host is not reflected due to limited number of studies. Even though echinococcosis affects

both public health and the domestic animal sector, therefore, it is important to devise new and strengthen implementation of the existing monitoring, judging, and control measures in this estimate.

Comparison of Isoenzyme pattern of *Echinococcus granulosus sensu stricto* (G1-G3) and *E. canadensis* (G6/G7) protoscoleces according to their Host Variation in Iran.

Dousti M, Sadjjadi SM, Solgi R, Vafafar A, Radfar A, Hatam GR.

08-02-2023

Iran Biomed J.

<https://pubmed.ncbi.nlm.nih.gov/37073115/>

Protoscolicidal effects of curcumin nanoemulsion against protoscoleces of *Echinococcus granulosus*.

Teimouri A, Jafarpour Azami S, Hashemi Hafshejani S, Ghanimatdan M, Bahreini MS, Alimi R, Sadjjadi SM.

18-04-2023

BMC Complement Med Ther.

<https://pubmed.ncbi.nlm.nih.gov/37072845/>

Background: The aim of the present study was to assess in vitro protoscolicidal effects of curcumin nanoemulsion (CUR-NE) against protoscoleces of cystic echinococcosis (CE)/hydatid cysts. **Methods:** The CUR-NE was prepared via spontaneous emulsification of soybean as the oil phase, a mixture of Tween 80 and Tween 85 as the surfactant, ethanol as the co-surfactant and distilled water. Various concentrations of CUR-NE (156, 312, 625 and 1250 µg/ml) were exposed to collected protoscoleces of infected sheep liver hydatid cysts for 10, 20, 30, 60 and 120 min. Viability of the protoscoleces were assessed using eosin exclusion test. Morphological changes of the protoscoleces were observed using differential interference contrast (DIC) microscopy. **Results:** The mean particle size and zeta potential of CUR-NE included 60.4 ± 14.8 nm and -16.1 ± 1.1 mV, respectively. Results showed that the viability of the protoscoleces decreased significantly with increases in CUR-NE concentrations ($p < 0.001$). The mortality rates of protoscoleces with exposure to concentrations of 1250 and 625 µg/ml of CUR-NE for 60 min were 94 and 73.33%, respectively. Mortality of the protoscoleces was 100% after 120 min of exposure to 1250 and 625 µg/ml concentrations of CUR-NE. Using NIC microscopy, extensively altered tegumental surface protoscoleces was observed after protoscoleces exposure to CUR-NE. **Conclusion:** The findings of the present study revealed the in vitro protoscolicidal potential of CUR-NE. Therefore, CUR-NEs are addressed as novel protoscolicidal agents, which can be used as an alternative natural medicine to kill the protoscoleces, owing to their low toxicity and significant inhibition potency. However, further studies are necessary to investigate pharmacologic and pharmacokinetics of CUR-NEs.

Can contrast-enhanced ultrasound differentiate the type of hepatic

echinococcosis: cystic echinococcosis or alveolar echinococcosis?

Zhang X, Suolang L, Ren Y, Wang Y, Jiang Y, Zhong X, Gou Z, Zhou W, Chen J, Li Y, Cai D.

17-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37069610/>

[Isolation of Cystic Echinococcosis Causative Agents of *Echinococcus equinus* and *Echinococcus ortleppi* Species from Humans in the Central Anatolia Region of Türkiye].

Eroglu F, Ordu M.

Apr-2023

Mikrobiyol Bul.

<https://pubmed.ncbi.nlm.nih.gov/37067210/>

Seropositivity Pattern of Human Cystic Echinococcosis at a Tertiary Care Hospital of India.

Das R, Gupta V, Khullar S, Verma N, Mirdha BR.

06-02-2023

J Lab Physicians.

<https://pubmed.ncbi.nlm.nih.gov/37064974/>

Cystic echinococcosis (CE), even after several control measures, causes significant morbidity throughout the world. Besides imaging investigation technology, the serological tests are essential for both diagnosis and management of this slowly progressive disease. The present study was a hospital-based retrospective study that examined the seropositivity rate for *Echinococcus granulosus sensu lato* antibody in patients suspected of CE at our tertiary health care center over 8 years from 2013 to 2020. Records of new visits to hospital/clinics and associated hospital discharge constituted the denominator of calculation. All samples were tested using commercially available indirect immunoglobulin G enzyme-linked immunosorbent assay kit. A total of 925 suspected patients with a clinical diagnosis of CE were screened. The age group that commonly tested positive for CE was 20 to 39 years, and liver was the predominant organ found to be affected. The seropositive rate was 41.2%. On further year-wise analysis, it was observed that the seropositivity rate had significantly declined from 61.4% in 2013 to 33.8% in 2020. This study clearly showed that there is a by 27.6% decline of CE seropositivity rate in 8 years. This declining rate may be attributed to improved socioeconomic status and better implementation of health programs.

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

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

13-02-2023

Microb Pathog.

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

Cystic echinococcosis (CE) is a zoonotic parasitic disease caused by the metacestode larva of *Echinococcus granulosus*. In this study, two-dimensional gel electrophoresis (2-DE) coupled with immunoblot analysis revealed that *E. granulosus* severin and 14-3-3zeta proteins (named EgSeverin and Eg14-3-3zeta, respectively) might be two potential biomarkers for serological diagnosis of echinococcosis. The recombinant EgSeverin (rEgSeverin, 45 kDa) and Eg14-3-3zeta (rEg14-3-3zeta, 35 kDa) were administered subcutaneously to BALB/c mice to obtain polyclonal antibodies for immunofluorescence analyses (IFAs). And IFAs showed that both proteins were located on the surface of protoscoleces (PSCs). Western blotting showed that both proteins could react with sera from *E. granulosus*-infected sheep, dog, and mice. Indirect ELISAs (rEgSeverin- and rEg14-3-3zeta-iELISA) were developed, respectively, with sensitivities and specificities ranging from 83.33% to 100% and a coefficient of variation (CV %) of less than 10%. The rEgSeverin-iELISA showed cross-reaction with both *E. granulosus* and *E. multilocularis*, while the rEg14-3-3zeta-iELISA showed no cross-reaction with other sera except for the *E. granulosus*-infected ones. The field sheep sera from Xinjiang and Qinghai were analyzed using rEgSeverin-iELISA, rEg14-3-3zeta-iELISA, and a commercial kit respectively, and no significant differences were found among the three methods ($p > 0.05$). However, the CE positive rates in sheep sera from Qinghai were significantly higher than those from Xinjiang ($p < 0.01$). Overall, the results suggest that EgSeverin and Eg14-3-3zeta could be promising diagnostic antigens for *E. granulosus* infection.

Chylothorax due to hepatic alveolar echinococcosis with infiltration of diaphragm and left pleura: a case report.

Schneider A, Klengel S, Lübbert C, Trawinski H.

14-04-2023

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37059979/>

Cystic Echinococcosis in Northern New Hampshire, USA.

AlSalman A, Mathewson A, Martin IW, Mahatanan R, Talbot EA.

May-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37044131/>

Filariose lymphatique

Biophysical and in-silico studies on the structure-function relationship of *Brugia malayi* protein disulfide isomerase.

Doharey PK, Verma P, Dubey A, Singh SK, Kumar M, Tripathi T, Alonazi M, Siddiqi NJ, Sharma B.

20-04-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37079006/>

Human Lymphatic filariasis is caused by parasitic nematodes *Wuchereria bancrofti*, *Brugia malayi*, and *Brugia timori*. Protein disulfide isomerase (PDI), a redox-active enzyme, helps to form and isomerize the disulfide bonds, thereby acting as a chaperone. Such activity is essential for activating many essential enzymes and functional proteins. *Brugia malayi* protein disulfide isomerase (BmPDI) is crucial for parasite survival and an important drug target. Here, we used a combination of spectroscopic and computational analysis to study the structural and functional changes in the BmPDI during unfolding. Tryptophan fluorescence data revealed two well-separated transitions during the unfolding process, suggesting that the unfolding of the BmPDI is non-cooperative. The binding of the fluorescence probe 8-anilino-1-naphthalene sulfonic acid dye (ANS) validated the results obtained by the pH unfolding. The dynamics of molecular simulation performed at different pH conditions revealed the structural basis of BmPDI unfolding. Detailed analysis suggested that under different pH, both the global structure and the conformational dynamics of the active site residues were differentially altered. Our multiparametric study reveals the differential dynamics and collective motions of BmPDI unfolding, providing insights into its structure-function relationship.

Burden of mosquito-borne diseases across rural versus urban areas in Cameroon between 2002 and 2021: prospective for community-oriented vector management approaches.

Alenou LD, Nwane P, Mbakop LR, Piameu M, Ekoko W, Mandeng S, Bikoy EN, Toto JC, Onguina H, Etang J.
19-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37076896/>

Background: Over the past two decades, Cameroon has recorded one of the highest rates of urban population growth in sub-Saharan Africa. It is estimated that more than 67% of Cameroon's urban population lives in slums, and the situation is far from improving as these neighbourhoods are growing at an annual rate of 5.5%. However, it is not known how this rapid and uncontrolled urbanization affects vector populations and disease transmission in urban versus rural areas. In this study, we analyse data from studies conducted on mosquito-borne diseases in Cameroon between 2002 and 2021 to determine the distribution of mosquito species and the prevalence of diseases they transmit with regards to urban areas versus rural areas. **Methods:** A search of various online databases, such as PubMed, Hinari, Google and Google Scholar, was conducted for relevant articles. A total of 85 publications/reports were identified and reviewed for entomological and epidemiological data from the ten regions of Cameroon. **Results:** Analysis of the findings from the reviewed articles revealed 10 diseases transmitted by mosquitoes to humans across the study regions. Most of these diseases were recorded in the Northwest Region, followed by the North, Far North and Eastern Regions. Data were collected from 37 urban and 28 rural sites. In the urban areas, dengue prevalence increased from 14.55% (95% confidence interval [CI] 5.2-

23.9%) in 2002-2011 to 29.84% (95% CI 21-38.7%) in 2012-2021. In rural areas, diseases such as Lymphatic filariasis and Rift valley fever, which were not present in 2002-2011, appeared in 2012-2021, with a prevalence of 0.4% (95% CI 0.0- 2.4%) and 10% (95% CI 0.6-19.4%), respectively. Malaria prevalence remained the same in urban areas (67%; 95% CI 55.6-78.4%) between the two periods, while it significantly decreased in rural areas from 45.87% (95% CI 31.1-60.6%) in 2002-2011 to 39% (95% CI 23.7-54.3%) in the 2012-2021 period (*P = 0.04). Seventeen species of mosquitoes were identified as involved in the transmission of these diseases, of which 11 were involved in the transmission of malaria, five in the transmission of arboviruses and one in the transmission of malaria and lymphatic filariasis. The diversity of mosquito species was greater in rural areas than in urban areas during both periods. Of the articles reviewed for the 2012-2021 period, 56% reported the presence of *Anopheles gambiae sensu lato* in urban areas compared to 42% reported in 2002-2011. The presence of *Aedes aegypti* increased in urban areas in 2012-2021 but this species was absent in rural areas. Ownership of long-lasting insecticidal nets varied greatly from one setting to another. **Conclusions:** The current findings suggest that, in addition to malaria control strategies, vector-borne disease control approaches in Cameroon should include strategies against lymphatic filariasis and Rift Valley fever in rural areas, and against dengue and Zika viruses in urban areas.

Human immune response against filarial HSP70 and its role in the diagnosis of lymphatic filariasis.

Ahmad F, Liebau E, Rathaur S.

18-04-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37073092/>

A sensitive and specific diagnostic kit is crucial for the detection of human lymphatic filariasis at the early stage of infection as the existing diagnostic tools are inefficient and expensive. In the present study, we have cloned and expressed *Brugia malayi* HSP70 (BmHSP70) protein and characterized it as a potential antigen for diagnosis of the asymptomatic microfilariae stage of *Wuchereria bancrofti* infection using ELISA, western blot, and bioinformatics tools. The antigenic efficacy of BmHSP70 was also compared with SchHSP70. The BmHSP70 and SchHSP70 peptide showed highly antigenic in nature and they showed immunogenic cross-reactivity endemic normal (EN) < chronic (CH) < microfilaraemic (MF) in IgG, IgG1, and IgG4 ELISA. IgG4-specific immunoblotting of BmHSP70 with MF sera further explicated its stage-specific antigenic cross-reactivity. These antigens (SchHSP70 and BmHSP70) showed a positive immunogenic correlation with the number of MF in blood samples. Thus, proposing BmHSP70 as a potential immunodiagnostic antigen against lymphatic filariasis. A triplet of GGMP tetrapeptide specific to the filarial HSP70 was also identified which was absent in human HSP70. In terms of sensitivity and specificity of antigens, these results suggest that recombinant BmHSP70 is a good antigen and could be used to diagnose early-stage of microfilariae infection.

Successful management of poisoning with ivermectin (Mectizan) in the Obala health district (Centre Region, Cameroon): a case report.

Donfo-Azafack C, Nana-Djeunga HC, Wafeu-Sadeu G, Dongmo-Yemele R, Kamgno J.

17-04-2023

J Med Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/37062821/>

Background: Ivermectin (Mectizan) is an anthelmintic drug that plays a major role in the fight against two major filarial diseases, onchocerciasis and lymphatic filariasis. Unlike previous drugs that had serious and sometimes fatal side effects, ivermectin has been considered to be safe and, therefore, is widely used. Data reporting the clinical presentation of poisoning with ivermectin are very scanty, even in experimental studies. **Case presentation:** In this paper, we report the case of a 19-year-old Black African female student residing in Obala (Centre Region, Cameroon) who was admitted to a health facility in Central Cameroon for a neurological disorder after intoxication with about 400 tablets of ivermectin 3 mg (~100 times the standard doses). This neurological disorder was characterized by somnolence, kinetic ataxia, increase of tendon reflex, and central visual disturbance. Management of this intoxication consisted of symptomatic treatment and monitoring of hemodynamic parameters for 5 days, with a favorable course. **Conclusions:** This is the first report of a poisoning with ivermectin at ~100 times the recommended dose. This case report confirms the safety and tolerability of ivermectin, even at exceptionally high dose.

Circulation of West Nile virus in mosquitoes approximate to the migratory bird stopover in West Coast Malaysia.

Natasha JA, Yasmin AR, Sharma RSK, Nur-Fazila SH, Nur-Mahiza MI, Arshad SS, Mohammed HO, Kumar K, Loong SK, Ahmad Khusaini MKS.

06-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37023172/>

Gale

Answer to April 2023 Photo Quiz.

Feng Y, Feng J, Qin B.

20-04-2023

J Clin Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37078716/>

Skin diseases in a nineteenth century English workhouse: analysis of the admission book for the Wakefield Workhouse Infirmary, 1826-1857.

Labbouze S, Manley AL, Gawkrödger DJ.

18-04-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37070391/>

Infectious diseases in the form of 'typhus' (74%) and 'fevers' (17%) were the commonest conditions accounting for entry to the Wakefield Workhouse Infirmary between 1826 and 1857, as recorded in the admissions book. Skin diseases were noted for 3.2% of admissions, principally scarlet fever (2%) and smallpox (1%). The mean age for primary dermatological admissions was 20 years (compared to 24 years for cases overall), with a mortality rate of 0.3%. The low number of smallpox cases may be the result of successful vaccination campaigns. The absence of admissions due to scabies (then known as 'the itch') might be due to exclusion of such cases from entry due to the known extreme infectivity of the condition. Workhouses played an important role in medical care in nineteenth century Britain but, in this example, skin diseases did not feature highly as causes of admission.

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

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

15-04-2023

Actas Dermosifiliogr.

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

[Outbreaks Due to Parasites: Examples from the World and Türkiye].

Ruh E, Taylan Özkan A.

Apr-2023

Mikrobiyol Bul.

<https://pubmed.ncbi.nlm.nih.gov/37067216/>

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

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

14-04-2023

Exp Appl Acarol.

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

Owing to difficulties in obtaining functional gene sequences, molecular pathogenic mechanisms in *Demodex* have been understudied. In this study, overlap extension PCR was used to obtain the sequences of cathepsin L (CatL), a pathogenicity-related gene, to provide a foundation for subsequent functional research. *Demodex folliculorum* and *Demodex brevis* mites were obtained from the face skin of Chinese individuals, and *Demodex canis* mites were isolated from the skin lesions of a dog. RNA was extracted and used to synthesise double-stranded cDNA. PCR amplification, cloning, sequencing, and bioinformatics analysis of CatL were performed. CatL gene sequences of 1005, 1008, and 1008 bp were successfully amplified for *D. brevis*, *D. folliculorum*, and *D. canis*, respectively. These sequences showed 99.9 or 100% identity with templates previously obtained by RNA-seq. The Maximum Likelihood (ML) phylogenetic tree showed that *D. folliculorum* clustered with *D. canis* first, then with *D. brevis*, and finally with

other Acariformes mite species. The three *Demodex* species had nine similar motifs to those of *Sarcoptes scabiei*, *Dermatophagoides pteronyssinus*, and *Dermatophagoides farinae*, and motifs 10-13 were valuable for identification. CatL proteins of *Demodex* species were predicted to be approximately 38 kDa, be located in lysosomes, have a signal peptide but no transmembrane region, and have two functional domains, I29 and Pept_C1. However, interspecific differences were observed in secondary and tertiary protein structures. In conclusion, we successfully obtained CatL sequences of three *Demodex* species by overlap extension PCR, which creates conditions for further pathogenic mechanism studies.

Scabies as a Neglected Tropical Disease in Iran: A Systematic Review with Meta-Analysis, during 2000-2022.

Khoobdel M, Azari-Hamidian S, Hanafi-Bojd AA, Bakhshi H, Jafari A, Moradi M.

30-09-2023

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37056644/>

Background: Scabies is referred to the infestation of skin by an ectoparasite, *Sarcoptes scabiei*. Having considerable financial consequences, this disease is a public health concern in several countries. In this review, we aimed to determine the current status of scabies in different provinces of Iran. **Methods:** Google Scholar, PubMed, Scopus, Science Direct, Scientific Information Database (SID), Sci-explore, Civilica, Magiran, Iranian Research Institute for Information Science and Technology and Elmnet databases were searched to find the related data in the time period within 2000-2022. To have a better insight into the status of prevalence of scabies in Iran, a meta-analysis and meta-regression was performed. **Results:** A total of 943 relevant studies were retrieved from the databases, and 62 eligible studies met all the needed criteria for inclusion in this systematic review. Scabies was investigated and reported in at least 22 and 21 provinces of Iran respectively. Most of the studies were conducted in Tehran, Razavi Khorasan, Hormozgan, Fars and Guilan Provinces. Positive samples of scabies belonged to humans, sheep, goats, dogs, rabbits, mice and gazelles. Meta-analysis showed that the overall estimated presence of scabies in Iran during 2000-2022 was 7% (95% CI 4.7-10.3%, $P < 0.001$). **Conclusion:** Infestations due to *S. scabiei* in Iran occur in different geographical locations and different climates. As a neglected tropical disease, the literature about the burden of scabies in Iran is inadequate. The present review highlights the importance of development of comprehensive strategies for the diagnosis and control of scabies, especially the provinces with high infestation rates.

Main mites associated with dermatopathies present in dogs and other members of the Canidae family.

Thomson P, Carreño N, Núñez A.

Feb-2023

Open Vet J.

<https://pubmed.ncbi.nlm.nih.gov/37073249/>

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

Genetic characterization of the zoonotic parasite *Ancylostoma caninum* in the central and eastern United States.

Quintana TA, Johnson WL, Ritchie D, Smith V, Martin KA, McMahan K, Brewer MT, Jesudoss Chelladurai JRJ.

18-04-2023

J Helminthol.

<https://pubmed.ncbi.nlm.nih.gov/37070361/>

Ancylostoma caninum is the most common nematode parasite of dogs in the United States. The present study aimed to describe the molecular epidemiology of *A. caninum* isolates from the central and eastern states of the United States using the partial mitochondrial cytochrome oxidase (*cox1*) gene and to compare them with those reported globally. We isolated eggs from faecal samples of dogs and characterized each isolate based on *cox1* sequences. A total of 60 samples originating from Kansas, Iowa, New York, Florida and Massachusetts were included. 25 haplotypes were identified in the United States dataset with high haplotype diversity (0.904). Sequence data were compared to sequences from other world regions available in GenBank. Global haplotype analysis demonstrated 35 haplotypes with a haplotype diversity of 0.931. Phylogenetic and network analysis provide evidence for the existence of moderate geographical structuring of *A. caninum* haplotypes. Our results provide an updated summary of *A. caninum* haplotypes and data for neutral genetic markers with utility for tracking hookworm populations. Sequences have been deposited in GenBank (ON980650-ON980674). Further studies of isolates from other regions are essential to understand the genetic diversity of this parasite.

Diversity and prevalence of gastrointestinal helminths of free-roaming dogs on coastal beaches in Ecuador: Potential for zoonotic transmission.

Calvopina M, Cabezas-Moreno M, Cisneros-Vásquez E, Paredes-Betancourt I, Bastidas-Caldes C.

May-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37068862/>

Free-roaming dogs are highly exposed to a range of zoonotic parasites, including helminths, which can be transmitted to humans, particularly in rural tropical settings of developing countries. To evidence the diversity and prevalence of gastrointestinal helminths in the stools of free-roaming dogs on the public Pacific coastal beaches of Ecuador, a cross-sectional study was conducted from August 2021 to August 2022. The sampling beaches are

located along the tropical Pacific coastal region. Stools were collected from the ground in containers with 10% formalin and processed using the Ritchie method; eggs were identified under a microscope. A total of 573 stools were examined from 20 beaches; the overall prevalence was 157 (27.4%) for one or more helminths. Ten parasites were identified, nine of which are potentially zoonotic. *Ancylostoma* spp. was the most prevalent (19.4%), followed by *Toxocara* spp. (7.2%). *Trichuris* spp., *Dipylidium caninum*, *Diphyllobothrium* spp., *Capillaria* spp., *Dicrocoelium* spp., *Heterobilharzia americana*, *Hymenolepis* spp. and *Spirocerca* spp. were also observed. Five of them are reported for the first-time infecting dogs in Ecuador. Hence, we evidenced that Ecuadorian beaches are highly contaminated with the dogs' zoonotic gastrointestinal helminths, posing a great risk to public health. Differences in the presence and prevalence were found in samples of tropical humid and dry climate zones. Therefore, based on our findings, we encourage the implementation of broad antiparasitic treatment and prevention strategies to reduce the zoonotic risk.

Prevalence and Risk Factors of Soil-Transmitted Helminthic Infections in the Pediatric Population in India: A Systematic Review and Meta-Analysis.

Chopra P, Shekhar S, Dagar VK, Pandey S.

17-08-2023

J Lab Physicians.

<https://pubmed.ncbi.nlm.nih.gov/37064993/>

Leishmaniose

Genome Analysis of Triploid Hybrid Leishmania Parasite from the Neotropics.

Van den Broeck F, Heeren S, Maes I, Sanders M, Cotton JA, Cupolillo E, Alvarez E, Garcia L, Tasia M, Marneffe A, Dujardin JC, Van der Auwera G.

May-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37081624/>

We discovered a hybrid *Leishmania* parasite in Costa Rica that is genetically similar to hybrids from Panama. Genome analyses demonstrated the hybrid is triploid and identified *L. braziliensis* and *L. guyanensis*-related strains as parents. Our findings highlight the existence of poorly sampled *Leishmania* (*Viannia*) variants infectious to humans.

Cutaneous Leishmaniasis Caused by Leishmania infantum, Israel, 2018-2021.

Solomon M, Astman N, Warshavsky K, Barzilai A, Meningher T, Avni D, Schwartz E.

May-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37081590/>

Cutaneous leishmaniasis (CL) is endemic to Israel. Previously, CL caused by *Leishmania infantum* had been

reported in Israel only once (in 2016). We report 8 *L. infantum* CL cases; 7 occurred during 2020-2021. None of the patients had systemic disease. *L. infantum* CL may be an emerging infection in Israel.

Leishmania donovani Transmission Cycle Associated with Human Infection, Phlebotomus alexandri Sand Flies, and Hare Blood Meals, Israel¹.

Studentsky L, Orshan L, Akad F, Ben Avi I, Diaz D, Elbaz S, Sagi O, Zagron G, Valinsky L, Davidovich-Cohen M, Baneth G.

May-2023

Emerg Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37080961/>

Canine visceral leishmaniasis diagnosis by UV spectroscopy of blood serum and machine learning algorithms.

Coelho ML, França T, Fontoura Mateus NL, da Costa Lima Junior MS, Cena C, do Nascimento Ramos CA.

18-04-2023

Photodiagnosis Photodyn Ther.

<https://pubmed.ncbi.nlm.nih.gov/37080349/>

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

Capasso C, Supuran CT.

20-04-2023

Expert Opin Ther Pat.

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

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

Using pentamidine to treat cutaneous leishmaniasis in children: a 10-year study in French Guiana.

Heleine M, Elenga N, Njueyon F, Martin E, Piat C, Pansart C, Couppie P, Hernandez M, Demar M, Blaizot R.
19-04-2023
Clin Exp Dermatol.
<https://pubmed.ncbi.nlm.nih.gov/37075241/>

Evaluation of Recombinase Polymerase Amplification assay for monitoring parasite load in patients with kala-azar and post kala-azar dermal leishmaniasis.

Roy M, Ceruti A, Kobialka RM, Roy S, Sarkar D, Wahed AAE, Chatterjee M.
19-04-2023
PLoS Negl Trop Dis.
<https://pubmed.ncbi.nlm.nih.gov/37075066/>

Background: The potential reservoirs of visceral leishmaniasis (VL) in South Asia include asymptomatic and relapsed cases of VL, along with patients with post kala-azar dermal leishmaniasis (PKDL). Accordingly, accurate estimation of their parasite load is pivotal for ensuring disease elimination, presently targeted for 2023. Serological tests cannot accurately detect relapses and/or monitor treatment effectiveness, and therefore, parasite antigen/nucleic acid based detection assays remain the only viable option. An excellent option is the quantitative polymerase chain reaction (qPCR) but the high cost, technical expertise and time involved precludes its wider acceptability. Accordingly, the recombinase polymerase amplification (RPA) assay operated in a mobile suitcase laboratory has emerged not simply as a diagnostic tool for leishmaniasis but also to monitor the disease burden.

Methodology/principal findings: Using total genomic DNA isolated from peripheral blood of confirmed VL cases (n = 40) and lesional biopsies of PKDL cases (n = 64), the kinetoplast-DNA based qPCR and RPA assay was performed and parasite load expressed as Cycle threshold (Ct) and Time threshold (Tt) respectively. Using qPCR as the gold standard, the diagnostic specificity and sensitivity of RPA in naïve cases of VL and PKDL was reiterated. To assess the prognostic potential of the RPA, samples were analyzed immediately at the end of treatment or ≥6 months following completion of treatment. In cases of VL, the RPA assay in terms of cure and detection of a relapse case showed 100% concordance with qPCR. In PKDL following completion of treatment, the overall detection concordance between RPA and qPCR was 92.7% (38/41). At the end of treatment for PKDL, 7 cases remained qPCR positive, whereas RPA was positive in only 4/7 cases, perhaps attributable to their low parasite load.

Conclusions/significance: This study endorsed the potential of RPA to evolve as a field applicable, molecular tool for monitoring parasite load, possibly at a point of care level and is worthy of consideration in resource limited settings.

Development of a Novel Enzyme-Linked Immunosorbent Assay and Lateral Flow Test System for Improved Serodiagnosis of Visceral Leishmaniasis in Different Areas of Endemicity.

Mahdavi R, Shams-Eldin H, Witt S, Latz A, Heinz D, Fresco-Taboada A, Aira C, Hübner MP, Sukyte D, Visekruna A, Teixeira HC, Abass E, Steinhoff U.
19-04-2023
Microbiol Spectr.
<https://pubmed.ncbi.nlm.nih.gov/37074181/>

Retrospective study of 613 canine cytologically normal bone marrows associated to altered hemograms: description, possible interpretation, and review of the principal physiological hematopoietic mechanisms.

Turinelli V, Rossi G, Gavazza A.
Feb-2023
Open Vet J.
<https://pubmed.ncbi.nlm.nih.gov/37073242/>

Background: In clinical routine, it can happen that to an abnormal hemogram corresponds an unexpected cytological normal bone marrow examination that can be difficult to interpret and to manage. **Aim:** This cytologically retrospective study wants to evaluate a consistent number of qualitative and quantitative normal bone marrow exams according to the hematological and clinical-pathological data to judge if this normality is by itself a pathologic state. **Methods:** Six hundred and thirteen bone marrow samples were examined. The bone marrow cytological examinations were performed using morphological and numerical criteria together with a complete hemogram, after the identification of clinical or hematological alterations such as multiple lymph nodes enlarged, positive leishmania serological result, staging of neoplasia, cytopenia, increased number of cells, or suspicion of malignant blood disorders. **Results:** Of the 613 bone marrow samples evaluated, 85 (14%) were classified as normal or without cytological abnormalities; however, only 28 (33%) of those cases had a normal hemogram associated, whereas 55 (65%) had one or more cytopenia and 2 (2%) had increased blood cells count. **Conclusion:** From this study emerges that cytological bone marrow examinations without any morphological or numerical abnormalities are often associated with altered hematological exams and for this reason, they should not be considered normal and should lead to other deepened investigations.

Structural Modelling of Platelet Activating Factor Acetyl Hydrolase in Leishmania donovani, Trypanosoma cruzi, and Trypanosoma brucei: Implications on Therapeutics for Leishmaniasis, Chagas Disease, and Sleeping Sickness.

Goswami A, Koley T, Rajan MV, Madhuri P, Upadhyay N, Das U, Kumar M, Ethayathulla AS, Hariprasad G.
11-04-2023
Infect Drug Resist.
<https://pubmed.ncbi.nlm.nih.gov/37070125/>

Purpose: Leishmaniasis, Chagas disease, and sleeping sickness are caused by protozoa *Leishmania donovani*, *Trypanosoma cruzi*, and *Trypanosoma brucei*, respectively.

Platelet activating factor acetyl hydrolase (PAF-AH) is an inflammatory protein implicated in pathogenesis of these three infections, thereby making them attractive drug targets. **Methods:** PAF-AH sequences were retrieved from UniProt and aligned using Clustal Omega. Homologous models of parasitic proteins were built based on crystal structure of human PAF-AH and validated using PROCHECK server. Volumes of substrate-binding channel were calculated using the ProteinsPlus program. High throughput virtual screening using Glide program in Schrodinger was done with ZINC drug library against parasitic PAF-AH enzymes. Complexes with best hits were energy-minimized and subjected to 100 ns molecular dynamic simulation and analyzed. **Results:** PAF-AH enzyme sequences from protozoa *Leishmania donovani*, *Trypanosoma cruzi*, *Trypanosoma brucei*, and human have a minimum of 34% sequence similarity with each other. Corresponding structures show a globular conformation consisting of twisted β -pleated sheets, flanked by α -helices on either side. Catalytic triad of serine-histidine-aspartate is conserved. Substrate-binding channel residues are conserved to an extent, with a lower channel volume in human as compared to target enzymes. Drug screening resulted in identification of three molecules that had better affinities than the substrate to the target enzymes. These molecules fulfill Lipinski's rules for drug likeness and also bind with less affinity to the human counterpart, thereby establishing a high selective index. **Conclusion:** Structures of PAF-AH from protozoan parasites and humans belong to the same family of enzymes and have a similar three-dimensional fold. However, they show subtle variations in residue composition, secondary structure composition, substrate-binding channel volume, and conformational stability. These differences result in certain specific molecules being potent inhibitors of the target enzymes while simultaneously having weaker binding to human homologue.

Clinical features, immunological interactions and household determinants of visceral leishmaniasis and malaria coinfections in West Pokot, Kenya: protocol for an observational study.

van Dijk N, Carter J, Omondi W, Mens P, Schallig H.
17-04-2023
BMJ Open.
<https://pubmed.ncbi.nlm.nih.gov/37068901/>

Immunological profile of two canine breeds in an endemic region of *Leishmania infantum*.

Macià M, Marín-García PJ, Ahuir-Baraja AE, Llobat L.
May-2023
Vet Parasitol Reg Stud Reports.
<https://pubmed.ncbi.nlm.nih.gov/37068864/>

Visceral leishmaniasis is the one of the most important protozoal zoonoses in Europe, and it is caused by *Leishmania infantum*, an intracellular protozoan parasite. The disease is endemic in dogs in the Mediterranean area.

The main goal of this work is to correlate the levels of several cytokines linked to immune response against *L. infantum* infection in two canine breeds. Thirty-one Boxer and twenty-eight Ibizan Hound dogs living in the Valencian Community (East coast of Spain) were analyzed for the presence of anti-*Leishmania* antibodies in serum by IFAT test. Cytokines IFN- γ , TNF- α , IL-2, IL-6, IL-8, and IL-18 were determined by ELISA commercial tests. The levels of IFN- γ , IL-2, and IL-18 in our study, cytokines linked to a cellular immune response, were higher ($p < 0.05$) in the Ibizan Hound breed; IL-6 levels were higher, although not significant, and only levels of IL-8 were higher in Boxer than in Ibizan Hound. No expression of TNF- α was found. These results corroborate that Ibizan Hound can develop a protective response against canine leishmaniasis, while Boxer is a susceptible breed. The study of immunological aspects in the different canine breeds may represent a useful tool in the prediction of the disease.

Molecular detection of vector-borne pathogens in cats tested for FIV and FeLV.

Melo TB, Silva TRM, Almeida TLAC, Tutija JF, Silva AOD, Lira MDS, Amorim D, Giannelli A, Ramos CADN, Alves LC, Carvalho GA, Ramos RAN.
May-2023
Vet Parasitol Reg Stud Reports.
<https://pubmed.ncbi.nlm.nih.gov/37068860/>

Nanoemulsions for increased penetrability and sustained release of leishmanicidal compounds.

García DJ, Fernández-Culma M, Upegui YA, Ríos-Vásquez LA, Quiñones W, Ocampo-Cardona R, Echeverri F, Vélez ID, Robledo SM.
17-04-2023
Arch Pharm (Weinheim).
<https://pubmed.ncbi.nlm.nih.gov/37068175/>

In the last decade, the World Health Organization has driven the development of drugs for topical use in patients with cutaneous leishmaniasis (CL), the most prevalent clinical form of leishmaniasis, a neglected tropical disease. The chemicals C₆ I, TC1, and TC2 were reported as promising antileishmanial drugs. We aimed to develop a topical nanoformulation that enhances the advantageous effect of C₆ I, TC1, and TC2, guaranteeing higher stability and bioavailability of the pharmacologically active components through the topical route. Nanoemulsions were prepared by ultrasonication based on oleic acid (0.5 g). A relation of Tween®-80/ethanol (1:3) and water was obtained; physicochemical characterization of all formulations was performed, and the preliminary stability and transdermal penetration of these nanoemulsions were also investigated. Newtonian-type fluids with high load capacity, 147-273 nm globule size, and -15 to -18 mV zeta potential were obtained with differential permeability rates in the first pig ear skin assay, first-order kinetics-release model for C₆ I, and Weibull for TC1 and TC2. The nanoemulsion showed good stability, high encapsulation efficiency, and higher leishmanicidal activity against *Leishmania braziliensis* with lower cytotoxicity in U937

macrophages. In conclusion, nanoemulsions of ethanol-oleic acid/Tween®-80 increase the activity of compounds with leishmanicidal activity by increasing their penetration and sustained release.

Dermis resident macrophages orchestrate localized ILC2-eosinophil circuitries to maintain their M2-like properties and promote non-healing cutaneous leishmaniasis.

Sacks D, Lee SH, Kang B, Kamenyeva O, Ferreira T, Cho K, Khillan J, Kabat J, Kelsall B.

05-04-2023

Res Sq.

<https://pubmed.ncbi.nlm.nih.gov/37066418/>

Tissue-resident macrophages (TRMs) are critical for tissue homeostasis/repair. We previously showed that dermal TRMs produce CCL24 (eotaxin2) which mediates their interaction with IL-4 producing eosinophils, required to maintain their number and M2-like properties in the T_H1 environment of the *Leishmania major* infected skin. Here, we unveil another layer of TRM self-maintenance involving their production of TSLP, an alarmin typically characterized as epithelial cell-derived. Both TSLP signaling and IL-5⁺ innate lymphoid cell 2 (ILC2s) were shown to maintain the number of dermal TRMs and promote infection. Single cell RNA sequencing identified the dermal TRMs as the sole source of TSLP and CCL24. Development of *Ccl24-cre* mice permitted specific labeling of dermal TRMs, as well as interstitial TRMs from other organs. Genetic ablation of TSLP from dermal TRMs reduced the number of dermal TRMs, and disease was ameliorated. Thus, by orchestrating localized type 2 circuitries with ILC2s and eosinophils, dermal TRMs are self-maintained as a replicative niche for *L. major*.

Corrigendum: Co-infection of Phlebotomus papatasi (Diptera: Psychodidae) gut bacteria with Leishmania major exacerbates the pathological responses of BALB/c mice.

Amni F, Maleki-Ravasan N, Nateghi-Rostami M, Hadighi R, Karimian F, Meamar AR, Badirzadeh A, Parvizi P.

29-03-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37065207/>

Autophagy in protists and their hosts: When, how and why?

Romano PS, Akematsu T, Besteiro S, Bindschedler A, Carruthers VB, Chahine Z, Coppens I, Descoteaux A, Alberto Duque TL, He CY, Heussler V, Le Roch KG, Li FJ, de Menezes JPB, Menna-Barreto RFS, Mottram JC, Schmuckli-Maurer J, Turk B, Tavares Veras PS, Salassa BN, Vanrell MC.

2023

Autophagy Rep.

<https://pubmed.ncbi.nlm.nih.gov/37064813/>

A difficult to treat Leishmania infantum relapse after allogeneic stem cell transplantation.

Arts RJW, Ector GICG, Bosch-Nicolau P, Molina I, McCall MBB, van der Velden WJFM, van Laarhoven A, de Mast Q, van Dorp S.

29-03-2023

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/37063784/>

Here we describe a complicated case of a relapsed *Leishmania infantum* infection after an allogeneic stem cell transplantation (allo-SCT) for primary myelofibrosis. Three years earlier the patient had been diagnosed with a hemophagocytic lymphohistiocytosis secondary to a visceral *Leishmania infantum* infection, for which he was effectively treated with a cumulative dose of 40 mg/kg liposomal amphotericin B. During the first disease episode he was also diagnosed with primary myelofibrosis for which he received medical follow-up. One year later ruxolitinib was started due to progressive disease. No *Leishmania* relapse occurred. Nevertheless, the marrow fibrosis progressed, and an allo-SCT was performed. Two months after allo-SCT prolonged fever and a persistent pancytopenia occurred, which was due to a relapse of visceral Leishmaniasis. The infection was refractory to a prolonged treatment with liposomal amphotericin B with a cumulative dose up to 100 mg/kg. Salvage treatment with miltefosine led to reduction of fever within a few days and was followed by a slow recovery of pancytopenia over the following months. The *Leishmania* parasite load by PCR started to decline and after 3.5 months no *Leishmania* DNA could be detected anymore and follow-up until ten months afterwards did not show a relapse.

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

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

06-04-2023

Eur J Med Chem.

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

Leishmania infection in patients with Inflammatory Bowel Disease: case series and literature review.

Pitarch LG, Almela P, Nos P.

13-04-2023

Gastroenterol Hepatol.

<https://pubmed.ncbi.nlm.nih.gov/37061089/>

Seroprevalence of Leishmania infantum in outdoor workers from southern Italian endemic regions.

Morea A, Stufano A, Sgroi G, De Benedictis L, Bezerra-Santos MA, Mendoza-Roldan JA, Veneziano V, Otranto D, Lovreglio P, Iatta R.

14-04-2023

Zoonoses Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37060161/>

Visceral leishmaniasis is a zoonotic vector-borne disease caused by *Leishmania infantum*. The infection often remains asymptomatic, though clinical forms may occur in immunosuppressed individuals. Although data on leishmaniasis in humans are available worldwide, the exposure to *L. infantum* of workers conducting outdoor activities has been scantily investigated, and it is limited to military personnel operating in endemic regions. This study aimed to assess the seroprevalence of *L. infantum* in different groups of outdoor workers and the occupational risk factors. The cross-sectional study was performed on 229 workers including forestry guards, farmers, veterinarians, geologists and agronomists from three regions of southern Italy (i.e., Apulia, Basilicata and Campania). All serum samples were screened for *L. infantum*-specific IgG/IgM by using automated indirect chemiluminescent immunoassays. Overall, 5.7% (13/229) of workers was positive to anti-*L. infantum* antibodies, with the highest seroprevalence in veterinarians (13.6%). An increased occupational health surveillance for *L. infantum* infection in outdoor workers is essential to better understand the risk of exposure in specific jobs. Furthermore, guidelines and education along with a One Health collaboration among veterinarians, physicians, parasitologists and occupational health care professionals are crucial for the prevention of this disease.

Genetic haplotypes associated with immune response to *Leishmania infantum* infection in dogs.

Álvarez L, Marín-García PJ, Llobat L.

14-04-2023

Vet Res Commun.

<https://pubmed.ncbi.nlm.nih.gov/37059873/>

Molecular Detection of *Leishmania* Infection in Phlebotomine Sand Flies from an Endemic Focus of Zoonotic Cutaneous Leishmaniasis in Iran.

Mohammadi-Azni S, Kalantari M, Pourmohammadi B.

30-09-2022

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37056645/>

Background: Due to the outbreak of zoonotic cutaneous leishmaniasis (ZCL), a disease caused by *Leishmania major* and mainly transmitted by *Phlebotomus papatasi*, in Damghan City, Semnan Province, the probable vectors of the disease were investigated in the city from 20 March 2016 to 20 January 2018. **Methods:** Sand flies were collected from indoors and outdoors biweekly by sticky traps in different parts of the city. The trapped sand flies were stored in 70% ethanol. They were identified and checked for *Leishmania* infections using nested-PCR method and specific primers; CSB1XR, CSB2XF, LiR, and 13Z. **Results:** Overall, 1862 phlebotomine sand flies of *Ph. papatasi* (48.8%), *Ph. andrejevi* (8.3%), *Ph. caucasicus* (7.7%), *Ph. mongolensis* (2%), *Ph. sergenti* (1.2%), *Ph. alexandri* (0.7%), *Sergentomyia murgabiensis sintoni* (29.3%), and *Se. sumbarica* (2%) were collected indoors

(31.1%) and outdoors (68.9%). The highest and lowest numbers of collected sand flies were belonging to *Ph. papatasi* (48.8%) and *Ph. alexandri* (0.7%) respectively. 2.2% of the examined sand flies were shown to be infected with *L. major* and all were belonging to *Ph. papatasi*. **Conclusion:** This study confirms the report of *Ph. papatasi* infection with *L. major* and also the existence of *Ph. sergenti* and *Ph. alexandri*, the potential vectors of *L. tropica* and *L. infantum* respectively, in Damghan City. According to the findings, it is necessary for health officials to plan and take action to prevent the occurrence of ZCL epidemic in the city as well as the occurrence of other forms of leishmaniasis.

A Sero-Epidemiological Study on Visceral Leishmaniasis among Volunteer Children and Adults in Rural Areas of Shahroud, Iran 2018-2019.

Ghodrati S, Akhoundi B, Mohebbali M, Zeinali M, Hajjarian H, Kakooei Z.

30-09-2023

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37056641/>

Background: Visceral leishmaniasis (VL) also known as Kala-azar is considered as one of the zoonotic infections in Mediterranean countries. The disease reservoir and vectors are dogs and sandflies respectively. Due to reported sporadic cases of Kala-azar in the past five years in Shahroud County, Semnan Province, Iran, this study aimed to investigate the status of this infection in this area and to determine its seroepidemiology to take required measurements for infection control and treatment. **Methods:** This study was conducted on 504 subjects residing in seven villages in Shahroud County. Blood samples were randomly selected using the cluster sampling method and were collected from subjects aged up to 13 years old (90%) and adults over 13 years old (10%) from September to May 2019. After separating sera from whole blood, samples were subjected to direct agglutination test (DAT) to detect anti-*Leishmania infantum* antibodies. A range of 1:10 to 1:800 dilutions were prepared from the samples. **Results:** Results of 1:800 titration indicated that no sample was positive for antibodies against *L. infantum*. After the secondary screening, 10 cases (1.98%) showed the antibody titer of 1:100, while four cases (0.79%) showed the antibody titer of 1:400. Of 14 cases with the *L. infantum* antibodies, all were detected from the children <13 years old. According to clinical findings, no patient was suffering from fever, weight loss, splenomegaly, hepatomegaly, and cachexia and therefore did not show the Kala-azar symptoms. **Conclusion:** The results of the current study indicate that Kala-azar is not prevalent in Shahroud County.

Molecular Identification of *Leishmania infantum* kDNA in Naturally Infected Dogs and Their Fleas in an Endemic Focus of Canine Visceral Leishmaniasis in Iran.

Azarm A, Dalimi A, Mohebbali M, Mohammadiha A, Pirestani M, Zarei Z, Zahraei-Ramazani A.

30-09-2023

J Arthropod Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37056639/>

Experimental feeding of *Sergentomyia minuta* on reptiles and mammals: comparison with *Phlebotomus papatasi*.

Ticha L, Volfova V, Mendoza-Roldan JA, Bezerra-Santos MA, Maia C, Sadlova J, Otranto D, Volf P.

13-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37055860/>

Evaluation of expression variations in virulence-related genes of *Leishmania major* after several culture passages compared with *Phlebotomus papatasi* isolated promastigotes.

Nemati Haravani T, Parvizi P, Hejazi SH, Sedaghat MM, Eskandarian A, Nateghi Rostami M.

13-04-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37053214/>

Cutaneous leishmaniasis (CL) is a prevalent infectious disease with considerable morbidity annually. Here, we aimed to investigate the likely variations in gene expression of glycoprotein63 (gp63), heat shock protein 70 (HSP70), histone, arginase, cysteine protease B (CPB), *Leishmania* homologue of receptors for activated C kinase (LACK), small hydrophilic endoplasmic reticulum-associated protein (SHERP) in metacyclic promastigotes of *L. major* isolated from *Phlebotomus papatasi* sand flies and promastigotes excessively cultured in culture medium. The parasites were collected from suspected CL cases in Pasteur Institute of Iran, cultured and inoculated into the female BALB/c mice (2×10⁶ promastigotes). Sand flies were trapped in Qom province, fed with the blood of euthanized infected mice and subsequently dissected in order to isolate the midgut including stomodeal valve. The metacyclic promastigotes were isolated from *Ph. papatasi* (Pro-Ppap) using peanut agglutinin test (PNA), then continuously cultured in RPMI-1640 medium enriched with fetal bovine serum, penicillin (100 U/ml) and streptomycin (100 mg/ml) to reach stationary phase (Pro-Stat). The gene expression was evaluated in both parasitic stages (Pro-Ppap and Pro-Stat) using qRT-PCR. Out results showed a significant increased gene expression at Pro-Ppap stage for gp63 ($P = 0.002$), SHERP ($P = 0.001$) and histone ($P = 0.026$) genes, in comparison with Pro-Stat stage. Noticeably, significant changes were, also, demonstrated in 10th to 15th passages [gp63 ($P = 0.041$), arginase ($P = 0.016$), LACK ($P = 0.025$)] and in 5th to 20th passage (SHERP) ($P = 0.029$). In conclusion, the findings of the present study seem to be essential in designing *Leishmania* studies, in particular regarding host-parasite interaction, immunization and infectivity studies.

The cytokine/chemokine response in *Leishmania*/HIV infection and co-infection.

Maksoud S, El Hokayem J.

01-04-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37082641/>

HIV infection progressively weakens the immune system by infecting and destroying cells involved in host defense. Viral infection symptoms are generated and aggravated as immunosuppression progresses, triggered by the presence of opportunistic infections: among these is leishmaniasis, a disease caused by the intracellular parasite *Leishmania*. The incidence of this co-infection is growing progressively due to the geographic distribution overlap. Both pathogens infect monocytes/macrophages and dendritic cells, although they can also modulate the activity of other cells without co-infecting, such as T and B lymphocytes. *Leishmania*/HIV co-infection could be described as a system comprising modulations of cell surface molecule expression, production of soluble factors, and intracellular death activities, leading ultimately to the potentiation of infectivity, replication, and spread of both pathogens. This review describes the cytokine/chemokine response in *Leishmania*/HIV infection and co-infection, discussing how these molecules modulate the course of the disease and analyzing the therapeutic potential of targeting this network.

Biophysical and modeling-based approach for the identification of inhibitors against DOHH from *Leishmania donovani*.

Katiki M, Sharma M, Neetu N, Rentala M, Kumar P.

13-04-2023

Brief Funct Genomics.

<https://pubmed.ncbi.nlm.nih.gov/35809341/>

Lèpre

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

Ghosh S, Saha S, Roy PK.

18-04-2023

J Theor Biol.

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

Methotrexate as a corticosteroid-sparing agent in leprosy reactions: A French multicenter retrospective study.

Jaume L, Hau E, Monsel G, Mahé A, Bertolotti A, Petit A, Le B, Chauveau M, Duhamel E, Maisonneuve T, Bagot M, Bouaziz JD, Mougari F, Cambau E, Jachiet M; Groupe d'infectiologie en dermatologie et des infections sexuellement transmissibles (GridIST).

20-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37079647/>

Introduction: Leprosy reactions (LRs) are inflammatory responses observed in 30%-50% of people with leprosy. First-line treatment is glucocorticoids (GCs), often

administered at high doses with prolonged courses, resulting in high morbi-mortality. Methotrexate (MTX) is an immunomodulating agent used to treat inflammatory diseases and has an excellent safety profile and worldwide availability. In this study, we describe the efficacy, GCs-sparing effect and safety of MTX in LR. **Methods:** We conducted a retrospective multicentric study in France consisting of leprosy patients receiving MTX for a reversal reaction (RR) and/or erythema nodosum leprosum (ENL) since 2016. The primary endpoint was the rate of good response (GR) defined as the complete disappearance of inflammatory cutaneous or neurological symptoms without recurrence during MTX treatment. The secondary endpoint was the GCs-sparing effect, safety and clinical relapse after MTX discontinuation. **Results:** Our study included 13 patients with LR (8 men, 5 women): 6 had ENL and 7 had RR. All patients had had at least one previous course of GCs and 2 previous treatment lines before starting MTX. Overall, 8/13 (61.5%) patients had GR, allowing for GCs-sparing and even GCs withdrawal in 6/11 (54.5%). No severe adverse effects were observed. Relapse after MTX discontinuation was substantial (42%): the median relapse time was 5.5 months (range 3-14) after stopping treatment. **Conclusion:** MTX seems to be an effective alternative treatment in LR, allowing for GCs-sparing with a good safety profile. Furthermore, early introduction during LR may lead to a better therapeutic response. However, its efficacy seems to suggest prolonged therapy to prevent recurrence.

Improvement and characterization of oral absorption behavior of clofazimine by SNEDDS: Quantitative evaluation of extensive lymphatic transport.

Yamanouchi K, Ishimaru T, Kakuno T, Takemoto Y, Kawatsu S, Kondo K, Maruyama M, Higaki K.

17-04-2023

Eur J Pharm Biopharm.

<https://pubmed.ncbi.nlm.nih.gov/37076052/>

Clofazimine, an anti-leprosy drug, has been anticipated for a candidate to treat tuberculosis, cryptosporidiosis, and coronavirus infection, but its low oral bioavailability is considered a reason for its limited activity. In the current study, we have tried to improve the oral bioavailability of clofazimine by several SNEDDS formulations and characterized the absorption behavior from various aspects. Among four SNEDDS formulations prepared, SNEDDS A, prepared with castor oil as an oil component, provided the highest bioavailability (around 61%) and SNEDDS D, prepared with Capryol 90, gave the second highest bioavailability. SNEDDS A formed the finest nanoparticles, which were maintained under gastric and intestinal luminal conditions. The comparison in oral bioavailability between the SNEDDS formulation and its corresponding preformed nanoemulsion suggested that SNEDDS A would efficiently form nanoemulsion in the gastrointestinal tract after oral administration. AUC of mesenteric lymph node concentration was the highest for SNEDDS A, which would be one of the reasons for SNEDDS A to reveal the highest oral bioavailability. A cycloheximide-treated oral absorption study and single-pass perfusion study by utilizing a vascular-luminal

perfused small intestine-liver preparation clearly indicated that over 90% of clofazimine absorbed to systemic circulation should be derived from lymphatic transport for both SNEDDS A and D. Furthermore, the fraction of dose absorbed was around 65% for SNEDDS D, but SNEDDS A achieved around 94%, indicating the excellent performance of SNEDDS A.

Burden of Typhoid and Paratyphoid Fever in India.

John J, Bavdekar A, Rongsen-Chandola T, Dutta S, Gupta M, Kanungo S, Sinha B, Srinivasan M, Shrivastava A, Bansal A, Singh A, Koshy RM, Jinka DR, Thomas MS, Alexander AP, Thankaraj S, Ebenezer SE, Karthikeyan AS, Kumar D, Njarekkattuvalappil SK, Raju R, Sahai N, Veeraraghavan B, Murhekar MV, Mohan VR, Natarajan SK, Ramanujam K, Samuel P, Lo NC, Andrews J, Grassly NC, Kang G; NSSEFI Study Team.

20-04-2023

N Engl J Med.

<https://pubmed.ncbi.nlm.nih.gov/37075141/>

Antimicrobial Stewardship Program: Time to be focused in speciality settings of leprosy institute and related health care setup.

Thangaraju P, Velmurugan H, Venkatesan S.

17-04-2023

Recent Adv Antiinfect Drug Discov.

<https://pubmed.ncbi.nlm.nih.gov/37070443/>

Inhibitory effect of natural compounds on Dihydropteroate synthase of Mycobacterium leprae: Molecular dynamic study.

Khan M, Khan S, Bushara NZA, Ali R, Tabassum Z, Ishrat R, Marouf HA, Sherwani S, Mirza S, Haque S.

17-04-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/37070201/>

Leprosy is a chronic infectious disease caused by a bacillus, *Mycobacterium leprae*. According to official data from 139 countries in the 6 WHO Regions, there were 127558 new leprosy cases worldwide in 2020. Leprosy mainly affects the skin, the peripheral nerves, mucosa of the upper respiratory tract, and the eyes. If this disease is left untreated, can harm the skin, nerves, limbs, eyes, and skin permanently. The disease is curable with multidrug therapy. Over a period of time *Mycobacterium leprae* has become resistant to these drugs. Therefore, new therapeutic molecules are warranted. This study was aimed to carry out the in-silico analysis to determine the inhibitory effect of natural compounds on Dihydropteroate synthase (DHPS) of *Mycobacterium leprae*. The DHPS is a key enzyme in the folate biosynthesis pathway in *M. leprae* and acts as a competitive inhibitor of PABA. The 3D structure of DHPS protein was modeled using homology modeling and was validated. Molecular docking and simulation along with other in-silico methods were employed to determine the inhibitory effect of ligand molecules towards DHPS target protein. Results revealed

ZINC03830554 molecule as a potential inhibitor of DHPS. Binding experiments and bioassays utilizing this strong inhibitor molecule against purified DHPS protein are necessary to validate these early findings. Communicated by Ramaswamy H. Sarma.

Obinutuzumab in Refractory Phospholipase A2 receptor-Associated Membranous Nephropathy With Severe CKD.

Naik S, Shukla S, Av N, Kumar V, Sekar A, Nada R, Rath M, Kohli HS, Ramachandran R.

31-01-2023

Kidney Int Rep.

<https://pubmed.ncbi.nlm.nih.gov/37069971/>

Association between asthma, rhinitis and atopic dermatitis with leprosy: A case-control study.

Tenório MDL, Araujo JMS, de Melo EV, Cazzaniga RA, Aragão AF, Valois LQ, Severo J, Santos-Filho MAA, Menezes-Silva L, Machado JA, Reed SG, Duthie MS, de Almeida RP, Bezerra-Santos M, de Jesus AR.

02-02-2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37067141/>

Background Considering the cross-regulation of Th1 and Th2 responses, we hypothesised that atopic diseases (Th2) inhibit the protective Th1 immune response to *Mycobacterium leprae* and exacerbates leprosy. **Objective** In this study, we aimed to evaluate the association between leprosy and atopic diseases. **Methods** To evaluate the association of atopic diseases with leprosy, we conducted a case-control study that included leprosy patients (n = 333) and their household contacts (n = 93). The questionnaire from the International Study of Asthma and Allergies in Childhood, which is validated in several countries for epidemiological diagnosis of atopic diseases, was applied to determine the occurrence of atopic diseases, allergic rhinitis, asthma, and atopic dermatitis among leprosy patients and the household contacts. **Results** Considering clinical and epidemiological data, among the leprosy group 51.6% (n = 172) were determined to have at least one atopic disease, while atopy was observed less frequently at 40.86% among household contacts (n = 38). When two or more atopic diseases were assessed, the frequency was significantly higher among the leprosy patients than in the household contacts (21.9% vs. 11.8%; P-value = 0.03). Likewise, the frequency of asthma was significantly higher among leprosy patients (21%) than in the household contacts (10.8%; P-value = 0.02). Thus, our analyses revealed an association of atopic diseases with leprosy, with a significant linear increase in the occurrence of leprosy with an increase in the number of atopic diseases (P-value = 0.01). **Limitation** Due to the difficulties in recruiting household contacts that have prolonged contact with patients, but are not genetically related to the patient, the household contacts group is smaller than the leprosy patient group. **Conclusion** The data reveal an association between atopic diseases and leprosy outcomes. This

knowledge could improve the treatment of leprosy patients with co-incident atopic diseases.

21-year trend of new leprosy cases in Guangdong, China: An analysis of surveillance data from 2000 to 2020.

Wang X, Lin X, Zhao P, Chen L, Zheng D, Yang B.

01-03-2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37067134/>

Lichens in dermatology.

Ramesh H, Somashekhar S, Kanathur S.

01-03-2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37067120/>

Recurrent targetoid hemosiderotic hemangioma with spontaneous resolution in a male.

Prashant Chopra S, Madke B, Bhardwaj M.

01-03-2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37067111/>

Students' perception of self-directed learning in dermatology: A survey.

Singh A, Rudrappa Kanthraj G, Shastry V, Gowdappa Hatthur B.

01-03-2023

Indian J Dermatol Venereol Leprol.

<https://pubmed.ncbi.nlm.nih.gov/37067108/>

Recurrent erythema nodosum leprosum leading to secondary renal amyloidosis and nephrotic syndrome in an Indian patient with lepromatous leprosy.

Ahuja R, Garg S, Barwad A, Subbiah A, Gupta V.

17-04-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37066445/>

Tuberculosis management and referral practices among traditional medicine practitioners in Lagos, Nigeria.

Adepoju VA, Oladimeji O, Sibiya MN, Inegbeboh J, Egesemba G.

01-03-2023

J Public Health Afr.

<https://pubmed.ncbi.nlm.nih.gov/37065812/>

Introduction: Despite the potential role of Traditional Birth Attendants (TBAs) and Traditional Healers (THs), little is known about their knowledge of tuberculosis (TB) management and referral practices in Nigeria. **Objective:** To determine knowledge and self-reported practices of traditional birth attendants and traditional healers in managing TB in Lagos, Nigeria. **Methods:** A cross-sectional study of 120 THs and TBAs in three high TB burden Local

Government Areas (LGAs) in Lagos, Nigeria. Data were collected between April 2018 to September 2018 through interviewer-administered questionnaires. We used Statistical Package for Social Sciences software for data analyses. Independent predictors of being TBA or TH were determined using logistic regression at the statistical significance of $P < 0.05$ and 95% confidence interval. **Results:** TB knowledge increased from 52.7% pre-test to 61.7% post-test and did not differ between TBAs and THs. Of the 120 Traditional Medical Practitioners studied, 70% (84) never treated TB; 57.3 % (69) ever referred chronic cough patients to a health facility; 90% (108) were willing to collaborate with National Tuberculosis, Leprosy and Buruli Ulcer Control Programme (NTBLCP), 85% (102) attached monetary and token incentive as a condition for the collaboration. THs had decreased odds of ever referring TB patient to the hospital (AOR: 0.3, 95% CI: 0.14-0.64, $P = 0.002$); currently referring TB patients (AOR: 0.06, 95% CI: 0.02-0.17, $P < 0.0001$) and consulting <40 patients in a year (AOR: 0.22, 95% CI: 0.09-0.53, $P < 0.0001$). **Conclusion:** Majority of the THs and TBAs were willing to collaborate with NTBLCP in the identification and referral of Presumptive TB patients. We suggest that NTBLCP empowers the TBAs and THs to help with an early referral of TB patients.

Valorization of *Adhatoda vasica* leaves: Extraction, in vitro analyses and in silico approaches.

Rudrapal M, Vallinayagam S, Aldosari S, Khan J, Albadrani H, Al-Shareeda A, Kamal M.
17-03-2023
Front Nutr.
<https://pubmed.ncbi.nlm.nih.gov/37063312/>

Leonine facies and madarosis in lepromatous leprosy.

Palaniappan V, Karthikeyan K.
01-12-2022
Postgrad Med J.
<https://pubmed.ncbi.nlm.nih.gov/37063004/>

Dermoscopy of Hailey-Hailey disease in dark skin: a multicentric observational controlled study by the International Dermoscopy Society Task Force on "Imaging in Skin of Color".

Ankad BS, Errichetti E, Lallas A, Chauhan P, Malani S, Neema S, Bhat YJ, Vinay K, Behera B, Khare S.
14-04-2023
Int J Dermatol.
<https://pubmed.ncbi.nlm.nih.gov/37057614/>

Obituary.

Khan AM.
Jun-2022
Indian J Med Res.
<https://pubmed.ncbi.nlm.nih.gov/37056080/>

JAK inhibitors in dermatology: the road travelled and path ahead, a narrative review.

Muddebihal A, Khurana A, Sardana K.
Apr-2023
Expert Rev Clin Pharmacol.
<https://pubmed.ncbi.nlm.nih.gov/36946306/>

Introduction: Numerous cutaneous dermatoses mediated by cytokines depend on the JAK STAT pathway for intracellular signaling. JAK inhibitors form a useful therapeutic approach in treating these conditions. The literature on effectiveness of JAK inhibitors in treatment of alopecia areata, vitiligo, atopic dermatitis, psoriasis and several other inflammatory and autoimmune diseases is growing although very few conditions have sufficiently well performed studies to their credit and, barring a few indications, their use in rest remains empirical as yet. **Areas covered:** A search of the PubMed database was made using the keywords Janus kinase inhibitors OR JAK inhibitors AND dermatology with the time duration limited to the last 5 years. Here, we review the JAK STAT pathway, the various conditions in which JAK inhibitors are currently used in dermatology, and other conditions their use is being explored in. **Expert opinion:** The pathology of a large number of dermatological disorders is mediated via inflammatory cytokines which signal via the JAK STAT pathway. JAKinibs have shown great promise in treating cutaneous disorders refractory to conventional therapy. Their current clinical use in dermatology is based on robust evidence (for some), and anecdotal evidence for most other dermatoses.

Treatment recalcitrant cases of tinea corporis/cruris caused by T. mentagrophytes - interdigitale complex with mutations in ERG11 ERG 3, ERG4, MDR1 MFS genes & SQLE and their potential implications.

Bhattacharyya A, Sadhasivam S, Sinha M, Gupta S, Saini S, Singh H, Khurana A, Sachdeva S, Sardana K, Ghosh S.
May-2023
Int J Dermatol.
<https://pubmed.ncbi.nlm.nih.gov/36929499/>

Background: Recalcitrant dermatophyte infections are being reported from various parts of the world due to varied causes including strain variation, steroid misuse, SQLE mutations, and variable quality of itraconazole pellet formulations. The oral drug preferred in endemic areas is itraconazole, to which MIC levels remain low, and clinical failures to itraconazole reported defy a sound scientific explanation. **Objectives:** The objective of the study was to conduct a proteomic and genomic analysis on isolates from therapeutically recalcitrant case with isolation of gene mutations and enzymatic abnormalities to explainazole failures. **Methods:** Trichophyton mentagrophyte interdigitale complex strains were isolated from seven clinically non-responding tinea corporis/cruris patients, who had failed a sequential course of 6 weeks of terbinafine 250 mg QD and itraconazole 100 mg BID. After AFST 1 strain, KA01 with high MIC to most drugs was characterized using whole genome sequencing,

comparative proteomic profiling, and total sterol quantification. **Results:** Sterol quantification showed that the standard strain of *Trichophyton mentagrophytes* (MTCC-7687) had half the ergosterol content than the resistant KA01 strain. Genomic analysis revealed mutations in SQLE, ERG4, ERG11, MDR1, MFS genes, and a novel ERG3 mutation. Proteomic analysis established the aberrant expression of acetyl Co-A transferase in the resistant strain and upregulation of thioredoxin reductase and peroxiredoxin. **Conclusion:** Our findings demonstrate possible reasons for multidrug resistance in the prevalent strain with mutations in genes that predict terbinafine (SQLE) and azole actions (ERG4, ERG11, ERG3) apart from efflux pumps (MDR1, MFS) that can explain multidrug clinical failures.

Development of treatment-decision algorithms for children evaluated for pulmonary tuberculosis: an individual participant data meta-analysis.

Gunasekera KS, Marcy O, Muñoz J, Lopez-Varela E, Sekadde MP, Franke MF, Bonnet M, Ahmed S, Amanullah F, Anwar A, Augusto O, Aurilio RB, Banu S, Batool I, Brands A, Cain KP, Carratalá-Castro L, Caws M, Click ES, Cranmer LM, García-Basteiro AL, Hesselning AC, Huynh J, Kabir S, Lecca L, Mandalakas A, Mavhunga F, Myint AA, Myo K, Nampijja D, Nicol MP, Orikiriza P, Palmer M, Sant'Anna CC, Siddiqui SA, Smith JP, Song R, Thuong Thuong NT, Ung V, van der Zalm MM, Verkuil S, Viney K, Walters EG, Warren JL, Zar HJ, Marais BJ, Graham SM, Debray TPA, Cohen T, Seddon JA.

May-2023

Lancet Child Adolesc Health.

<https://pubmed.ncbi.nlm.nih.gov/36924781/>

Mindin (SPON2) Is Essential for Cutaneous Fibrogenesis in a Mouse Model of Systemic Sclerosis.

Rana I, Kataria S, Tan TL, Hajam EY, Kashyap DK, Saha D, Ajnabi J, Paul S, Jayappa S, Ananthan ASHP, Kumar P, Zaarour RF, Haarshaadri J, Kansagara G, Rizvi A, Zirmire RK, Badarinath K, Khedkar SU, Chandra Y, Samuel R, George R, Danda D, Jacob PM, Dey R, Dhandapany PS, He YW, Varga J, Varghese S, Jamora C.

May-2023

J Invest Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36528128/>

Systemic sclerosis is a fibrotic disease that initiates in the skin and progresses to internal organs, leading to a poor prognosis. Unraveling the etiology of a chronic, multifactorial disease such as systemic sclerosis has been aided by various animal models that recapitulate certain aspects of the human pathology. We found that the transcription factor SNAI1 is overexpressed in the epidermis of patients with systemic sclerosis, and a transgenic mouse recapitulating this expression pattern is sufficient to induce many clinical features of the human disease. Using this mouse model as a discovery platform, we have uncovered a critical role for the matricellular protein Mindin (SPON2) in fibrogenesis. Mindin is produced by SNAI1 transgenic skin keratinocytes and aids

fibrogenesis by inducing early inflammatory cytokine production and collagen secretion in resident dermal fibroblasts. Given the dispensability of Mindin in normal tissue physiology, targeting this protein holds promise as an effective therapy for fibrosis.

Severe iron deficiency anemia causing trichorrhhexis nodosa - an unusual presentation.

Sakthibalan R, Menon R, David BG.

May-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36518006/>

Generalised cutaneous plasmacytomas as initial manifestation in a patient of IgA multiple myeloma.

Batra A, Vaniyath S, Kumar S, Melanda H, Kumari N, Hazarika N, Nath UK.

Feb-2022

Postgrad Med J.

<https://pubmed.ncbi.nlm.nih.gov/37066582/>

Morsures de serpent

Effect of the snake venom component crotamine on lymphatic endothelial cell responses and lymph transport.

Si H, Yin C, Wang W, Davies P, Sanchez E, Suntravat M, Zawieja D, Cromer W.

Apr-2023

Microcirculation.

<https://pubmed.ncbi.nlm.nih.gov/35689804/>

Objective: The pathology of snake envenomation is closely tied to the severity of edema in the tissue surrounding the area of the bite. Elucidating the mechanisms that promote the development of such severe edema is critical to a better understanding of how to treat this life-threatening injury. We focused on one of the most abundant venom components in North American viper venom, crotamine, and the effects it has on the cells and function of the lymphatic system. **Methods:** We used RT-PCR to identify the location and relative abundance of crotamine's cellular targets (Kvα channels) within the tissues and cells of the lymphatic system. We used calcium flux, nitrate production, and cell morphometry to determine the effects of crotamine on lymphatic endothelial cells. We used tracer transport, node morphometry, and node deposition to determine the effects of crotamine on lymph transport in vivo. **Results:** We found that genes that encode targets of crotamine are highly present in lymphatic tissues and cells and that there is a differential distribution of those genes that correlates with phasic contractile activity. We found that crotamine potentiates calcium flux in human dermal lymphatic endothelial cells in response to stimulation with histamine and sheer stress (but not alone) and that it alters the production of nitric oxide in response to shear as well as changes the level of F-actin polymerization of those same cells. Crotamine alters lymphatic transport of large molecular weight

tracers to local lymph nodes and is deposited within the node mostly in the immediate subcapsular region.

Conclusion: This evidence suggests that snake venom components may have an impact on the function of the lymphatic system. This needs to be studied in greater detail as there are numerous venom components that may have effects on aspects of the lymphatic system. This would not only provide basic information on the pathobiology of snakebite but also provide targets for improved therapeutics to treat snakebite.

Mycétome

Genetic variability of the 16S rRNA gene of *Nocardia brasiliensis*, the most common causative agent of actinomycetoma in Latin America and the Caribbean.

Cruz-Medrano MG, Manzanares-Leal GL, González-Nava J, Moreno-Pérez PA, Sandoval-Trujillo H, Ramírez-Durán N.

14-04-2023

Rev Inst Med Trop Sao Paulo.

<https://pubmed.ncbi.nlm.nih.gov/37075338/>

Knowledge and attitudes towards cervical cancer prevention among women in Khartoum state, Sudan.

Siddig EE, Ahmed A, Ahmed ES, Mohammed MA, Kunna E, El-Sadig SM, Ali Y, Hassan RA, Ali ET, Mohamed NS.

Jan-Dec 2023

Womens Health (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37070544/>

Background: Cervical cancer is considered the third leading cause of death among women worldwide, and human papillomavirus was identified as a major causative agent for developing cervical cancer. **Objectives:** This study aimed to assess the knowledge and attitudes towards cervical cancer prevention among women in Khartoum state, Sudan. **Design:** A community-based cross-sectional study implemented in Khartoum state, Sudan, from 1 August 2020 to 1 September 2020. **Methods:** We conducted a descriptive cross-sectional community-based study using an electronic questionnaire for data collection. Descriptive statistics, frequency, mean, and percentage were computed. **Results:** The study included 716 female participants with a mean age of 27.6 + 8.7 years. 580 (81.0%) and 229 (32.0%) had heard about cervical cancer and Pap test, respectively. cervical cancer was assumed related to alcohol consumption 109 (15.2%), giving birth to many children 51 (7.1%), ageing 118 (16.5%), and having many sexual partners 335 (46.8%). In addition, 300 (41.9%) attributed cervical cancer to having human papillomavirus infection, 256 (35.6%) to the prolonged use of contraceptives, and 162 (22.6%) to smoking. Knowledge about the best time to be vaccinated against human papillomavirus, 110 (15.4%) stated it is better after marriage. Regression models to predict the effectors on participants' knowledge and attitudes showed a low standard deviation of the estimates with higher values of the adjusted R² [R: 0.041, 0.017, and 0.006; std: 1.527,

0.417, and 0.426]. This indicates the combined influence of occupation, educational level, family income, and marital status on the participant's knowledge and attitude levels. **Conclusion:** This study revealed that the participant's knowledge and attitudes levels are mainly driven by their occupation, educational level, family income, and marital status altogether. This underscores the need for a countrywide community engagement campaign through health education and raising awareness sessions, and massive social media to sensitize the community and healthcare providers about the risk of cervical cancer and the available prevention and control measures.

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

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

17-04-2032

Chem Biodivers.

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

Eumycetoma, the fungal form of the neglected tropical disease mycetoma, is a crippling infectious disease with low response rates to currently available antifungal drugs. In this study, a series of natural naphthoquinones and anthraquinones was evaluated for their activity against *Madurella mycetomatis*, which is the most common causative agent of eumycetoma. The metabolic activity of *Madurella mycetomatis* as well as the viability of *Galleria mellonella* larvae upon treatment with quinones was investigated. Several hydroxy-substituted naphthoquinones exhibited activity against *Madurella mycetomatis*. In particular, naphthazarin (5,8-dihydroxy-1,4-naphthoquinone) was identified as a considerably active antifungal compound against *Madurella mycetomatis* (IC₅₀ = 1.4 µM), while it showed reduced toxicity to *Galleria mellonella* larvae, which is a well-established in vivo invertebrate model for mycetoma drug studies.

Rage

Clinical characterization and placental pathology of mpox infection in hospitalized patients in the Democratic Republic of the Congo.

Pittman PR, Martin JW, Kingebeni PM, Tamfum JM, Mwema G, Wan Q, Ewala P, Alonga J, Bilulu G, Reynolds MG, Quinn X, Norris S, Townsend MB, Satheshkumar PS, Wadding J, Soltis B, Honko A, Güereña FB, Korman L, Patterson K, Schwartz DA, Huggins JW; Kole Human Mpox Infection Study Group.

20-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37079637/>

Quantifying the interconnectedness between poverty, health access, and rabies mortality.

Taylor E, George K, Johnson E, Whitelegg H, Prada JM, Horton DL.

20-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37079553/>

The global 2030 goal set by the World Organization for Animal Health (WOAH), the World Health Organization (WHO), and the Food and Agriculture Organization (FAO), to eliminate dog-mediated human rabies deaths, has undeniably been a catalyst for many countries to re-assess existing dog rabies control programmes. Additionally, the 2030 agenda for Sustainable Development includes a blueprint for global targets which will benefit both people and secure the health of the planet. Rabies is acknowledged as a disease of poverty, but the connections between economic development and rabies control and elimination are poorly quantified yet, critical evidence for planning and prioritisation. We have developed multiple generalised linear models, to model the relationship between health care access, poverty, and death rate as a result of rabies, with separate indicators that can be used at country-level; total Gross Domestic Product (GDP), and current health expenditure as a percentage of the total gross domestic product (% GDP) as an indicator of economic growth; and a metric of poverty assessing the extent and intensity of deprivation experienced at the individual level (Multidimensional Poverty Index, MPI). Notably there was no detectable relationship between GDP or current health expenditure (% GDP) and death rate from rabies. However, MPI showed statistically significant relationships with per capita rabies deaths and the probability of receiving lifesaving post exposure prophylaxis. We highlight that those most at risk of not being treated, and dying due to rabies, live in communities experiencing health care inequalities, readily measured through poverty indicators. These data demonstrate that economic growth alone, may not be enough to meet the 2030 goal. Indeed, other strategies such as targeting vulnerable populations and responsible pet ownership are also needed in addition to economic investment.

Addressing vaccine-preventable encephalitis in vulnerable populations.

Piamonte BLC, Easton A, Wood GK, Davies NWS, Granerod J, Michael BD, Solomon T, Thakur KT.

20-04-2023

Curr Opin Neurol.

<https://pubmed.ncbi.nlm.nih.gov/37078664/>

Purpose of review: Vaccinations have been pivotal in lowering the global disease burden of vaccine-preventable encephalitides, including Japanese encephalitis, tick-borne encephalitis, measles encephalitis, and rabies encephalitis, among others. **Recent findings:** Populations vulnerable to vaccine-preventable infections that may lead to encephalitis include those living in endemic and rural areas, military members, migrants, refugees, international travelers, younger and older persons, pregnant women, the immunocompromised, outdoor, healthcare and laboratory workers, and the homeless. There is scope for improving the availability and distribution of vaccinations, vaccine equity, surveillance of

vaccine-preventable encephalitides, and public education and information. **Summary:** Addressing these gaps in vaccination strategies will allow for improved vaccination coverage and lead to better health outcomes for those most at risk for vaccine-preventable encephalitis.

Distribution of *Baylisascaris procyonis* in Raccoons (*Procyon lotor*) in Florida, USA.

Cunningham MW, Wolf DP, Sayler KA, Milleson M, Bankovich B, Schueller P, Haley BS, Stura S, Yabsley MJ.

20-04-2023

J Wildl Dis.

<https://pubmed.ncbi.nlm.nih.gov/37074793/>

Coinfection of Canine Distemper Virus and Rabies Virus in Wildlife Samples Submitted for Routine Rabies Testing.

Moessner H, Brunt S, Diaz A, Davis A.

20-04-2023

J Wildl Dis.

<https://pubmed.ncbi.nlm.nih.gov/37074768/>

Transmission dynamics of lyssavirus in *Myotis myotis*: mechanistic modelling study based on longitudinal seroprevalence data.

Kim Y, Leopardi S, Scaravelli D, Zecchin B, Priori P, Festa F, Drzewnioková P, De Benedictis P, Nouvellet P.

26-04-2023

Proc Biol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37072038/>

We investigated the transmission dynamics of lyssavirus in *Myotis myotis* and *Myotis blythii*, using serological, virological, demographic and ecological data collected between 2015 and 2022 from two maternity colonies in northern Italian churches. Despite no lyssavirus detection in 556 bats sampled over 11 events by reverse transcription-polymerase chain reaction (RT-PCR), 36.3% of 837 bats sampled over 27 events showed neutralizing antibodies to *European bat lyssavirus 1*, with a significant increase in summers. By fitting sets of mechanistic models to seroprevalence data, we investigated factors that influenced lyssavirus transmission within and between years. Five models were selected as a group of final models: in one model, a proportion of exposed bats (median model estimate: 5.8%) became infectious and died while the other exposed bats recovered with immunity without becoming infectious; in the other four models, all exposed bats became infectious and recovered with immunity. The final models supported that the two colonies experienced seasonal outbreaks driven by: (i) immunity loss particularly during hibernation, (ii) density-dependent transmission, and (iii) a high transmission rate after synchronous birthing. These findings highlight the importance of understanding ecological factors, including colony size and synchronous birthing timing, and potential infection heterogeneities to enable more robust assessments of lyssavirus spillover risk.

Rabies virus infection is associated with variations in calbindin D-28K and calretinin mRNA expression levels in mouse brain tissue.

Korie GC, Sallau AB, Kanu B, Kia GSN, Kwaga JKP.

18-04-2023

Arch Virol.

<https://pubmed.ncbi.nlm.nih.gov/37069450/>

Rabies virus (RABV) infection leads to a fatal neurological outcome in humans and animals and is associated with major alterations in cellular gene expression. In this study, we describe the effects of RABV infection on the mRNA expression levels of two genes, encoding the Ca²⁺-binding proteins (Ca-BPs) calbindin D-28K (Calb1) and calretinin (Calb2), in the brains of BALB/c mice. Sixty 4-week-old mice were divided into two test groups and one control group. Mice were inoculated intramuscularly with either a street rabies virus (SRV) strain or a challenge virus standard (CVS-11) strain and sacrificed at 3-day intervals up to day 18 postinfection. A direct fluorescent antibody test (DFAT) was used to verify the presence of RABV antigen in brain tissues, and real-time quantitative PCR (RT-PCR) was used to assess gene expression. Infection with both RABV strains resulted in significant ($p < 0.05$) increases in Calb1 and Calb2 expression in the test animals when compared with the controls at various time points in the study. Correlation analysis indicated very weak insignificant ($p > 0.05$) negative and positive relationships, respectively, between Calb1 expression ($r = -0.04$) and Calb2 expression ($r = 0.08$) with viral load (CVS-11 strain). Insignificant ($p > 0.05$) relationships were also observed Calb1 expression ($r = -0.28$) and Calb2 expression ($r = 0.06$) and viral load for the SRV strain. The observed alterations in Calb1 and Calb2 expression in this study indicate possible impairments in neuronal Ca²⁺ buffering and Ca²⁺ homeostasis as a result of RABV infection and, consequently, possible involvement of calbindin-D28K and calretinin in the neuropathogenesis of rabies.

Monosynaptic inputs to ventral tegmental area glutamate and GABA co-transmitting neurons.

Pr Vost ED, Phillips A, Lauridsen K, Enserro G, Rubinstein B, Alas D, McGovern DJ, Ly A, Banks M, McNulty C, Kim YS, Fenno LE, Ramakrishnan C, Deisseroth K, Root DH.

07-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37066408/>

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

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

31-03-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37065250/>

Altered connectomes of adult-born granule cells following engraftment of

GABAergic progenitors in the mouse hippocampus.

Arshad MN, Pinto A, van Praag H, Naegle JR.

13-04-2023

Prog Neurobiol.

<https://pubmed.ncbi.nlm.nih.gov/37061022/>

Adult neurogenesis occurs in the dentate gyrus (DG) of the rodent hippocampus throughout life, producing new granule cells (GCs) that migrate from a stem cell niche called the subgranular zone (SGZ) into the adjacent granule cell layer (GCL). Seizures associated with temporal lobe epilepsy alter adult neurogenesis and promote the formation of hyperexcitable circuits. Stem cell therapies for treating intractable seizure disorders are based on the premise that transplantation of GABAergic interneurons will strengthen inhibitory connections within the hippocampus and reduce hyperexcitability. Grafts of medial ganglionic eminence (MGE)-derived fetal GABAergic progenitors into the DG of adult mice with pilocarpine-induced TLE have been shown to suppress spontaneous recurrent seizures. In addition, the transplanted cells formed functional inhibitory synaptic connections with hippocampal neurons, including adult-born GCs. However, it is unknown whether MGE grafts change adult-born GC connectivity. To address this question, we compared the first-order monosynaptic inputs to adult-born GCs in TLE mice with or without MGE-derived interneuron grafts. Here we show that TLE increased excitatory inputs from endogenous hippocampal, entorhinal cortex, and medial septum/diagonal band neurons onto adult-born GCs. In contrast, in TLE mice with grafts, these excitatory inputs were reduced, coinciding with transplanted GABAergic interneuron innervation of adult-born GCs. These findings indicate that GABAergic interneuron transplantation into the dentate gyrus may prevent epilepsy-associated alterations in the connectivity of adult-born GCs.

SARS-CoV-2 spike ectodomain targets $\alpha 7$ nicotinic acetylcholine receptors.

O'Brien BCV, Weber L, Hueffer K, Weltzin MM.

13-04-2023

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/37061001/>

Virus entry into animal cells is initiated by attachment to target macromolecules located on host cells. The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) trimeric spike glycoprotein targets host angiotensin converting enzyme 2 to gain cellular access. The SARS-CoV-2 glycoprotein contains a neurotoxin-like region that has sequence similarities to the rabies virus and the human immunodeficiency virus glycoproteins, as well as to snake neurotoxins, which interact with nicotinic acetylcholine receptor (nAChR) subtypes via this region. Using a peptide of the neurotoxin-like region of SARS-CoV-2 (SCoV2P), we identified that this area moderately inhibits $\alpha 3\beta 2$, $\alpha 3\beta 4$ and $\alpha 4\beta 2$ subtypes, while potentiating and inhibiting $\alpha 7$ nAChRs. These nAChR subtypes are found in target tissues including the nose, lung, central nervous system and immune cells. Importantly, SCoV2P potentiates and inhibits ACh-induced $\alpha 7$ nAChR responses

by an allosteric mechanism, with nicotine enhancing these effects. Live-cell confocal microscopy was used to confirm that SCoV2P interacts with $\alpha 7$ nAChRs in transfected neuronal-like N2a and human embryonic kidney 293 cells. The SARS-CoV-2 ectodomain functionally potentiates and inhibits the $\alpha 7$ subtype with nanomolar potency. Our functional findings identify that the $\alpha 7$ nAChR is a target for the SARS-CoV-2 glycoprotein, providing a new aspect to our understanding of SARS-CoV-2 and host cell interactions, in addition to disease pathogenesis.

Portable reduced graphene oxide biosensor for detection of rabies virus in bats using nasopharyngeal swab samples.

Chalhua R, Akashi L, Zuñiga J, Beatriz de Carvalho Ruthner Batista H, Moratelli R, Champi A.

31-03-2023

Biosens Bioelectron.

<https://pubmed.ncbi.nlm.nih.gov/37060864/>

The pathogenesis of zoonotic viral infections: Lessons learned by studying reservoir hosts.

Begeman L, van Riel D, Koopmans MPG, Kuiken T.

28-03-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37056741/>

Schistosomiasis

Ultrasound aspects and risk factors associated with urogenital schistosomiasis among primary school children in Mali.

Agniwo P, Sidibé B, Diakité A, Niaré SD, Guindo H, Akplogan A, Ibikounlé M, Boissier J, Dabo A.

30-04-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/37081494/>

Background: Urogenital schistosomiasis is endemic in Mali and is a major cause of serious morbidity in large parts of the world. This disease is responsible for many socio-economic and public health issues. The aim of this study was to investigate the impact of the disease on morbidity and to describe demographic and socioeconomic factors in relation to the status of children with urogenital schistosomiasis in Mali. **Methods:** We conducted a cross-sectional study in November 2021 of 971 children aged 6 to 14 years selected at random from six schools in three districts in the Kayes Region of Mali. Demographic and socioeconomic data were collected on survey forms. Clinical data were collected following a medical consultation. Hematuria was systematically searched for through the use of strips. The search for *Schistosoma haematobium* eggs in urine was done via the filtration method. The urinary tract was examined by ultrasound. Associations between each of these variables and disease infection were tested using multivariate logistic regression. **Results:** The overall prevalence of urinary

schistosomiasis detected was 50.2%. The average intensity of infection was 36 eggs/10 ml of urine. The associated risk factors for urogenital schistosomiasis showed that children who bathed, used the river/pond as a domestic water source, and who habitually urinated in the river/pond were more affected ($P < 0.05$). Children with farming parents were most affected ($P = 0.032$). The collection of clinical signs revealed that boys had more pollakiuria (58.6%) and dysuria (46.4%) than girls. Ultrasound data showed that focal lesion rates were recorded in all villages with the lowest rate in Diakalel (56.1%). Ultrasound and parasitological findings showed that irregularity and thickening were strongly associated with urinary schistosomiasis ($P < 0.0001$). **Conclusions:** *Schistosoma haematobium* infection was still endemic in the study site despite more than a decade of mass treatment with praziquantel. However, the high percentage of symptoms associated with high intensity reinforces the idea that further studies in terms of schistosomiasis-related morbidity are still needed.

Development and assessment of a novel gold immunochromatographic assay for the diagnosis of schistosomiasis japonica.

Mu Y, McManus DP, Gordon CA, You H, Ross AG, Olveda RM, Cai P.

03-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37077910/>

Descriptive Analysis of Transient-State Observations for Thioredoxin/Glutathione Reductase (Sec597Cys) from *Schistosoma mansoni*.

Smith MM, Alt TB, Williams DL, Moran GR.

18-04-2023

Biochemistry.

<https://pubmed.ncbi.nlm.nih.gov/37071546/>

Dissection of schistosome tissues under LC-MS compatible preservative condition for quantitative proteomics.

Neves LX, Wilson RA, Castro-Borges W.

17-04-2023

Rapid Commun Mass Spectrom.

<https://pubmed.ncbi.nlm.nih.gov/37070167/>

Schistosomes are blood flukes with specialised tissues and organs, each one playing a pivotal role in perpetuating the parasite life cycle. Herein, we describe a detailed methodology for preserving the proteome of adult *Schistosoma mansoni* worms during manual dissection for enrichment of tissues associated with the parasite's alimentary tract. We provide step-by-step directions for specimen storage and dissection while in preservative solution, tissue homogenisation, protein extraction and digestion using a methodology fully compatible with downstream quantitative LC-MS analysis. Our methodology uses label-free and QconCAT-based absolute quantification for detection of *S. mansoni* esophageal gland products proposed as vaccine candidates. Through

stabilisation of the proteome and minimizing sample degradation during dissection our approach has allowed us to access the hidden proteome of target tissues not readily available from total lysates because of their small volume. This protocol can be replicated or adapted to other *Schistosoma* species lacking quantitative proteomics characterisation of specialised tissues for discovery of proteins with potential diagnostic and therapeutic utility.

No evidence for schistosome parasite fitness trade-offs in the intermediate and definitive host.

Le Clec'h W, Chevalier FD, Jutzeler K, Anderson TJC.

17-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37069704/>

Epidemiology of pediatric schistosomiasis in hard-to-reach areas and populations: a scoping review.

Isaiah PM, Sólveig Palmeirim M, Steinmann P.

17-04-2023

Infect Dis Poverty.

<https://pubmed.ncbi.nlm.nih.gov/37069632/>

T cell subsets, regulatory T, regulatory B cells and proinflammatory cytokine profile in *Schistosoma haematobium* associated bladder cancer: First report from Upper Egypt.

Mohammed SA, Hetta HF, Zahran AM, Tolba MEM, Attia RAH, Behnsawy HM, Algammal AM, Batiha GE, Mohammed AQ, Ahmad AA.

17-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37068081/>

Background: Schistosomiasis affects over 250 million people worldwide. Despite children and the poor being key risk groups, limited research and control activities target pre-school aged children (PSAC) and hard-to-reach populations. As endemic countries shift the goals of their schistosomiasis programs from morbidity control to disease elimination, there is a need for inclusive planning to cover all affected age groups from all geographical areas and populations to achieve sustainable impact and health equity. **Methods:** We conducted searches in MEDLINE, Web of Science, Embase (Ovid), and LILACS per the Preferred Reporting Items for Systematic Reviews and Meta-Analyses-Extension for Scoping Reviews (PRISMA-ScR) guidelines. Quality assessment of identified articles was done using the Joanna Briggs Institute Prevalence Critical Appraisal Tool. Relevant study data were extracted from the articles and entered into Microsoft Excel 2016 for descriptive analysis. **Results:** From the 17,179 screened articles, we identified 13 eligible studies on schistosomiasis in PSAC living in hard-to-reach areas and populations. All identified studies were from sub-Saharan Africa. The mean sample size of the retained studies was 572, with a balanced sex distribution among the young children sampled in each study. Ten studies investigated *Schistosoma mansoni*, one investigated *Schistosoma*

haematobium, while two covered both *S. mansoni* and *S. haematobium* in the target population. The prevalence of *S. mansoni* among PSAC in the included studies was estimated at 12.9% in Ghana, 80.3-90.5% in Kenya, 35.0% in Madagascar, 9.6-78.0% in Senegal, 11.2-35.4% in Sierra Leone, 44.4-54.9% in Tanzania and 39.3-74.9% in Uganda. Out of the three studies that investigated *S. haematobium*, the presence of the infection was reported in only one study carried out in Nigeria. Schistosome infections reported in nearly all studies included in this review were of light intensity. Only one study conducted in Nigeria documented visible hematuria in 17.7% of the PSAC studied. **Conclusions:** The findings document the high prevalence of schistosomiasis among PSAC in hard-to-reach populations and underscore the need to consider this population subgroup when designing the expansion of preventive chemotherapy and schistosomiasis control activities.

Corrigendum: *Schistosoma mansoni* coactivator associated arginine methyltransferase 1 (SmCARM1) effect on parasite reproduction.

Coelho FS, Gava SG, Andrade LF, Geraldo JA, Tavares NC, Lunkes FMN, Neves RH, Machado-Silva JR, Pierce RJ, Oliveira G, Mourão MM.

29-03-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37065155/>

Anti-schistosomal immunity to core xylose/fucose in N-glycans.

Prasanphanich NS, Leon K, Secor WE, Shoemaker CB, Heimbürg-Molinari J, Cummings RD.

04-04-2023

Front Mol Biosci.

<https://pubmed.ncbi.nlm.nih.gov/37081851/>

Background: The function of different populations of the immune system in bladder cancer (BCa) is well established. However, the cohesive role of the immune cell profile of schistosomal BCa at systemic and tissue levels is still lacking, especially in endemic countries. The balance hypothesized between protumorigenic and antitumor molecules determines the prognosis of tumor progression. This study aimed to investigate the frequency of T cell subsets at both blood and tumor tissue, regulatory T(Treg), regulatory B cells (Breg) and proinflammatory cytokines in *S. haematobium*-related BCa patients in Egypt. **Methodology/principal findings:** The frequency of T cell subsets at both blood and tumor tissue, regulatory T(Treg), regulatory B cells (Breg) were studied by flow cytometry and proinflammatory cytokines by ELISA in *S. haematobium*-related BCa patients in Egypt. The results indicated a significant increase in the activity of T-cell populations, particularly CD3+, CD4+, and regulatory T cells (Tregs), and a decrease in cytotoxic CD8+ T cells in the patient group. An increased proportion of CD19+CD24+CD38+ Bregs and proinflammatory cytokines (IL-1 β , IL-6, and TNF- α) was also observed. However, T-cell subpopulations in the tumor microenvironment showed a significant reduction in cancer patients compared to

controls. Moreover, positive correlations were observed between the frequencies of Bregs and Tregs, suggesting the promotion of cancer progression besides their relation to the intensity of schistosomal infection. **Conclusions/significance:** Trapped *Schistosoma haematobium* eggs in bladder tissue might lead to persistent inflammation that contributes to immunomodulation and promotes tumor progression, as evidenced by the increase in peripheral T helper, Tregs, Bregs and serum tumor-promoting cytokines. Considering the role and integrated functions of specific immune responses in BCa could help future diagnostic and therapeutic implications.

Trachome

TFOS Lifestyle Report: Impact of environmental conditions on the ocular surface.

Alves M, Asbell P, Dogru M, Giannaccare G, Grau A, Gregory D, Kim DH, Marini MC, Ngo W, Nowinska A, Saldanha JJ, Villani E, Wakamatsu TH, Yu M, Stapleton F. 14-04-2023
Ocul Surf.
<https://pubmed.ncbi.nlm.nih.gov/37062427/>

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

CsHscB Derived from a Liver Fluke *Clonorchis Sinensis* Ameliorates Cholestatic Hepatic Fibrosis in a Mouse Model of Sclerosing Cholangitis.

Yu Q, Koda S, Xu N, Li J, Wang JL, Liu M, Liu JX, Zhang Y, Yang HM, Zhang BB, Li XY, Li XC, Tang RX, Zheng KY, Yan C. 18-04-2023
Curr Mol Med.
<https://pubmed.ncbi.nlm.nih.gov/37076961/>

Background: Primary sclerosing cholangitis (PSC) is a chronic cholestatic liver disease characterized by inflammatory fibrosis usually involving the whole biliary tree. However, there are very limited treatment options to treat this disease. Our previous study found a lipid-protein rCsHscB from a liver fluke - *Clonorchis sinensis*, which had full capacities of immune regulation. Therefore, we investigated the role of rCsHscB in a mouse model of sclerosing cholangitis induced by xenobiotic 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC) to explore whether this protein had potential therapeutic value for PSC. **Methods:** Mice were fed 0.1% DDC for 4 weeks and treated with CsHscB (30 µg/mouse, intraperitoneal

injection, once every 3 days); the control group was given an equal amount of PBS or CsHscB under normal diet conditions. All the mice were sacrificed at 4 weeks for the evaluation of biliary proliferation, fibrosis, and inflammation. **Results:** rCsHscB treatment attenuated DDC-induced liver congestion and enlargement and significantly decreased the upregulation of serum AST and ALT levels. The administration of rCsHscB to DDC-fed mice significantly decreased cholangiocyte proliferation and pro-inflammatory cytokine production compared to mice fed with DDC alone. Also, rCsHscB treatment showed a decreased expression of α-SMA in the liver and other markers of liver fibrosis (Masson staining, Hydroxyproline content, and collagen deposit). More interestingly, DDC-fed mice treated with rCsHscB showed a significant up-regulation of PPAR-γ expression, which was similar to control mice, indicating the involvement of PPAR-γ signaling in the protective action of rCsHscB. **Conclusion:** Overall, our data show that rCsHscB attenuates the progression of cholestatic fibrosis induced by DDC and supports the potential for manipulating the parasite-derived molecule to treat certain immune-mediated disorders.

Examining ecosystem (dis-)services on liver fluke infection in rural Northeast Thailand.

Wang YC, Law A, Namsanor J, Sithithaworn P. 19-04-2023
Infect Dis Poverty.
<https://pubmed.ncbi.nlm.nih.gov/37076937/>

Background: The direct reliance of humans on and their interactions with freshwater ecosystems in the Lower Mekong Basin have given rise to parasitic infections, which is particularly prevalent in Northeast Thailand where raw fish consumption is practiced. This study examined the interactions between environments, ecosystem (dis-)services, human raw fish consumption habits, and raw fish dish sharing on liver fluke infection risk. **Method:** Water fecal contents and the first intermediate snail host were sampled between June and September of 2019. One hundred twenty questionnaires were surveyed in two villages of different environmental surroundings, one next to a river and the other located inland, in Northeast Thailand. Multivariate regression analyses using linear mixed effect models assessed the influence of social, behavioral and perceptual factors on raw fish consumption frequency, willingness to avoid consumption and liver fluke infection status. Social network analysis compared the degree of raw fish dish sharing between the villages and assessed the probable influence of connections to fish procurement locations and sharing activities on liver fluke infection risk. **Results:** High abundance of the first intermediate snail host and presence of fecal contamination in water could endanger both villages to ecosystem disservices of parasitic transmission. The river-side village relied more on provisioning ecosystem services than the inland village (29.7% vs. 16.1% of villages) to consume raw fish as their main source of protein. Males in both villages (64.5 and 40.4 days/year for the respective villages) are also likely to consume koi pla and pla som, higher risk fish dishes, more

frequently than females (4.1 and 4.3 days/year for the respective villages). The consumption habits of both villages were driven mostly by deriving cultural ecosystem services. Participation in raw fish dish sharing activities significantly reduced the odds of an individual being willing to avoid the consumption (Odds ratio = 0.19). Network analysis suggested that river-side villagers had a more direct raw fish dish sharing interaction and they procured fish from multiple locations; these characteristics might potentially account for more liver fluke infected households in the village. **Conclusion:** Villagers' raw fish consumption is driven by deriving cultural ecosystem services, and the geographic settings of the villages potentially affect villagers' fish procurement locations and infection risk. The findings underscore the linkages between villagers and their surrounding ecosystem environments as pertinent determinants for foodborne parasitic disease risk.

Extracellular vesicles from the trematodes *Fasciola hepatica* and *Dicrocoelium dendriticum* trigger different responses in human THP-1 macrophages.

Sánchez-López CM, González-Arce A, Soler C, Ramírez-Toledo V, Trelis M, Bernal D, Marcilla A.

Apr-2023

J Extracell Vesicles.

<https://pubmed.ncbi.nlm.nih.gov/37073796/>

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

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

19-04-2023

Parasitol Res.

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

Multispecies helminth parasitism of grazing dairy cows in Germany and Austria, examined in the housing period.

Rehbein S, Hamel D, Lackerschmid J, Mayr S, Visser M.

May-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37068863/>

Helminth composition and burden data for dairy cows have not been reported for >40 years for Germany and even less information is available for Austria. In the context of two recent studies, helminth parasitism was studied in 32 cows (23 from six farms in Bavaria and Tyrol; 9 from one farm in Saxony) from pasture-based dairy farms necropsied during the housing period. Helminths were enumerated and identified based on morphological characters (all helminths but rumen flukes) or molecular techniques (rumen flukes). Thirteen species of gastrointestinal nematodes and two species each of liver flukes (*Fasciola hepatica*, *Dicrocoelium dendriticum*) and rumen flukes (*Calicophoron daubneyi*, *Paramphistomum leydeni*) were recorded; no lungworms were recovered

from any cow. Early fourth-stage (inhibited) larval *Ostertagia* species nematodes (210 to 140,600) were recovered from all cows, 31 each had adult *Ostertagia ostertagi*/*Ostertagia lyrata* (40 to 2020) and *Trichostrongylus axei* (10 to 53,400), 23 *Oesophagostomum radiatum* (1 to 242) and 20 *Cooperia punctata* (10 to 3330). Other nematodes present in descending order of prevalence were: *Cooperia oncophora*/*Cooperia surnabada*, *Ostertagia leptospicularis*/*Ostertagia kolchida*, *Oesophagostomum venulosum*, *Bunostomum phlebotomum*, *Chabertia ovina*, *Nematodirus helvetianus*, *Trichostrongylus longispicularis*, *Haemonchus contortus* and *Aonchotheca bilobata*. The cows from Bavaria and Tyrol harbored more total gastrointestinal nematodes than that from Saxony (geometric mean adult plus inhibited larval nematodes, 6510 vs. 2051, respectively). However, in both cohorts of cows abomasal nematodes accounted for ~97% of the total nematode burden with inhibited larval *Ostertagia* species nematodes contributing over 70% of the total gastrointestinal nematode burden and ~96% of the *Ostertagia* species burden. Approximately 44%, 37% and 19% of the cows harbored <5000, 5000 to 10,000 or >10,000 total gastrointestinal nematodes, respectively. Fecal nematode egg and coproculture nematode larval counts significantly correlated with the cows' total adult nematode burden ($r_s = 0.354$, $p < 0.05$, and $r_s = 0.608$, $p < 0.001$, respectively). Although the magnitude of nematode burden to exert production effects on dairy cows is not well defined and may vary relative to several factors including nutritional supplementation, the level of mixed parasitism found in this investigation supports consideration of grazing dairy cows in helminth control measures, especially at the time of housing in autumn.

Paragonimiasis Misdiagnosed as Pulmonary Tuberculosis: A Case Report.

Villanueva-Villegas R, Diaz-Mendoza J, Salas-Lopez J, Espiche C.

15-05-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37065342/>

Trypanosomes (trypanosomiasis et maladie de Chagas)

Metabolomic profile, anti-trypanosomal potential and molecular docking studies of *Thunbergia grandifolia*.

El-Nashar HAS, Sayed AM, El-Sherief HAM, Rateb ME, Akil L, Khadra I, Majrashi TA, Al-Rashood ST, Binjubair FA, El Hassab MA, Eldehna WM, Abdelmohsen UR, Mostafa NM.

Dec-2023

J Enzyme Inhib Med Chem.

<https://pubmed.ncbi.nlm.nih.gov/37080775/>

Trypanosomiasis is a protozoan disease transmitted via *Trypanosoma brucei*. This study aimed to examine the

metabolic profile and anti-trypanosomal effect of methanol extract of *Thunbergia grandifolia* leaves. The liquid chromatography-high resolution electrospray ionisation mass spectrometry (LC-HRESIMS) revealed the identification of fifteen compounds of iridoid, flavonoid, lignan, phenolic acid, and alkaloid classes. The extract displayed a promising inhibitory activity against *T. brucei* TC 221 with MIC value of 1.90 µg/mL within 72 h. A subsequent in silico analysis of the dereplicated compounds (i.e. inverse docking, molecular dynamic simulation, and absolute binding free energy) suggested both rhodesain and farnesyl diphosphate synthase as probable targets for two compounds among those dereplicated ones in the plant extract (i.e. diphyllin and avacennone B). The absorption, distribution, metabolism, excretion, and toxicity (ADMET) profiling of diphyllin and avacennone were calculated accordingly, where both compounds showed acceptable drug-like properties. This study highlighted the antiparasitic potential of *T. grandifolia* leaves.

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

Capasso C, Supuran CT.

20-04-2023

Expert Opin Ther Pat.

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

Occurrence of triatomines in public spaces: An atypical case in the Southwestern Brazilian Amazon.

Cruz KSD, Ribeiro MAL, Madeira FP, Paixão DDS, Jesus AC, Camargo LMA, Rosa JAD, Oliveira J, Bernarde PS, Meneguetti DUO.

14-04-2023

Rev Soc Bras Med Trop.

<https://pubmed.ncbi.nlm.nih.gov/37075450/>

Electrophysiological detection of visible wavelengths of artificial lights inducing take-off in adults of *Rhodnius prolixus* (Hemiptera: Triatominae).

Ortiz MI, Hincapié-Peñaloza E, Molina J.

14-04-2023

Rev Inst Med Trop Sao Paulo.

<https://pubmed.ncbi.nlm.nih.gov/37075332/>

Rhodnius prolixus is the most important vector of *Trypanosoma cruzi* in the northern part of South America. The compound eyes in adults of *R. prolixus* are involved in the nocturnal flight dispersion from sylvatic environments into human dwellings. During this behavior, the artificial lights play an important role in attracting *R. prolixus*; however, it is still not clear whether the compound eyes of this species use different visible wavelengths as a cue during active dispersion. We applied electrophysiological (electroretinography or ERG) and behavioral (take-off) experiments in a controlled laboratory setting to determine the spectral sensitivity of the compound eyes and the attraction of *R. prolixus* adults to discrete visible wavelengths. For the ERG experiments, flashes of 300 ms

at wavelengths ranging between 350 and 700 nm at a constant intensity of 3.4 µW/cm² were tested after adaptation to darkness and to blue and yellow lights. For the behavioral experiments, the adults were exposed to nine visible wavelengths at three different intensities, and their direction of take-off in an experimental arena was established with circular statistics. The ERG results showed peaks of spectral sensitivity at 470-490 nm and 520-550 nm in adults, while behavioral experiments showed attractions to blue, green and red lights, depending on the intensity of the light stimuli. The electrophysiological and behavioral results confirm that *R. prolixus* adults can detect certain wavelengths in the visible spectrum of light and be attracted to them during take-off.

A comprehensive review on potential candidates for the treatment of chagas disease.

Pathak S, Bhardwaj M, Agrawal N, Bhardwaj A.

18-04-2023

Chem Biol Drug Des.

<https://pubmed.ncbi.nlm.nih.gov/37070386/>

The RNA export factor TbMex67 connects transcription and RNA export in *Trypanosoma brucei* and sets boundaries for RNA polymerase I.

Pozzi B, Naguleswaran A, Florini F, Rezaei Z, Roditi I.

18-04-2023

Nucleic Acids Res.

<https://pubmed.ncbi.nlm.nih.gov/37070196/>

TbMex67 is the major mRNA export factor known to date in trypanosomes, forming part of the docking platform within the nuclear pore. To explore its role in co-transcriptional mRNA export, recently reported in *Trypanosoma brucei*, pulse labelling of nascent RNAs with 5-ethynyl uridine (5-EU) was performed with cells depleted of TbMex67 and complemented with a dominant-negative mutant (TbMex67-DN). RNA polymerase (Pol) II transcription was unaffected, but the procyclin loci, which encode mRNAs transcribed by Pol I from internal sites on chromosomes 6 and 10, showed increased levels of 5-EU incorporation. This was due to Pol I readthrough transcription, which proceeded beyond the procyclin and procyclin-associated genes up to the Pol II transcription start site on the opposite strand. Complementation by TbMex67-DN also increased Pol I-dependent formation of R-loops and γ-histone 2A foci. The DN mutant exhibited reduced nuclear localisation and binding to chromatin compared to wild-type TbMex67. Together with its interaction with chromatin remodelling factor TbRRM1 and Pol II, and transcription-dependent association of Pol II with nucleoporins, our findings support a role for TbMex67 in connecting transcription and export in *T. brucei*. In addition, TbMex67 stalls readthrough by Pol I in specific contexts, thereby limiting R-loop formation and replication stress.

Structural Modelling of Platelet Activating Factor Acetyl Hydrolase in *Leishmania donovani*, *Trypanosoma*

cruzi, and Trypanosoma brucei: Implications on Therapeutics for Leishmaniasis, Chagas Disease, and Sleeping Sickness.

Goswami A, Koley T, Rajan MV, Madhuri P, Upadhyay N, Das U, Kumar M, Ethayathulla AS, Hariprasad G.

11-04-2023

Infect Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37070125/>

Allylpolyalkoxybenzene Inhibitors of Galactonolactone Oxidase from Trypanosoma cruzi.

Chudin AA, Zlotnikov ID, Krylov SS, Semenov VV, Kudryashova EV.

Jan-2023

Biochemistry (Mosc).

<https://pubmed.ncbi.nlm.nih.gov/37068875/>

Circulation of Trypanosoma evansi antibodies and risk variables among dromedary camels in Al Batinah governorates, Sultanate of Oman.

Al-Harrasi M, Al-Habsi K, Ali H, Al-Marzooqi W, Al-Kharousi K, Al-Hamrashdi A, El-Tahir HA, Elshafie EI.

May-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37068866/>

Trypanosoma evansi is a blood protozoan infects camels with Surra disease and causes high economic losses. The current study was focused on estimating the seroprevalence and associated risk factors of Surra disease among camels, using 425 blood samples collected from 45 farms in nine Wilayats of Al Batinah governorates in the Sultanate of Oman. Host and environmental risk factors associated with *T. evansi* seroprevalence were analyzed by questionnaire arranged during sample collection. The overall seroprevalence by the serological CATT/*T. evansi* was 19.5% (83/425, CI: 16.0-23.6%). The seroconversion rate between the two governorates of north and south Al Batinah was not statistically significant ($p > 0.05$). However, the highest frequency was in Al Musannah at 41.7% (10/24, CI: 22.1-63.4%), and the lowest was in Al Khaburah at 10.5% (6/57, CI: 4.0-21.5%). Most of the owners in Al Khaburah (82.5%) were aware of *T. evansi* importance, and therefore they kept camels separate from ruminants. The ticks-free camels, racing camels and camels less than five years old showed higher *T. evansi* seroprevalence than other camels. The mean total protein was significantly ($t = 2.817$, $p = 0.006$) higher in seropositive camels (6.49 ± 0.75) compared to seronegative ones (6.25 ± 0.55), whereas PCV was not statistically different between the positive (28.96 ± 4.33) and negative camels (29.83 ± 3.63). Further studies are highly recommended to determine the prevalence and type of *T. evansi* in camels and ruminants in different governorates in Oman, especially in the Dhofar region, where the highest camel density is reported in the country.

Molecular detection of vector-borne pathogens in cats tested for FIV and FeLV.

Melo TB, Silva TRM, Almeida TLAC, Tutija JF, Silva AOD, Lira MDS, Amorim D, Giannelli A, Ramos CADN, Alves LC, Carvalho GA, Ramos RAN.

May-2023

Vet Parasitol Reg Stud Reports.

<https://pubmed.ncbi.nlm.nih.gov/37068860/>

The aim of this study was to detect molecularly vector borne pathogens (VBPs) in domiciled cats tested for Feline immunodeficiency virus (FIV) and Feline leukemia virus (FeLV). Blood samples ($n = 119$) were analyzed microscopically and molecularly through PCR and sequenced for the detection of the following pathogens: piroplasmids, *Bartonella henselae*, *Cytauxzoon felis*, *Ehrlichia canis*, *Leishmania* spp., hemotropic *Mycoplasma* spp., *Trypanosoma* spp., and *Rickettsia* spp. Animals were also serological assessed for detection of antibodies against FIV and FeLV. Out of all animals, 20.16% (24/119) tested positive for at least one VBPs at molecular examination. Conversely, no animal resulted positive at microscopic analysis. The most prevalent pathogen was hemotropic *Mycoplasma haemofelis* (8.40%; 10/119), followed by *Candidatus Mycoplasma haemominutum* (5.88%; 7/119), *E. canis* (5.04%; 6/119), *C. felis* (0.84%; 1/119) and *B. henselae* (0.84%; 1/119). One animal (0.84%; 1/119) was co-infected with *E. canis* and *B. henselae*. A total of 5.88% (7/119) and 1.68% (2/119) tested positive for FIV and FeLV, respectively. Data of this study demonstrate that owned cats can be at risk of hemotropic *Mycoplasma* spp., *E. canis*, *C. felis* and *B. henselae*. Therefore, preventive measures against vectors of these pathogens should be implemented in order to reduce the risk of exposition and consequently infection. Additionally, aggressive behaviors among cats should be avoided, especially because hemotropic *Mycoplasma* spp. may be transmitted through the bite of animals.

Benzonidazole treatment has a beneficial effect on cells infected with the Colombian strain of Trypanosoma cruzi.

Rafael Moreira L, Dos Santos Oliveira KK, Torres DJL, da Silva Barros M, de Arruda TR, Nascimento AV, Soares AKA, Higino TMM, Diniz GTN, Souza VMO, de Moraes CNL, de Lorena VMB.

17-04-2023

Parasite Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37066749/>

Tc HRG plays a central role in orchestrating heme uptake in Trypanosoma cruzi epimastigotes.

Tevere E, Di Capua CB, Chasen NM, Etheridge RD, Cricco JA.

05-04-202

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37066141/>

Trypanosoma cruzi, a heme auxotrophic parasite, can control intracellular heme content by modulating Tc HRG

expression when a free heme source is added to axenic culture. Herein, we explore the role of *Tc* HRG protein in regulating the uptake of heme derived from hemoglobin in epimastigotes. It was found that the parasite's endogenous *Tc* HRG (protein and mRNA) responds similarly to bound (hemoglobin) and free (hemin) heme. Additionally, the overexpression of *Tc* HRG leads to an increase in intracellular heme content. The localization of *Tc* HRG is also not affected in parasites supplemented with hemoglobin as the sole heme source. Endocytic null epimastigotes do not show a significant difference in growth profile, intracellular heme content and *Tc* HRG protein accumulation compared to WT when feeding with hemoglobin or hemin as a source of heme. These results suggest that the uptake of hemoglobin-derived heme likely occurs through extracellular proteolysis of hemoglobin *via* the flagellar pocket, and this process is governed by *Tc* HRG. In sum, *T. cruzi* epimastigotes controls heme homeostasis by modulating *Tc* HRG expression independently of the source of available heme.

Autophagy in protists and their hosts: When, how and why?

Romano PS, Akematsu T, Besteiro S, Bindschedler A, Carruthers VB, Chahine Z, Coppens I, Descoteaux A, Alberto Duque TL, He CY, Heussler V, Le Roch KG, Li FJ, de Menezes JPB, Menna-Barreto RFS, Mottram JC, Schmuckli-Maurer J, Turk B, Tavares Veras PS, Salassa BN, Vanrell MC.

2023

Autophagy Rep.

<https://pubmed.ncbi.nlm.nih.gov/37064813/>

Pathogenic protists are a group of organisms responsible for causing a variety of human diseases including malaria, sleeping sickness, Chagas disease, leishmaniasis, and toxoplasmosis, among others. These diseases, which affect more than one billion people globally, mainly the poorest populations, are characterized by severe chronic stages and the lack of effective antiparasitic treatment. Parasitic protists display complex life-cycles and go through different cellular transformations in order to adapt to the different hosts they live in. Autophagy, a highly conserved cellular degradation process, has emerged as a key mechanism required for these differentiation processes, as well as other functions that are crucial to parasite fitness. In contrast to yeasts and mammals, protist autophagy is characterized by a modest number of conserved autophagy-related proteins (ATGs) that, even though, can drive the autophagosome formation and degradation. In addition, during their intracellular cycle, the interaction of these pathogens with the host autophagy system plays a crucial role resulting in a beneficial or harmful effect that is important for the outcome of the infection. In this review, we summarize the current state of knowledge on autophagy and other related mechanisms in pathogenic protists and their hosts. We sought to emphasize when, how, and why this process takes place, and the effects it may have on the parasitic cycle. A better understanding of the significance of autophagy for the protist life-cycle will potentially be helpful to design novel anti-parasitic strategies.

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

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

06-04-2023

Eur J Med Chem.

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

Fatty acid elongases 1-3 have distinct roles in mitochondrial function, growth, and lipid homeostasis in *Trypanosoma cruzi*.

Pagura L, Dumoulin PC, Ellis CC, Mendes MT, Estevao IL, Almeida IC, Burleigh BA.

13-04-2023

J Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/37061002/>

Trypanosomatids are a diverse group of unflagellate protozoan parasites that include globally relevant pathogens such as *Trypanosoma cruzi*, the causative agent of Chagas disease. Trypanosomes lack the fatty acid synthase (FAS)-I system typically used for *de novo* fatty acid (FA) synthesis in other eukaryotes. Instead, these microbes have evolved a modular fatty acid elongase (ELO) system comprised of individual ELO enzymes (ELO1-4) that can operate processively to generate long chain- and very long chain-fatty acids. The importance of ELO's for maintaining lipid homeostasis in trypanosomatids is currently unclear, given their ability to take up and utilize exogenous fatty acids for lipid synthesis. To assess ELO function in *T. cruzi*, we generated individual knockout lines, Δ elo1, Δ elo2 and Δ elo3, in which the genes encoding ELO1-3 were functionally disrupted in the parasite insect stage (epimastigote). Using unbiased lipidomic and metabolomic analyses, in combination with metabolic tracing and biochemical approaches, we demonstrate that ELO2 and ELO3 are required for global lipid homeostasis, whereas ELO1 is dispensable for this function. Instead, ELO1 activity is needed to sustain mitochondrial activity and normal growth in *T. cruzi* epimastigotes. The cross-talk between microsomal ELO1 and the mitochondrion is a novel finding that, we propose, merits further examination of the trypanosomatid ELO pathway as critical for central metabolism.

Combination of ultra-rapid DNA purification (PURE) and loop-mediated isothermal amplification (LAMP) for rapid detection of *Trypanosoma cruzi* DNA in dried blood spots.

Longhi SA, García Casares LJ, Muñoz-Calderón AA, Alonso-Padilla J, Schijman AG.

14-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37058542/>

Ulcère de Buruli

Research article network analysis of polymicrobial chronic wound infections in Masanga, Sierra Leone.

Sandmann S, Nunes JV, Grobusch MP, Sesay M, Kriegel MA, Varghese J, Schaumburg F.

18-04-2032

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37072717/>

Background: Chronic wounds are frequently colonized or infected with multiple bacterial or fungal species, which can both promote or inhibit each other. Network analyses are helpful to understand the interplay of these species in polymicrobial infections. Our aim was to analyse the network of bacterial and fungal species in chronic wounds.

Methods: Swabs (n = 163) from chronic wound infections (Masanga, Sierra Leone, 2019-2020) were screened for bacterial and fungal species using non-selective agars. Some of these wounds were suspected but not confirmed Buruli ulcer. Species identification was done with MALDI-TOF mass spectrometry. Network analysis was performed to investigate co-occurrence of different species within one patient. All species with n ≥ 10 isolates were taken into account. **Results:** Of the 163 patients, 156 had a positive wound culture (median of three different species per patient; range 1-7). *Pseudomonas aeruginosa* (n = 75) was the dominating species with frequent co-detections of *Klebsiella pneumoniae* (21 cases; OR = 1.36, 95%CI: 0.63-2.96, p = 0.47), *Staphylococcus aureus* (14 cases; OR = 1.06, 95%CI: 0.44-2.55, p = 1) and *Proteus mirabilis* (13 cases; OR = 0.84, 95%CI: 0.35-1.99, p = 0.69). **Conclusion:** The culturome of chronic wounds in Sierra Leonean patients is highly diverse and characterized by the co-occurrence of *P. aeruginosa*, *K. pneumoniae* and *S. aureus*.

Buruli ulcer: application of thermography for remote diagnosis of a neglected disease.

Yotsu RR, Vagamon B, Almamy D, Aka N, Yeboue LKG, Yao A, Blanton RE.

18-04-2023

Br J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37071786/>

Tuberculosis management and referral practices among traditional medicine practitioners in Lagos, Nigeria.

Adepoju VA, Oladimeji O, Sibiya MN, Inegbeboh J, Egesemba G.

01-03-2023

J Public Health Afr.

<https://pubmed.ncbi.nlm.nih.gov/37065812/>

Introduction: Despite the potential role of Traditional Birth Attendants (TBAs) and Traditional Healers (THs), little is known about their knowledge of tuberculosis (TB) management and referral practices in Nigeria. **Objective:** To determine knowledge and self-reported practices of traditional birth attendants and traditional healers in

managing TB in Lagos, Nigeria. **Methods:** A cross-sectional study of 120 THs and TBAs in three high TB burden Local Government Areas (LGAs) in Lagos, Nigeria. Data were collected between April 2018 to September 2018 through interviewer-administered questionnaires. We used Statistical Package for Social Sciences software for data analyses. Independent predictors of being TBA or TH were determined using logistic regression at the statistical significance of P<0.05 and 95% confidence interval.

Results: TB knowledge increased from 52.7% pre-test to 61.7% post-test and did not differ between TBAs and THs. Of the 120 Traditional Medical Practitioners studied, 70% (84) never treated TB; 57.3 % (69) ever referred chronic cough patients to a health facility; 90% (108) were willing to collaborate with National Tuberculosis, Leprosy and Buruli Ulcer Control Programme (NTBLCP), 85% (102) attached monetary and token incentive as a condition for the collaboration. THs had decreased odds of ever referring TB patient to the hospital (AOR: 0.3, 95% CI: 0.14-0.64, P=0.002); currently referring TB patients (AOR: 0.06, 95% CI: 0.02-0.17, P<0.0001) and consulting <40 patients in a year (AOR: 0.22, 95% CI: 0.09-0.53, P<0.0001).

Conclusion: Majority of the THs and TBAs were willing to collaborate with NTBLCP in the identification and referral of Presumptive TB patients. We suggest that NTBLCP empowers the TBAs and THs to help with an early referral of TB patients.

Statistical modelling based on structured surveys of Australian native possum excreta harbouring *Mycobacterium ulcerans* predicts Buruli ulcer occurrence in humans.

Vandelannoote K, Buultjens AH, Porter JL, Velink A, Wallace JR, Blasdel KR, Dunn M, Boyd V, Fyfe JAM, Tay EL, Johnson PDR, Windecker SM, Golding N, Stinear TP.

1404-2023

Elife.

<https://pubmed.ncbi.nlm.nih.gov/37057888/>

Background: Buruli ulcer (BU) is a neglected tropical disease caused by infection of subcutaneous tissue with *Mycobacterium ulcerans*. BU is commonly reported across rural regions of Central and West Africa but has been increasing dramatically in temperate southeast Australia around the major metropolitan city of Melbourne, with most disease transmission occurring in the summer months. Previous research has shown that Australian native possums are reservoirs of *M. ulcerans* and that they shed the bacteria in their fecal material (excreta). Field surveys show that locales where possums harbor *M. ulcerans* overlap with human cases of BU, raising the possibility of using possum excreta surveys to predict the risk of disease occurrence in humans. **Methods:** We thus established a highly structured 12-month possum excreta surveillance program across an area of 350 km² in the Mornington Peninsula area 70 km south of Melbourne, Australia. The primary objective of our study was to assess using statistical modelling if *M. ulcerans* surveillance of possum excreta provided useful information for predicting future human BU case locations. **Results:** Over two sampling campaigns in summer and winter, we collected 2282 possum excreta specimens of which 11% were PCR

positive for *M. ulcerans*-specific DNA. Using the spatial scanning statistical tool *SaTScan*, we observed non-random, co-correlated clustering of both *M. ulcerans* positive possum excreta and human BU cases. We next trained a statistical model with the Mornington Peninsula excreta survey data to predict the future likelihood of human BU cases occurring in the region. By observing where human BU cases subsequently occurred, we show that the excreta model performance was superior to a null model trained using the previous year's human BU case incidence data (AUC 0.66 vs 0.55). We then used data unseen by the excreta-informed model from a new survey of 661 possum excreta specimens in Geelong, a geographically separate BU endemic area to the southwest of Melbourne, to prospectively predict the location of human BU cases in that region. As for the Mornington Peninsula, the excreta-based BU prediction model outperformed the null model (AUC 0.75 vs 0.50) and pinpointed specific locations in Geelong where interventions could be deployed to interrupt disease spread. **Conclusions:** This study highlights the *One Health* nature of BU by confirming a quantitative relationship between possum excreta shedding of *M. ulcerans* and humans developing BU. The excreta survey-informed modeling we have described will be a powerful tool for efficient targeting of public health responses to stop BU.