



Veille scientifique

Maladies tropicales négligées

Semaine 18
01 au 07 mai 2023

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Cysticercose

Older Age in Subarachnoid Neurocysticercosis Reflects a Long Prepatent Period.

Nateros F, Saenz E, Saavedra H, Gonzales I, Pretell EJ, Perez E, Castillo Y, Bustos JA, Garcia HH; Cysticercosis Working Group in Peru.

Am J Trop Med Hyg. 2023 May 1

<https://pubmed.ncbi.nlm.nih.gov/37127275/>

Knowledge and practices about taeniasis/cysticercosis complex within the framework of the national plan for its elimination in Colombia, 2019.

Gamarra-Rueda R, Knudson-Ospina RA, Olaya LA, Gómez N, Orellano AI, Navarro LF, Apráez NG, Fernández-Niño JA, López MC.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36963599/>

The taeniasis/cysticercosis complex (TCC) belongs to the group of neglected infectious diseases with a multifactorial transmission that includes hosts such as humans and pigs of the parasitic tapeworm (*Taenia solium*) and environmental factors. This study represents the first phase of the National and Cross-sectoral Plan for TCC Elimination. **Objectives:** To obtain data about knowledge and practices in relation to the TCC from knowledge, attitudes, and practices (KAP) surveys applied in two pilot localities for building a baseline of the potential risk factors related to identification, prevention, and control of TCC in Colombia. **Methods:** A descriptive cross-sectional survey from October to November in 2019 was carried out using a structured questionnaire and random sampling by single-stage conglomerates in the municipalities of Mahates, Bolívar (n = 152) (Atlantic Region) and Mercaderes, Cauca (n = 152) (Andean Region). **Results:** Respondents in Mahates showed moderate knowledge about TCC compared to those in Mercaderes, however, risky practices were identified in both places (consumption of pork with cysts and defecation in places other than the bathroom or latrine). Deficiency in infrastructure and failure in basic services were observed as potential risk factors for TCC transmission in both municipalities. **Conclusion:** Based on the framework of the National and Cross-sectoral Plan for TCC Elimination, adequate knowledge on identification, prevention, and control of the disease must be reinforced; cultural and ecological differences should be considered when designing communication and knowledge transmission tools. We consider that major investment should be made in improving basic services and creating sustainable modernized pig farming in Mahates and Mercaderes.

The challenges of detecting *Taenia solium* and neurocysticercosis in low and middle-income countries: A scoping review of Lao People's Democratic Republic.

Larkins A, Keatley S, Insisiengmay B, Phetsouvanh R, Bruce M, Ash A.

Mai-2023

Trop Med Int Health.

<https://pubmed.ncbi.nlm.nih.gov/36898844/>

Dengue, chikungunya et maladie à virus Zika

Phytochemical profiling of the essential oils from three *Curcuma* species and their *in vitro* and *in silico* dengue protease inhibition activity.

Jani NA, Maarof NI, Zahari MMFM, Jamil M, Zakaria II, Mohamad Zobir SZ, Kasim N, Salin NH, Mohamad Ali NA, Khalid WEFW, Pungot NH.

05-05-2023

Nat Prod Res.

<https://pubmed.ncbi.nlm.nih.gov/37144399/>

The chemical compositions, *in vitro* and *in silico* anti-dengue activity of the essential oils of the rhizomes of *Curcuma longa* Linn., *C. aeruginosa* Roxb., and *C. xanthorrhiza* Roxb. had been investigated. The *C. longa* oil was mainly composed of ar-turmerone (54.0%) and curlone (17.7%), while the *C. aeruginosa* oil was rich in curzerenone (23.4%), 1,8-cineole (21.2%), and camphor (7.1%). Xanthorrhizol (21.6%), β -curcumene (19.5%), ar-curcumene (14.2%), and camphor (9.2%) were the major compounds in the *C. xanthorrhiza* oil. Among the oils, the *C. longa* oil was found to be the most active NSB-NS3 protease inhibitor (IC₅₀ 1.98 μ g/mL). PLS biplot disclosed that the essential oils were classified into three separated clusters based on their characteristic chemical compositions, with *C. longa* positioned closest to the *in vitro* anti-dengue activity. Four compounds from the *C. longa* oil have both hydrogen and hydrophobic bonds that could be responsible for the DENV-2 NS2B-NS3 inhibitory effect.

Contributions of musculoskeletal rehabilitation in patients after chikungunya fever: a systematic review.

Sales WB, Leite DG, Truta Ramalho CS, Macêdo SGGF, de Souza GF, Cavalcanti Maciel AC.

04-05-2023

BMC Musculoskelet Disord.

<https://pubmed.ncbi.nlm.nih.gov/37143009/>

Exploring allosteric hits of the NS2B-NS3 protease of DENV2 by structure-guided screening.

Gangopadhyay A, Saha A.

29-04-2023

Comput Biol Chem.

<https://pubmed.ncbi.nlm.nih.gov/37141792/>

Infection of the maternal-fetal interface and vertical transmission following low-dose inoculation of pregnant rhesus

macaques (*Macaca mulatta*) with an African-lineage Zika virus.

Koenig MR, Mitzey AM, Morgan TK, Zeng X, Simmons HA, Mejia A, Leyva Jaimes F, Keding LT, Crooks CM, Weiler AM, Bohm EK, Aliota MT, Friedrich TC, Mohr EL, Golos TG.

04-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37141276/>

Background: Congenital Zika virus (ZIKV) infection can result in birth defects, including malformations in the fetal brain and visual system. There are two distinct genetic lineages of ZIKV: African and Asian. Asian-lineage ZIKVs have been associated with adverse pregnancy outcomes in humans; however, recent evidence from experimental models suggests that African-lineage viruses can also be vertically transmitted and cause fetal harm.

Methodology/principal findings: To evaluate the pathway of vertical transmission of African-lineage ZIKV, we inoculated nine pregnant rhesus macaques (*Macaca mulatta*) subcutaneously with 44 plaque-forming units of a ZIKV strain from Senegal, (ZIKV-DAK). Dams were inoculated either at gestational day 30 or 45. Following maternal inoculation, pregnancies were surgically terminated seven or 14 days later and fetal and maternal-fetal interface tissues were collected and evaluated. Infection in the dams was evaluated via plasma viremia and neutralizing antibody titers pre- and post- ZIKV inoculation. All dams became productively infected and developed strong neutralizing antibody responses. ZIKV RNA was detected in maternal-fetal interface tissues (placenta, decidua, and fetal membranes) by RT-qPCR and in situ hybridization. In situ hybridization detected ZIKV predominantly in the decidua and revealed that the fetal membranes may play a role in ZIKV vertical transmission. Infectious ZIKV was detected in the amniotic fluid of three pregnancies and one fetus had ZIKV RNA detected in multiple tissues. No significant pathology was observed in any fetus; and ZIKV did not have a substantial effect on the placenta.

Conclusions/significance: This study demonstrates that a very low dose of African-lineage ZIKV can be vertically transmitted to the macaque fetus during pregnancy. The low inoculating dose used in this study suggests a low minimal infectious dose for rhesus macaques. Vertical transmission with a low dose in macaques further supports the high epidemic potential of African ZIKV strains.

Urban mosquito distributions are modulated by socioeconomic status and environmental traits in the USA.

Yitbarek S, Chen K, Celestin M, McCary M.

04-05-2023

Ecol Appl.

<https://pubmed.ncbi.nlm.nih.gov/37140135/>

[Dengue fever is knocking on the doors of Europe].

Filali A, D'Acremont V.

03-05-2023

Rev Med Suisse.

<https://pubmed.ncbi.nlm.nih.gov/37139880/>

Comparative study of three herbal formulations against dengue vectors *Aedes aegypti*.

Alyahya HS.

Juin-2023

Saudi J Biol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37138927/>

The efficacy of three formulations (i.e., natural lavender crude, essential oil, and gel) extracted from *Lavender angustifolia* was tested against vectors of the epidemic dengue virus, *Aedes aegypti*, to evaluate their larvicidal activity effect. The ethanolic extract of the lavender crude was prepared using a rotary evaporator, while the other extracts, such as essential oil and gel, were obtained from iHerb, a supplier of medicinal herbs in the US. The mortality rate of larvae was evaluated 24 h after exposure. Larvicidal activity of the lavender crude was 91% mortality at 150 ppm, 94% for essential oil at a concentration of 3000 ppm, and 97% for lavender gel at a 1000 ppm. Natural lavender crude was one of the most promising extracts tested against *Ae. aegypti* larvae, with lethal concentrations at LC₅₀ and LC₉₀ of 76.4 and 174.5 ppm post-treatment. The essential oil had the least effect on mosquito larvae, with LC₅₀ and LC₉₀ reaching 1814.8 and 3381.9 ppm, respectively. The lavender gel was moderately effective against *Ae. aegypti* larvae, with LC₅₀ and LC₉₀ values reaching 416.3 and 987.7 ppm after exposure. The occurrence of morphological abnormalities in the larvae treated with the three compounds, in turn, resulted in an incomplete life cycle. Therefore, our results indicated that natural lavender crude displayed the highest larvicidal activity against larvae, followed by gel and essential oil. Thus, this study concluded that lavender crude is an effective, eco-friendly compound that can be used as an alternative to chemical products to control vector-borne epidemic diseases.

The epidemiology and evolutionary dynamics of massive dengue outbreak in China, 2019.

Sang S, Yue Y, Wang Y, Zhang X.

17-04-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37138627/>

Introduction: In 2019, China experienced massive dengue outbreaks with high incidence and expanded outbreak areas. The study aims to depict dengue's epidemiology and evolutionary dynamics in China and explore the possible origin of these outbreaks. **Methods:** Records of confirmed dengue cases in 2019 were obtained from the China Notifiable Disease Surveillance System. The sequences of complete envelope gene detected from the outbreak provinces in China in 2019 were retrieved from GenBank. Maximum Likelihood trees were constructed to genotype the viruses. The median-joining network was used to visualize fine-scale genetic relationships. Four methods were used to estimate the selective pressure. **Results:** A total of 22,688 dengue cases were reported, 71.4% of which were indigenous cases and 28.6% were

imported cases (including from abroad and from other domestic provinces). The abroad cases were predominantly imported from Southeast Asia countries (94.6%), with Cambodia (3,234 cases, 58.9%), and Myanmar (1,097 cases, 20.0%) ranked as the top two. A total of 11 provinces with dengue outbreaks were identified in the central-south of China, of which Yunnan and Guangdong provinces had the highest number of imported and indigenous cases. The primary source of imported cases in Yunnan was from Myanmar, while in the other ten provinces, the majority of imported cases were from Cambodia. Guangdong, Yunnan and Guangxi provinces were China's primary sources of domestically imported cases. Phylogenetic analysis of the viruses in outbreak provinces revealed three genotypes: (I, IV, and V) in DENV 1, Cosmopolitan and Asian I genotypes in DENV 2, and two genotypes (I and III) in DENV 3. Some genotypes concurrently circulated in different outbreak provinces. Most of the viruses were clustered with those from Southeast Asia. Haplotype network analysis showed that Southeast Asia, possibly Cambodia and Thailand, was the respective origin of the viruses in clade 1 and 4 for DENV 1. Positive selection was detected at codon 386 in clade 1. **Conclusion:** Dengue importation from abroad, especially from Southeast Asia, resulted in the dengue epidemic in China in 2019. Domestic transmission between provinces and positive selection on virus evolution may contribute to the massive dengue outbreaks.

Investigation of the activity of baicalein towards Zika virus.

Sawadpongpan S, Jaratsittisin J, Hitakarun A, Roytrakul S, Wikan N, Smith DR.

03-05-2023

BMC Complement Med Ther.

<https://pubmed.ncbi.nlm.nih.gov/37138273/>

Author Correction: Model-based assessment of Chikungunya and O'nyong-nyong virus circulation in Mali in a serological cross-reactivity context.

Hozé N, Diarra I, Sangaré AK, Pastorino B, Pezzi L, Kouriba B, Sagara I, Dabo A, Djimé A, Thera MA, Doumbo OK, de Lamballerie X, Cauchemez S.

03-05-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37137917/>

Long-Term Safety Analysis of the ChAdOx1-nCoV-19 Corona Virus Vaccine: Results from a Prospective Observational Study in Priority Vaccinated Groups in North India.

Kaur U, Fatima Z, Maheshwari K, Sahni V, Dehade A, KI A, Yadav AK, Kansal S, Jaisawal V, Chakrabarti SS.

03-05-2023

Drug Saf.

<https://pubmed.ncbi.nlm.nih.gov/37133805/>

Introduction: Various vaccines for protection against COVID-19 were provided emergency approval in late 2020 to early 2021. There is a scarcity of long-term safety data

for many of these. **Objective:** The main aim of this study is to provide the one-year safety results of the ChAdOx1-nCoV-19/AZD1222 vaccine and determine the risk factors of adverse events of special interest (AESIs) and persistent AESIs. **Methods:** This was a prospective observational study conducted from February 2021 to April 2022 in a tertiary hospital in North India and its two associated centers. Health care workers, other frontline workers, and the elderly vaccinated with the ChAdOx1-nCoV-19 vaccine constituted the study population. Individuals were contacted telephonically at pre-decided intervals for one year and health issues of significant concern were recorded. Atypical adverse events developing after a booster dose of the COVID-19 vaccine were assessed. Regression analysis was conducted to determine risk factors of AESI occurrence and determinants of AESIs persisting for at least one month at the time of final telephonic contact.

Results: Of 1650 individuals enrolled, 1520 could be assessed at one-year post-vaccination. COVID-19 occurred in 44.1% of participants. Dengue occurred in 8% of participants. The majority of the AESIs belonged to the MedDRA® SOC of musculoskeletal disorders (3.7% of 1520). Arthropathy (knee joint involvement) was the most common individual AESI (1.7%). Endocrinal disorders such as thyroid abnormalities and metabolic disorders such as newly diagnosed diabetes developed in 0.4% and 0.3% of individuals, respectively. Regression analysis showed females, individuals with a pre-vaccination history of COVID-19, diabetes, hypothyroidism, and arthropathy had 1.78-, 1.55-, 1.82-, 2.47- and 3.9-times higher odds of AESI development. Females and individuals with hypothyroidism were at 1.66- and 2.23-times higher risk of persistent AESIs. Individuals receiving the vaccine after COVID-19 were at 2.85- and 1.94 times higher risk of persistent AESIs compared, respectively, to individuals with no history of COVID-19 and individuals developing COVID-19 after the vaccine. Among participants receiving a booster dose of the COVID-19 vaccine (n = 185), 9.7% developed atypical adverse events of which urticaria and new-onset arthropathy were common. **Conclusion:** Nearly half of the ChAdOx1-nCoV-19 vaccine recipients developed COVID-19 over one year. Vigilance is warranted for AESIs such as musculoskeletal disorders. Females, individuals with hypothyroidism, diabetes, and pre-vaccination history of COVID-19 are at higher risk of adverse events. Vaccines received after natural SARS-CoV-2 infection may increase the risk of persistence of adverse events. Sex and endocrinal differences and timing of the COVID-19 vaccine with respect to natural infection should be explored as determinants of AESIs in the future. Pathogenetic mechanisms of vaccine-related adverse events should be investigated along with comparisons with an unvaccinated arm to delineate the overall safety profile of COVID-19 vaccines.

Prevalence and Risk Factors of Acute Kidney Injury in Hospitalized Children with Dengue Infection Using Kidney Disease Improving Global Outcomes Criteria: Authors' Reply.

Mekangkul E, Siripen N, Rianthavorn P.

03-05-2023

Indian J Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/37133750/>

Colocalization of Chikungunya Virus with Its Receptor MXRA8 during Cell Attachment, Internalization, and Membrane Fusion.

Feng F, Bouma EM, Hu G, Zhu Y, Yu Y, Smit JM, Diamond MS, Zhang R.

01-05-2023

J Virol.

<https://pubmed.ncbi.nlm.nih.gov/37133449/>

Arthritogenic alphaviruses, including chikungunya virus (CHIKV), preferentially target joint tissues and cause chronic rheumatic disease that adversely impacts the quality of life of patients. Viruses enter target cells via interaction with cell surface receptor(s), which determine the viral tissue tropism and pathogenesis. Although MXRA8 is a recently identified receptor for several clinically relevant arthritogenic alphaviruses, its detailed role in the cell entry process has not been fully explored. We found that in addition to its localization on the plasma membrane, MXRA8 is present in acidic organelles, endosomes, and lysosomes. Moreover, MXRA8 is internalized into cells without a requirement for its transmembrane and cytoplasmic domains. Confocal microscopy and live cell imaging revealed that MXRA8 interacts with CHIKV at the cell surface and then enters cells along with CHIKV particles. At the moment of membrane fusion in the endosomes, many viral particles are still colocalized with MXRA8. These findings provide insight as to how MXRA8 functions in alphavirus internalization and suggest possible targets for antiviral development. **IMPORTANCE** The globally distributed arthritogenic alphaviruses have infected millions of humans and induce rheumatic disease, such as severe polyarthralgia/polyarthritis, for weeks to years. Alphaviruses infect target cells through receptor(s) followed by clathrin-mediated endocytosis. MXRA8 was recently identified as an entry receptor that shapes the tropism and pathogenesis for multiple arthritogenic alphaviruses, including chikungunya virus (CHIKV). Nonetheless, the exact functions of MXRA8 during the process of viral cell entry remain undetermined. Here, we have provided compelling evidence for MXRA8 as a bona fide entry receptor that mediates the uptake of alphavirus virions. Small molecules that disrupt MXRA8-dependent binding of alphaviruses or internalization steps could serve as a platform for unique classes of antiviral drugs.

Dirofilaria immitis is endemic in rural areas of the Brazilian Amazonas state capital, Manaus.

Barbosa UC, Nava AFD, Ferreira Neto JV, Dias CA, Silva VCD, Mesquita HG, Sampaio RTM, Barros WG, Farias ES, Silva TRRD, Crainey JL, Tadei WP, Koolen HHH, Pessoa FAC.

28-04-2023

Rev Bras Parasitol Vet.

<https://pubmed.ncbi.nlm.nih.gov/37132734/>

The canine filarial parasite *Dirofilaria immitis* has not been reported in Brazil's Amazonas state capital, Manaus, for over a century. Here, we report one imported and 27 autochthonous *D. immitis* infections from a microfilarial survey of 766 domestic dog blood samples collected between 2017 and 2021 in Manaus. An Overall prevalence estimate of 15.44% (23/149) was calculated from our two rural collection sites; a prevalence of 1.22% (4/328) was estimated at our periurban collection site, and an overall prevalence of 0.35% (1/289) was calculated from our two urban clinic collections. Our data suggest that in the urban areas of Manaus, where the parasites are very likely vectored by the same species of mosquito that historically vectored *Wuchereria bancrofti* (*Culex quinquefasciatus*), prevalence levels are very low and possibly maintained by an influx from rural areas where sylvatic reservoirs and/or more favorable vector transmission dynamics maintain high prevalences.

Targeting Sex Determination to Suppress Mosquito Populations.

Li M, Kandul NP, Sun R, Yang T, Benetta ED, Brogan DJ, Antoshechkin I, Sánchez C HM, Zhan Y, DeBeaubien NA, Loh YM, Su MP, Montell C, Marshall JM, Akbari OS.

20-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37131747/>

Rapid epidemic expansion of chikungunya virus-ECSA lineage in Paraguay.

Giovanetti M, Vazquez C, Lima M, Castro E, Rojas A, de la Fuente AG, Aquino C, Cantero C, Fleitas F, Torales J, Barrios J, Ortega MJ, Gamarra ML, Villalba S, Alfonso T, Xavier J, Adelino T, Fritsch H, Iani FCM, Pereira GC, de Oliveira C, Schuab G, Rodrigues ES, Kashima S, Leite J, Gresh L, Franco L, Tegally H, Van Voorhis WC, Lessels R, de Filippis AMB, Ojeda A, Sequera G, Montoya R, Holmes EC, de Oliveira T, Rico JM, Lourenço J, Fonseca V, Junior Alcantara LC.

17-04-2023

medRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37131602/>

The spread of vector-borne viruses, such as CHIKV, is a significant public health concern in the Americas, with over 120,000 cases and 51 deaths in 2023, of which 46 occurred in Paraguay. Using a suite of genomic, phylodynamic, and epidemiological techniques, we characterized the ongoing large CHIKV epidemic in Paraguay.

Integrated clinical and metabolomic analysis of dengue infection shows molecular signatures associated with host-pathogen interaction in different phases of the disease.

Rathnakumar S, Kambhampati NSV, Saiswaroop R, Pradhan SS, Ramkumar G, Beeraka N, Muddu GK, Kumar S, Javvaji SK, Parangoankar A, Sivaramakrishnan V, Ramamurthy SS.

02-05-2023

Metabolomics.

<https://pubmed.ncbi.nlm.nih.gov/37130982/>

High 4-1BB Expression in PBMCs and Tumor Infiltrating Lymphocytes (TILs) in Patients with Head and Neck Squamous Cell Carcinoma.

Bin-Alee F, Chunthagonesupawit N, Meesakul T, Diloktaweewattana A, Mahattanasakul P, Mutirangura A, Ruangritchankul K, Keelawat S, Kitkumthorn N.

02-05-2023

Eur J Dent.

<https://pubmed.ncbi.nlm.nih.gov/37130554/>

Chikungunya virus infection in *Aedes aegypti* is modulated by L-cysteine, taurine, hypotaurine and glutathione metabolism.

Kumar A, Shrinet J, Sunil S.

02-05-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37130109/>

Background: Blood meal and infections cause redox imbalance and oxidative damage in mosquitoes which triggers the mosquito's system to produce antioxidants in response to increased oxidative stress. Important pathways activated owing to redox imbalance include taurine, hypotaurine and glutathione metabolism. The present study was undertaken to evaluate the role of these pathways during chikungunya virus (CHIKV) infection in *Aedes aegypti* mosquitoes. **Methodology:** Using a dietary L-cysteine supplement system, we upregulated these pathways and evaluated oxidative damage and oxidative stress response upon CHIKV infection using protein carbonylation and GST assays. Further, using a dsRNA based approach, we silenced some of the genes involved in synthesis and transport of taurine and hypotaurine and then evaluated the impact of these genes on CHIKV infection and redox biology in the mosquitoes. **Conclusions:** We report that CHIKV infection exerts oxidative stress in the *A. aegypti*, leading to oxidative damage and as a response, an elevated GST activity was observed. It was also observed that dietary L-cysteine treatment restricted CHIKV infection in *A. aegypti* mosquitoes. This L-cysteine mediated CHIKV inhibition was coincided by enhanced GST activity that further resulted in reduced oxidative damage during the infection. We also report that silencing of genes involved in synthesis of taurine and hypotaurine modulates CHIKV infection and redox biology of *Aedes* mosquitoes during the infection.

Association of viral kinetics, infection history, NS1 protein with plasma leakage among Indonesian dengue infected patients.

Nainggolan L, Dewi BE, Hakiki A, Pranata AJ, Sudiro TM, Martina B, van Gorp E.

02-05-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37130105/>

Objectives: Plasma leakage, a hallmark of disease in Dengue virus (DENV) infection, is an important clinical manifestation and is often associated with numerous factors such as viral factors. The aim of this study is to investigate the association of virus serotype, viral load kinetics, history of infection, and NS1 protein with plasma leakage. **Methods:** Subjects with fever \leq 48 hours and positive DENV infection were included. Serial laboratory tests, viral load measurements, and ultrasonography examination to assess plasma leakage were performed. **Results:** DENV-3 was the most common serotype found in the plasma leakage group (35%). Patients with plasma leakage demonstrated a trend of higher viral load and a longer duration of viremia compared to those without. This was significantly observed on the fourth day of fever ($p = 0.037$). We found higher viral loads on specific days in patients with plasma leakage in both primary and secondary infections compared to those without. In addition, we also observed more rapid viral clearance in patients with secondary infection. NS1 protein, especially after 4 days of fever, was associated with higher peak viral load level, even though it was not statistically significant ($p = 0.470$). However, pairwise comparison demonstrated that peak viral load level in the group of patients with circulating NS1 detected for 7 days was significantly higher than the 5-day group ($p = 0.037$). **Conclusion:** DENV-3 was the most common serotype to cause plasma leakage. Patients with plasma leakage showed a trend of higher viral load and a longer duration of viremia. Higher level of viral load was observed significantly on day 5 in patients with primary infection and more rapid viral clearance was observed in patients with secondary infection. Longer duration of circulating NS1 protein was also seen to be positively correlated with higher peak viral load level although not statistically significant.

Limited Effect of Ground Floor Fogging on Mosquito Distribution in High-Rise Condominia.

Lee JM, Wasserman RJ, Wilson RF, Cuthbert RN, Rahman S, Yek SH.

02-05-2023

Ecohealth.

<https://pubmed.ncbi.nlm.nih.gov/37129695/>

Impact, health care utilization, and costs of travel-associated mosquito-borne diseases in international travellers: a prospective study.

Tozan Y, Headley TY, Javelle E, Gautret P, Grobusch M, Pijper C, Asgeirsson H, Chen LH, Bourque D, Menéndez MD, Moro L, Gobbi F, Sánchez-Montalvá A, Connor BA, Matteelli A, Crosato V, Huits R, Libman M, Hamer DH.

02-05-2023

J Travel Med.

<https://pubmed.ncbi.nlm.nih.gov/37129519/>

Using compartmental models and Particle Swarm Optimization to assess Dengue basic reproduction number R_0 .

for the Republic of Panama in the 1999-2022 period.

Navarro Valencia

VA, Díaz Y, Pascale JM, Boni MF, Sanchez-Galan JE.
13-04-2023

Heliyon.

<https://pubmed.ncbi.nlm.nih.gov/37128312/>

Nowadays, the ability to make data-driven decisions in public health is of utmost importance. To achieve this, it is necessary for modelers to comprehend the impact of models on the future state of healthcare systems. Compartmental models are a valuable tool for making informed epidemiological decisions, and the proper parameterization of these models is crucial for analyzing epidemiological events. This work evaluated the use of compartmental models in conjunction with Particle Swarm Optimization (PSO) to determine optimal solutions and understand the dynamics of Dengue epidemics. The focus was on calculating and evaluating the rate of case reproduction, R_0 , for the Republic of Panama. Three compartmental models were compared: Susceptible-Infected-Recovered (SIR), Susceptible-Exposed-Infected-Recovered (SEIR), and Susceptible-Infected-Recovered Human-Susceptible-Infected Vector (SIR Human-SI Vector, SIR-SI). The models were informed by demographic data and Dengue incidence in the Republic of Panama between 1999 and 2022, and the susceptible population was analyzed. The SIR, SEIR, and SIR-SI models successfully provided R_0 estimates ranging from 1.09 to 1.74. This study provides, to the best of our understanding, the first calculation of R_0 for Dengue outbreaks in the Republic of Panama.

Development of disposable electrode for the detection of mosquito-borne viruses.

Nasrin F, Khoris IM, Chowdhury AD, Muttaqin SE, Park EY.

01-05-2023

Biotechnol J.

<https://pubmed.ncbi.nlm.nih.gov/37127933/>

Development of disposable, rapid, and convenient biosensor with high sensitivity and reliability is the most desired method of viral disease prevention. To achieve this goal, in this work, a practical impedimetric biosensor has been implemented into a disposable electrode on a screen-printed carbon electrode (SPCE) for the detection of two mosquito-borne viruses. The biosensor fabrication has step-wisely carried out on the disposable electrode surface at room temperature: starting from conductive film formation, physical binding of the gold nanoparticles (AuNPs)-polyaniline (PANI) into the conductive film, and biofunctionalization. To get the maximum efficiency of the antibody, biotinylated antibody has been conjugated on the surface of AuNP-PANI/PANI-SPCE via the streptavidin-biotin conjugation method which is a critical factor for the high sensitivity. Using the antibody-antigen interaction, this disposable electrode has designed to detect mosquito-borne infectious viruses, Chikungunya virus (CHIKV), and Zika virus (ZIKV) separately in a wide linear

range of 100 fg mL⁻¹ to 1 ng mL⁻¹ with a low detection limit of 1.33 and 12.31 fg mL⁻¹, respectively.

Chikungunya seroprevalence in population-based studies: a systematic review and meta-analysis.

Skalinski LM, Santos AES, Paixão E, Itaparica M, Barreto F, da Conceição Nascimento Costa M, Teixeira MG.

01-05-2023

Arch Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37127721/>

Background: Seroprevalence studies about chikungunya infection are usually conducted after epidemics to estimate the magnitude of the attack. This study aimed to estimate the seroprevalence of CHIKV by WHO region, considering the periods of introduction of the virus in these regions and its potential to lead to epidemics.

Methods: We systematically reviewed Medline/Pubmed, Embase, Lilacs, Scopus and Web of Science for original articles published up to 2020. Cohort, case-control and cross-sectional studies were eligible for inclusion, based on the results of laboratory diagnosis of previous or previous and recent infection. Those conducted with symptomatic individuals were excluded. **Results:** 596 articles were identified, 197 full-text were reviewed and 64 were included, resulting in 71 seroprevalences. Most were cross-sectional studies (92%), between 2001 and 2020 (92%), with population of all ages (55%), conducted in Kenya (10.9%), Brazil (9.4%) and French Polynesia (7.8%). The pooled estimates were 24% (95%CI 19-29; $I^2 = 99.7\%$; $p < 0.00$), being 21% (95%CI 13-30; $I^2 = 99.5\%$; $p < 0.00$) for adults, 7% (95%CI 0-23; $I^2 = 99.7\%$; $p < 0.00$) for children and 30% (95%CI 23-38; $I^2 = 99.7\%$; $p < 0.00$) for all ages. The higher seroprevalences were found in African, the Americas and South-East Asian Regions. **Conclusions:** The great heterogeneity of seroprevalences points to the persistence of viral circulation. Even where the seroprevalence is high, the population replacement and the absence of vaccines mean that the risk of virus spread and epidemics remains.

Comparative assessment of the bacterial communities associated with Anopheles darlingi immature stages and their breeding sites in the Brazilian Amazon.

Mosquera KD, Nilsson LKJ, de Oliveira MR, Rocha EM, Marinotti O, Håkansson S, Tadei WP, de Souza AQL, Terenius O.

01-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37127597/>

Background: The neotropical anopheline mosquito *Anopheles darlingi* is a major malaria vector in the Americas. Studies on mosquito-associated microbiota have shown that symbiotic bacteria play a major role in host biology. Mosquitoes acquire and transmit microorganisms over their life cycle. Specifically, the microbiota of immature forms is largely acquired from their aquatic environment. Therefore, our study aimed to describe the microbial communities associated with *An. darlingi* immature forms and their breeding sites in the

Coari municipality, Brazilian Amazon. **Methods:** Larvae, pupae, and breeding water were collected in two different geographical locations. Samples were submitted for DNA extraction and high-throughput 16S rRNA gene sequencing was conducted. Microbial ecology analyses were performed to explore and compare the bacterial profiles of *An. darlingi* and their aquatic habitats. **Results:** We found lower richness and diversity in *An. darlingi* microbiota than in water samples, which suggests that larvae are colonized by a subset of the bacterial community present in their breeding sites. Moreover, the bacterial community composition of the immature mosquitoes and their breeding water differed according to their collection sites, i.e., the microbiota associated with *An. darlingi* reflected that in the aquatic habitats where they developed. The three most abundant bacterial classes across the *An. darlingi* samples were Betaproteobacteria, Clostridia, and Gammaproteobacteria, while across the water samples they were Gammaproteobacteria, Bacilli, and Alphaproteobacteria. **Conclusions:** Our findings reinforce the current evidence that the environment strongly shapes the composition and diversity of mosquito microbiota. A better understanding of mosquito-microbe interactions will contribute to identifying microbial candidates impacting host fitness and disease transmission.

Applying a multi-strain dengue model to epidemics data.

de Araújo RGS, Jorge DCP, Dorn RC, Cruz-Pacheco G, Esteva MLM, Pinho STR.

29-04-2023

Math Biosci.

<https://pubmed.ncbi.nlm.nih.gov/37127090/>

A conserved Y-shaped RNA structure in the 3'UTR of chikungunya virus genome as a host-specialized element that modulates viral replication and evolution.

Bardossy ES, Volpe S, Alvarez DE, Filomatori CV.

01-05-2023

PLoS Pathog.

<https://pubmed.ncbi.nlm.nih.gov/37126493/>

Hyperferritinemia in Severe Dengue Infection: Single-Center Retrospective Cohort Study.

Lakshmanan C, Ranjit S, Natraj R, Venkatachalapathy P, Kumar VS, Lum LCS.

01-05-2023

Pediatr Crit Care Med.

<https://pubmed.ncbi.nlm.nih.gov/37125796/>

Objectives: Hyperferritinemia in the critical phase of dengue infections may correlate with severe dengue (SD) disease, and our primary objective was to examine the association between ferritin level on day 1 of PICU admission and 2009 World Health Organization (WHO) criteria for SD. Our secondary objective was outcome in relation to care. It is unclear whether immunomodulatory

therapy during the critical phase may restore immune homeostasis and mitigate disease severity. **Design, setting, and patients:** Retrospective cohort study of children with dengue 1 month to 16 years old with admission ferritin greater than or equal to 500 ng/mL requiring PICU admission. Demographics, clinical, and laboratory parameters, presence of the 2009 WHO SD criteria and outcomes were analyzed. Immunomodulatory therapy was used when there was persistent hyperinflammation beyond the critical phase of plasma leakage. **Interventions:** None. **Measurements and main results:** Fifty-five patients were admitted in the critical phase of dengue with median (interquartile range) ferritin levels of 8,105 ng/mL (2,350-15,765 ng/mL). Patients with at least one WHO SD category had higher ferritin levels compared to those without any SD criteria, with the highest levels in eight patients with all three SD categories. In our cohort of 55, 52 patients (94%) recovered with standard supportive therapy. Recovery was associated with decreased ferritin levels that occurred in parallel with improved circulation and platelet counts; this included 22 of 24 patients with admission ferritin levels greater than or equal to 10,000 ng/mL and two with ferritin greater than 1,00,000 ng/mL. Immunomodulation was used in three patients with unremitting fever, persistent hyperferritinemia, and progressive multiple organ dysfunction beyond the critical phase, of whom two died. **Conclusions:** Hyperferritinemia in the critical phase of SD is associated with the number of 2009 WHO SD criteria present. Our data also indicate that many patients with SD recover well with supportive care.

Pathophysiology and mechanisms of hearing impairment related to neonatal infection diseases.

Capra D, DosSantos MF, Sanz CK, Acosta Filha LG, Nunes P, Heringer M, Ximenes-da-Silva A, Pessoa L, de Mattos Coelho-Aguiar J, da Fonseca ACC, Mendes CB, da Rocha LS, Devalle S, Niemeyer Soares Filho P, Moura-Neto V.

14-04-2023

Front Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37125179/>

The inner ear, the organ of equilibrium and hearing, has an extraordinarily complex and intricate arrangement. It contains highly specialized structures meticulously tailored to permit auditory processing. However, hearing also relies on both peripheral and central pathways responsible for the neuronal transmission of auditory information from the cochlea to the corresponding cortical regions. Understanding the anatomy and physiology of all components forming the auditory system is key to better comprehending the pathophysiology of each disease that causes hearing impairment. In this narrative review, the authors focus on the pathophysiology as well as on cellular and molecular mechanisms that lead to hearing loss in different neonatal infectious diseases. To accomplish this objective, the morphology and function of the main structures responsible for auditory processing and the immune response leading to hearing loss were explored. Altogether, this information permits the proper understanding of each infectious disease discussed.

Dengue: Update on Clinically Relevant Therapeutic Strategies and Vaccines.

Palanichamy Kala M, St John AL, Rathore APS.
2023

Curr Treat Options Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37124673/>

Dengue viruses (DENV) continue to circulate worldwide, resulting in a significant burden on human health. There are four antigenically distinct serotypes of DENV, an infection of which could result in a potentially life-threatening disease. Current treatment options are limited and rely on supportive care. Although one dengue vaccine is approved for dengue-immune individuals and has modest efficacy, there is still a need for therapeutics and vaccines that can reduce dengue morbidities and lower the infection burden. There have been recent advances in the development of promising drugs for the treatment of dengue. These include direct antivirals that can reduce virus replication as well as host-targeted drugs for reducing inflammation and/or vascular pathologies. There are also new vaccine candidates that are being evaluated for their safety and efficacy in preventing dengue disease. This review highlights nuances in the current standard-of-care treatment of dengue. We also discuss emerging treatment options, therapeutic drugs, and vaccines that are currently being pursued at various stages of preclinical and clinical development.

Retrospective investigation of the origin and epidemiology of the dengue outbreak in Yunnan, China from 2017 to 2018.

Cao L, Yu Z, He H, Guo X, Wei C, Zhang X, Bao J, Li C, Zhou H, Xin J, Nan F.

03-04-2023

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/37124563/>

Population structure and invasion history of *Aedes aegypti* (Diptera: Culicidae) in Southeast Asia and Australasia.

Maynard AJ, Ambrose L, Bangs MJ, Ahmad R, Butafa C, Beebe NW.

25-03-2023

Evol Appl.

<https://pubmed.ncbi.nlm.nih.gov/37124090/>

The Threat of Impending Pandemics: A Proactive Approach.

Mishra B, Rath S, Mohanty M, Mohapatra PR.

27-03-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37123718/>

The incessant occurrence of devastating health-related events, either on a large scale, such as pandemics, or in a local community in the form of sporadic outbreaks due to infectious agents, warrants a rapid, target-oriented, well-organized response team to combat the demonic consequences. While the world has been recovering from

the clutches of the recent disastrous COVID-19 pandemic, the struggles against novel emerging and re-emerging pathogens such as monkeypox (mpox), newer evolving strains of influenza, Ebola, Zika, and the yellow fever virus continue to date. Therefore, a multisectoral, intercontinental, collaborative, interdisciplinary, and highly dedicated approach should always be implemented to achieve optimal health and avert future threats.

Determination of the best multivariate adaptive geographically weighted generalized Poisson regression splines model employing generalized cross-validation in dengue fever cases.

Sriningsih R, Otok BW, Sutikno.

07-04-2023

MethodsX.

<https://pubmed.ncbi.nlm.nih.gov/37122365/>

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

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

19-04-2023

Carbohydr Res.

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

Single-cell RNA sequencing reveals the fragility of male spermatogenic cells to Zika virus-induced complement activation.

Yang W, Liu LB, Liu FL, Wu YH, Zhen ZD, Fan DY, Sheng ZY, Song ZR, Chang JT, Zheng YT, An J, Wang PG.

29-04-2023

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/37120617/>

Zika virus (ZIKV) is a potential threat to male reproductive health but the mechanisms underlying its influence on testes during ZIKV infection remain obscure. To address this question, we perform single-cell RNA sequencing using testes from ZIKV-infected mice. The results reveal the fragility of spermatogenic cells, especially spermatogonia, to ZIKV infection and show that the genes of the complement system are significantly upregulated mainly in infiltrated S100A4 + monocytes/macrophages. Complement activation and its contribution to testicular damage are validated by ELISA, RT-qPCR and IFA and further verify in ZIKV-infected northern pigtailed macaques by RNA genome sequencing and IFA, suggesting that this might be the common response to ZIKV infection in primates. On this basis, we test the complement inhibitor C1INH and S100A4 inhibitors sulindac and niclosamide for their effects on testis protection. C1INH alleviates the pathological change in the testis but deteriorates ZIKV infection in general. In contrast, niclosamide effectively reduces S100A4 + monocyte/macrophage infiltration, inhibits complement

activation, alleviates testicular damage, and rescues the fertility of male mice from ZIKV infection. This discovery therefore encourages male reproductive health protection during the next ZIKV epidemic.

Virus Infections in Older People.

Soiza RL, Scicluna C, Bilal S.

2023

Subcell Biochem.

<https://pubmed.ncbi.nlm.nih.gov/37120468/>

Innate immune pathway modulator screen identifies STING pathway activation as a strategy to inhibit multiple families of arbo and respiratory viruses.

Garcia G Jr, Irudayam JI, Jeyachandran AV, Dubey S, Chang C, Castillo Cario S, Price N, Arumugam S, Marquez AL, Shah A, Fanaei A, Chakravarty N, Joshi S, Sinha S, French SW, Parcells MS, Ramaiah A, Arumugaswami V.

25-04-2023

Cell Rep Med.

<https://pubmed.ncbi.nlm.nih.gov/37119814/>

Sonication and heat-mediated synthesis, characterization and larvicidal activity of sericin-based silver nanoparticles against dengue vector (Aedes aegypti).

Summer M, Tahir HM, Ali S.

29-04-2023

Microsc Res Tech.

<https://pubmed.ncbi.nlm.nih.gov/37119431/>

Fabrication, characterization and evaluation of the larvicidal potential of novel silk protein (sericin)-based silver nanoparticles (Se-AgNPs) were the prime motives of the designed study. Furthermore, investigation of the sericin as natural reducing or stabilizing agent was another objective behind this study. Se-AgNPs were synthesized using sonication and heat. Fabricated Se-AgNPs were characterized using particle size analyzer, UV spectrophotometry, FTIR and SEM which confirmed the fabrication of the Se-AgNPs. Size of sonication-mediated Se-AgNPs was smaller (7.49 nm) than heat-assisted Se-AgNPs (53.6 nm). Being smallest in size, sonication-assisted Se-AgNPs revealed the significantly highest ($F_{4,10} = 39.20$, $p = .00$) larvicidal activity against fourth instar lab and field larvae ($F_{4,10} = 1864$, $p = .00$) of dengue vector (*Aedes aegypti*) followed by heat-assisted Se-AgNPs and positive control (temephos). Non-significant larvicidal activity was showed by silver (without sericin) which made the temperature stability of silver, debatable. Furthermore, findings of biochemical assays (glutathione-S transferase, esterase, and acetylcholinesterase) showed the levels of resistance in field strain larvae. Aforementioned findings of the study suggests the sonication as the best method for synthesis of Se-AgNPs while the larvicidal activity is inversely proportional to the size of Se-AgNPs, i.e., smallest the size, highest the larvicidal activity. Conclusively, status of the sericin as a natural reducing/stabilizing agent has been endorsed by the findings of this study.

Impact of tetravalent dengue vaccination with screening, ADE, and altered infectivity on single-serotype dengue and Zika transmission.

Kribs C, Greenhalgh D.

29-04-2023

J Math Biol.

<https://pubmed.ncbi.nlm.nih.gov/37119296/>

Acquired immunity to a dengue virus serotype (whether by infection or the only licensed dengue vaccine) can produce antibody-dependent enhancement (ADE) in later infections with another dengue serotype, resulting in higher viral loads and more severe symptoms such as dengue hemorrhagic fever, unless the person already has immunity to multiple dengue serotypes. Screening to confirm dengue seropositivity is therefore recommended before vaccination. Recent studies suggest that the closely-related Zika virus may also interact with dengue through ADE. This study uses a mathematical model to evaluate the likely impact of imperfect screening and dengue vaccination on the spread of both viruses in a population where only one dengue serotype circulates, although the vaccine may take against any or all of the four recognized serotypes. Analysis focuses on the reproductive numbers of the viruses. Results indicate that vaccination increases the spread of Zika through induced ADE, while its impact on the spread of dengue depends on screening specificity and serotype-specific vaccine efficacies, as well as the intensity of ADE. Numerical analysis identifies the roles played by age-in and catch-up vaccination as well as screening characteristics and prior dengue exposure.

Synergism between chikungunya virus infection and rheumatoid arthritis on cytokine levels: Clinical implications?

Bezerra LA, da Silva Bastos YC, Gonçalves JP, Silva Júnior JVI, de Lorena VMB, Duarte ALBP, Marques CDL, Coêlho MRCD.

29-04-2023

Braz J Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37118056/>

Empowering Communities During the COVID-19 Pandemic Through Mothers' Support Groups: Evidence From a Community Engagement Initiative in Sri Lanka.

Wijesinghe M, Gunawardana B, Weerasinghe W, Karunarathne S, Vithana V, Rajapaksha R, Batuwanthudawe R, Karunapema R.

28-04-2023

Glob Health Sci Pract.

<https://pubmed.ncbi.nlm.nih.gov/37116926/>

Community empowerment has previously been used to mitigate the effects of health emergencies, such as outbreaks of Ebola virus disease and Zika virus. In Sri Lanka, mothers' support groups (MSGs) aim to promote community health, well-being, and nutrition practices through community engagement. With the emergence of

the COVID-19 pandemic, MSGs were mobilized by the Health Promotion Bureau in response to the pandemic. Key activities MSGs engaged in during the COVID-19 response included establishing communication networks, creating a supportive environment for preventive behaviors, organizing vaccination clinics, distributing essential food and medicine, organizing recreational activities, promoting home gardening, and monitoring community activities. We examine how these community-based empowerment initiatives successfully assisted in the pandemic response. Health officials can help to build more resilient communities that are better prepared for future health emergencies by valuing the community-level methods used in overcoming COVID-19 and further strengthening the skills of community group members.

Potential use of high-resolution melting analyses for SARS-CoV-2 genomic surveillance.

de Souza Andrade A, Freitas EF, de Castro Barbosa E, Guimarães N, de Melo Iani FC, da Costa AVB, Bernardes AFL, Adelino TER, Ataíde ACZ, Gregianini TS, Nunes JD, Stringari LL, Riediger IN, Fernandes SB, de Jesus R, Fonseca V, Caldas S.

26-04-2023

J Virol Methods.

<https://pubmed.ncbi.nlm.nih.gov/37116586/>

Editorial: Insights in virus and host: 2021.

Hiscott J, Brandt CR.

11-04-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37113129/>

Intrahost Genetic Diversity of Dengue Virus in Human Hosts and Mosquito Vectors under Natural Conditions Which Impact Replicative Fitness In Vitro.

Nonyong P, Ekalaksananan T, Phanthanawiboon S, Overgaard HJ, Alexander N, Thaewongiew K, Sawaswong V, Nimsamer P, Payungporn S, Phadungsombat J, Nakayama EE, Shioda T, Pientong C.

17-04-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112962/>

Dengue virus (DENV) is an arbovirus whose transmission cycle involves disparate hosts: humans and mosquitoes. The error-prone nature of viral RNA replication drives the high mutation rates, and the consequently high genetic diversity affects viral fitness over this transmission cycle. A few studies have been performed to investigate the intrahost genetic diversity between hosts, although their mosquito infections were performed artificially in the laboratory setting. Here, we performed whole-genome deep sequencing of DENV-1 ($n = 11$) and DENV-4 ($n = 13$) derived from clinical samples and field-caught mosquitoes from the houses of naturally infected patients, in order to analyze the intrahost genetic diversity of DENV between host types. Prominent differences in DENV intrahost diversity were observed in the viral population structure

between DENV-1 and DENV-4, which appear to be associated with differing selection pressures. Interestingly, three single amino acid substitutions in the NS2A (K81R), NS3 (K107R), and NS5 (I563V) proteins in DENV-4 appear to be specifically acquired during infection in *Ae. aegypti* mosquitoes. Our *in vitro* study shows that the NS2A (K81R) mutant replicates similarly to the wild-type infectious clone-derived virus, while the NS3 (K107R), and NS5 (I563V) mutants have prolonged replication kinetics in the early phase in both Vero and C6/36 cells. These findings suggest that DENV is subjected to selection pressure in both mosquito and human hosts. The NS3 and NS5 genes may be specific targets of diversifying selection that play essential roles in early processing, RNA replication, and infectious particle production, and they are potentially adaptive at the population level during host switching.

T Cells in Tick-Borne Flavivirus Encephalitis: A Review of Current Paradigms in Protection and Disease Pathology.

13-04-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112938/>

The family *Flaviviridae* is comprised of a diverse group of arthropod-borne viruses that are the etiological agents of globally relevant diseases in humans. Among these, infection with several of these flaviviruses—including West Nile virus (WNV), Zika virus (ZIKV), Japanese encephalitis virus (JEV), tick-borne encephalitis virus (TBEV), and Powassan virus (POWV)—can result in neuroinvasive disease presenting as meningitis or encephalitis. Factors contributing to the development and resolution of tick-borne flavivirus (TBEV, POWV) infection and neuropathology remain unclear, though many recently undertaken studies have described the virus-host interactions underlying encephalitic disease. With access to neural tissues despite the selectively permeable blood-brain barrier, T cells have emerged as one notable contributor to neuroinflammation. The goal of this review is to summarize the recent advances in tick-borne flavivirus immunology—particularly with respect to T cells—as it pertains to the development of encephalitis. We found that although T cell responses are rarely evaluated in a clinical setting, they are integral in conjunction with antibody responses to restricting the entry of TBFV into the CNS. The extent and means by which they can drive immune pathology, however, merits further study. Understanding the role of the T cell compartment in tick-borne flavivirus encephalitis is instrumental for improving vaccine safety and efficacy, and has implications for treatments and interventions for human disease.

Dengue Exposure and Wolbachia wMel Strain Affects the Fertility of Quiescent Eggs of *Aedes aegypti*.

Petersen MT, Couto-Lima D, Garcia GA, Pavan MG, David MR, Maciel-de-Freitas R.

12-04-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112932/>

(1) Background: The deployment of the bacterium *Wolbachia* to reduce arbovirus transmission is ongoing in several countries worldwide. When *Wolbachia*-carrying *Aedes aegypti* are released and established in the field, females may feed on dengue-infected hosts. The effects of simultaneous exposure on life-history traits of *Ae. aegypti* to *Wolbachia* wMel strain and dengue-1 virus DENV-1 remain unclear. (2) Methods: We monitored 4 groups (mosquitoes with either DENV-1 or *Wolbachia*, coinfecting with DENV-1 and *Wolbachia*, as well as negative controls) to estimate *Ae. aegypti* survival, oviposition success, fecundity, collapsing and fertility of quiescent eggs for 12 weeks. (3) Results: Neither DENV-1 nor *Wolbachia* had a significant impact on mosquito survival nor on mosquito fecundity, although the last parameter showed a tendency to decrease with ageing. There was a significant decrease in oviposition success in individuals carrying *Wolbachia*. *Wolbachia* infection and storage time significantly increased egg collapse parameter on the egg viability assay, while DENV-1 had a slight protective effect on the first four weeks of storage. (4) Conclusions: Despite limitations, our results contribute to better understanding of the tripartite interaction of virus, bacteria and mosquito that may take place in field conditions and aid in guaranteeing the *Wolbachia* strategy success.

Isolation of Flaviviruses and Alphaviruses with Encephalitogenic Potential Diagnosed by Evandro Chagas Institute (Pará, Brazil) in the Period of 1954-2022: Six Decades of Discoveries.

Wanzeller ALM, da Silva FS, Hernández LHA, Barros LIL, Freitas MNO, Santos MM, Gonçalves EJ, Pantoja JAS, Lima CS, Lima MF, Costa LRO, das Chagas LL, Silva IF, da Cunha TCADS, do Nascimento BLS, Vasconcelos HB, da Rosa EST, Rodrigues SG, Azevedo RDS, Martins LC, Casseb LMN, Chiang JO, Nunes Neto JP, Cruz ACR, Carvalho VL, Vasconcelos PFDC, da Silva EVP.

10-04-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112917/>

Laboratory Evaluation and Field Testing of Dengue NS1 and IgM/IgG Rapid Diagnostic Tests in an Epidemic Context in Senegal.

Ndiaye O, Woolston K, Gaye A, Loucoubar C, Cocozza M, Fall C, Dia F, Adams ER, Samb M, Camara D, Sadio BD, Diagne CT, Weidmann M, Faye O, Fitchett JRA, Sall AA, Diagne CT.

31-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112887/>

Grape Seed Proanthocyanidins Inhibit Replication of the Dengue Virus by Targeting NF-κB and MAPK-Mediated Cyclooxygenase-2 Expression.

Chen WC, Hossen M, Liu W, Yen CH, Huang CH, Hsu YC, Lee JC.

30-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112864/>

Dengue virus (DENV) infection is a serious global health issue as it causes severe dengue hemorrhagic fever and dengue shock syndrome. Since no approved therapies are available to treat DENV infection, it is necessary to develop new agents or supplements that can do this. In this study, grape seed proanthocyanidins extract (GSPE), which is widely consumed as a dietary supplement, dose-dependently suppressed the replication of four DENV serotypes. The inhibitory mechanism demonstrated that GSPE downregulated DENV-induced aberrant cyclooxygenase-2 (COX-2) expression, revealing that the inhibitory effect of the GSPE on DENV replication involved targeting DENV-induced COX-2 expression. Mechanistic studies on signaling regulation have demonstrated that GSPE significantly reduced COX-2 expression by inactivating NF-κB and ERK/P38 MAPK signaling activities. Administering GSPE to DENV-infected suckling mice reduced virus replication, mortality, and monocyte infiltration of the brain. In addition, GSPE substantially reduced the expression of DENV-induced inflammatory cytokines associated with severe dengue disease, including tumor necrosis factor-α, nitric oxide synthase, interleukin (IL)-1, IL-6, and IL-8, suggesting that GSPE has potential as a dietary supplement to attenuate DENV infection and severe dengue.

A Perspective on Current Flavivirus Vaccine Development: A Brief Review.

Dutta SK, Langenburg T.

28-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112840/>

Differences in Longevity and Temperature-Driven Extrinsic Incubation Period Correlate with Varying Dengue Risk in the Arizona-Sonora Desert Region.

Ernst KC, Walker KR, Castro-Luque AL, Schmidt C, Joy TK, Brophy M, Reyes-Castro P, Díaz-Caravantes RE, Encinas VO, Aguilera A, Gameros M, Cuevas Ruiz RE, Hayden MH, Alvarez G, Monaghan A, Williamson D, Arnbrister J, Gutiérrez EJ, Carrière Y, Riehle MA.

26-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112832/>

The Others: A Systematic Review of the Lesser-Known Arboviruses of the Insular Caribbean.

Ali I, Alarcón-Elbal PM, Mundle M, Noble SAA, Oura CAL, Anzinger JJ, Sandiford SL.

25-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112824/>

The Caribbean enjoys a long-standing eminence as a popular tourist destination; however, over the years it has also amassed the sobriquet "arbovirus hotspot". As the

planet warms and vectors expand their habitats, a cognizant working knowledge of the lesser-known arboviruses and the factors that influence their emergence and resurgence becomes essential. The extant literature on Caribbean arboviruses is spread across decades of published literature and is quite often difficult to access, and, in some cases, is obsolete. Here, we look at the lesser-known arboviruses of the insular Caribbean and examine some of the drivers for their emergence and resurgence. We searched the scientific literature databases PubMed and Google Scholar for peer-reviewed literature as well as scholarly reports. We included articles and reports that describe works resulting in serological evidence of the presence of arboviruses and/or arbovirus isolations in the insular Caribbean. Studies without serological evidence and/or arbovirus isolations as well as those including dengue, chikungunya, Zika, and yellow fever were excluded. Of the 545 articles identified, 122 met the inclusion criteria. A total of 42 arboviruses were identified in the literature. These arboviruses and the drivers that affect their emergence/resurgence are discussed.

The Anti-Dengue Virus Peptide DV2 Inhibits Zika Virus Both In Vitro and In Vivo.

Castro-Amarante MF, Pereira SS, Pereira LR, Santos LS, Venceslau-Carvalho AA, Martins EG, Balan A, Souza Ferreira LC.

25-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112820/>

Alphavirus Evasion of Zinc Finger Antiviral Protein (ZAP) Correlates with CpG Suppression in a Specific Viral nsP2 Gene Sequence.

Nguyen LP, Aldana KS, Yang E, Yao Z, Li MMH.

24-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112813/>

Certain re-emerging alphaviruses, such as chikungunya virus (CHIKV), cause serious disease and widespread epidemics. To develop virus-specific therapies, it is critical to understand the determinants of alphavirus pathogenesis and virulence. One major determinant is viral evasion of the host interferon response, which upregulates antiviral effectors, including zinc finger antiviral protein (ZAP). Here, we demonstrated that Old World alphaviruses show differential sensitivity to endogenous ZAP in 293T cells: Ross River virus (RRV) and Sindbis virus (SINV) are more sensitive to ZAP than o'nyong'nyong virus (ONNV) and CHIKV. We hypothesized that the more ZAP-resistant alphaviruses evade ZAP binding to their RNA. However, we did not find a correlation between ZAP sensitivity and binding to alphavirus genomic RNA. Using a chimeric virus, we found the ZAP sensitivity determinant lies mainly within the alphavirus non-structural protein (nsP) gene region. Surprisingly, we also did not find a correlation between alphavirus ZAP sensitivity and binding to nsP RNA,

suggesting ZAP targeting of specific regions in the nsP RNA. Since ZAP can preferentially bind CpG dinucleotides in viral RNA, we identified three 500-bp sequences in the nsP region where CpG content correlates with ZAP sensitivity. Interestingly, ZAP binding to one of these sequences in the nsP2 gene correlated to sensitivity, and we confirmed that this binding is CpG-dependent. Our results demonstrate a potential strategy of alphavirus virulence by localized CpG suppression to evade ZAP recognition.

Transient Blockade of Type I Interferon Signalling Promotes Replication of Dengue Virus Strain D2Y98P in Adult Wild-Type Mice.

Wilken L, Stelz S, Prajeeth CK, Rimmelzwaan GF.

23-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112795/>

Dengue virus serotypes 1 to 4 (DENV1-4) place nearly half the global population at risk of infection and the licensed tetravalent dengue vaccine fails to protect individuals who have not previously been exposed to DENV. The development of intervention strategies had long been hampered by the lack of a suitable small animal model. DENV does not replicate in wild-type mice due to its inability to antagonise the mouse type I interferon (IFN) response. Mice deficient in type I IFN signalling (*Ifnar1*^{-/-} mice) are highly susceptible to DENV infection, but their immunocompromised status makes it difficult to interpret immune responses elicited by experimental vaccines. To develop an alternative mouse model for vaccine testing, we treated adult wild-type mice with MAR1-5A3-an IFNAR1-blocking, non-cell-depleting antibody-prior to infection with the DENV2 strain D2Y98P. This approach would allow for vaccination of immunocompetent mice and subsequent inhibition of type I IFN signalling prior to challenge infection. While *Ifnar1*^{-/-} mice quickly succumbed to infection, MAR1-5A3-treated mice did not show any signs of illness but eventually seroconverted. Infectious virus was recovered from the sera and visceral organs of *Ifnar1*^{-/-} mice, but not from those of mice treated with MAR1-5A3. However, high levels of viral RNA were detected in the samples of MAR1-5A3-treated mice, indicating productive viral replication and dissemination. This transiently immunocompromised mouse model of DENV2 infection will aid the pre-clinical assessment of next-generation vaccines as well as novel antiviral treatments.

Recent Advancements in Mosquito-Borne Flavivirus Vaccine Development.

Wu B, Qi Z, Qian X.

23-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112794/>

Antiviral Activity of Quercetin Hydrate against Zika Virus.

Saivish MV, Menezes GL, da Silva RA, Fontoura MA, Shimizu JF, da Silva GCD, Teixeira IDS, Mistrão NFB,

Hernandes VM, Rahal P, Sacchetto L, Pacca CC, Marques RE, Nogueira ML.

19-04-2023

Int J Mol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37108665>

Physiological and developmental dysfunctions in the dengue vector *Culex pipiens* (Diptera: Culicidae) immature stages following treatment with zinc oxide nanoparticles.

Ibrahim AMA, Thabet MA, Ali AM.

Mai-2023

Pestic Biochem Physiol.

<https://pubmed.ncbi.nlm.nih.gov/37105619/>

The medical value of mosquitoes attracted researchers worldwide to search for a valuable way to control such serious insects. The continuous development of resistance against chemical insecticides pushed toward looking for novel and promising compounds against mosquitoes. In this study, the toxicity and physio-developmental effects of 10-30 nm spherical zinc oxide nanoparticles (ZnONPs) in aqueous suspension was addressed against the first larval instar of *Culex pipiens* mosquito. The calculated value of LC_{50} was about 0.892 g/L while the sub lethal concentration LC_{20} recorded about 0.246 g/L. Larvae treated with ZnONPs suffered reduced growth rate, longer developmental period and malformations in the breathing tube. Furthermore, the treated larvae showed clear abnormal appearance of the gastric caeca and midgut epithelia under transmission electron microscope (TEM). These abnormalities appeared as condensation of the nuclear chromatin, abnormal shape or absence of microvilli, highly increased amount of smooth endoplasmic reticulum in the cytoplasm and appearance of numerous vacuoles. Additionally, ZnONPs interfered with several biochemical pathways such as induction of oxidative stress which appeared in the form of increased levels of hydrogen peroxide and inability to activate the detoxifying enzymes alkaline phosphatase (ALP), catalase and glutathione peroxidase (GPX). On the contrary, the activity of the antioxidant enzyme superoxide dismutase (SOD) increased in treated larvae. Furthermore, LC_{20} and LC_{50} of ZnONPs inhibited the growth rate of the larval gut fauna in vitro. These results clearly show that ZnONPs target several tissues leading to serious alteration in the physiological and developmental processes in *C. pipiens* mosquito larvae.

Long-term projections of the impacts of warming temperatures on Zika and dengue risk in four Brazilian cities using a temperature-dependent basic reproduction number.

Van Wyk H, Eisenberg JNS, Brouwer AF.

27-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37104296/>

For vector-borne diseases the basic reproduction number [Formula: see text], a measure of a disease's epidemic potential, is highly temperature-dependent. Recent work

characterizing these temperature dependencies has highlighted how climate change may impact geographic disease spread. We extend this prior work by examining how newly emerging diseases, like Zika, will be impacted by specific future climate change scenarios in four diverse regions of Brazil, a country that has been profoundly impacted by Zika. We estimated a [Formula: see text], derived from a compartmental transmission model, characterizing Zika (and, for comparison, dengue) transmission potential as a function of temperature-dependent biological parameters specific to *Aedes aegypti*. We obtained historical temperature data for the five-year period 2015-2019 and projections for 2045-2049 by fitting cubic spline interpolations to data from simulated atmospheric data provided by the CMIP-6 project (specifically, generated by the GFDL-ESM4 model), which provides projections under four Shared Socioeconomic Pathways (SSP). These four SSP scenarios correspond to varying levels of climate change severity. We applied this approach to four Brazilian cities (Manaus, Recife, Rio de Janeiro, and São Paulo) that represent diverse climatic regions. Our model predicts that the [Formula: see text] for Zika peaks at 2.7 around 30°C, while for dengue it peaks at 6.8 around 31°C. We find that the epidemic potential of Zika will increase beyond current levels in Brazil in all of the climate scenarios. For Manaus, we predict that the annual [Formula: see text] range will increase from 2.1-2.5, to 2.3-2.7, for Recife we project an increase from 0.4-1.9 to 0.6-2.3, for Rio de Janeiro from 0-1.9 to 0-2.3, and for São Paulo from 0-0.3 to 0-0.7. As Zika immunity wanes and temperatures increase, there will be increasing epidemic potential and longer transmission seasons, especially in regions where transmission is currently marginal. Surveillance systems should be implemented and sustained for early detection.

Spatiotemporal and Seasonal Trends of Class A and B Notifiable Infectious Diseases in China: Retrospective Analysis.

Zheng J, Zhang N, Shen G, Liang F, Zhao Y, He X, Wang Y, He R, Chen W, Xue H, Shen Y, Fu Y, Zhang WH, Zhang L, Bhatt S, Mao Y, Zhu B.

27-04-2023

JMIR Public Health Surveill.

<https://pubmed.ncbi.nlm.nih.gov/37103994/>

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/>

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/>

Background: Since 2018, a dengue epidemic has been raging annually in Reunion Island, which poses the major problem of its morbidity and mortality. However, there is no consensus in the literature on factors associated with severity of illness. The objective of this study was to identify the factors associated with the occurrence of severe dengue (SD) according to the criteria adopted in 2009 by the World Health Organization (WHO), during the 2019 epidemic. **Methodology/principal findings:** A total of 163 patients with RT-PCR-confirmed dengue were included in a multicenter prospective cohort study in Reunion Island between January and June 2019. Of these, 37 (23%) were classified as SD, which involves presentation dominated by at least one organ failure, and 126 (77%) classified as non-SD (of which 90 (71%) had warning signs). Confusion, dehydration, and relative hypovolemia were significantly associated with SD in bivariate analysis ($p < 0.05$). The factors associated with SD in multivariate analysis were a time from first symptom to hospital consultation over 2 days (OR: 2.46, CI: 1.42-4.27), a history of cardiovascular disease (OR: 2.75, 95%CI: 1.57-4.80) and being of Western European origin (OR: 17.60, CI: 4.15-74). **Conclusions/significance:** This study confirms that SD is a frequent cause of hospitalization during dengue epidemics in Reunion Island. It suggests that cardiovascular disease, Western European origin, and delay in diagnosis and management are risk factors associated with SD fever, and that restoration of blood volume and correction of dehydration must be performed early to be effective.

Impact of prior flavivirus vaccination on immunogenicity and efficacy of an inactivated Zika vaccine in Indian rhesus macaques.

Young G, Zahralban-Steele M, Dean HJ.

05-05-2023

Vaccine.

<https://pubmed.ncbi.nlm.nih.gov/37055345/>

The Burden of Arboviral Infections in the Military Health System 2012-2019.

Wellington T, Fraser JA, Kuo HC, Hickey PW, Lindholm DA.

10-04-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37037439/>

Arboviral infections, including dengue (DNV), chikungunya (CHIKV), and Zika (ZIKV), impact both travelers and native populations of endemic regions. We sought to assess the disease burden of arboviral infections in the Military Health System, the validity of arboviral diagnostic codes, and the role of pretravel counseling on insect avoidance precautions. We searched for diagnostic codes consistent with arboviral infection and grouped them into DNV, CHIKV, ZIKV, Japanese encephalitis virus (JEV), and Other. Demographic data were evaluated. A subset of charts in each category were reviewed for diagnostic validity and travel characteristics. In all, 10,547 unique subjects carried

17,135 arboviral diagnostic codes, including 1,606 subjects (15.2%) coded for DNV, 230 (2.2%) for ZIKV, 65 (0.6%) for CHIKV, and 4,317 (40.9%) for JEV. A chart review was performed on 807 outpatient charts, yielding outpatient diagnostic code positive predictive values of 60.5% (DNV), 15.3% (ZIKV), and 64.5% (CHIKV); there were no valid cases of JEV. Dengue represented the greatest burden of arboviral infections with 2.2 cases per 100,000 military healthcare enrollees over the 2012-2019 fiscal years. More than 80% of subjects with arboviral infection did not have documented pretravel counseling. Arboviral infections represent a significant disease burden in young travelers to endemic regions. After adjustment for diagnostic validity, DNV represented the greatest burden. Diagnostic codes for ZIKV and JEV overestimate the burden of these diseases. Low rates of pretravel visits represent an opportunity for increased emphasis on insect exposure precautions.

Tropical infections as occupational diseases among young volunteers in social projects.

Kölsch Y, Phiri BSJ, Küpper T.

Mai-2023

Int J Hyg Environ Health.

<https://pubmed.ncbi.nlm.nih.gov/37030087/>

Insecticide susceptibility and detection of kdr-gene mutations in *Aedes aegypti* of Peshawar, Pakistan.

Tanzila G, Rasheed SB, Khan NH, Kausar A, Jahan F, Wahid S.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37028585/>

Dengue is an endemic disease in Peshawar, Pakistan and its primary vector is *Aedes aegypti* mosquito. Due to absence of vaccines and proper treatment for dengue, vector control becomes a necessary tool for disease management. Reported insecticide resistance in vectors is a serious threat to the control of dengue. This study presents the susceptibility status of *Ae. aegypti* to eight insecticides in district Peshawar along with one of the first attempts to screen mutations in the vector's knock down resistant gene (*kdr*). Local *Ae. aegypti* was found to be highly resistant to DDT and Deltamethrin while they were susceptible to Cyfluthrin and Bendiocarb. DNA sequencing of domains II and III of *kdr*-gene detected four SNPs in domain IIS6 at positions S989P and V1016G while two mutations were reported at position T1520I and F1534C in domain IIIS6. Lowest allele frequency was observed for S989P and V1016G positions while it was highest for F1534C. Among mutational combinations SSVVTICC (43%) was evidently the most predominant combination, where T1520I was heterozygous and F1534C was homozygous mutant. The study concludes insecticide resistance in local dengue population of Peshawar, Pakistan. The resistance observed is to some extent also corroborated in the molecular study of *kdr* gene. Findings herein can be utilized in designing dengue vector control strategies in Peshawar.

Current thoughts on cellular functions of numb-associated kinases.

Huang C, Ji C, Wang J.

Mai-2023

Mol Biol Rep.

<https://pubmed.ncbi.nlm.nih.gov/37014568/>

Members of the Numb-associated kinase family of serine/threonine kinases play an essential role in many cellular processes, such as endocytosis, autophagy, dendrite morphogenesis, osteoblast differentiation, and the regulation of the Notch pathway. Numb-associated kinases have been relevant to diverse diseases, including neuropathic pain, Parkinson's disease, and prostate cancer. Therefore, they are considered potential therapeutic targets. In addition, it is reported that Numb-associated kinases have been involved in the life cycle of multiple viruses such as hepatitis C virus (HCV), Ebola virus (EBOV), and dengue virus (DENV). Recently, Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) continues to threaten global health. Studies show that Numb-associated kinases are implicated in the infection of SARS-CoV-2 which can be suppressed by Numb-associated kinases inhibitors. Thus, Numb-associated kinases are proposed as potential host targets for broad-spectrum antiviral strategies. We will focus on the recent advances in Numb-associated kinases-related cellular functions and their potential as host targets for viral infections in this review. Questions that remained unknown on the cellular functions of Numb-associated kinases will also be discussed.

Infectivity of three Mayaro Virus geographic isolates in human cell lines.

Patel AR, Dulcey M, Abid N, Cash MN, Dailey J, Salemi M, Mavian C, Vittor AY.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36965613/>

A sero-epidemiological investigation of West Nile virus among patients without any records of their symptoms from three different hospitals from Tunisia.

Nasraoui N, Ben Moussa ML, Ayedi Y, Mastouri M, Trabelsi A, Raies A, Wölfel R, Moussa MB.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36948235/>

The Development and Evaluation of a Combined Infection-Rheumatology Assessment Service in Response to the Chikungunya Fever Epidemic.

Krutikov M, Donovan J, Lambourne J, Ciurtin C, Brown M, Bailey R, Manson JJ.

20-03-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36940667/>

The chikungunya virus is an arthritogenic alphavirus. Acute infection may be followed by persistent arthralgia, often causing significant functional impairment. The 2014-2015 chikungunya fever (CHIKF) epidemic resulted in a marked increase in cases presenting to rheumatology and tropical diseases services. A combined multidisciplinary rheumatology-tropical diseases service for assessment, management, and follow-up of patients with proven CHIKF and persistent (≥ 4 weeks) arthralgia was proposed and rapidly developed at The Hospital for Tropical Diseases in London. Rapid set up of a multidisciplinary clinic in response to the epidemic was achieved. Of a total of 54 patients, 21 (38.9%) patients with CHIKF developed persistent arthralgia and were reviewed by the multidisciplinary service. A combined assessment approach enabled comprehensive multidisciplinary assessment of CHIKF, assessment of joint pathology through ultrasound, and appropriate follow-up. A combined rheumatology-tropical diseases service was successfully used to identify and assess CHIKF-associated morbidity. Future outbreaks may be approached by establishing tailored multidisciplinary clinics.

First report of natural Wolbachia infections in mosquitoes from Cuba.

Ruiz A, Gutiérrez-Bugallo G, Rodríguez-Roche R, Pérez L, González-Broche R, Piedra LA, Martínez LC, Menéndez Z, Vega-Rúa A, Bisset JA.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36907292/>

Quantifying Aedes aegypti Host Odor Preference Using a Two-Port Olfactometer.

Metz HC, Zung JL, McBride CS.

02-05-2023

Cold Spring Harb Protoc.

<https://pubmed.ncbi.nlm.nih.gov/36669857/>

Blood-feeding mosquitoes are a leading threat to global public health-vectoring dangerous infections including Zika, dengue, and malaria. Mosquitoes identify and target hosts for blood meals by using visual, thermal, and chemical cues. Here we describe an assay for measuring odor-based host-preference behavior-that is, the preferential approach toward one host over another based on differences in the volatile compounds they emit. The assay can be adapted for use with diverse odor sources, from live animals and their breath to odor-scented sleeves with controlled amounts of CO₂. Mosquitoes in this assay fly upwind to within 30 cm of the odor source and then enter a small trap. We therefore believe this assay best replicates medium- to short-range host-seeking, when females approach and are preparing to land on a host animal. We also find that relative response in a two-choice test shows less trial-to-trial variation than the absolute number of responsive mosquitoes, which appears more sensitive to exogenous factors such as rearing conditions. This assay has been used to better understand mosquito host-seeking decisions, which can provide fundamental insight into the

brain and behavior as well as information useful for the design of novel vector control strategies.

Splicing factor SF3B3, a NS5-binding protein, restricts ZIKV infection by targeting GCH1.

Chen T, Yang H, Liu P, Hamiti M, Zhang X, Xu Y, Quan W, Zhang Y, Yu W, Jiao L, Du T, Xi J, Yin B, Zhou W, Lu S, Peng X.

Avr-2023

Virol Sin.

<https://pubmed.ncbi.nlm.nih.gov/36572150/>

Transfusion transmitted virus and dengue virus among healthy blood donors: A prevalence report from Jordan.

Swedan S, Al-Saleh D.

01-05-2023

Biomol Biomed.

<https://pubmed.ncbi.nlm.nih.gov/36475356/>

Transfusion transmitted virus (TTV) is thought to contribute to non-A non-E hepatitis and other diseases. Dengue virus (DENV) is a serious mosquito-borne pathogen. Reports on TTV and DENV in Jordan and the Middle East and North Africa region are limited. Herein, the prevalence of TTV antigen and anti-DENV IgG antibodies among apparently healthy blood donors from Northern Jordan and the Northern Agwar region of Jordan was investigated using an enzyme-linked immunosorbent assay. Chi-square test and binary logistic regression were used to correlate positivity with possible infection risk factors (age, sex, residence location, and occupation). One hundred ninety apparently healthy blood donors were included in the study (age 18 - 54 years). TTV antigen was detected in 17.9% of the samples. Lower antigen positivity was observed among Agwar residents than non-residents (7.1% vs 24.5%; chi-square test $P < 0.001$), which was confirmed by regression analysis (odds ratio 0.262 [95% confidence interval 0.086-0.805]; $P = 0.019$). Antigen positivity did not differ by age, sex, or occupation. Seropositivity for anti-DENV IgG was 17.9%. Seropositivity did not differ by age, sex, or occupation. Higher seropositivity was observed among Agwar residents than non-residents (36.1% vs 9.4%; chi-square test $P < 0.001$), which was confirmed by regression analysis (odds ratio 5.420 [95% confidence interval 2.377-12.359]; $P < 0.001$). Overall, low TTV antigen prevalence and DENV seroprevalence were found among blood donors from Northern Jordan and the Northern Agwar region of Jordan.

Molecular characterization of recombinant premembrane protein of dengue virus serotype-2 for development of diagnostic assay.

Munir R, Rafique S, Ali A, Amin I, Ahmed S, Vajeheha A, Shahid M, Samiullah TR, Idrees M, Tao YJ, Khan MU.

Mai-2023

J Basic Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36356225/>

Bilateral Ciliochoroidal Effusion with Secondary Angle Closure and Myopic Shift in Dengue Fever.

Dhoot SK.

Mai-2023

Ocul Immunol Inflamm.

<https://pubmed.ncbi.nlm.nih.gov/35324371/>

Purpose: To describe a case of bilateral ciliochoroidal effusion with secondary angle closure and myopic shift early in course of Dengue Fever. **Case description:** A 36-year-old, female complaints of painless loss of vision few days after being diagnosed dengue fever. Her best corrected visual acuity is 6/6 with refractive correction of -3.00 DS and -2.75 DS in right and left eye respectively. On examination her anterior chambers are shallow with closed angles on anterior segment optical coherence tomography and high intraocular pressure. Fundus examination revealed macular striae with peripheral choroidal oedema suggestive of ciliochoroidal effusion with angle closure and acute myopic shift. Few days after starting on topical intraocular pressure lowering drugs, cycloplegics and topical steroid eye drops along with low dose systemic steroids her condition improved with resolution of choroidal effusion and return of vision to normal levels. **Discussion:** This case report represents interesting patient who developed transient loss of vision due to accumulation of fluid in suprachoroidal space resulting in secondary angle closure and myopia after being diagnosed with dengue fever, for which one should have high index of suspicion to facilitate timely management.

In silico identification of small molecule protein-protein interaction inhibitors: targeting hotspot regions at the interface of MXRA8 and CHIKV envelope protein.

Verma J, Subbarao N.

Mai-2023

J Biomol Struct Dyn.

<https://pubmed.ncbi.nlm.nih.gov/35272566/>

Dracunculose

Characterization of the physico-chemical properties of the natural habitat and in vitro culture effects on the biochemistry, proliferation and morphology of *Lemna minuta*.

Maissour A, Bouqadida M, Oualili H, El Omari R, Belfaiza M, Makroum K.

03-05-2023

BMC Plant Biol.

<https://pubmed.ncbi.nlm.nih.gov/37138221/>

In this study, the ecological conditions of the natural habitat of *Lemna minuta* Kunth in Morocco were investigated, and the impact of five synthetic growth media (Murashige-Skoog (MS), Schenk-Hildebrand (SH), Hoagland medium (HM), 10X Algal Assay Procedure (AAP), and Swedish Standard Institute medium (SIS)) on the

morphophysiological and biochemical parameters was analysed. The morphophysiological parameters included root length, frond surface area, and fresh weight, while the biochemical parameters included photosynthetic pigments, carbohydrates, and protein content. The study was conducted in vitro in two phases: an uncontrolled aeration system (Phase I) and a controlled aeration system (Phase II). The results showed that the pH, conductivity, salinity, and ammonium levels in the natural habitat were within the optimal range for duckweed growth. The measured orthophosphate concentrations were higher compared to previous observations, while the recorded chemical oxygen demand values were low. The study also revealed a significant effect of the culture medium composition on the morphophysiological and biochemical parameters of the duckweed. The fresh weight biomass, relative growth rate in fronds, relative growth rate in surface area, root length, protein content, carbohydrates, chlorophyll (a), chlorophyll (b), total chlorophyll, carotenoids, and the chlorophyll (a/b) ratio were all affected by the culture medium. The most accurate regression models described the growth index GI(F) based on time and in vitro culture conditions in both phases. In Phase I, the best models for MS, SIS, AAP, and SH media were linear, weighted quadratic, cubic, and weighted cubic, respectively. In Phase II, the best models for all growth media were linear. The time coefficients (in days) for Phase II were 0.321, 0.547, 1.232, 1.470, and 0.306 for AAP, HM, MS, SH, and SIS, respectively. Comparing the morphophysiological and biochemical parameters of fronds from different media and analysing the regression model results showed that the SH and MS media were the best among the tested media for the in vitro culture of *L. minuta* in controlled aeration conditions. However, further research is needed to develop new synthetic media that best promote the growth and maintenance of this duckweed in long-term culture.

Physiological and transcriptional responses to heat stress in a typical phenotype of *Pinellia ternata*.

Wang J, Chen J, Zhang X, Feng X, Li X.

Avr-2023

Chin J Nat Med.

<https://pubmed.ncbi.nlm.nih.gov/37120243/>

Pinellia ternata is an important medicinal plant, and its growth and development are easily threatened by high temperature. In this study, comprehensive research on physiological, cytological and transcriptional responses to different levels of heat stress were conducted on a typical phenotype of *P. ternata*. First, *P. ternata* exhibited tolerance to the increased temperature, which was supported by normal growing leaves, as well as decreased and sustained photosynthetic parameters. Severe stress aggravated the damages, and *P. ternata* displayed an obvious leaf senescence phenotype, with significantly increased SOD and POD activities (46% and 213%). In addition, mesophyll cells were seriously damaged, chloroplast thylakoid was fuzzy, grana lamellae and stroma lamellae were obviously broken, and grana thylakoids were stacked, resulting in a dramatically declined photosynthetic rate (74.6%). Moreover, a total of 16 808

genes were significantly differential expressed during this process, most of which were involved in photosynthesis, transmembrane transporter activity and plastid metabolism. The number of differentially expressed transcription factors in MYB and bHLH families was the largest, indicating that these genes might participate in heat stress response in *P. ternata*. These findings provide insight into the response to high temperature and facilitate the standardized cultivation of *P. ternata*.

Integrated transcriptomics and metabolomics reveal key metabolic pathway responses in *Pistia stratiotes* under Cd stress.

Wei Z, Zhongbing C, Xiuqin Y, Luying S, Huan M, Sixi Z.

15-06-2023

J Hazard Mater.

<https://pubmed.ncbi.nlm.nih.gov/36989786/>

Cadmium (Cd) can interfere with plant gene expression, change the content of metabolites and affect plant growth. In this study, untargeted metabolomics (LC-MS) and RNA-Seq sequencing were performed on root tissues of *Pistia stratiotes* exposed to Cd stress. The results showed that cadmium stress affected the accumulation and transport of cadmium in plants and increased the content of soluble sugar, the activities of ascorbate peroxidase (APX), and peroxidase (POD) by 34.89%, 41.45%, and 6.71% on average, and decreased the activity of superoxide dismutase (SOD) by 51.51% on average. At the same time, the contents of carotenoid, chlorophyll a, and chlorophyll b decreased by 29.52%, 20.11%, and 13.14%, respectively, thus affecting the growth and development of plants. Metabolomic analysis showed that Cd stress affected eight metabolic pathways, involving 27 differentially expressed metabolites, mainly including unsaturated fatty acids, amino acids (phenylalanine), nucleotides, sulfur compounds, and flavonoids. By transcriptome analysis, a total of 3107 differentially expressed genes (DEGs, 2666 up-regulated genes, and 441 down-regulated genes) were identified, which were mainly involved in four pathways, among which glutathione metabolism and lignin biosynthesis were the key metabolic pathways. In conclusion, this study reveals the metabolic and transcriptional response mechanisms of *P. stratiotes* to Cd stress through multi-omics, providing the theoretical basis for the phytoremediation of water contaminated by Cd.

Aerial roots elevate indoor plant health: Physiological and morphological responses of three high-humidity adapted Araceae species to indoor humidity levels.

Sheeran L, Rasmussen A.

Juin-2023

Plant Cell Environ.

<https://pubmed.ncbi.nlm.nih.gov/36786325/>

Echinococcosis

Extracellular vesicles secreted by *Echinococcus multilocularis*: Important players in angiogenesis promotion.

Liu C, Cao J, Zhang H, Field MC, Yin J.

02-05-2023

Microbes Infect.

<https://pubmed.ncbi.nlm.nih.gov/37142117/>

The involvement of *Echinococcus multilocularis*, and other parasitic helminths, in regulating host physiology is well recognized, but molecular mechanisms remain unclear. Extracellular vesicles (EVs) released by helminths play important roles in regulating parasite-host interactions by transferring materials to the host. Analysis of protein cargo of EVs from *E. multilocularis* protoscoleces in the present study revealed a unique composition exclusively associated with vesicle biogenesis. Common proteins in various *Echinococcus* species were identified, including the classical EVs markers tetraspanins, TSG101 and Alix. Further, unique tegumental antigens were identified which could be exploited as *Echinococcus* EV markers. Parasite- and host-derived proteins within these EVs are predicted to support important roles in parasite-parasite and parasite-host communication. In addition, the enriched host-derived protein payloads identified in parasite EVs in the present study suggested that they can be involved in focal adhesion and potentially promote angiogenesis. Further, increased angiogenesis was observed in livers of mice infected with *E. multilocularis* and the expression of several angiogenesis-regulated molecules, including VEGF, MMP9, MCP-1, SDF-1 and serpin E1 were increased. Significantly, EVs released by the *E. multilocularis* protoscolex promoted proliferation and tube formation by human umbilical vein endothelial cells (HUVECs) in vitro. Taken together, we present the first evidence that tapeworm-secreted EVs may promote angiogenesis in *Echinococcus*-infections, identifying central mechanisms of *Echinococcus*-host interactions.

Effect and mechanism of reactive oxygen species-mediated NOD-like receptor family pyrin domain-containing 3 inflammasome activation in hepatic alveolar echinococcosis.

Chen CS, Zhang YG, Wang HJ, Fan HN.

14-04-2023

World J Gastroenterol.

<https://pubmed.ncbi.nlm.nih.gov/37122606/>

Ex vivo Immuno-modulatory effect of *Echinococcus granulosus* laminated layer during allergic rhinitis and allergic asthma: A study in Algerian Patients.

Benazzouz S, Amri M, Ketfi A, Boutemine IM, Sellam SL, Benkhalifa S, Ameer F, Djebbara S, Achour K, Soufli I, Belguendouz H, Gharnaout M, Touil-Boukoffa C.

26-04-2023

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37116772/>

The effect of helminthic infections on allergic diseases and asthma is still inconclusive. Moreover, there is considerable evidence suggesting that nitric oxide (NO), metalloproteinases and pro-inflammatory cytokines play a significant role in the physiopathology of these diseases. In this sense, the aim of our study is to investigate the ex vivo immunomodulatory effect of the laminated layer (LL, outside layer of parasitic cyst) of the helminth *Echinococcus granulosus* on NO, IL-17A and IL-10 production. In the first step of our study, we evaluated in vivo the NO, MMP-9, IL-17A, IL-10 levels in Algerian patients with allergic asthma and allergic rhinitis and their changes in relation with exacerbation status of the patients. In the principal part of our work, we assessed NO, IL-10 and IL-17A levels in supernatants of patients PBMC cultures before and after stimulation with LL. Our results indicate a significant reduction in NO production by PBMC of patients with allergic rhinitis and allergic asthma whether mild, moderate or severe after stimulation with LL. Interestingly, LL induces a significant decrease in the production of NO and IL-17A levels as well as an increase in the production of IL-10 in the cultures performed with PBMC of patients with severe allergic asthma. Importantly, our data indicate that LL exert a down-modulatory effect on inflammatory mediators (NO, IL-17A) and up immune-regulatory effect on IL-10 production. Collectively, our study supports the hygiene hypothesis suggesting that *Echinococcus granulosus* infection like other helminths could prevent and/or modulate inflammation responses during inflammatory diseases.

Can *Echinococcus Granulosus* Infestation Prevent Pancreatic Cancer? An in vivo Experimental Study.

Doğan S, Çakır M, Kartal A, Öztaş H, Oltulu P.

01-04-2023

Asian Pac J Cancer Prev.

<https://pubmed.ncbi.nlm.nih.gov/37116153/>

Hydatid cyst is a zoonotic infestation caused by *Echinococcus granulosus*, and it is known that some parasites found in humans cause cancer in humans or some may have a protective effect against cancer. Cancer is one of the most serious health problems of today and it has been shown in some studies that parasites such as *Echinococcus granulosus* can have an inhibitory effect. The aim of this study was determined as whether *Echinococcus granulosus* has an inhibitory effect on exocrine pancreatic cancer with the help of the azaserine-rat model used in different cancer studies. Material and Methods: During experimental process a total of 45 male Wistar rats used, 14-day-old male Wistar rats were divided into groups according to the experimental protocol, administered azaserine injection protocol or kept as a control group without azaserine injection. Animals are grouped as Group 1, Control Group (group not treated with Azaserine and not injected with protoscolex.) (E-A-) (n=7); Group 2, Group injected with (IP) Azaserine only (30mg/kg) (E-A+) (n=8); Group 3, Group injected (IP) with protoscolex suspension of 1 cc only (E+A-) (n=15); Group 4, Group injected both Azaserine (IP) and protoscolex suspension (IP) (E+A+) (n=15). Atypical Acinar Cell Foci (AACF) load in the exocrine pancreas of each rat was

measured quantitatively with the help of a video image analyzer and the AACF load was calculated with the help of a mathematical model. Results: Findings showed that the Atypical Acinar Cell Foci (AACF) burden was statistically significantly lower in the Azaserine+ protoscolex (Azaserine-injected-protoscolex-implanted) rat group compared to the other groups, suggesting that Echinococcosis in the azaserine-rat model could inhibit the development of precursor foci of neoplastic changes in the exocrine pancreas. Conclusion: The most significant aspect of our study is that it contributes new insights into the controversy that Echinococcosis suppresses pancreatic cancer.

Identification of Omega-class glutathione transferases in helminths of the Taeniidae family.

Miles S, Mourglia-Ettlin G, Fernández V.

Juin-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37024059/>

Metabolomic profiling of early inactive hepatic alveolar and cystic echinococcosis.

Bai Z, Ma X, Yan R, Lei W, Zhang Y, Ren Y, Liu S.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36940858/>

Hepatic alveolar echinococcosis (AE) and cystic echinococcosis (CE) are severe helminthic zoonoses and leading causes of parasitic liver damage. They pose a high mortality risk due to invisible clinical signs, especially at the early inactive stage. However, the specific metabolic profiles induced by inactive AE and CE lesions remain largely unclear. Therefore, we used gas chromatography-mass spectrometry-based metabolomic profiling to identify the global metabolic variations in AE and CE patient sera to differentiate between the two diseases and reveal the mechanisms underlying their pathogenesis. In addition, specific serum biomarkers of inactive hepatic AE and CE were screened using receiver operating curves, which can contribute to the clinical diagnosis of both diseases, especially in the earlier phase. These differential metabolites are involved in glycine, serine, tyrosine, and phenylalanine metabolism. Further analysis of key metabolic pathways showed that inactive AE lesions strongly alter amino acid metabolism in the host. CE lesions have an altered metabolism of oxidative stress response. These changes suggest these metabolite-associated pathways can serve as biomarkers to distinguish individuals with inactive AE and CE from healthy populations. This study also investigated the differences in serum metabolic profiles in patients with CE and AE. The biomarkers identified belonged to different metabolic pathways, including lipid, carnitine, androgen, and bile acid metabolism. Taken together, by investigating the different phenotypes of CE and AE with metabolomic profiling, serum biomarkers facilitating early diagnosis were identified.

Analysis of sheep peripheral blood mononuclear cells in response to *Echinococcus granulosus* microRNA-71 overexpression.

Li Y, Yan L, Ci D, Li R, Li W, Xia T, Shi H, Ayaz M, Zheng Y, Wang P.

Juin-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36739092/>

Giant renal hydatid cyst in an 8-year-old girl.

Cai Q, Tang Y, Zhanghuang C, Li S.

Mai-2023

Asian J Surg.

<https://pubmed.ncbi.nlm.nih.gov/36504152/>

Filariose lymphatique

Morbidity hotspot surveillance: A novel approach to detect lymphatic filariasis transmission in non-endemic areas of the Tillabéry region of Niger.

Badia-Rius X, Adamou S, Taylor MJ, Kelly-Hope LA.

18-04-2023

Parasite Epidemiol Control.

<https://pubmed.ncbi.nlm.nih.gov/37138586/>

The Niger Lymphatic Filariasis (LF) Programme is making good progress towards the elimination goal and scaling up morbidity management and disability prevention (MMDP) activities. Clinical case mapping and the increased availability of services has prompted patients to come forward in both endemic and non-endemic districts. The latter included Filingué, Balewara and Abala districts of the Tillabéry region, and in 2019, 315 patients were found during a follow-up active case finding activity, suggesting it may have low transmission. The aim of this study was to assess the endemicity status in areas reporting clinical cases, 'morbidity hotspots', in three non-endemic districts of the Tillabéry region. A cross-sectional survey was conducted in 12 villages in June 2021. Filarial antigen was detected using the rapid Filariasis Test Strip (FTS) diagnostic, and information obtained on gender, age, residency length, bed net ownership and usage, and presence of hydrocoele and/or lymphoedema. Data were summarised and mapped using QGIS software. A total of 4058 participants between 5 and 105 years old were surveyed, with 29 (0.7%) participants found to be FTS positive. Balewara district had significantly higher FTS positive rates than the other districts. No significant differences were found by gender (male 0.8%; female 0.6%), age group (<26 years 0.7%; ≥26 years 0.7%), and residency length (<5 years 0.7%; ≥5 years 0.7%). Three villages reported no infections; seven villages <1%, one village 1.1% and one village 4.1%, which was on the border of an endemic district. Bed net ownership (99.2%) and usage (92.6%) was very high and there was no significant difference between FTS infection rates. The results indicate that there are low levels of transmission in populations, including children, living in districts

previously classified as non-endemic. This has implications for the Niger LF programme in terms of delivering targeted mass drug administration (MDA) in transmission hotspots, and MMDP services, including hydrocoele surgery to patients. The use of morbidity data may be a practical proxy to trigger mapping of ongoing transmission in low endemic areas. Continued efforts to study morbidity hotspots, post-validation transmission, cross-border and cross-district endemicity are needed to meet the WHO NTD 2030 roadmap targets.

Combination of conservative and surgical methods in the treatment of giant lymphedema of the scrotum: A case report.

Istranov AL, Makarov IG, Makarova NV, Tulina I, Ulasov IV, Isakova YI.

12-04-2023

Front Surg.

<https://pubmed.ncbi.nlm.nih.gov/37123541/>

Objective: Genital lymphedema is a severe, disabling condition associated with a malfunction of the lymphatic system. Primary lymphedema of the scrotum is a variant of congenital dysplasia of lymphatic vessels. Secondary genital lymphedema is much more common and can be caused by parasitic invasion (filariasis) or damage to the lymphatic system during the treatment of cancer (radiation therapy, lymphadenectomy). Healthcare providers are frequently unable to detect and treat this illness successfully in ordinary clinical practice. This paper uses the case of a patient with stage 3 secondary lymphedema (unknown genesis) of both lower extremities and lymphedema of the scrotum, complicated by recurrent erysipelas, a history of lymphorrhoea, impaired skin trophic and multiple papillomatosis, to demonstrate the efficacy of a combination of conservative and surgical methods in the treatment of giant lymphedema of the scrotum. **Methods:** In the treatment, the combination of decongestant physical therapy (CDPT, CDT) according to M. Földi was used at pre-surgery and post-surgery stages, combined with a reconstructive operation, including the removal of the affected tissues of the urogenital region, phalloplasty, and scrotoplasty with rotational skin flaps. **Results:** A decrease in the circumference of the lowest extremities in the lower leg area by 68 cm on the right and by 69 cm on the left was achieved by conservative treatment. Due to the combination of conservative and surgical treatment, the patient's body weight decreased by 69.4 kg, and the scrotum decreased by 63 cm. Subsequently, the patient fully recovered his sexual function. **Conclusion:** A combination of complex decongestive physical therapy and surgery is necessary for patients with advanced genital edema. The isolated use of surgical or conservative treatment does not provide a sufficient improvement in the patient's quality of life. Modern plastic surgery technologies enable patients to achieve complete functional and cosmetic recovery, while proper selection and usage of compression hosiery help preserve and improve the outcomes acquired following treatment.

Knowledge and participation in mass drug administration against lymphatic filariasis and soil-transmitted helminth infections among the community members in Dar es Salaam, Tanzania.

Ngunyali DA, Mpomele SS, Kilonzi M, Mutagonda RF, Mikomangwa WP, Mlyuka HJ, Kibanga W, Marealle AI.

02-05-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36563099/>

Gale

[Infectious diseases in migrants].

Stich A.

04-05-2023

Inn Med (Heidelb).

<https://pubmed.ncbi.nlm.nih.gov/37140630/>

The current influx of refugees and the high rate of immigration increase the prevalence and impact of infectious diseases in Europe. Infections may be detected at first contact, as a result of systematic screening or as part of general medical care. Diagnosis and treatment require special expertise and, in some cases, special precautions. The spectrum of imported infections is determined by the countries of origins of the migrants and the circumstances associated with their escape to Germany. In this article, diagnosis and treatment of the most important infectious diseases will be presented. As far as infectious diseases are concerned, refugees and migrants are not a threat to the host population, but instead have to be perceived and cared for as a highly vulnerable group.

Diagnostic concordance of telemedicine as compared to face-to-face care in primary health care clinics in rural India: a randomized crossover trial.

Verma N, Buch B, Taralekar R, Acharya S.

11-04-2023

JMIR Form Res.

<https://pubmed.ncbi.nlm.nih.gov/37130015/>

In Vitro Efficacy of Terpenes from Essential Oils against *Sarcoptes scabiei*.

Li M, Feng S, Huang S, Guillot J, Fang F.

11-04-2023

Molecules.

<https://pubmed.ncbi.nlm.nih.gov/37110595/>

The mite *Sarcoptes scabiei* is responsible for the emerging or re-emerging skin disease called scabies in humans and sarcoptic mange in animals. Essential oils represent an appealing alternative strategy for the control of *Sarcoptes* infections, but the commercial development of essential oils may be hampered by their inconsistency in efficacy due to their varied chemical compositions. In order to address this issue, we assessed the efficacy of six components (carvacrol, eugenol, geraniol, citral, terpinen-4-ol, and linalool) against *S. scabiei*. At a concentration of

0.5%, carvacrol presented the best miticidal efficacy, with a median lethal time (LT₅₀) value of 6.7 min, followed by eugenol (56.3 min), geraniol (1.8 h), citral (6.1 h), terpinen-4-ol (22.3 h), and linalool (39.9 h). The LC₅₀ values at 30 min for carvacrol, eugenol, and geraniol were 0.24, 0.79, and 0.91%, respectively. In conclusion, carvacrol, eugenol, and geraniol represent potential complementary or alternative agents for *S. scabiei* infections in humans or animals. Our study provides a scientific basis for the development of scabicial products based on essential oils.

Standardized cotton swab sampling with nested quantitative polymerase chain reaction is effective for diagnosing ordinary scabies.

Chung HC, Chun EJ, Kim JK, Kim SS, Kim CW.

27-04-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36715503/>

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

Development of a hookworm egg hatching assay to determine the ovicidal effects of anthelmintics.

Easland E, Biendl S, Keiser J.

04-05-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37143169/>

Background: Few anthelmintics are currently available, manifesting the urgent need for new treatment options. In vitro profiling of current anthelmintics against larval and adult stage helminths displayed varying effects on closely related worm species and between life stages of the same species. Conversely, limited research has been performed on the egg stage of human hookworms, and the effects of investigational compounds on the egg stage are not routinely assessed. **Methods:** We profiled the development and hatching of *Heligmosomoides polygyrus*, *Ancylostoma duodenale* and *Necator americanus* eggs isolated from rodent faeces in liquid media with various nutrient levels, osmolar concentrations, and acidities in dependence on incubation temperature and light exposure. Incubation conditions were optimised to allow the study of drug effect on immature and embryonated eggs. We analysed concentration-effect relationships of commercially available anthelmintics over 72 h. **Results:** Rapid embryonation and hatching were observed at room temperature with and without light exposure without nutrient supplementation in a wide range of acidities. Hookworms hatched optimally at room temperature in PBS achieving > 75% hatching over 34 h. Developmental delays were seen when eggs were stored at 4 °C with no effect on viability. Similar delays were also seen with

increased osmolar concentrations resulting in decreased viability. Benzimidazole anthelmintics effectively reduced the viability and prevented hatching of hookworm eggs, with albendazole and thiabendazole eliciting particularly potent effects at EC₅₀ values below 1 µM. Macrolide anthelmintics as well as emodepside, oxantel pamoate, and pyrantel pamoate were inactive while monepantel, levamisole, and tribendimidine displayed varied potencies among the hookworm species.

Conclusion: The presented egg-hatching assay will complement ongoing anthelmintic drug discovery and allow a full characterisation of drug activity against all life stages. In the development and application of the egg-hatching assay, good accordance was observed between the three hookworm species evaluated. Marketed anthelmintics show differences of drug action compared to larval and adult stages highlighting the importance of profiling drug activity against all life stages.

Prevalence of helminths in fresh vegetables: a narrative literature review.

da Costa Dantas LM, de Medeiros Maia CM, da Silva Chaves Damasceno KSF, Mont'Alverne Jucá Seabra L, Chaves G, de Assis CF, de Sousa Júnior FC.

Juin-2023

J Sci Food Agric.

<https://pubmed.ncbi.nlm.nih.gov/36208474/>

The consumption of fresh vegetables is related to healthy lifestyle habits present in culinary preparations in different regions. The presence of pathogenic parasites in these foods can cause gastrointestinal disorders. Thus, the objective of the present study was to carry out a narrative review of the literature on the prevalence of helminths in fresh vegetable samples. The analysis of the studies published from 2016 to 2022 showed that hookworms and *Ascaris lumbricoides* are the most common pathogenic helminths in fresh vegetable samples, with a prevalence of up to 73.8% and 55.1%, respectively. In addition, studies have shown associations between the presence of helminths and pathogenic protozoa. The results obtained in this review indicate the urgent need to implement actions at all stages of the vegetable production chain, from the water used in planting irrigation to cleaning before sale to the final consumer.

Leishmaniose

Host competence of Algerian Gerbillus amoenus for Leishmania major.

Benallal KE, Mezai G, Mefissel M, Klari N, Lardjane C, Khardine AF, Kherachi I, Dib Y, Brahmi K, Sadlova J, Volf P, Harrat Z.

18-04-2023

Int J Parasitol Parasites Wildl.

<https://pubmed.ncbi.nlm.nih.gov/37144140/>

New cocrystals of heterocyclic drugs: structural, antileishmanial, larvicidal and urease inhibition studies.

Murtaza G, Khan M, Farooq S, Choudhary MI, Yousuf S.

01-06-2023

Acta Crystallogr C Struct Chem.

<https://pubmed.ncbi.nlm.nih.gov/37140892/>

Many heterocycles have been developed as drugs due to their capacity to interact productively with biological systems. The present study aimed to synthesize cocrystals of the heterocyclic antitubercular agent pyrazinamide (PYZ, 1, BCS III) and the commercially available anticonvulsant drug carbamazepine (CBZ, 2, BCS class II) to study the effect of cocrystallization on the stability and biological activities of these drugs. Two new cocrystals, namely, pyrazinamide-homophthalic acid (1/1) (PYZ:HMA, 3) and carbamazepine-5-chlorosalicylic acid (1/1) (CBZ:5-SA, 4), were synthesized. The single-crystal X-ray diffraction-based structure of carbamazepine-trans-cinnamic acid (1/1) (CBZ:TCA, 5) was also studied for the first time, along with the known cocrystal carbamazepine-nicotinamide (1/1) (CBZ:NA, 6). From a combination drug perspective, these are interesting pharmaceutical cocrystals to overcome the known side effects of PYZ (1) therapy, and the poor biopharmaceutical properties of CBZ (2). The purity and homogeneity of all the synthesized cocrystals were confirmed by single-crystal X-ray diffraction, powder X-ray diffraction and FT-IR analysis, followed by thermal stability studies based on differential scanning calorimetry (DSC) and thermogravimetric analysis (TGA). Detailed intermolecular interactions and the role of hydrogen bonding towards crystal stability were evaluated quantitatively via Hirshfeld surface analysis. The solubility of CBZ at pH 6.8 and 7.4 in 0.1 N HCl and H₂O were compared with the values of cocrystal CBZ:5-SA (4). The solubility of CBZ:5-SA was found to be significantly improved at pH 6.8 and 7.4 in H₂O. All the synthesized cocrystals 3-6 exhibited a potent urease inhibition (IC₅₀ values range from 17.32 ± 0.89 to 12.3 ± 0.8 µM), several times more potent than standard acetohydroxamic acid (IC₅₀ = 20.34 ± 0.43 µM). PYZ:HMA (3) also exhibited potent larvicidal activity against *Aedes aegypti*. Among the synthesized cocrystals, PYZ:HMA (3) and CBZ:TCA (5) were found to possess antileishmanial activity against the miltefosine-induced resistant strain of *Leishmania major*, with IC₅₀ values of 111.98 ± 0.99 and 111.90 ± 1.44 µM, respectively, in comparison with miltefosine (IC₅₀ = 169.55 ± 0.20 µM).

Photodynamic therapy mediated by a red LED and methylene blue inactivates resistant *Leishmania amazonensis*.

Cabral FV, Yoshimura TM, Teixeira da Silva DF, Cortez M, Ribeiro MS.

01-05-2023

J Opt Soc Am A Opt Image Sci Vis.

<https://pubmed.ncbi.nlm.nih.gov/37133199/>

Cutaneous leishmaniasis is a neglected parasitic disease that leads to destructive lesions. The emergence of drug resistance has been a global concern over the past years. Photodynamic therapy (PDT) mediated by a red LED and methylene blue (MB) involves the overproduction of oxidative stress, which oxidizes several cellular biomolecules and prevents the selection of resistant strains. Herein, we investigated the potential of PDT mediated by MB against wild-type and miltefosine-

resistant strains of *Leishmania amazonensis*. As a result, both strains were susceptible to PDT, thus encouraging us to seek the best conditions to overcome the drug resistance problem in cutaneous leishmaniasis.

Synthesis of 4-(4-chlorophenyl)thiazole compounds: in silico and in vitro evaluations as leishmanicidal and trypanocidal agents.

Cruz Filho IJD, Oliveira JF, Santos ACS, Pereira VRA, Lima MCA.

Mai-2023

An Acad Bras Cienc.

<https://pubmed.ncbi.nlm.nih.gov/37132749/>

Visceral leishmaniasis in Kosovo: A case of misdiagnosis and diagnostic challenges.

Tolaj I, Mehmeti M, Gashi H, Berisha F, Gashi V, Fejza H, Shala N.

12-04-2023

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/37131489/>

Introduction: Visceral leishmaniasis (VL) is a parasitic disease caused by various *Leishmania* species and is a potentially life-threatening condition. The disease is highly endemic in several regions, including the Balkans, yet information regarding its prevalence in Kosovo is limited.

Case presentation: In this case presentation, a 62-year-old man was admitted to a hospital in Kosovo due to a persistent high fever, and after extensive evaluations and treatments, he was diagnosed with fever of unknown origin (FUO) and transferred to a hospital in Turkey. An abscess of the psoas muscle caused by MRSA was found, however, pancytopenia persisted despite antibiotic treatment. Six months later, the patient was hospitalized again due to fever, chills, and night sweats. Microscopic examination and serological tests revealed the presence of *Leishmania infantum* in the bone marrow. Liposomal amphotericin B treatment resulted in a significant improvement in the patient's condition. **Discussion:** The diagnosis of VL can be challenging, and it can easily be misdiagnosed as other diseases, resulting in diagnostic delays and potentially fatal outcomes. In endemic regions such as the Balkans, it is crucial for physicians to be aware of this infection to avoid misdiagnosis or diagnostic delay. Early diagnosis and prompt treatment of VL are essential in preventing morbidity and mortality. **Conclusion:** This case highlights the significance of considering VL as a possible diagnosis in patients presenting with febrile illnesses accompanied by pancytopenia and splenomegaly, especially in endemic regions.

Prevalence of *Trypanosoma lainsoni* and its effects of parasitism on the health of non-volant small mammals from the Brazilian Cerrado.

de Oliveira MM, Ferrando CPR, Gómez-Hernández C, de Oliveira KR, Araújo IAC, Ribeiro PVA, Mineo TWP, Leiner NO, Mineo JR, da Silva SM.

02-05-2023

Small mammals are important hosts and/or reservoirs of *Trypanosoma* spp. This study aimed to verify the prevalence of *Trypanosoma* spp. in non-volant small mammals from the Brazilian Cerrado and to test the effects of *T. lainsoni* on the neutrophil/lymphocyte ratio (N/L) and body condition in rodent and marsupial populations. For this, we collected blood samples of 293 individuals captured in five forest fragments between 2019 and 2020. Blood was used to prepare the blood smears and packed on filter paper for DNA extraction. Generalized linear models were performed to test the effects of *T. lainsoni* on host health. The DNA was submitted to nested PCR targeting the *Trypanosoma* spp. 18S rRNA gene. From blood smears analyzed by microscopy, we obtained a positivity rate of 7.2% for *Trypanosoma* spp. About 31.1% of *Gracilinanus agilis*, *Didelphis albiventris*, and *Rhipidomys macrurus* samples were positive in nested PCR. From the obtained sequences, 83.3% were genetically identical to *T. lainsoni* and about 11% to *T. cruzi* TcI. In addition, we reported the infection of *T. lainsoni* in *Hylaeamys megacephalus*. We suggest that *T. lainsoni* does not influence the body condition and N/L ratio for either *G. agilis* or *R. macrurus*. Overall, our results expand the host list of *T. lainsoni* and demonstrate the infection of small mammals by *T. cruzi* TcI in peri-urban areas.

CryoEM reveals oligomeric isomers of a multienzyme complex and assembly mechanics.

Lee JKI, Liu YT, Hu JJ, Aphasizheva I, Aphasizhev R, Zhou ZH.

08-04-2023

J Struct Biol X.

<https://pubmed.ncbi.nlm.nih.gov/37128595/>

Intracellular persistence of *Leishmania tarentolae* in primary canine macrophage cells.

Louzada-Flores VN, Latrofa MS, Lucente MS, Dambrós BP, Mendoza-Roldan JA, Varotto-Bocazzi I, Cattaneo GM, Späth GF, Buonavoglia A, Otranto D.

9-04-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37127215/>

Leishmania tarentolae is a non-pathogenic species first isolated from geckoes in the Mediterranean basin. The finding that dogs test positive against both *Leishmania infantum* and *L. tarentolae* raises questions regarding the ability of the latter species to persist and adapt to new hosts. This study aimed to evaluate in vitro the capability of *L. tarentolae* to colonize, survive and persist in canine primary monocyte-derived mononuclear cells. Monocytes were isolated from dog whole blood samples and placed in 24-well plates for differentiation into macrophages and for incubation with *L. tarentolae* field-isolated strains (RI-325 and SF-178) and laboratory (LEM-124) strain; the parasite burden was assessed at different time points post-infection. The *L. infantum* laboratory strain (MON-1)

was used as control. Infection parameters were evaluated by microscopy, counting the number of amastigotes/200 infected cells, and by duplex real-time PCR from supernatants and detached cells. Similar to *L. infantum*, *L. tarentolae* strains developed into round-shaped amastigote-like forms, with higher infection rates detected at 4 h followed by an overall decrease until 48 h. RI-325 presented also a higher infection rate at 72 h. Data showed that *L. tarentolae* strains infect and persist inside in vitro primary canine mononuclear cells, opening new perspectives for further laboratory studies.

Molecular detection of *Leishmania* (*Sauroleishmania*) *adleri* (*Trypanosomatida: Trypanosomatidae*) in *Sergentomyia* sp. sand flies (*Diptera: Psychodidae*) in Mali and Niger.

Krüger A, Balczun C, Scheid PL, Hagen RM, Eisenbarth A.
29-04-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37127214/>

Phlebotomine sand flies of the genus *Sergentomyia* are considered to be of minor importance as vectors of *Leishmania* parasites pathogenic to humans, but are known to transmit lizard parasites of the subgenus *Sauroleishmania*, including *L. (S.) adleri*. However, knowledge on the geographic distribution of *Sauroleishmania* spp. and the infection rates in the vectors is very limited. Therefore, our study aimed (1) to further elucidate the distribution and prevalence of *Sauroleishmania* spp. in their respective vectors and (2) to assess the potential risk for occasional transmission of *Leishmania* parasites to international military personnel deployed in camps in Mali and Niger. A total of 1,482 wild-caught sand flies (*Sergentomyia* spp. and closely related *Grassomyia* spp.) were screened by real-time PCR for the presence of *Leishmania* DNA. Thirty-two sand fly pools were tested positive, with six from Mali and 26 from Niger. The DNA of four representative isolates was sequenced. The resulting sequences revealed a homology to *L. adleri*, which leads to the first report of this species from Mali and Niger to the best of our knowledge. The results suggest that *Sergentomyia* (*Sintonius*) *clydei* might be the natural sand fly vector, while *Grassomyia* spp. appear to be refractory. No *Leishmania* sp. pathogenic to humans was detected in these sand flies.

***Leishmania donovani* Attenuates Dendritic Cell Trafficking to Lymph Nodes by Inhibiting C-Type Lectin Receptor 2 Expression via Transforming Growth Factor- β .**

Yadav M, Akhtar MN, Mishra M, Kumar S, Kumar R, Shubham, Nandal A, Sen P.

01-05-2023

Microbiol Spectr.

<https://pubmed.ncbi.nlm.nih.gov/37125906/>

MicroRNA-21 and microRNA-148a affects PTEN, NO and ROS in canine leishmaniasis.

De Freitas JH, Bragato JP, Rebech GT, Costa SF, Dos Santos MO, Soares MF, Eugênio FR, Dos Santos PSP, De Lima VMF.

13-04-2023

Front Genet.

<https://pubmed.ncbi.nlm.nih.gov/37124626/>

Canine Visceral leishmaniasis (CanL) poses a severe public health threat in several countries. Disease progression depends on the degree of immune response suppression. MicroRNAs (miRs) modulate mRNA translation into proteins and regulate various cellular functions and pathways associated with immune responses. MiR-21 and miR-148a can alter the parasite load and M1 macrophages are the principal cells in dogs' leishmanicidal activity. A previous study found increased miR-21 and miR-148a in splenic leukocytes (SL) of dogs with CanL using microarray analysis and *in silico* analysis identified PTEN pathway targets. PTEN is involved in the immune regulation of macrophages. We measured PTEN and the production of reactive oxygen species (ROS) and nitric oxide (NO) before and after transfection SLs of dogs with CanL with mimic and inhibition of miR-21 and miR-148a. PTEN levels increased, NO and ROS decreased in SLs from dogs with CanL. Inhibition of miRNA-21 resulted in PTEN increase; in contrast, PTEN decreased after miR-148a inhibition. Nitrite (NO₂) levels increased after transfection with miR-21 inhibitor but were decreased with miR-148a inhibitor. The increase in miR-21 promoted a reduction in ROS and NO levels, but miR-148a inhibition increased NO and reduced ROS. These findings suggest that miR-21 and miR-148a can participate in immune response in CanL, affecting PTEN, NO, and ROS levels.

New antiprotozoal sesquiterpene derivatives from *Dorema glabrum* Fisch & C.A.Mey.

Delnavazi MR, Ebrahimi SN, Hadjiakhoondi A, Yassa N.

28-04-2023

Fitoterapia.

<https://pubmed.ncbi.nlm.nih.gov/37121409/>

Live attenuated *Leishmania infantum* centrin deleted mutant (LiCen^{-/-}) as a novel vaccine candidate: A field study on safety, immunogenicity, and efficacy against canine leishmaniasis.

Zarei Z, Mohebbi M, Dehghani H, Khamesipour A, Tavakkol-Afshari J, Akhoundi B, Abbaszadeh-Afshar MJ, Alizadeh Z, Skandari SE, Asl AD, Razmi GR.

25-04-2023

Comp Immunol Microbiol Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37119594/>

This study was designed to evaluate the safety, immunogenicity, and efficacy of a single dose of *L. infantum* (LiCen^{-/-}) live attenuated candidate vaccine against canine leishmaniasis (CanL). Eighteen healthy domestic dogs with no anti-*Leishmania* antibodies and negative leishmanin skin test (LST) were randomly inoculated intravenously with either *L. infantum* (LiCen^{-/-}) vaccine candidate in 10 dogs or phosphate-buffered saline (PBS) in 8 dogs. The safety, immunogenicity, and efficacy

rate of *L. infantum* (LiCen^{-/-}) vaccine candidate against CanL were evaluated by different criteria, including clinical manifestations, injection-site lesion, hematology and biochemistry values, anti-*Leishmania* antibodies using direct agglutination test (DAT), delayed-type hypersensitivity (DTH) using LST, and CD4⁺ and CD8⁺ T-cells subsets, as well as by measuring interferon (IFN-γ), interleukin (IL-23), IL-17, and IL-10 cytokines. Spleen aspiration and detection of *Leishmania* parasite using parasitological examinations (microscopy and culture) were performed in both vaccinated and control groups. Two months after intervention, each dog was challenged intraperitoneally (IP) with wide type (WT) *L. infantum*. Two-month follow-up post vaccination showed no clinical signs and serious side effects associated with the vaccination. A significant increase was found in the expression of IL-17, CD4⁺, and CD8⁺ gene transcripts in PBMCs, as well as increased levels of Th1 cytokines, and reduction of Th2 cytokine. The efficacy of the vaccine candidate was calculated to be 42.85%. While the time window for assessing the vaccine's effectiveness was too limited to draw any real conclusions but the preliminary results showed a moderate efficacy rate due to inoculation a single dose of *L. infantum* (LiCen^{-/-}) vaccine candidate. Further investigations with more sample sizes and multiple doses of the vaccine candidate using natural challenges in the endemic areas of CanL are recommended.

Investigating potential sand fly vectors after the first reported outbreak of cutaneous leishmaniasis in Ghana.

de Souza DK, Addo SO, Desewu K, Nzelu CO, Mosore MT, Nimo-Paintsil S, Attram N, Appawu M, Wilson MD, Boakye DA.

28-04-2023

Parasit Vectors.

<https://pubmed.ncbi.nlm.nih.gov/37118766/>

Background: Leishmaniasis is a parasitic disease caused by species of the genus *Leishmania*, which are transmitted through the bite of infected female sand flies. Since the first reported outbreak of cutaneous leishmaniasis in Ghana, in 1999, there has been limited published information on its vectors and reservoir hosts there. Previous studies have shown strong dominance of the sand fly genus *Sergentomyia* over the genus *Phlebotomus* in Ghana. Thus the aim of this study was to determine the possible sand fly vector species in Ghana, as well as their human-feeding behavior, from the time of the first reported outbreak of CL in the country. **Methods:** Sand flies were collected from randomly selected houses in three communities. They were identified and used for blood meal source identification and the detection of *Leishmania* infection using molecular methods. **RESULTS:** A total of 1051 female sand flies were morphologically identified, of which *Sergentomyia africana africana* (29%) was the predominant species. Among the 275 female sand flies that had blood-fed, the identified blood meal sources included chicken (33.8%) and goat (12.4%); the percentage of human blood meals was 32%. Single-source and mixed-source blood meals were identified in *Sergentomyia africana africana* (11.6%), *Sergentomyia ingrami* (14.9%) and *Sergentomyia simillima* (20%), with *S.*

simillima having the highest proportion of blood meals that included human blood (14.6%). Using molecular methods, unfed sand flies and identified human-feeding species were examined for the presence of *Leishmania* DNA. Pool screening analysis revealed three pools of *S. ingrami* positive for *Leishmania* major DNA, with an infection rate of 1.27% (95% confidence interval 2.467-3.647). **Conclusions:** The findings suggest that some *Sergentomyia* species may be involved in the transmission of cutaneous leishmaniasis in Ghana. However, the role of *S. ingrami* as a vector of leishmaniasis in Ghana needs to be conclusively validated by isolating the parasite from this species and through experimental transmission studies.

In-vitro biological evaluation of 3,3',5,5'-tetramethoxy-biphenyl-4,4'-diol and molecular docking studies on trypanothione reductase and Gp63 from *Leishmania amazonensis* demonstrated anti-leishmania potential.

Schirmann JG, Bortoleti BTS, Gonçalves MD, Tomiotto-Pellissier F, Camargo PG, Miranda-Sapla MM, Lima CHS, Bispo MLF, Costa IN, Conchon-Costa I, Pavanelli WR, Dekker RFH, Barbosa-Dekker AM.

28-04-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37117253/>

Vaterite microparticle-loaded methylene blue for photodynamic activity in macrophages infected with *Leishmania braziliensis*.

Marmo VLM, Ambrósio JAR, Gonçalves EP, Raniero LJ, Beltrame Junior M, Pinto JG, Ferreira-Strixino J, Simioni AR.

28-04-2023

Photochem Photobiol Sci.

<https://pubmed.ncbi.nlm.nih.gov/37115408/>

Role of Natural plant extracts for potential Antileishmanial targets-In-depth review of the molecular mechanism.

Naik N, Kaushal RS, Upadhyay TKU, Kahrizi D, Al-Najjar MAA, Khan MS, Siddiqui S.

20-09-2023

Cell Mol Biol (Noisy-le-grand).

<https://pubmed.ncbi.nlm.nih.gov/37114261/>

A group of protozoan parasites known as *Leishmania* species can cause a variety of chronic illnesses, ranging from self-healing lesions to fatal outcomes. Drug-resistant pathogens have become common due to the lack of safe and effective medications, which has sparked the development of new therapeutic interventions, particularly plant-based natural extracts. As a way to avoid chemotherapy's side effects, natural herbal remedies have drawn more attention. In addition to having anti-inflammatory, anticancer, and cosmetic properties, the secondary metabolites of plants, such as phenolic compounds, flavonoids, alkaloids, and terpenes, have a

number of positive effects on our health. Natural metabolites such as naphthoquinone, alkaloids, benzophenones, etc. that have antileishmanial and antiprotozoal activity have been the subject of extensive research. In this review paper, it can be concluded that these natural extracts can be developed into excellent therapeutic agents against Leishmaniasis.

The Role of the *Leishmania infantum* Infected Dogs as a Potential Reservoir Host for Toscana Virus in a Zoonotic Visceral Leishmaniasis Focus of Northern Tunisia.

Dachraoui K, Chelbi I, Labidi I, Ben Osman R, Sayadi A, Ben Said M, Cherni S, Abbas MAS, Charrel R, Zhioua E.

20-04-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112992/>

A QSAR Study for Antileishmanial 2-Phenyl-2,3-dihydrobenzofurans [†].

Bernal FA, Schmidt TJ.

12-04-2023

Molecules.

<https://pubmed.ncbi.nlm.nih.gov/37110632/>

Leishmaniasis, a parasitic disease that represents a threat to the life of millions of people around the globe, is currently lacking effective treatments. We have previously reported on the antileishmanial activity of a series of synthetic 2-phenyl-2,3-dihydrobenzofurans and some qualitative structure-activity relationships within this set of neolignan analogues. Therefore, in the present study, various quantitative structure-activity relationship (QSAR) models were created to explain and predict the antileishmanial activity of these compounds. Comparing the performance of QSAR models based on molecular descriptors and multiple linear regression, random forest, and support vector regression with models based on 3D molecular structures and their interaction fields (MIFs) with partial least squares regression, it turned out that the latter (i.e., 3D-QSAR models) were clearly superior to the former. MIF analysis for the best-performing and statistically most robust 3D-QSAR model revealed the most important structural features required for antileishmanial activity. Thus, this model can guide decision-making during further development by predicting the activity of potentially new leishmanicidal dihydrobenzofurans before synthesis.

***Leishmania infantum* (JPCM5) Transcriptome, Gene Models and Resources for an Active Curation of Gene Annotations.**

Camacho E, González-de la Fuente S, Solana JC, Tabera L, Carrasco-Ramiro F, Aguado B, Requena JM.

04-04-2023

Genes (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37107624/>

In vitro and in vivo evaluation of efficacy of berberine chloride: Phyto-alternative approach against Trypanosoma evansi infection.

Gupta S, Vohra S, Sethi K, Rani R, Gupta S, Kumar S, Kumar R.

Juin-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37084956/>

Current chemotherapy against the Surra organism, *Trypanosoma evansi* has several limitations in terms of efficacy, toxicity, availability and emerging resistance. These reasons make the search of new chemo-preventive and chemo-therapeutic agent with high potency and low toxicity. Alkaloid phyto-molecules, berberine has shown promising anti-kinetoplastid activity against *T. cruzi*, *T. congolense*, *T. brucei*, *Leishmania donovani* and *L. tropica*. However, till date, there is no investigation of therapeutic efficacy of berberine chloride (BC) against *T. evansi*. The IC₅₀ value of BC for growth inhibition of *T. evansi* at 24 h of culture was calculated as 12.15 µM. The specific selectivity index (SSI) of BC was calculated as 19.01 and 10.43 against Vero cell line and Equine PBMC's, respectively. Thirteen drug target genes affecting various metabolic pathways were studied to investigate the mode of trypanocidal action of BC. In transcript analysis, the mRNA expression of arginine kinase 1 remained refractory to exposure with BC, which provides metabolic plasticity in adverse environmental conditions. In contrary, rest all the drug target gene were down-regulated, which indicates that drug severely affect DNA replication, cell proliferation, energy homeostasis, redox homeostasis and calcium homeostasis of *T. evansi*, leading to the death of parasite in low concentrations. It is the first attempt to investigate in vitro anti-trypanosomal activity of BC against *T. evansi*. These data imply that phytochemicals as alternative strategies can be explored in the future as an alternative treatment for Surra in animal.

A review of nemorosone: Chemistry and biological properties.

Cuesta-Rubio O, Monzote L, Fernández-Acosta R, Pardo-Andreu GL, Rastrelli L.

Juin-2023

Phytochemistry.

<https://pubmed.ncbi.nlm.nih.gov/37044362/>

Genomic analysis of two phlebotomine sand fly vectors of Leishmania from the New and Old World.

Labbé F, Abdeladhim M, Abrudan J, Araki AS, Araujo RN, Arensburger P, Benoit JB, Brazil RP, Bruno RV, Bueno da Silva Rivas G, Carvalho de Abreu V, Charamis J, Coutinho-Abreu IV, da Costa-Latgé SG, Darby A, Dillon VM, Emrich SJ, Fernandez-Medina D, Figueiredo Gontijo N, Flanley CM, Gatherer D, Genta FA, Gesing S, Giraldo-Calderón GI, Gomes B, Aguiar ERGR, Hamilton JGC, Hamarsheh O, Hawksworth M, Hendershot JM, Hickner PV, Imler JL, Ioannidis P, Jennings EC, Kamhawi S, Karageorgiou C, Kennedy RC, Krueger A, Latorre-Estivalis JM, Ligoxygakis P, Meireles-Filho ACA, Minx P, Miranda JC, Montague

MJ, Nowling RJ, Oliveira F, Ortigão-Farias J, Pavan MG, Horacio Pereira M, Nobrega Pitaluga A, Provetti Olmo R, Ramalho-Ortigao M, Ribeiro JMC, Rosendale AJ, Sant'Anna MRV, Scherer SE, Secundino NFC, Shoue DA, da Silva Moraes C, Gesto JSM, Souza NA, Syed Z, Tadros S, Teles-de-Freitas R, Telleria EL, Tomlinson C, Traub-Csekö YM, Marques JT, Tu Z, Unger MF, Valenzuela J, Ferreira FV, de Oliveira KPV, Vigoder FM, Vontas J, Wang L, Weedall GD, Zhioua E, Richards S, Warren WC, Waterhouse RM, Dillon RJ, McDowell MA.

12-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37043542/>

TLR9 agonist CpG ODN 2395 promotes the immune response against Leishmania donovani in obesity and undernutrition mice.

He J, Huang F, Liao X, Zhang J, Wei S, Xiao Y, Zheng X, Zhu Z, Chen D, Chen J.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37030488/>

As important immunomodulators, CpG ODNs have broad application prospects in the treatment and prevention of leishmaniasis. In order to explore the immunomodulatory effect of CpG ODNs on mice infected with *Leishmania* parasites in different nutritional status, TLR9 agonist CpG ODN 2395 or TLR9 antagonist CpG ODN 2088 was injected into normal, obesity and undernutrition BALB/c mice infected with *Leishmania donovani*, respectively. Subsequently, spleen and liver parasite loads, spleen and liver immune gene expression, spleen T cell subsets proportion and PD-1 expression, serum lipids, serum cytokines, and anti-*Leishmania* antibodies were measured to assess the immune response of mice with different nutritional status. The results displayed that at the 8th week after infection, the spleen parasite load of obesity and undernutrition mice was significantly higher than that of normal mice, but the liver parasite load showed no statistical difference among the three groups. The treatment of CpG ODN 2395 or CpG ODN 2088 significantly reduced the spleen parasite load of obesity and undernutrition infected mice, but did not reduce that of normal infected mice. In obesity infected mice, CpG ODN 2395 promoted the up-regulation of TCR, ICOS and TLR4 in spleen, promoted the secretion of IFN-γ and anti-*Leishmania* total IgG and IgG1 antibodies, and increased the content of serum HDL-C. In undernutrition infected mice, CpG ODN 2395 promoted the up-regulation of spleen CD28 and TLR9, increased the proportion of spleen CD3⁺ T cells, and decreased the content of serum IL-10. Our results demonstrated that CpG ODN 2395 enhanced the immune response and clearance of *Leishmania* parasites in obesity and undernutrition mice, which might be used as a therapeutic agent for obesity and undernutrition leishmaniasis patients in the future.

Evasion of the complement system by Leishmania through the uptake of C4bBP, a complement regulatory protein, and probably by the action of

GP63 on C4b molecules deposited on parasite surface.

Pereira-Filho AA, Queiroz DC, Saab NAA, D'Ávila Pessoa GC, Koerich LB, Pereira MH, Sant'Anna MRV, Araújo RN, Bartholomeu DC, Gontijo NF.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36963597/>

The complement system is a primary component of the vertebrate innate immune system, and its activity is harmful to microorganisms and parasites. To evade complement attack, some pathogens, such as viruses, bacteria, and protozoa, can interact with complement regulatory proteins from their hosts. Our research group has described the ability of *Leishmania* species to bind Factor H from human serum and use it as a tool to evade the complement system. However, there is no description of the interaction of *Leishmania* with other complement regulatory proteins, such as the C4b-binding protein (C4bBP), a negative regulator of classical and lectins complement system pathways. The results presented in this manuscript suggest that *Leishmania infantum*, *L. amazonensis*, and *L. braziliensis* recruit C4bBP from human serum. The uptake of C4bBP by *L. infantum* was studied in detail to improve our understanding of this inhibitory mechanism. When exposed to this complement regulator, parasites with inactivated GP63 bind to C4bBP and inactivate C4b deposited on their surface after serum exposure. This inactivation occurs by the action of Factor I, a complement system protease. In addition to the C4bBP-Factor I inactivation mechanism, the surface parasite protease GP63 can also inactivate soluble C4b molecules and probably that C4b molecules deposited on the parasites surface. This manuscript shows that *Leishmania* has two independent strategies to inactivate C4b molecules, preventing the progress of classical and lectins pathways. The identification of the C4bBP receptor on the *Leishmania* membrane may provide a new vaccine target to fight leishmaniasis.

Diversity and geographical distribution of *Leishmania* species and the emergence of *Leishmania (Leishmania) infantum* and *L. (Viannia) panamensis* in Central-Western Venezuela.

Delgado-Noguera LA, Hernández-Pereira CE, Castillo-Castañeda AC, Patiño LH, Castañeda S, Herrera G, Mogollón E, Muñoz M, Duran A, Loyo D, Pacheco M, Arena L, Isquiel G, Yopez L, Colmenarez B, Caviedes M, Mendez Y, Herrera S, Ramírez JD, Paniz-Mondolfi AE.

Juin-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/36940857/>

Mutilating localized cutaneous leishmaniasis caused by *Leishmania guyanensis*.

Silva DFD, Gadelha SQ, Cavalcante AS, Andrade RV, Guerra JAO, Gadelha ADR.

Mai-Juin 2023

An Bras Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36863980/>

Antiparasitic Activity of Two Natural Terpenes from *Salvia cuspidata* against *Leishmania amazonensis*.

Troncoso ME, Germanó MJ, Arrieta VJ, García Bustos MF, Cifuentes D, Cargnelutti DE, Lozano ES.

28-04-2023

J Nat Prod.

<https://pubmed.ncbi.nlm.nih.gov/36857574/>

Leishmaniasis is a neglected disease caused by flagellated parasites of the *Leishmania* genus affecting more than 10 million people worldwide. Current treatments for leishmaniasis involve the administration of poorly tolerated drugs with toxic side effects in patients. There is an imperative necessity for novel compounds to treat this disease. One of the most used strategies in the search for different antiparasitic compounds is the screening of purified plant molecules. The diterpenes 12-hydroxy-11,14-diketo-6,8,12-abietatrien-19,20-olide (HABTO) and 5-epi-icetexone (ICTX) isolated from *Salvia cuspidata* were shown to be effective against *Leishmania amazonensis* *in vitro* and *in vivo*. They displayed an antiproliferative effect against *L. amazonensis* promastigotes. They also induce an increase in ROS levels and affect the mitochondrial activity of parasites. HABTO and ICTX in an *in vivo* model of cutaneous leishmaniasis decrease footpad swelling, parasite load, and splenic index. Moreover, they induce significant reduction in the O.D. of total anti-*Leishmania* IgG and IgG1 subtype antibody responses against *L. amazonensis* compared to the PBS group but maintain high levels of IgG2a. This suggests that in HABTO- or ICTX-treated mice, there is a slowdown in the progression of the disease. These terpenes could be considered as possible novel antileishmanial agents against *L. amazonensis* and thus treat cutaneous leishmaniasis.

Lèpre

Leprosy in French Guiana, 2015 to 2021: Dynamics of a Persistent Public Health Problem.

Petiot A, Drak Alsibai K, Dossou C, Couppie P, Blaizot R.

05-05-2023

Acta Derm Venereol.

<https://pubmed.ncbi.nlm.nih.gov/37144514/>

A resurgence of leprosy as a public health problem in French Guiana was reported over the period 2007 to 2014, particularly among Brazilians gold miners. Prolonged multidrug therapy and reversal reactions represent a therapeutic challenge. The objective of this study was to assess the evolution of leprosy in this European overseas territory. All patients with leprosy confirmed in histopathology between 1 January 2015 and 31 December 2021 were included. A total of 86 patients were included, including 64 new cases and 22 previously diagnosed cases. Sixty patients (70%) were male, 6 cases were paediatric. Brazilian gold miners represented 44.1% of reported occupations (15/34). Maroons represented the second community (13 patients, 15%). Multibacillary and

paucibacillary forms were found in 53 (71%) and 22 (29%) patients, respectively. The annual prevalence never exceeded the threshold of 1/10,000. The mean incidence and prevalence were significantly lower than during the period 2007 to 2014 ($p < 0.0001$). Reversal reactions were found in 29 patients and almost always required a long course of steroids. Infliximab allowed a reduction in the length of treatment with steroids in 2/2 cases. In conclusion, the prevalence of leprosy has decreased significantly in French Guiana, but remains driven by the population of illegal gold miners. Anti-tumour necrosis factor (anti-TNF) drugs represent a promising option in the management of reversal reactions.

Use of local data to evaluate TB contact investigation in Malawi.

Kaswaswa K, Mlauzi L, Mpunga J, Mandambwe C, Kawatsu L, Uchimura K.

01-05-2023

Int J Tuberc Lung Dis.

<https://pubmed.ncbi.nlm.nih.gov/37143224/>

Cutaneous paecilomyces infection in an immunocompetent patient.

Dsouza PA, Monteiro RC, Martis J, Fernandes S.

04-05-2023

Int J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37140100/>

Efficacy and Safety of a Protein-Based SARS-CoV-2 Vaccine: A Randomized Clinical Trial.

Mostafavi E, Eybpoosh S, Karamouzian M, Khalili M, Haji-Maghsoudi S, Salehi-Vaziri M, Khamesipour A, Jalali T, Nakhaeizadeh M, Sharifi H, Mansoori Y, Keramat F, Ghodrati S, Javanian M, Doroud D, Omrani MD, Asadi H, Pouriayeali MH, Ghasemian R, Farshidi H, Pourahmad M, Ghasemzadeh I, Mounesan L, Darvishian M, Mirjalili MR, Toledo-Romani ME, Valenzuela-Silva C, Verez-Bencomo V, Gouya MM, Emadi-Koochak H, Haghdooost AA, Biglari A; Soberana Study Group.

01-05-2023

JAMA Netw Open.

<https://pubmed.ncbi.nlm.nih.gov/37133864/>

Importance: The protein-based SARS-CoV-2 vaccines FINLAY-FR-2 (Soberana 02) and FINLAY-FR-1A (Soberana Plus) showed good safety and immunogenicity in phase 1 and 2 trials, but the clinical efficacy of the vaccine remains unknown. **Objective:** To evaluate the efficacy and safety of a 2-dose regimen of FINLAY-FR-2 (cohort 1) and a 3-dose regimen of FINLAY-FR-2 with FINLAY-FR-1A (cohort 2) in Iranian adults. **Design, setting, and participants:** A multicenter, randomized, double-blind, placebo-controlled, phase 3 trial was conducted at 6 cities in cohort 1 and 2 cities in cohort 2. Participants included individuals aged 18 to 80 years without uncontrolled comorbidities, coagulation disorders, pregnancy or breastfeeding, recent immunoglobulin or immunosuppressive therapy, and clinical presentation or laboratory-confirmed COVID-19 on enrollment. The study was conducted from April 26 to September 25, 2021. **Interventions:** In cohort 1, 2 doses of

FINLAY-FR-2 ($n = 13\ 857$) or placebo ($n = 3462$) were administered 28 days apart. In cohort 2, 2 doses of FINLAY-FR-2 plus 1 dose of FINLAY-FR-1A ($n = 4340$) or 3 placebo doses ($n = 1081$) were administered 28 days apart. Vaccinations were administered via intramuscular injection. **Main outcomes and measures:** The primary outcome was polymerase chain reaction-confirmed symptomatic COVID-19 infection at least 14 days after vaccination completion. Other outcomes were adverse events and severe COVID-19. Intention-to-treat analysis was performed. **Results:** In cohort 1 a total 17 319 individuals received 2 doses and in cohort 2 5521 received 3 doses of the vaccine or placebo. Cohort 1 comprised 60.1% men in the vaccine group and 59.1% men in the placebo group; cohort 2 included 59.8% men in the vaccine group and 59.9% in the placebo group. The mean (SD) age was 39.3 (11.9) years in cohort 1 and 39.7 (12.0) years in cohort 2, with no significant difference between the vaccine and placebo groups. The median follow-up time in cohort 1 was 100 (IQR, 96-106) days and, in cohort 2, 142 (137-148) days. In cohort 1, 461 (3.2%) cases of COVID-19 occurred in the vaccine group and 221 (6.1%) in the placebo group (vaccine efficacy: 49.7%; 95% CI, 40.8%-57.3%) vs 75 (1.6%) and 51 (4.3%) in cohort 2 (vaccine efficacy: 64.9%; 95% CI, 49.7%-59.5%). The incidence of serious adverse events was lower than 0.1%, with no vaccine-related deaths. **Conclusions and relevance:** In this multicenter, randomized, double-blind, placebo-controlled, phase 3 trial of the efficacy and safety of FINLAY-FR-2 and FINLAY-FR-1A, 2 doses of FINLAY-FR-2 plus the third dose of FINLAY-FR-1A showed acceptable vaccine efficacy against symptomatic COVID-19 as well as COVID-19-related severe infections. Vaccination was generally safe and well tolerated. Therefore, Soberana may have utility as an option for mass vaccination of the population, especially in resource-limited settings, because of its storage condition and affordable price.

Phylogenetic relationship of Fusarium species isolated from keratitis using TEF1 and RPB2 gene sequences.

Yassin Z, Salehi Z, Soleimani M, Lotfali E, Fattahi M, Sharifynia S.

Juin-2023

Iran J Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37124860/>

Epidemiological characteristics of leprosy from 2000 to 2019 in a state with low endemicity in southern Brazil.

Moraes PC, Eidt LM, Koehler A, Ransan LG, Scrofeneker ML.

27-04-2023

An Bras Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/37120406/>

Background: Leprosy is an infectious and contagious disease caused by *Mycobacterium leprae* and is mainly characterized by lesions in the skin and peripheral nerves. In Brazil, it is a public health problem due to its high endemicity. However, the state of Rio Grande do Sul presents low endemicity of this disease. **Objective:** To

characterize the epidemiological profile of leprosy in the state of Rio Grande do Sul from 2000 to 2019. **Methods:** This was a retrospective observational study. Epidemiological data were collected from the Notifiable Diseases Information System (SINAN, Sistema de Informação de Agravos de Notificação). **Results:** Among the 497 municipalities in the state, 357 (71.8%) registered cases of leprosy in the assessed period, with an average of 212 (81.5%) new cases per year. The average detection rate was 1.61 new cases per 100,000 inhabitants. The male sex was predominant (51.9%) and the mean age was 50.4 years. Regarding the epidemiological clinical profile; 79.0% of the patients were multibacillary; 37.5% presented the borderline clinical form; 16% had grade 2 physical disability at diagnosis and bacilloscopy was positive in 35.4% of cases. As for treatment, 73.8% of the cases were treated with the standard multibacillary therapeutic regimen. **Study limitations:** There were missing/inconsistent data in the database available. **Conclusions:** The findings observed in this study indicate that the state presents a low endemicity profile of the disease and these results can support adequate health policies relevant to the reality of Rio Grande do Sul, inserted in a national scenario of highly endemic leprosy.

Live attenuated *Leishmania infantum* centrin deleted mutant (LiCen^{-/-}) as a novel vaccine candidate: A field study on safety, immunogenicity, and efficacy against canine leishmaniasis.

Zarei Z, Mohebbi M, Dehghani H, Khamesipour A, Tavakkol-Afshari J, Akhoundi B, Abbaszadeh-Afshar MJ, Alizadeh Z, Skandari SE, Asl AD, Razmi GR.
25-04-2023

Comp Immunol Microbiol Infect Dis.
<https://pubmed.ncbi.nlm.nih.gov/37119594/>

This study was designed to evaluate the safety, immunogenicity, and efficacy of a single dose of *L. infantum* (LiCen^{-/-}) live attenuated candidate vaccine against canine leishmaniasis (CanL). Eighteen healthy domestic dogs with no anti-*Leishmania* antibodies and negative leishmanin skin test (LST) were randomly inoculated intravenously with either *L. infantum* (LiCen^{-/-}) vaccine candidate in 10 dogs or phosphate-buffered saline (PBS) in 8 dogs. The safety, immunogenicity, and efficacy rate of *L. infantum* (LiCen^{-/-}) vaccine candidate against CanL were evaluated by different criteria, including clinical manifestations, injection-site lesion, hematology and biochemistry values, anti-*Leishmania* antibodies using direct agglutination test (DAT), delayed-type hypersensitivity (DTH) using LST, and CD4⁺ and CD8⁺ T-cells subsets, as well as by measuring interferon (IFN- γ), interleukin (IL-23), IL-17, and IL-10 cytokines. Spleen aspiration and detection of *Leishmania* parasite using parasitological examinations (microscopy and culture) were performed in both vaccinated and control groups. Two months after intervention, each dog was challenged intraperitoneally (IP) with wide type (WT) *L. infantum*. Two-month follow-up post vaccination showed no clinical signs and serious side effects associated with the vaccination. A significant increase was found in the expression of IL-17, CD4⁺, and CD8⁺ gene transcripts in

PBMCs, as well as increased levels of Th1 cytokines, and reduction of Th2 cytokine. The efficacy of the vaccine candidate was calculated to be 42.85%. While the time window for assessing the vaccine's effectiveness was too limited to draw any real conclusions but the preliminary results showed a moderate efficacy rate due to inoculation a single dose of *L. infantum* (LiCen^{-/-}) vaccine candidate. Further investigations with more sample sizes and multiple doses of the vaccine candidate using natural challenges in the endemic areas of CanL are recommended.

Immunogenicity and protective efficacy of an inactivated Newcastle disease virus vaccine encapsulated in poly-(lactic-co-glycolic acid) nanoparticles.

Ananda Kumar BS, Panickan S, Bindu S, Kumar V, Ramakrishnan S, Saxena S, Shrivastava S, Dandapat S.
30-03-2023

Poult Sci.
<https://pubmed.ncbi.nlm.nih.gov/37116285/>

CD11b⁺Gr-1^{low} cells that accumulate in *M.leprae*-induced granulomas of the footpad skin of nude mice have the characteristics of monocytic-myeloid-derived suppressor cells.

Jin SH, Lee SB.
14-04-2023
Tuberculosis (Edinb).
<https://pubmed.ncbi.nlm.nih.gov/37116235/>

Genomic analysis unveils genome degradation events and gene flux in the emergence and persistence of *S. Paratyphi A* lineages.

Jacob JJ, Pragasam AK, Vasudevan K, Velmurugan A, Priya Teekaraman M, Priya Thirumoorthy T, Ray P, Gupta M, Kapil A, Bai SP, Nagaraj S, Saigal K, Chandola TR, Thomas M, Bavdekar A, Ebenezer SE, Shastri J, De A, Dutta S, Alexander AP, Koshy RM, Jinka DR, Singh A, Srivastava SK, Anandan S, Dougan G, John J, Kang G, Veeraraghavan B, Mutreja A.
28-04-2023

PLoS Pathog.
<https://pubmed.ncbi.nlm.nih.gov/37115804/>

Paratyphoid fever caused by *S. Paratyphi A* is endemic in parts of South Asia and Southeast Asia. The proportion of enteric fever cases caused by *S. Paratyphi A* has substantially increased, yet only limited data is available on the population structure and genetic diversity of this serovar. We examined the phylogenetic distribution and evolutionary trajectory of *S. Paratyphi A* isolates collected as part of the Indian enteric fever surveillance study "Surveillance of Enteric Fever in India (SEFI)." In the study period (2017-2020), *S. Paratyphi A* comprised 17.6% (441/2503) of total enteric fever cases in India, with the isolates highly susceptible to all the major antibiotics used for treatment except fluoroquinolones. Phylogenetic analysis clustered the global *S. Paratyphi A* collection into seven lineages (A-G), and the present study isolates were distributed in lineages A, C and F. Our analysis highlights

that the genome degradation events and gene acquisitions or losses are key molecular events in the evolution of new *S. Paratyphi* A lineages/sub-lineages. A total of 10 hypothetically disrupted coding sequences (HDCS) or pseudogenes-forming mutations possibly associated with the emergence of lineages were identified. The pan-genome analysis identified the insertion of P2/PSP3 phage and acquisition of IncX1 plasmid during the selection in 2.3.2/2.3.3 and 1.2.2 genotypes, respectively. We have identified six characteristic missense mutations associated with lipopolysaccharide (LPS) biosynthesis genes of *S. Paratyphi* A, however, these mutations confer only a low structural impact and possibly have minimal impact on vaccine effectiveness. Since *S. Paratyphi* A is human-restricted, high levels of genetic drift are not expected unless these bacteria transmit to naive hosts. However, public-health investigation and monitoring by means of genomic surveillance would be constantly needed to avoid *S. Paratyphi* A serovar becoming a public health threat similar to the *S. Typhi* of today.

Unveiling the TGF- β 1 paradox: Significant implication of TGF- β 1 promoter variants and its mRNA and protein expression in atopic dermatitis.

Shafi T, Rasool R, Ayub S, Bhat IA, Shah IH, Hussain S, Shah ZA, Baba SM, Makhdoomi R, Bashir SA.

Mai-2023

Mol Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37084506/>

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, Maisonnobe 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.

ML Flow serological test: complementary tool in leprosy.

Montanha JOM, Nardi SMT, Binhardi FMT, Pedro HDSP, Santi MP, Paschoal VDA.

Mai-Juin-2023

An Bras Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36890048/>

Shorter regimens improved treatment outcomes of multidrug-resistant tuberculosis patients in Tanzania in 2018 cohort.

Mleoh L, Mziray SR, Tsere D, Koppelaar I, Mulder C, Lyakurwa D.

Mai-2023

Trop Med Int Health.

<https://pubmed.ncbi.nlm.nih.gov/36864011/>

Objective: In 2018, shorter treatment regimens (STR) for people with drug-resistant tuberculosis (DR-TB) were introduced in Tanzania and included kanamycin, high-dose moxifloxacin, prothionamide, high-dose isoniazid, clofazimine, ethambutol and pyrazinamide. We describe treatment outcomes of people diagnosed with DR-TB in a cohort initiating treatment in 2018 in Tanzania. **Methods:** This was a retrospective cohort study conducted at the National Centre of Excellence and decentralised DR-TB treatment sites for the 2018 cohort followed from January 2018 to August 2020. We reviewed data from the National Tuberculosis and Leprosy Program DR-TB database to assess clinical and demographic information. The association between different DR-TB regimens and treatment outcome was assessed using logistic regression analysis. Treatment outcomes were described as treatment complete, cure, death, failure or lost to follow-up. A successful treatment outcome was assigned when the patient achieved treatment completion or cure. **Results:** A total of 449 people were diagnosed with DR-TB of whom 382 had final treatment outcomes: 268 (70%) cured; 36 (9%) treatment completed; 16 (4%) lost to follow-up; 62 (16%) died. There was no treatment failure. The treatment success rate was 79% (304 patients). The 2018 DR-TB treatment cohort was initiated on the following regimens: 140 (46%) received STR, 90 (30%) received the standard longer regimen (SLR), 74 (24%) received a new drug regimen. Normal nutritional status at

baseline [adjusted odds ratio (aOR) = 6.57, 95% CI (3.33-12.94), $p < 0.001$] and the STR [aOR = 2.67, 95% CI (1.38-5.18), $p = 0.004$] were independently associated with successful DR-TB treatment outcome. **Conclusion:** The majority of DR-TB patients on STR in Tanzania achieved a better treatment outcome than on SLR. The acceptance and implementation of STR at decentralised sites promises greater treatment success. Assessing and improving nutritional status at baseline and introducing new shorter DR-TB treatment regimens may strengthen favourable treatment outcomes.

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

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

Mai-2032

Int J STD AIDS.

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

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

Miliaria crystallina.

Palaniappan V, Sadhasivamohan A, Sankarapandian J, Karthikeyan K.

27-04-2023

Clin Exp Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36692206/>

Morsures de serpent

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

Ralph R, Garg D, Balachandran A, Ganesh SR, Lamb T.

29-04-2023

Toxicon.

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

India is home to a diverse spectrum of medically-significant snakes accounting for one of the world's largest burdens of envenoming, morbidity and mortality. Indian polyspecific antivenom is derived from the venom of four snake species (*Daboia russelii*, *Echis carinatus*, *Naja naja* and *Bungarus caeruleus*), considered to be responsible for the majority of snakebite morbidity and mortality in India. The treatment of envenoming from other less-commonly encountered venomous snake species can be challenging. In this report, we describe the case of a 32-year-old male who presented with local swelling and coagulopathy

following a bite from *Ovophis monitcola* (mountain pit-viper) in Nagaland, Northeast India. Local and systemic envenoming, failed to respond to Indian polyspecific antivenom and venom-induced consumption coagulopathy, confirmed by bedside and laboratory-based clotting assays, persisted for more than three weeks. Remote consultation with a national-level Poison Control Centre helped establish the responsible snake species and guide appropriate medical management.

The chemistry of snake venom and its medicinal potential.

Oliveira AL, Viegas MF, da Silva SL, Soares AM, Ramos MJ, Fernandes PA.

Juillet-2023

Nat Rev Chem.

<https://pubmed.ncbi.nlm.nih.gov/37117308/>

Changes in Serum Enzymes and Related Mechanisms of Respiratory Dysfunction in Patients after Venomous Snake Bite and Analysis of Anti-Venomous Snake Serum Treatment.

Nong J, Huang Z, Huang Z, Yang J, Li J, Huang D, Wang W.

30-09-2022

Cell Mol Biol (Noisy-le-grand).

<https://pubmed.ncbi.nlm.nih.gov/37114264/>

To explore the changes in serum enzymes in patients with a snake bite, the treatment of respiratory dysfunction, and the clinical effect of anti-snake serum treatment. Fifty snake bite patients admitted to the emergency medicine department were selected and rolled into a light group (n=27), heavy group (n=15), and critical group (n=8). Anti-venomous snake serum was injected intravenously. Patients with severe respiratory dysfunction were treated with mechanical ventilation. The white blood cell (WBC), C-reactive protein (CRP), interleukin-6 (IL-6), alanine aminotransferase (ALT), aspartate aminotransferase (AST), blood urea nitrogen (BUN), and creatinine (Cr) counts of the heavy group and the critical group were higher versus light group ($P < 0.05$). The WBC, CRP, IL-6, ALT, AST, BUN, and Cr of the critical group were higher versus the heavy group ($P < 0.05$). The prothrombin time (PT), activated partial thrombin time (APTT), and thrombin time (TT) of the heavy group and critical group were longer versus the light group ($P < 0.05$). The PT, APTT, and TT of the critical group were longer than the heavy group ($P < 0.05$). The fibrinogen (FIB) of the light group was higher in contrast to that in the other two groups ($P < 0.05$), while the critical group was the lowest ($P < 0.05$). In summary, the severity of snakebites in patients can be evaluated according to the indexes of WBC, IL-6, coagulation function, and liver and kidney function.

Application of an Extracellular Matrix-Mimicking Fluorescent Polymer for the Detection of Proteolytic Venom Toxins.

Wachtel E, Bittenbinder MA, van de Velde B, Slagboom J, de Monts de Savasse A, Alonso LL, Casewell NR, Vonk FJ, Kool J.

18-04-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37104232/>

The cytotoxicity caused by snake venoms is a serious medical problem that greatly contributes to the morbidity observed in snakebite patients. The cytotoxic components found in snake venoms belong to a variety of toxin classes and may cause cytotoxic effects by targeting a range of molecular structures, including cellular membranes, the extracellular matrix (ECM) and the cytoskeleton. Here, we present a high-throughput assay (384-well plate) that monitors ECM degradation by snake venom toxins via the application of fluorescent versions of model ECM substrates, specifically gelatin and collagen type I. Both crude venoms and fractionated toxins of a selection of medically relevant viperid and elapid species, separated via size-exclusion chromatography, were studied using the self-quenching, fluorescently labelled ECM-polymer substrates. The viperid venoms showed significantly higher proteolytic degradation when compared to elapid venoms, although the venoms with higher snake venom metalloproteinase content did not necessarily exhibit stronger substrate degradation than those with a lower one. Gelatin was generally more readily cleaved than collagen type I. In the viperid venoms, which were subjected to fractionation by SEC, two (*B. jararaca* and *C. rhodostoma*, respectively) or three (*E. ocellatus*) active proteases were identified. Therefore, the assay allows the study of proteolytic activity towards the ECM in vitro for crude and fractionated venoms.

Proteomic Analysis, Immuno-Specificity and Neutralization Efficacy of Pakistani Viper Antivenom (PVAV), a Bivalent Anti-Viperid Antivenom Produced in Pakistan.

Lim ASS, Tan KY, Quraishi NH, Farooque S, Khoso ZA, Ratanabanangkoon K, Tan CH.

03-04-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37104203/>

Anti-Metalloproteases: Production and Characterization of Polyclonal IgG Anti-F2 Fraction Antibodies Purified from the Venom of the Snake *Bitis arietans*.

Godoi KS, Guidolin FR, Portaro FCV, Spencer PJ, da Silva WD.

01-04-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37104202/>

Bitis arietans is a medically important snake found in Sub-Saharan Africa. The envenomation is characterized by local and systemic effects, and the lack of antivenoms aggravates the treatment. This study aimed to identify venom toxins and develop antitoxins. The F2 fraction obtained from *Bitis arietans* venom (BaV) demonstrated the presence of several proteins in its composition, including metalloproteases. Titration assays carried out together with the immunization of mice demonstrated the development of anti-F2 fraction antibodies by the animals. The determination of the affinity of antibodies against

different *Bitis* venoms was evaluated, revealing that only BaV had peptides recognized by anti-F2 fraction antibodies. In vivo analyses demonstrated the hemorrhagic capacity of the venom and the effectiveness of the antibodies in inhibiting up to 80% of the hemorrhage and 0% of the lethality caused by BaV. Together, the data indicate: (1) the prevalence of proteins that influence hemostasis and envenomation; (2) the effectiveness of antibodies in inhibiting specific activities of BaV; and (3) isolation and characterization of toxins can become crucial steps in the development of new alternative treatments. Thus, the results obtained help in understanding the envenoming mechanism and may be useful for the study of new complementary therapies.

Multilevel Comparison of Indian Naja Venoms and Their Cross-Reactivity with Indian Polyvalent Antivenoms.

Deka A, Bhatia S, Santra V, Bharti OK, Lalremsanga HT, Martin G, Wüster W, Owens JB, Graham S, Doley R, Malhotra A.

01-04-2023

Toxins (Basel).

<https://pubmed.ncbi.nlm.nih.gov/37104196/>

Clinical features of snake envenomation in South Korea.

Moon JM, Chun BJ, Cho YS.

Avr-2023

Clin Toxicol (Phila).

<https://pubmed.ncbi.nlm.nih.gov/36939139/>

Traditional remedies and other characteristics among human snakebite survivors in Baringo county, Kenya, 2010-2020: a case series.

Kung'u PN, Chweya RN, Gachohi JM.

02-05-2023

Int Health.

<https://pubmed.ncbi.nlm.nih.gov/35724263/>

Background: Seeking traditional remedies following snakebites leads to avoidable deaths in rural settings in developing countries. **Methods:** In this case series study, we identified and recruited 169 snakebite survivors in Baringo county, a hard-to-reach region in northwestern Kenya, who experienced snakebites from 2010 to 2020 using a snowballing technique. We explored associations between traditional and hospital care in managing snakebites and other characteristics. χ^2 tests assessed these categorical differences. **Results:** Fifty-four (33%) of the survivors used traditional remedies to manage snakebites. The majority (56%) were men and aged >18 y (72%); 59% had low education levels and income. They sourced water from rivers or lakes (93%) and used charcoal as an energy source (74%). These survivors (>67%) resided in households practicing free-range and stall-feeding animal husbandry systems and in houses with thatch roofing or an earthen floor structure. Also, >62% reported muscle tremors, fever and chills, while 80% visited health facilities for further treatment. **Conclusion:** Community sensitization covering the risks of non-

effective remedies and escalation of training to traditional healers could improve the speed of referrals in hard-to-reach snakebite hotspots. Medical anthropology studies could explore the enablers of continued use of traditional remedies in snakebite management in rural communities.

Response to: Risk of hemorrhagic stroke after venomous snakebite: correspondence.

Hung WH, Hung YM, Yip HT, Wei JC, Chang R.

29-04-2023

QJM.

<https://pubmed.ncbi.nlm.nih.gov/35640993/>

Risk of hemorrhagic stroke after venomous snakebite: correspondence.

Yeh WB, Lee WK, Jou IM, Chou MC.

29-04-2023

QJM.

<https://pubmed.ncbi.nlm.nih.gov/35640973/>

Mycétome

A Detailed Review of Surgical Management of Uncommon Cutaneous Disorders.

Tolat A, Kalwaniya DS, Sharma A, Kumar D, Rana S, Ahluwalia C.

27-03-2023

Cureus.

<https://pubmed.ncbi.nlm.nih.gov/37123679/>

A variety of cutaneous disorders can present to the general surgeon either directly or by referral for surgical intervention. Some conditions are commonly seen and operated on by general surgeons which include lipoma, epidermoid cyst, etc. On the other hand, some are uncommon conditions like dermatofibrosarcoma protuberans and chondroid syringoma which require a high index of suspicion to diagnose. Most general surgeons are not familiar with the latest guidelines to treat such uncommon conditions. In this article, we provide a review of uncommon cutaneous disorders requiring surgical intervention that were encountered at our high-volume tertiary care center and a discussion about their etiology, presentation, diagnosis, management and follow-up with one case report of each condition. The objective of this article is to familiarize the general surgeon with these cutaneous disorders which though uncommon, will present in their practice at some point.

Using a *Madurella mycetomatis*-specific PCR on grains obtained via non-invasive fine-needle aspirated material is more accurate than cytology.

Siddig EE, Ahmed A, Hassan OB, Bakhiet SM, Verbon A, Fahal AH, van de Sande WWJ.

Juin-2023

Mycoses.

<https://pubmed.ncbi.nlm.nih.gov/36740735/>

Background: Eumycetoma is a chronic subcutaneous inflammatory fungal infection most often caused by the fungus *Madurella mycetomatis*. Using a species-specific PCR on DNA directly isolated from grains is currently the most reliable method for species identification. However, so far, PCR has been performed on grains obtained through deep-seated surgical biopsies, which are invasive procedures. Grains can also be obtained via ultrasound-guided fine-needle aspiration (US-FNA). Here we determined the diagnostic performance of species-specific PCRs performed on samples obtained through US-FNA. **Methods:** From 63 patients, US-FNA was performed to obtain eumycetoma grains; 34 patients also underwent a deep-seated biopsy. From the grains, DNA was isolated, and one pan-fungal and two *M. mycetomatis*-specific PCRs were performed. The sensitivity and specificity were determined. **Results:** Of the 63 patients who underwent US-FNA, 78% (49/63) had evidence of eumycetoma based on cytology and 93.7% (59/63) based on species-specific PCRs. In the 34 patients for whom surgical biopsies were performed as well, 31 patients had a positive PCR for *M. mycetomatis* when DNA was isolated from the deep-seated biopsy, and 30 had a positive PCR when DNA was obtained from the US-FNA material. This resulted in a 96.8% sensitivity, and 100% specificity with 97.1% diagnostic accuracy for PCR performed on US-FNA. **Conclusion:** PCR performed on the US-FNA material has a similar sensitivity and specificity as PCR performed on deep-seated biopsies. Therefore, when using PCR, a deep-seated biopsy may not be necessary to obtain grains.

Onchocercose

***Wolbachia* Ferrochelatase as a potential drug target against filarial infections.**

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

26-04-2023

J Mol Graph Model.

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

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

resulting in their death. This study which involved targeting enzymes in biosynthetic pathways of the parasitic worms' endosymbiont (Wolbachia), has proven to be an alternative therapeutic option leading to the discovery of new drugs, which will help facilitate the elimination of parasitic infections.

Pian

Solubility and Thermodynamics Profile of Benzethonium Chloride in Pure and Binary Solvents at Different Temperatures.

Bhola R, Ghumara R, Patel C, Parsana V, Bhatt K, Kundariya D, Vaghani H.

14-04-2023

ACS Omega.

<https://pubmed.ncbi.nlm.nih.gov/37125112/>

Benzethonium chloride (BTC) has various applications in several industries. The solubility and solution thermodynamic properties of BTC were measured. The solubility of BTC in methanol, ethanol, 1-propanol, 2-propanol, 1-butanol, water, dimethyl sulfoxide, acetic acid, and dimethyl formamide neat solvents and methanol + water and ethanol + water binary solvents at 298.15-318.15 K over an atmospheric pressure was measured. The solubility data of BTC is positively related to the temperature in all selected solvents. The solubility data was fitted by the Apelblat model, λh model, Yaws model, Van't Hoff equation, CNIBS/R-K model, and modified Jouyban-Acree equation. The RMSD and ARD were chosen to evaluate the fitting of each model. The dissolution thermodynamic parameters, enthalpy of the solution, entropy of the solution, and Gibbs energy of the solution were calculated. The solubility data and dissolution thermodynamic parameters of BTC will provide significant guidance for purification, crystallization, and separation in various areas.

Treponemal Antibody Seroprevalence Using a Multiplex Bead Assay from Samples Collected during the 2018 Nigeria HIV/AIDS Indicator and Impact Survey: Searching for Yaws in Nigeria.

Guagliardo SAJ, Parameswaran N, Agala N, Abubakar A, Cooley G, Ye T, Kamb M, Mba N, William N, Greby S, Iriemenam N, Alagi M, Okoye M, Martin D.

10-04-2023

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/37037444/>

Rage

Double-stranded RNA immunohistochemistry as a screening tool for viral encephalitis.

Piantadosi A, Shariatzadeh N, Bombin A, Arkun K, Alexandrescu S, Kleinschmidt-DeMasters BK, Solomon IH.

04-05-2023

Am J Clin Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37141170/>

Analysis of a multi-type resurgence of *Mycobacterium bovis* in cattle and badgers in Southwest France, 2007-2019.

Bouchez-Zacria M, Ruetten S, Richomme C, Lesellier S, Payne A, Boschirol ML, Courcoul A, Durand B.

05-03-2023

Vet Res.

<https://pubmed.ncbi.nlm.nih.gov/37138355/>

Although control measures to tackle bovine tuberculosis (bTB) in cattle have been successful in many parts of Europe, this disease has not been eradicated in areas where *Mycobacterium bovis* circulates in multi-host systems. Here we analyzed the resurgence of 11 *M. bovis* genotypes (defined based on spoligotyping and MIRU-VNTR) detected in 141 farms between 2007 and 2019, in an area of Southwestern France where wildlife infection was also detected from 2012 in 65 badgers. We used a spatially-explicit model to reconstruct the simultaneous diffusion of the 11 genotypes in cattle farms and badger populations. Effective reproduction number R was estimated to be 1.34 in 2007-2011 indicating a self-sustained *M. bovis* transmission by a maintenance community although within-species R_s were both < 1 , indicating that neither cattle nor badger populations acted as separate reservoir hosts. From 2012, control measures were implemented, and we observed a decrease of R below 1. Spatial contrasts of the basic reproduction ratio suggested that local field conditions may favor (or penalize) local spread of bTB upon introduction into a new farm. Calculation of generation time distributions showed that the spread of *M. bovis* has been more rapid from cattle farms (0.5-0.7 year) than from badger groups (1.3-2.4 years). Although eradication of bTB appears possible in the study area (since $R < 1$), the model suggests it is a long-term prospect, because of the prolonged persistence of infection in badger groups (2.9-5.7 years). Supplementary tools and efforts to better control bTB infection in badgers (including vaccination for instance) appear necessary.

Autophagy and unfolded protein response induction: a crosstalk between street rabies virus and the host.

Poorghobadi S, Baesi K, Gharibzadeh S, Shirzad R, Khosravy MS, Fazeli M, Sheikholeslami F.

03-05-2023

Cell Stress Chaperones.

<https://pubmed.ncbi.nlm.nih.gov/37133695/>

The endoplasmic reticulum (ER) response mechanism to cellular stress is mediated by the unfolded protein response/ER-associated degradation (UPR/ERAD) pathway. A viral infection can trigger ER stress and engage some transcription factors, depending on the host cell and virus type, activating or inhibiting autophagy. The relationship between ER response and autophagy in rabies has not been investigated yet. In the present study, the mouse brain was infected with street rabies virus (SRABV).

Total RNA was extracted from the brains of animals, and cDNA was synthesized. Next, real-time PCR assay was performed using specific primers. The expression of hypoxanthine-guanine phosphoribosyltransferase (Hprt), CCAAT/enhancer binding protein homologous protein (CHOP), apoptosis signal-regulating kinase 1 (ASK1), activating transcription factor 6 (ATF6), and caspase 3 (CASP3) genes was also investigated. Based on the results, SRABV caused significant changes in the mRNA expression of ATF6, CHOP, and ASK1 genes in the brains of infected mice in the control group (group V). Treatment of infected cells with the pIRES-EGFP-Beclin-1 vector and rapamycin caused changes in nearly most of the parameters. However, alterations in CASP3 gene expression were only observed when the vector and the virus were simultaneously injected into the cells. Overall, protection and autophagy against cell death induced by SRABV infection can be achieved by activating the ER stress pathway, followed by a marked increase in the expression of ATF6, CHOP, ASK1, and CASP3 genes.

Design and characterization of chimeric Rabies-SARS-CoV-2 virus-like particles for vaccine purposes.

Garay E, Fontana D, Villarraza J, Fuselli A, Gugliotta A, Antuña S, Tardivo B, Rodríguez MC, Gastaldi V, Battagliotti JM, Alvarez D, Castro E, Cassataro J, Ceaglio N, Prieto C.

01-05-2023

Appl Microbiol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/37126083/>

Editorial: Immunopathogenesis and infection characteristics of zoonotic viral diseases.

Arshad MI, Wensman JJ, Munir M.

14-04-2023

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/37124049/>

Structure and Function of Neuronal Circuits linking Ventrolateral Preoptic Nucleus and Lateral Hypothalamic Area.

Prokofeva K, Saito YC, Niwa Y, Mizuno S, Takahashi S, Hirano A, Sakurai T.

27-04-2023

J Neurosci.

<https://pubmed.ncbi.nlm.nih.gov/37117013/>

Orthopoxvirus Circulation in an Endemic Area in Brazil: Investigation of Infections in Small Mammals during an Absence of Outbreaks.

Domingos IJS, Rocha KLS, Graciano JM, Almeida LR, Doty JB, Paglia AP, Oliveira DB, Nakazawa YJ, Trindade GS.

25-03-2023

Viruses.

<https://pubmed.ncbi.nlm.nih.gov/37112823/>

Vaccinia virus (VACV) is the causative agent of an emerging viral zoonosis called bovine vaccinia (BV). Several studies

have documented characteristics of VACV infections in Brazil; however, the manner in which this virus is maintained in wildlife remains unknown. This work investigated the presence of viral DNA and anti-orthopoxvirus (OPXV) antibodies in samples collected from small mammals in a VACV-endemic area in Minas Gerais, Brazil, in the absence of current outbreaks. Samples did not show amplification of OPXV DNA in molecular tests. However, 5/142 serum samples demonstrated the presence of anti-OPXV neutralizing antibodies in serological tests. These data reinforce the involvement of small mammals in the natural cycle of VACV, highlighting the need for further ecological studies to better understand how this virus is maintained in nature and to develop measures to prevent BV outbreaks.

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/>

We describe the results of a prospective observational study of the clinical natural history of human monkeypox (mpox) virus (MPXV) infections at the remote L'Hopital General de Reference de Kole (Kole hospital), the rainforest of the Congo River basin of the Democratic Republic of the Congo (DRC) from March 2007 until August 2011. The research was conducted jointly by the Institute National de Recherche Biomedical (INRB) and the US Army Medical Research Institute of Infectious Diseases (USAMRIID). The Kole hospital was one of the two previous WHO Mpox study sites (1981-1986). The hospital is staffed by a Spanish Order of Catholic Nuns from La Congregation Des Soeurs Missionnaires Du Christ Jesus including two Spanish physicians, who were members of the Order as well, were part of the WHO study on human mpox. Of 244 patients admitted with a clinical diagnosis of MPXV infection, 216 were positive in both the Pan-Orthopox and MPXV specific PCR. The cardinal observations of these 216 patients are summarized in this report. There were three deaths (3/216) among these hospitalized patients; fetal death occurred in 3 of 4 patients who were pregnant at admission, with the placenta of one fetus demonstrating prominent MPXV infection of the chorionic villi. The most common complaints were rash (96.8%), malaise (85.2%), sore throat (78.2%), and lymphadenopathy/adenopathy (57.4%). The most common physical exam findings were mpox rash (99.5%) and lymphadenopathy (98.6%). The single patient without the classic mpox rash had been previously vaccinated against smallpox. Age group of less than 5 years had the highest lesion count. Primary household cases tended to have higher lesion counts than secondary or later same household cases. Of the 216 patients, 200 were tested for IgM & IgG antibodies (Abs)

to Orthopoxviruses. All 200 patients had anti-orthopoxvirus IgG Abs; whereas 189/200 were positive for IgM. Patients with hypoalbuminemia had a high risk of severe disease. Patients with fatal disease had higher maximum geometric mean values than survivors for the following variables, respectively: viral DNA in blood (DNAemia); maximum lesion count; day of admission mean AST and ALT.

Schistosomiasis

The association of systemic inflammation and cognitive functions of pre-school aged children residing in a *Schistosoma haematobium* endemic area in Zimbabwe.

Kasambala M, Mukaratirwa S, Vengesai A, Mduluzza-Jokonya T, Jokonya L, Midzi H, Makota RB, Mutemeri A, Maziti E, Dube-Marimbe B, Chibanda D, Mutapi F, Mduluzza T.

18-04-2023

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/37143686/>

Background: Cognitive function is negatively impacted by schistosomiasis and might be caused by systemic inflammation which has been hypothesized to be one of the mechanisms driving cognitive decline. This study explored the association of systemic inflammatory biomarkers; interleukin (IL)-10, IL-6, IL-17, transforming growth factor (TGF- β), tumor necrosis factor (TNF- α), C-reactive protein (CRP) and hematological parameters with cognitive performance of preschool-aged children (PSAC) from an *Schistosoma haematobium* endemic area.

Methods: The Griffith III tool was used to measure the cognitive performance of 136 PSAC. Whole blood and sera were collected and used to quantify levels of IL-10, TNF- α , IL-6, TGF- β , IL-17 A and CRP using the enzyme-linked immunosorbent assay and hematological parameters using the hematology analyzer. Spearman correlation analysis was used to determine the relationship between each inflammatory biomarker and cognitive performance. Multivariate logistic regression analysis was used to determine whether systemic inflammation due to *S. haematobium* infection affected cognitive performance in PSAC. **Results:** Higher levels of TNF- α and IL-6, were correlated with lower performance in the Foundations of Learning domain ($r = -0.30$; $p < 0.001$ and $r = -0.26$; $p < 0.001$), respectively. Low cognitive performance in the Eye-Hand-Coordination Domain was observed in PSAC with high levels of the following inflammatory biomarkers that showed negative correlations to performance; TNF- α ($r = -0.26$; $p < 0.001$), IL-6 ($r = -0.29$; $p < 0.001$), IL-10 ($r = -0.18$; $p < 0.04$), WBC ($r = -0.29$; $p < 0.001$), neutrophils ($r = -0.21$; $p = 0.01$) and lymphocytes ($r = -0.25$; $p = 0.003$). The General Development Domain correlated with TNF- α ($r = -0.28$; $p < 0.001$) and IL-6 ($r = -0.30$; $p < 0.001$). TGF- β , IL-17A and MXD had no significant correlations to performance in any of the cognitive domains. The overall general development of PSAC was negatively impacted by *S. haematobium* infections (OR = 7.6; $p = 0.008$) and (OR = 5.6; $p = 0.03$) where the PSAC had higher levels of TNF- α

and IL-6 respectively. **Conclusion:** Systemic inflammation and *S. haematobium* infections are negatively associated with cognitive function. We recommend the inclusion of PSAC into mass drug treatment programs.

A mini-review on ELISA-Based Diagnosis of Schistosomiasis.

Dos Santos M, Teixeira de Faria M, Oliveira da Silva J, Braga Gandra I, Julia Ribeiro A, Alves Silva K, Moreira Nogueira L, Martins Machado J, Maria da Silveira Mariano R, Maia Gonçalves AA, Ludolf F, Antonio Candia-Puma M, Chávez-Fumagalli MA, Campos-da-Paz M, Cordeiro Giunchetti R, Sobreira Galdino A.

04-05-2023

Curr Mol Med.

<https://pubmed.ncbi.nlm.nih.gov/37143281/>

Schistosoma haematobium urinary tract complications in African migrants attending primary care facilities in Paris, France: a retrospective cohort study (2004-2018).

Deniaud F, Vignier N, Raynal G, Boo N, Collignon A, Hennequin C.

02-05-2023

Infect Dis Now.

<https://pubmed.ncbi.nlm.nih.gov/37142230/>

Enhancing the antischistosomal activity of carvacryl acetate using nanoemulsion.

de Souza RL, Mengarda AC, Roquini DB, Melo CO, de Moraes MC, C Espírito-Santo MC, de Sousa DP, Moraes J, Oliveira EE.

04-05-2023

Nanomedicine (Lond).

<https://pubmed.ncbi.nlm.nih.gov/37140262/>

Aim: To formulate a carvacryl acetate nanoemulsion (CANE) and test its antischistosomal activity. **Materials & methods:** CANE was prepared and tested *in vitro* on *Schistosoma mansoni* adult worms and both human and animal cell lines. Next, CANE was administered orally to mice infected with either a prepatent infection or a patent infection of *S. mansoni*. **Results:** CANE was stable during 90 days of analysis. CANE showed *in vitro* anthelmintic activity, and no cytotoxic effects were observed. *In vivo*, CANE was more effective than the free compounds in reducing worm burden and egg production. Treatment with CANE was more effective for prepatent infections than praziquantel. **Conclusion:** CANE improves antiparasitic properties and may be a promising delivery system for schistosomiasis treatment.

Sentinel Surveillance of Schistosomiasis - China, 2021.

Guo S, Dang H, Li Y, Zhang L, Yang F, He J, Cao C, Xu J, Li S.

24-03-2023

China CDC Wkly.

<https://pubmed.ncbi.nlm.nih.gov/37138895/>

The Impact of Targeted Treatment and Mass Drug Administration Delivery Strategies on the Prevalence and Intensity of Schistosomiasis in School Aged Children in Africa: A Systematic Review.

Chanhanga N, Mindu T, Mogaka J, Chimbari M.

25-04-2023

Infect Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37138838/>

Schistosomiasis is a public health problem in more than 78 countries in the world. The disease is most prevalent among children than adults due to their high exposure to infectious water sources. Various interventions such as mass drug administration (MDA), snail control, safe water provision and health education have been implemented independently or jointly to control, reduce and ultimately eliminate Schistosomiasis. This scoping review focused on studies reporting the impact of different delivery strategies of targeted treatment and MDA on the prevalence and intensity of schistosomiasis infection in school aged children in Africa. The review focused on *Schistosoma haematobium* and *Schistosoma mansoni* species. A systematic search for eligible literature from peer-reviewed articles was done from Google Scholar, Medline, PubMed and EBSCO host databases. The search yielded twenty-seven peer-reviewed articles. All articles found reported a decrease in the prevalence of schistosomiasis infection. Five studies (18.5%) reported a prevalence change below 40%, eighteen studies (66.7%) reported a change between 40% and 80%, and four studies (14.8%) reported a change above 80%. The infection intensity post-treatment was varied: twenty-four studies reported a decrease, while two studies reported an increase. The review showed that the impact of targeted treatment on the prevalence and intensity of schistosomiasis depended on the frequency at which it was offered, complementary interventions, and its uptake by the target population. Targeted treatment can significantly control the infection burden, but cannot eliminate the disease. Constant MDA programs coupled with preventative and health promotional programs are required to reach the elimination stage.

Epididymal bilharzia simulating a testicular tumor: A case report.

Ido FAHA, Ouedraogo AS, Savadogo I, Hafing T, Ouattara S.

20-04-2023

IDCases.

<https://pubmed.ncbi.nlm.nih.gov/37131488/>

Bilharzia or schistosomiasis is a parasitic disease due to infestation by a hematophagous trematode of the genus *Schistosoma*. It is the second most frequent parasitic endemic in the world after malaria. The most frequent tissue infections are intestinal and genitourinary. Testicular localizations of schistosoma are very rare. When lesions become chronic, they present as non-specific masses, bilharziomas, posing enormous problems of differential diagnosis with other benign and malignant pathologies, which impacts management. We report a

case of epididymal schistosomiasis in a 37 years old patient simulating a malignant tumor. This case allowed us to review the diagnostic difficulties of this rare localization and the challenges of management.

Multi-strain compatibility polymorphism between a parasite and its snail host, a neglected vector of schistosomiasis in Africa.

Spaan JM, Pennance T, Laidemitt MR, Sims N, Roth J, Lam Y, Rawago F, Ogara G, Loker ES, Odiere MR, Steinauer ML.

31-03-2023

Curr Res Parasitol Vector Borne Dis.

<https://pubmed.ncbi.nlm.nih.gov/37128285/>

Schistosoma transmission: scaling-up competence from hosts to ecosystems.

Douchet P, Gourbal B, Loker ES, Rey O.

27-04-2023

Trends Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37120369/>

Biogenic silver nanoparticle exhibits schistosomicidal activity in vitro and reduces the parasitic burden in experimental schistosomiasis mansoni.

Detoni MB, Bortoleti BTDS, Tomiotto-Pellissier F, Concato VM, Gonçalves MD, Silva TF, Ortiz LSF, Gomilde AC, Rodrigues ACJ, de Matos RLN, Bracarense APFRL, de Matos AMRN, Simão ANC, Endo TH, Kobayashi RKT, Nakazato G, Costa IN, Conchon-Costa I, Oliveira FJA, Pavanelli WR, Miranda-Sapla MM.

27-04-2023

Microbes Infect.

<https://pubmed.ncbi.nlm.nih.gov/37120010/>

Schistosomiasis is a neglected tropical parasitic disease that affects millions of people, being the second most prevalent parasitic disease worldwide. The current treatment has limited effectiveness, drug-resistant strains, and is not effective in different stages of the disease. This study investigated the antischistosomal activity of biogenic silver nanoparticles (Bio-AgNp) against *Schistosoma mansoni*. Bio-AgNp presented direct schistosomicidal activity on newly transformed schistosomula causing plasma membrane permeabilization. In *S. mansoni* adult worms, reduced the viability and affected the motility, increasing oxidative stress parameters, and inducing plasma membrane permeabilization, loss of mitochondrial membrane potential, lipid bodies accumulation, and autophagic vacuoles formation. During the experimental schistosomiasis mansoni model, Bio AgNp restored body weight, reduced hepatosplenomegaly, and decrease the number of eggs and worms in feces and liver tissue. The treatment also ameliorates liver damage and reduces macrophage and neutrophil infiltrates. A reduction in count and size was evaluated in the granulomas, as well as a change to an exudative-proliferative phase, with a local increase of IFN- γ . Together our results showed that Bio-

AgNp is a promising therapeutic candidate for studies of new therapeutic strategies against schistosomiasis.

Correlation of Cytokines with Parasitic Infections, Undernutrition and Micronutrient Deficiency among Schoolchildren in Rural Tanzania: A Cross-Sectional Study.

Mrimi EC, Palmeirim MS, Minja EG, Long KZ, Keiser J.

15-04-2023

Nutrients.

<https://pubmed.ncbi.nlm.nih.gov/37111135/>

Malnutrition and parasitic infections are often interconnected in a vicious cycle. Malnutrition can lead to changes in immune response, which may affect cytokine concentrations and potentially increase susceptibility to infections. In turn, parasitic infections can exacerbate malnutrition by impairing nutrient absorption. This cross-sectional study aimed to explore this interplay. Schoolchildren aged 6-12 years living in rural Tanzania ($n = 120$) provided blood, stool and urine samples to determine the relationship between cytokine concentrations (interleukin 4 (IL-4), interferon gamma (IFN γ) and interleukin 17A (IL-17A)), parasitic infections, undernutrition and micronutrient deficiency adjusting for sex, age, inflammatory markers, socioeconomic status and school categories. All schoolchildren had a normal blood cell count. The concentration of IL-4 was significantly higher in schoolchildren diagnosed with stunting, *Schistosoma mansoni* infection, a high C-reactive protein concentration, nausea, poor housing and increasing age. The concentration of IFN γ was associated with *Plasmodium falciparum* and *Entamoeba histolytica*/*Entamoeba dispar*/*Entamoeba moshkovskii* infections, vitamin A deficiency, attending the most remote schools and low socioeconomic status. Our study confirms a potential relationship between cytokine concentrations and parasitic infections, malnutrition and low socioeconomic status. A better understanding of long-term effects of parasitic infections and malnutrition on the immune function could help in designing tailored and effective interventions.

Characteristics of Th9 cells in Schistosoma japonicum-infected C57BL/6 mouse mesenteric lymph node.

Qiu H, Wang R, Xing J, Li L, Gao Z, Li J, Fang C, Shi F, Mo F, Liu L, Zhao Y, Xie H, Zhao S, Huang J.

Juin-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37086898/>

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

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

02-05-2023

Biochemistry

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

Thioredoxin/glutathione reductase from *Schistosoma mansoni* (SmTGR) catalyzes the reduction of both oxidized thioredoxin and glutathione with electrons from reduced nicotinamide adenine dinucleotide phosphate (NADPH). SmTGR is a drug target for the treatment of Schistosomiasis, an infection caused by *Schistosoma* platyhelminths residing in the blood vessels of the host. *Schistosoma* spp. are reliant on TGR enzymes as they lack catalase and so use reduced thioredoxin and glutathione to regenerate peroxiredoxins consumed in the detoxification of reactive oxygen species. SmTGR is a flavin adenine dinucleotide (FAD)-dependent enzyme, and we have used the flavin as a spectrophotometric reporter to observe the movement of electrons within the enzyme. The data show that NADPH fractionally reduces the active site flavin with an observed rate constant estimated in this study to be $\sim 3000 \text{ s}^{-1}$. The flavin then reoxidizes by passing electrons at a similar rate to the proximal Cys159-Cys154 disulfide pair. The dissociation of NADP $^{+}$ occurs with a rate of $\sim 180 \text{ s}^{-1}$, which induces the deprotonation of Cys159, and this coincides with the accumulation of an intense FAD-thiolate charge transfer band. It is proposed that the electrons then pass to the Cys596-Cys597 disulfide pair of the associated subunit in the dimer with a net rate constant of $\sim 2 \text{ s}^{-1}$. (Note: Cys597 is Sec597 in wild-type (WT) SmTGR.) From this position, the electrons can be passed to oxidized thioredoxin or further into the protein to reduce the Cys28-Cys31 disulfide pair of the originating subunit of the dimer. From the Cys28-Cys31 center, electrons can then pass to oxidized glutathione that has a binding site directly adjacent.

Association between polymorphisms of IL4, IL13, IL10, STAT6 and IFNG genes, cytokines and immunoglobulin E levels with high burden of Schistosoma mansoni in children from schistosomiasis endemic areas of Cameroon.

Mewamba EM, Noyes H, Tiofack AAZ, Kamga RMN, Kamdem CN, Mengoue LET, Ofon E, Ngassam RIK, Nyangiri O, Bucheton B, Njiokou F, Womeni MH, Matovu E, MacLeod A, Simo G; TrypanoGEN+ research group of the H3Africa consortium.

Juillet-2023

Infect Genet Evol.

<https://pubmed.ncbi.nlm.nih.gov/36889485/>

Molecular detection of Schistosoma species in unusual snail hosts: a note of caution.

Pinto HA.

02-05-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36594275/>

The interaction between snails and species of *Schistosoma* results from an evolutionary process with an intrinsic host-parasite specificity to the snail genus. Faced with this fact, the recent molecular-based report on the potential infection of the thiarid *Melanoides tuberculata* with human schistosome should be cautiously interpreted. The

high sensibility of molecular tools can result in false positives, perhaps by amplifying DNA from an external (contaminant) or invasive stage of schistosome found in this non-permissive snail host. Thus, parasitological data are mandatory to extrapolate the importance of the finding for the epidemiology and control of schistosomiasis.

Schistosomiasis mansonii and hydrographical conditions in São Carlos, São Paulo, Brazil.

De Sousa Dos Santos S, Chachá SGF, da Rocha BC, Spiller KR, de Toledo CF, Aníbal FF, de Avó LRDS, Luporini RL, Cereda Junior A, Melanda EA.

02-05-2023

Trans R Soc Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36576498/>

Schistosoma haematobium infection in a returning Chinese worker.

Wang N, Li J, Zheng Y, Wang L.

Mai-2023

Asian J Surg.

<https://pubmed.ncbi.nlm.nih.gov/36517256/>

Trachome

Validation of immunoassays for the Chlamydia trachomatis antigen Pgp3 using a chimeric monoclonal antibody.

Goodhew B, Tang X, Goldstein J, Lee J, Martin D, Gwyn S.

04-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37142607/>

How well do coverage surveys and programmatically reported mass drug administration coverage match? Results from 214 mass drug administration campaigns in 15 countries, 2008-2017.

Zoerhoff KL, Mbabazi PS, Gass K, Kraemer J, Fuller BB, Blair L, Bougma R, Meite A, Negussu N, Gashaw B, Nash SD, Biritwum NK, Lemoine JF, Ulliyartha Pangaribuan H, Wijayanti E, Kollie K, Rasoamananjana CF, Juziwele L, Mkwanda S, Rimal P, Gnanadou I, Diop B, Dorkenoo AM, Bronzan R, Tukahebwa EM, Kabole F, Yevstigneyeva V, Bisanzio D, Courtney L, Koroma J, Endayishimye E, Reithinger R, Baker MC, Fleming FM.

Mai-2023

BMJ Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/37142297/>

Introduction: Delivering preventive chemotherapy through mass drug administration (MDA) is a central approach in controlling or eliminating several neglected tropical diseases (NTDs). Treatment coverage, a primary indicator of MDA performance, can be measured through routinely reported programmatic data or population-based coverage evaluation surveys. Reported coverage is

often the easiest and least expensive way to estimate coverage; however, it is prone to inaccuracies due to errors in data compilation and imprecise denominators, and in some cases measures treatments offered as opposed to treatments swallowed. **Objective:** Analyses presented here aimed to understand (1) how often coverage calculated using routinely reported data and survey data would lead programme managers to make the same programmatic decisions; (2) the magnitude and direction of the difference between these two estimates, and (3) whether there is meaningful variation by region, age group or country. **Methods:** We analysed and compared reported and surveyed treatment coverage data from 214 MDAs implemented between 2008 and 2017 in 15 countries in Africa, Asia and the Caribbean. Routinely reported treatment coverage was compiled using data reported by national NTD programmes to donors, either directly or via NTD implementing partners, following the implementation of a district-level MDA campaign; coverage was calculated by dividing the number of individuals treated by a population value, which is typically based on national census projections and occasionally community registers. Surveyed treatment coverage came from post-MDA community-based coverage evaluation surveys, which were conducted as per standardised WHO recommended methodology. **Results:** Coverage estimates using routine reporting and surveys gave the same result in terms of whether the minimum coverage threshold was reached in 72% of the MDAs surveyed in the Africa region and in 52% in the Asia region. The reported coverage value was within ± 10 percentage points of the surveyed coverage value in 58/124 of the surveyed MDAs in the Africa region and 19/77 in the Asia region. Concordance between routinely reported and surveyed coverage estimates was 64% for the total population and 72% for school-age children. The study data showed variation across countries in the number of surveys conducted as well as the frequency with which there was concordance between the two coverage estimates. **Conclusions:** Programme managers must grapple with making decisions based on imperfect information, balancing needs for accuracy with cost and available capacity. The study shows that for many of the MDAs surveyed, based on the concordance with respect to reaching the minimum coverage thresholds, the routinely reported data were accurate enough to make programmatic decisions. Where coverage surveys do show a need to improve accuracy of routinely reported results, NTD programme managers should use various tools and approaches to strengthen data quality in order to use data for decision-making to achieve NTD control and elimination goals.

Determinants of Trachomatous Inflammation-Follicular Among Children Aged 1 to 9 Years Old in a Rural Area of Gozamn District, Northwestern Ethiopia: A Matched Case-Control Study.

Adane B, Malede A, Sewunet B, Kumlachew L, Moges M, Woretaw L, Temesgen T, Bewket Y, Gete M, Yirdaw G, Ayele A, Adane M.

25-04-2023

Background: Approximately 1.9 million people worldwide are blind or visually impaired due to trachoma, and trachoma remains endemic in 44 countries. Amhara in Ethiopia has the highest burden of trachoma in the world. A key indicator of whether active trachoma requires public health intervention is the incidence of trachomatous inflammation-follicular in children aged 1 to 9 years. However, limited study has been conducted on the determinants in rural communities. This study therefore aimed to fill this gap by identifying determinants in the Gozamn district of northwestern Ethiopia. **Methods:** A community-based case-control study was carried out between March 15 and April 30, 2021. Five or more follicles on the epitaxial conjunctivae that are larger than 0.5 mm were considered a case. Controls were free of any sign of trachoma. A semi-structured questionnaire and an observational checklist were used to gather the data, and STATA version 14 was used for the analysis. Using a 95% confidence interval, both bivariable and multivariable conditional logistic regression was performed. **Results:** A total of 726 mothers/caregivers participated in this study, with a participation rate of 98.4%. Children from poor families (mAOR = 4.68; CI: 2.80-6.21), households where the water source is far from home (>30 minutes) (mAOR = 4.91; CI: 1.37-12.56), mean daily water consumption (<20 l/c/d) (mAOR = 4.42; CI: 1.71-11.39), face washing frequency less than once a day (mAOR = 10.64; CI: 2.58-18.84), cloth washing frequency once a month or less (mAOR = 9.18; CI: 2.20-18.62), and mothers or caregivers with poor knowledge of active trachoma (mAOR = 3.88; CI: 1.47-10.22) were determinants of trachomatous inflammation-follicular. **Conclusions:** We conclude that infrequent faces and clothes washing; unavailability of water, children in poor families, and poor knowledge of mothers/caregivers were risk factors. Health education initiatives about active trachoma, its prevention, and control methods focusing on personal hygiene are so required.

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

Pneumothorax with Eosinophilia is an Important Diagnostic Clue for Distinguishing Paragonimiasis from Chronic Eosinophilic Pneumonia: A Case Report.

Sakakura S, Yamaguchi F, Abe T, Cho H, Shimizu S, Mase A, Shikama Y, Maruyama H.

25-04-2023

Infect Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/37138842/>

The *Paragonimus westermani* infection is a parasitic foodborne infection that induces systemic symptoms with eosinophilia in humans. Here, we described pneumothorax in addition to pulmonary opacities with eosinophilia in a man with a positive *P. westermani* serology. He was misdiagnosed with chronic eosinophilic pneumonia (CEP) during the initial phase. Paragonimiasis can share similar clinical findings with CEP in cases where the worm is confined to the lungs. The findings of the current study suggest that paragonimiasis and CEP can be distinguished from each other by the presence of various symptoms. Notably, eosinophilia with pneumothorax should be an important diagnostic factor for paragonimiasis.

Current status and progress in the omics of *Clonorchis sinensis*.

Wang N, Zhang Z, Huang L, Chen T, Yu X, Huang Y.

29-04-2023

Mol Biochem Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/37127222/>

Characterization of Monoamine Oxidase-A in tropical liver fluke, *Fasciola gigantica*.

Beg MA, Rehman A, Rehman L, Ullah R, Farhat F, Wasim S, Abidi SMA.

27-04-2023

PLoS One.

<https://pubmed.ncbi.nlm.nih.gov/37104309/>

Fasciola gigantica, responsible for the zoonotic disease fasciolosis, pose a great threat to the livestock and human health worldwide. The triclabendazole (TCBZ) has been used for decades as a broad spectrum anthelmintic to control this perilous disease but the emergence of resistance in flukes against TCBZ has prompted researchers across the world to explore for new drugs and antigenic targets. World Health Organization has strongly recommended the utilization of neurobiologically significant biomolecules as new drug/antigenic targets because of their significant role in the physiology of parasites. Monoamine Oxidase (MAO) is an important neurobiological enzyme which catabolizes aminergic neurotransmitters thus preventing prolonged excitation of neurons and in non-neuronal cells it prevents cellular toxicity due to accumulation of toxic monoamines. Owing to the important role of MAO in the survival and perpetuation of parasites, multipronged approaches were undertaken for the characterization of MAO-A in *F. gigantica*. The activity of MAO was found to be 1.5 times higher in the mitochondrial samples than the whole homogenate samples. The adult worms of the *F. gigantica* appeared to possess both the isoforms of MAO i.e., MAO-A and MAO-B. The zymographic studies revealed strong enzyme activity in its native state as assessed through prominent dark bands at 250KDa in the zymogram. The enzyme was also found to be highly immunogenic as revealed by high antibody titer at 1:6400 dilution. The immunogenicity of MAO-A enzyme was further established in the Western Blots in which a strong band of 50KDa was distinctly evident. Despite ubiquitous presence

of MAO in *F. gigantica* some regions like tegumental surface and intestinal caecae displayed strong immunofluorescence as compared to other regions. The detection of MAO-A in the *F. gigantica* samples in Dot-Blot assay indicate a great potential of this molecule for the immunodiagnosics of fasciolosis, particularly in the field conditions. The enzyme activity was sensitive to the specific inhibitor clorgyline in a concentration dependant manner, particularly in the late incubation period. The zymographic results also exhibited similar trend. The strong intensity of spots in Dot-blots indicate high immunogenicity of the MAO protein. The intensity of bands/spots in the samples of worms treated with clorgyline also declined, clearly indicating that the tropical liver fluke possesses prominent MAO-A activity.

Fasciola hepatica juveniles interact with the host fibrinolytic system as a potential early-stage invasion mechanism.

Serrat J, Becerro-Recio D, Torres-Valle M, Simón F, Valero MA, Bargues MD, Mas-Coma S, Siles-Lucas M, González-Miguel J.

21-04-2023

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/37083884/>

Background: The trematode *Fasciola hepatica* is the most widespread causative agent of fasciolosis, a parasitic disease that mainly affects humans and ruminants worldwide. During *F. hepatica* infection, newly excysted juveniles (FhNEJ) emerge in the duodenum of the mammalian host and migrate towards their definitive location, the intra-hepatic biliary ducts. Understanding how *F. hepatica* traverses the intestinal wall and migrates towards the liver is pivotal for the development of more successful strategies against fasciolosis. The central enzyme of the mammalian fibrinolytic system is plasmin, a serine protease whose functions are exploited by a number of parasite species owing to its broad spectrum of substrates, including components of tissue extracellular matrices. The aim of the present work is to understand whether FhNEJ co-opt the functions of their host fibrinolytic system as a mechanism to facilitate trans-intestinal migration. **Methodology/principal findings:** A tegument-enriched antigenic extract of FhNEJ (FhNEJ-Teg) was obtained in vitro, and its capability to bind the zymogen plasminogen (PLG) and enhance its conversion to the active protease, plasmin, were analyzed by a combination of enzyme-linked immunosorbent, chromogenic and immunofluorescence assays. Additionally, PLG-binding proteins in FhNEJ-Teg were identified by bidimensional electrophoresis coupled to mass spectrometry analysis, and the interactions were validated using FhNEJ recombinant proteins. **Conclusions/significance:** Our results show that FhNEJ-Teg contains proteins that bind PLG and stimulate its activation to plasmin, which could facilitate the traversal of the intestinal wall by FhNEJ and contribute to the successful establishment of the parasite within its mammalian host. Altogether, our findings contribute to a better understanding of host-parasite relationships during early fasciolosis and may be exploited from a pharmacological and/or immunological perspective for the development of

treatment and control strategies against this global disease.

Trypanosomes (trypanosomiasis et maladie de Chagas)

Severe Chagas disease in Ecuador: a countrywide geodemographic epidemiological analysis from 2011 to 2021.

Vásconez-González J, Izquierdo-Condoy JS, Fernandez-Naranjo R, Gamez-Rivera E, Tello-De-la-Torre A, Guerrero-Castillo GS, Ruiz-Sosa C, Ortiz-Prado E.

18-04-2023

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/37143984/>

Background: Chagas disease is a neglected and often forgotten tropical disease caused by the *Trypanosoma cruzi*. This parasite can be transmitted through the direct contact of human skin with feces and urine of the triatomine insect. According to the World Health Organization (WHO), an estimated 6-7 million people are infected worldwide, killing at least 14,000 every year. The disease has been reported in 20 of the 24 provinces of Ecuador, with El Oro, Guayas, and Loja being the most affected. **Methodology:** We analyzed the morbidity and mortality rates of severe Chagas disease in Ecuador on a nationwide, population-based level. Hospitalization cases and deaths were also examined based on altitude, including low (< 2,500 m) and high (> 2,500 m) altitudes, according to the International Society. Data was retrieved from the National Institute of Statistics and Census hospital admissions and in-hospital mortality databases from 2011 to 2021. **Results:** A total of 118 patients have been hospitalized in Ecuador since 2011 due to Chagas disease. The overall in-hospital mortality rate was 69.4% ($N = 82$). Men have a higher incidence rate (4.8/1,000,000) than women, although women have a significantly higher mortality rate than men (6.9/1,000,000). **Conclusion:** Chagas disease is a severe parasitic condition that primarily affects rural and poorer areas of Ecuador. Men are more likely to be infected due to differences in work and sociocultural activities. Using average elevation data, we conducted a geodemographic analysis to assess incidence rates by altitude. Our findings indicate that the disease is more common at low and moderate altitudes, but recent increases in cases at higher altitudes suggest that environmental changes, such as global warming, could be driving the proliferation of disease-carrying vectors in previously unaffected areas.

Microbiome Alterations Driven by Trypanosoma cruzi Infection in Two Disjunctive Murine Models.

Castañeda S, Muñoz M, Hotez PJ, Bottazzi ME, Paniz-Mondolfi AE, Jones KM, Mejia R, Poveda C, Ramírez JD.

04-05-2023

Microbiol Spectr.

<https://pubmed.ncbi.nlm.nih.gov/37140369/>

Biochemical and genotyping analyses of camels (*Camelus dromedaries*) trypanosomiasis in North Africa.

Darwish AM, Sharaf A, Gaouar SBS, Ali NI, El-Aziz THA, Abushady AM, Kaouadji Z, Othman OE, Obornik M.

03-05-2023

Sci Rep.

<https://pubmed.ncbi.nlm.nih.gov/37137920/>

Synthesis of 4-(4-chlorophenyl)thiazole compounds: in silico and in vitro evaluations as leishmanicidal and trypanocidal agents.

Cruz Filho IJD, Oliveira JF, Santos ACS, Pereira VRA, Lima MCA.

01-05-2023

An Acad Bras Cienc.

<https://pubmed.ncbi.nlm.nih.gov/37132749/>

Neglected tropical diseases are a diverse group of communicable pathologies that mainly prevail in tropical and subtropical regions. Thus, the objective of this work was to evaluate the biological potential of eight 4-(4-chlorophenyl)thiazole compounds. Tests were carried out in silico to evaluate the pharmacokinetic properties, the antioxidant, cytotoxic activities in animal cells and antiparasitic activities were evaluated against the different forms of *Leishmania amazonensis* and *Trypanosoma cruzi* in vitro. The in silico study showed that the evaluated compounds showed good oral availability. In a preliminary in vitro study, the compounds showed moderate to low antioxidant activity. Cytotoxicity assays show that the compounds showed moderate to low toxicity. In relation to leishmanicidal activity, the compounds presented IC50 values that ranged from 19.86 to 200 µM for the promastigote form, while for the amastigote forms, IC50 ranged from 101 to more than 200 µM. The compounds showed better results against the forms of *T. cruzi* with IC50 ranging from 1.67 to 100 µM for the trypomastigote form and 1.96 to values greater than 200 µM for the amastigote form. This study showed that thiazole compounds can be used as future antiparasitic agents.

Multiple domains of the integral KREPA3 protein are critical for the structure and precise functions of RNA Editing Catalytic Complexes in *Trypanosoma brucei*.

Davidge B, McDermott SM, Carnes J, Lewis I, Tracy M, Stuart KD.

19-04-2023

bioRxiv.

<https://pubmed.ncbi.nlm.nih.gov/37131796/>

The gRNA directed U-insertion and deletion editing of mitochondrial mRNAs that is essential in different life cycle stages for the protozoan parasite *Trypanosoma brucei* is performed by three similar multi-protein catalytic complexes (CCs) that contain the requisite enzymes. These CCs also contain a common set of eight proteins that have no apparent direct catalytic function, including six that have an OB-fold domain. We show here that one of these

OB-fold proteins, KREPA3 (A3), has structural homology to other editing proteins, is essential for editing and is multifunctional. We investigated A3 function by analyzing the effects of single amino acid loss of function mutations most of which were identified by screening bloodstream form (BF) parasites for loss of growth following random mutagenesis. Mutations in the ZFs, an intrinsically disordered region (IDR) and several within or near the C-terminal OB-fold domain variably impacted CC structural integrity and editing. Some mutations resulted in almost complete loss of CCs and its proteins and editing whereas others retained CCs but had aberrant editing. All but a mutation which is near the OB-fold affected growth and editing in BF but not procyclic form (PF) parasites. These data indicate that multiple positions within A3 have essential functions that contribute to the structural integrity of CCs, the precision of editing and the developmental differences in editing between BF and PF stages.

Prevalence of *Trypanosoma lainsoni* and its effects of parasitism on the health of non-volant small mammals from the Brazilian Cerrado.

de Oliveira MM, Ferrando CPR, Gómez-Hernández C, de Oliveira KR, Araújo IAC, Ribeiro PVA, Mineo TWP, Leiner NO, Mineo JR, da Silva SM.

02-05-2023

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/37129625/>

Hematologic parameters and the effect of hemoparasites of wild anurans in Northern Sinaloa, Mexico.

Isaak Delgado AB, Zavala-Norzagaray AA, Espinoza-Romo BA, Ortega-Anaya JG, Ley-Quirón CP, Aguirre A, Rendón-Franco E.

01-05-2023

Vet Clin Pathol.

<https://pubmed.ncbi.nlm.nih.gov/37127551/>

Background: Few hematologic profiles for free-ranging amphibians are available. Hematologic evaluation is a useful tool for determining the health of amphibian populations and providing further knowledge for conservation actions. **Objectives:** Hematologic variables and the presence and effect of hemoparasites in anuran species were evaluated in Northern Sinaloa, Mexico. **Methods:** Blood samples were collected from wild anurans of eight species to perform blood cell counts, leukocyte differential counts, and serum protein concentrations using manual methods and refractometry. In addition, morphologic identification and quantification of the hemoparasites were performed on blood smears. **Results:** Differences were observed by sex, age, and season for the hematologic values of *Incilius alvarius* (n = 23), *Incilius mazatlanensis* (n = 46), *Rhinella horribilis* (n = 64), *Leptodactylus melanonotus* (n = 46), *Lithobates forreri* (n = 135), *Lithobates catesbeianus* (n = 20), *Smilisca fodiens* (n = 42), and *Scaphiopus couchii* (n = 7). Intra- and extra-erythrocytic hemoparasites were found in 56.2% of amphibian hosts; the hemoparasite infection of R.

horribilis and *L. melanonotus* was higher in the dry season, showing increases in erythroplastids and monocytes. For *L. forreri*, males were more infected than females, and increases in leukocytes were associated with infections of different types of hemoparasites species. **Conclusions:** Hematologic values, hemoparasite prevalence, and the response to hemoparasite infection vary among amphibian species, sex, and age, as well as on season and hemoparasite type. This highlights the importance of hematologic evaluations in wild amphibian populations to determine the subclinical effects of hemoparasite infections.

Type-I like metalloproteinase in the venom of the West African saw-scaled carpet viper (*Echis ocellatus*) has anti-trypanosomal activity against African trypanosomes.

Ilu A, Chia MA, Cataldi TR, Labate CA, Ebiloma GU, Yusuf PO, Shuaibu MN, Balogun EO.

29-04-2023

Toxicon.

<https://pubmed.ncbi.nlm.nih.gov/37127124/>

New antiprotozoal sesquiterpene derivatives from *Dorema glabrum* Fisch & C.A.Mey.

Delnavazi MR, Ebrahimi SN, Hadjiakhoondi A, Yassa N.

28-04-2023

Fitoterapia.

<https://pubmed.ncbi.nlm.nih.gov/37121409/>

Marginal risk of domestic vector-borne *Trypanosoma cruzi* transmission after improved vector control of *Triatoma infestans* across a rural-to-urban gradient in the Argentine Chaco.

Alvedro A, Gaspé MS, Enriquez GF, Macchiaverna NP, Gürtler RE, Cardinal MV.

28-04-2023

Acta Trop.

<https://pubmed.ncbi.nlm.nih.gov/37119837/>

The interruption of domestic vector-borne transmission of *Trypanosoma cruzi* in the Americas remains one of the main goals of the World Health Organization 2021-2030 road map for neglected tropical diseases. We implemented a longitudinal intervention program over 2015-2022 to suppress (peri)domestic *Triatoma infestans* in the municipality of Avia Terai, Chaco Province, Argentina and found that house infestation (3851 houses inspected) and triatomine abundance decreased over the first 2 years post-intervention (YPI), and remained stable thereafter associated to moderate pyrethroid resistant foci. Here we assessed selected components of transmission risk after interventions across the rural-to-urban gradient. We used multistage random sampling to select a municipality-wide sample of *T. infestans*. We examined 356 insects collected in 87 houses for *T. cruzi* infection using kDNA-PCR and identified their bloodmeal sources using an indirect ELISA. The overall prevalence of *T. cruzi* infection post-intervention was 1.7% (95% CI 0.7-3.6). Few houses (5.7%)

(95% CI 2.5-12.8) harbored infected triatomines across the gradient. Infected triatomines were found in 5 peri-urban or rural dwellings over 1-4 years post-intervention. No infected insect was found in the urban area. The human blood index decreased from 66.2 at baseline to 42.8 at 1YPI and then increased to 92.9 at 4-5 YPI in the few infested domiciles detected. The percentage of houses with human-fed bugs displayed a similar temporal trend. Our results indicate marginal risks of domestic vector-borne transmission across the district after implementation of the intervention program. Ensuring sustainable vector surveillance coupled with human etiological diagnosis and treatment in hiperendemic areas like the Gran Chaco region, is urgently needed.

Amplicon sequencing reveals complex infection in infants congenitally infected with *Trypanosoma cruzi* and informs the dynamics of parasite transmission.

Hakim JMC, Waltemann A, Tinajeros F, Kharabara O, Málaga Machaca E, Calderon M, Mendiña MDC, Wang J, Rueda D, Zimic M, Verástegui M, Juliano JJ, Gilman RH, Mugnier MR, Bowman NM; Chagas working group.

29-04-2023

J Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/37119236/>

Congenital transmission of *Trypanosoma cruzi* is an important source of new Chagas infections worldwide. The mechanisms of congenital transmission remain poorly understood, but there is evidence that parasite factors are involved. Investigating changes in parasite strain diversity during transmission could provide insight into the parasite factors that influence the process. Here we use amplicon sequencing of a single copy *T. cruzi* gene to evaluate the diversity of infection in clinical samples from Chagas positive mothers and their infected infants. Several infants and mothers were infected with multiple parasite strains, mostly of the same TcV lineage, and parasite strain diversity was higher in infants than mothers. Two parasite haplotypes were detected exclusively in infant samples, while one haplotype was never found in infants. Together, these data suggest multiple parasites initiate a congenital infection and that parasite factors influence the probability of vertical transmission.

Sulfonamide derived from anacardic acid as potential antichagasic: a theoretical approach based on molecular docking, molecular dynamics, and density functional theory calculations.

da Silva LP, Almeida-Neto FWQ, Bezerra LL, Silva J, Monteiro NKV, Marinho MM, Dos Santos HS, Teixeira AMR, Marinho ES, de Lima-Neto P.

29-04-2023

J Mol Model.

<https://pubmed.ncbi.nlm.nih.gov/37117952/>

Ulcère de Buruli

Floristic Diversity as an Indicator in Low and High Endemic Buruli Ulcer Areas in Côte d'Ivoire.

Ehouman E, Soro D, Ouattara DN, Cissé CB, Bakayoko A, Dosso M, Zo-Bi IC, Kouassi AF, Koné MW.

2023

Int J Environ Res.

<https://pubmed.ncbi.nlm.nih.gov/37128551/>

Mycobacterium ulcerans is an environmental bacterium responsible for Buruli ulcer. This disease has a high frequency index in humid tropical regions, with a high incidence in Sub-Saharan Africa. The ecology and mode of transmission of this disease is not well established. Based on dilution effect hypothesis, acting as lowering disease transmission due to greater biodiversity, floristic inventory was carried out in the Health Districts of Daloa and Bouaké in Côte d'Ivoire. In each district, high and low endemic sites were investigated. A total of 169 plant species were inventoried for both low and high endemicity of Buruli ulcer sites in the districts. The Indval index revealed that 13 plant species were good indicators for Buruli ulcer highly endemic areas. The plants which correlate with high endemicity area were *Leersia hexandra*, *Panicum laxum*, *Mimosa pudica*, *Paspalum distichum*, *Persicaria senegalensis*, *Calopogonium mucunoides*, *Echinochloa colona*, *Ipomoea sagittata*, and *Eichhornia crassipes*. For low endemic sites, a strong relationship was recorded for 37 plants. The indices revealed low similarity between high and low endemicity sites. Low endemicity sites expressed the highest plant species diversity. These results suggest the hypothesis that floristic richness is more important in sites of low endemicity than in those of high endemicity. Moreover, we observed a co-occurrence of some plant species and Buruli ulcer endemicity. This finding may lead to the fact that it is important to care about the biodiversity to prevent outbreak of Buruli ulcer cases.

Statistical modeling based on structured surveys of Australian native possum excreta harboring *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.

14-04-2023

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 modeling 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 2,282 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 the efficient targeting of public health responses to stop BU. **Funding:** This research was supported by the National Health and Medical Research Council of Australia and the Victorian Government Department of Health (GNT1152807 and GNT1196396).