Réseau MTN Francophone

Veille scientifique
Maladies tropicales négligées

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04 au 10 septembre 2023

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Cysticercose

Revisiting extracranial cysticercosis: A rare case series of mycoparasitism affecting the cervicofacial region from an endemic zone.

Singh S, Jaiswal V, Tiwari S, Yadav S.
Mai-Auût 2023
Natl J Maxillofac Surg.
https://pubmed.ncbi.nlm.nih.gov/37661975/

Evaluation of a point-of-care test for the diagnosis of Taenia solium neurocysticercosis in rural southern Tanzania: a diagnostic accuracy study.

Stelzle D, Makasi CE, Schmidt V, Van Damme I, Trevisan C, Ruether C, Fleury A, Noh J, Handali S, Dorny P, Magnussen P, Zulu G, Mwape KE, Bottieau E, Gabriël S, Ngowi BJ, Winkler AS; SOLID collaborators.
31-08-2023
Lancet Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37660709/

Background: Neurocysticercosis is a common cause of epilepsy in Taenia solium-endemic areas in sub-Saharan Africa but is often undiagnosed because of an absence of affordable diagnostic tools. This study evaluated the diagnostic accuracy of a T solium cysticercosis antibody-detecting lateral-flow point-of-care assay (TS POC test) for the neuroimaging-based diagnosis of neurocysticercosis. Methods: Patients with epileptic seizures or severe progressive headache were recruited consecutively from three hospitals in southern Tanzania. All patients were tested with the TS POC test. All patients positive for cysticercosis on the TS POC test and every tenth patient who was negative for cysticercosis received a brain CT examination and underwent reference testing for T solium cysticercosis (ie, rT24H-EITB, LLGP-EITB, and antigen ELISA). The primary outcome of the study was the sensitivity of the TS POC test for the diagnosis of neurocysticercosis. Findings: Of the 601 recruited participants, 102 (17%) tested positive for cysticercosis with the TS POC test. Overall, 48 (62%) of the 77 patients positive for cysticercosis and five (17%) of the 29 patients negative for cysticercosis on the TS POC test had CT-confirmed neurocysticercosis. The TS POC test yielded a sensitivity of 49% (uncertainty interval [UI] 41-58) for neurocysticercosis. Sensitivity was similar to that of the rT24H-EITB (44%, UI 37-51) and the antigen ELISA (50%, 43-56). For the subset of neurocysticercosis cases with at least one active (ie, vesicular) lesion, sensitivity was above 98% for the TS POC test, the rT24H-ETIB, and the antigen ELISA. Interpretation: The TS POC test showed promising results for the diagnosis of neurocysticercosis in patients with vesicular lesions, which need to be confirmed in a larger study. This test could be considered to support policies on screening patients with suspected neurocysticercosis in clinical settings, which would allow appropriate referral for neuroimaging and early treatment. Funding: German Federal Ministry of Education and Research and the European & Developing Countries Clinical Trials Partnership.

Knowledge, attitudes and practices regarding porcine cysticercosis control among smallholder pig farmers in Kongwa and Songwe districts, Tanzania: A cross-sectional study.

Wilson C, Nonga HE, Mdegela RH, Churi AJ, Mkupasi EM, Winkler AS, Ngowi HA.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652629/

Taenia solium taeniasis/cysticercosis (TSTC) is a parasitic zoonotic disease that is endemic in several developing countries, causing serious public health and economic impacts. A cross-sectional study was conducted to assess knowledge, attitudes and practices (KAP) related to porcine cysticercosis (PCC) transmission, prevention and control among smallholder pig farmers in Kongwa and Songwe Districts in Tanzania. A semi-structured questionnaire was administered to 692 smallholder pig farmers from randomly selected households. STATA software version 17 was used to analyse quantitative data, summarize farmers' KAP about PCC and calculate performance scores. Nearly half (42%) of the respondents had little knowledge regarding PCC, only 17% of the respondents had good practices towards prevention/control of PCC and 72% had a positive attitude towards PCC- prevention/control measures. The majority (73%) of smallholder pig farmers admitted deworming their pigs regularly, whereas 76% reported deworming themselves and their family members regularly. Albendazole and ivermectin are the most commonly used medications for deworming people and pigs, respectively. According to the findings, the majority of smallholder pig farmers in Kongwa and Songwe Districts showed a good attitude towards PCC prevention/control measures but had limited knowledge of the PCC life cycle and control. In addition, only one in five farmers was engaged in good practices. The findings revealed further that farmers are engaged in risky behaviours that aid the spread and perpetuation of the T. solium parasite in the study area. It is recommended that farmers should be given proper health education on the T. solium transmission cycle and preventive/control practices to limit PCC transmission.

Dengue, chikungunya et maladie à virus Zika

Analysis of the dynamics of a vector-borne infection with the effect of imperfect vaccination from a fractional perspective.

Tang TQ, Jan R, Khurshaid A, Shah Z, Vrinceanu N, Racheriu M.
01-09-2023
Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37658134/

The burden of vector-borne infections is significant, particularly in low- and middle-income countries where vector populations are high and healthcare infrastructure may be inadequate. Further, studies are required to

investigate the key factors of vector-borne infections to provide effective control measure. This study focuses on formulating a mathematical framework to characterize the spread of chikungunya infection in the presence of vaccines and treatments. The research is primarily dedicated to descriptive study and comprehension of dynamic behaviour of chikungunya dynamics. We use Banach's and Schaefer's fixed point theorems to investigate the existence and uniqueness of the suggested chikungunya framework resolution. Additionally, we confirm the Ulam-Hyers stability of the chikungunya system. To assess the impact of various parameters on the dynamics of chikungunya, we examine solution pathways using the Laplace-Adomian method of disintegration. Specifically, to visualise the impacts of fractional order, vaccination, bite rate and treatment computer algorithms are employed on the infection level of chikungunya. Our research identified the framework's essential input settings for managing chikungunya infection. Notably, the intensity of chikungunya infection can be reduced by lowering mosquito bite rates in the affected area. On the other hand, vaccination, memory index or fractional order, and treatment could be used as efficient controlling variables.

Outcomes up to age 36 months after congenital Zika virus infection-U.S. states.

Neelam V, Woodworth KR, Chang DJ, Roth NM, Reynolds MR, Akosa A, Carr CP, Anderson KN, Mulkey SB, DeBiasi RL, Biddle C, Lee EH, Elmore AL, Scotland SJ, Sowunmi S, Longcore ND, Ahmed M, Langlois PH, Khuwaja S, Browne SE, Lind L, Shim K, Gosciminski M, Blumenfeld R, Khuntia S, Halai UA, Locklear A, Chan M, Willabus T, Tonzel J, Marzec NS, Barreto NA, Sanchez C, Fornoff J, Hale S, Nance A, Iguchi L, Adibhatla SN, Potts E, Schiffman E, Raman D, McDonald MF, Stricklin B, Ludwig E, Denson L, Contreras D, Romitti PA, Ferrell E, Marx M, Signs K, Cook A, Leedom VO, Beauregard S, Orantes LC, Cronquist L, Roush L, Godfred-Cato S, Gilboa SM, Meaney-Delman D, Honein MA, Moore CA, Tong VT.
01-09-2023
Pediatr Res.
https://pubmed.ncbi.nlm.nih.gov/37658124/

Background: To characterize neurodevelopmental abnormalities in children up to 36 months of age with congenital Zika virus exposure. Methods: From the U.S. Zika Pregnancy and Infant Registry, a national surveillance system to monitor pregnancies with laboratory evidence of Zika virus infection, pregnancy outcomes and presence of Zika associated birth defects (ZBD) were reported among infants with available information. Neurologic sequelae and developmental delay were reported among children with ≥1 follow-up exam after 14 days of age or with ≥1 visit with development reported, respectively. Results: Among 2248 infants, 10.1% were born preterm, and 10.5% were small-for-gestational age. Overall, 122 (5.4%) had any ZBD; 91.8% of infants had brain abnormalities or microcephaly, 23.0% had eye abnormalities, and 14.8% had both. Of 1881 children ≥1 follow-up exam reported, neurologic sequelae were more common among children with ZBD (44.6%) vs. without ZBD (1.5%). Of children with ≥1 visit with development reported, 46.8% (51/109) of children with ZBD and 7.4% (129/1739) of children without ZBD had confirmed or possible developmental delay. Conclusion: Understanding the prevalence of developmental delays and healthcare needs of children with congenital Zika virus exposure can inform health systems and planning to ensure services are available for affected families. Impact: We characterize pregnancy and infant outcomes and describe neurodevelopmental abnormalities up to 36 months of age by presence of Zika associated birth defects (ZBD). Neurologic sequelae and developmental delays were common among children with ZBD. Children with ZBD had increased frequency of neurologic sequelae and developmental delay compared to children without ZBD. Longitudinal follow-up of infants with Zika virus exposure in utero is important to characterize neurodevelopmental delay not apparent in early infancy, but logistically challenging in surveillance models.

Direct mosquito feedings on dengue-2 virus-infected people reveal dynamics of human infectiousness.

Lambrechts L, Reiner RC Jr, Briesemeister MV, Barrera P, Long KC, Elson WH, Vizcarra A, Astete H, Bazan I, Siles C, Vilcarromero S, Leguia M, Kawiecki AB, Perkins TA, Lloyd AL, Waller LA, Kitron U, Jenkins SA, Hontz RD, Campbell WR, Carrington LB, Simmons CP, Ampuero JS, Vasquez G, Elder JP, Paz-Soldan VA, Vazquez-Prokopec GM, Rothman AL, Barker CM, Scott TW, Morrison AC.
01-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37656759/

LGP2 directly interacts with flavivirus NS5 RNA-dependent RNA polymerase and downregulates its pre-elongation activities.

Tan Z, Wu J, Huang L, Wang T, Zheng Z, Zhang J, Ke X, Zhang Y, Liu Y, Wang H, Tao J, Gong P.
01-09-2023
PLoS Pathog.
https://pubmed.ncbi.nlm.nih.gov/37656756/

LGP2 is a RIG-I-like receptor (RLR) known to bind and recognize the intermediate double-stranded RNA (dsRNA) during virus infection and to induce type-I interferon (IFN)-related antiviral innate immune responses. Here, we find that LGP2 inhibits Zika virus (ZIKV) and tick-borne encephalitis virus (TBEV) replication independent of IFN induction. Co-immunoprecipitation (Co-IP) and confocal immunofluorescence data suggest that LGP2 likely colocalizes with the replication complex (RC) of ZIKV by interacting with viral RNA-dependent RNA polymerase (RdRP) NS5. We further verify that the regulatory domain (RD) of LGP2 directly interacts with RdRP of NS5 by biolayer interferometry assay. Data from in vitro RdRP assays indicate that LGP2 may inhibit polymerase activities of NS5 at pre-elongation but not elongation stages, while an RNA-binding-defective LGP2 mutant can still inhibit RdRP activities and virus replication. Taken together, our work suggests that LGP2 can inhibit flavivirus replication

through direct interaction with NS5 protein and downregulates its polymerase pre-elongation activities, demonstrating a distinct role of LGP2 beyond its function in innate immune responses.

Correction to: Persistence of Immunogenicity of a Purified Inactivated Zika Virus Vaccine Candidate in Healthy Adults: 2 Years of Follow-up Compared With Natural Infection.

[No authors listed]
01-09-2023
J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37656480/

Factors that impact on recruitment to vaccine trials in the context of a pandemic or epidemic: a qualitative evidence synthesis.

Meskell P, Biesty LM, Dowling M, Roche K, Meehan E, Glenton C, Devane D, Shepperd S, Booth A, Cox R, Chan XHS, Houghton C.
01-09-2023
Cochrane Database Syst Rev.
https://pubmed.ncbi.nlm.nih.gov/37655964/

Background: The World Health Organization declared the COVID-19 pandemic on 11 March 2020. Vaccine development and deployment were swiftly prioritised as a method to manage and control disease spread. The development of an effective vaccine relies on people's participation in randomised trials. Recruitment to vaccine trials is particularly challenging as it involves healthy volunteers who may have concerns around the potential risks and benefits associated with rapidly developed vaccines. Objectives: To explore the factors that influence a person's decision to participate in a vaccine trial in the context of a pandemic or epidemic. Search methods: We used standard, extensive Cochrane search methods. The latest search date was June 2021. Selection criteria: We included qualitative studies and mixed-methods studies with an identifiable qualitative component. We included studies that explored the perspectives of adults aged 18 years or older who were invited to take part in vaccine trials in the context of a pandemic or epidemic. Data collection and analysis: We assessed the title, abstracts and full texts identified by the search. We used a sampling frame to identify data-rich studies that represented a range of diseases and geographical spread. We used QSR NVivo to manage extracted data. We assessed methodological limitations using an adapted version of the Critical Skills Appraisal Programme (CASP) tool for qualitative studies. We used the 'best-fit framework approach' to analyse and synthesise the evidence from our included studies. We then used the Confidence in the Evidence from Reviews of Qualitative research (GRADE-CERQual) assessment to assess our confidence in each finding and develop implications for practice. Main results: We included 34 studies in our review. Most studies related to HIV vaccine trials. The other studies related to Ebola virus, tuberculosis, Zika virus and COVID-19. We developed 20 key findings, under three broad themes (with seven subthemes), that described the factors that people consider when deciding whether to take part in a vaccine trial for a pandemic or epidemic disease. Our GRADE-CERQual confidence was high in nine of the key findings, moderate in 10 key findings and low in one key finding. The main reason for downgrading review findings were concerns regarding the relevance and adequacy of the underlying data. As a result of the over-representation of HIV studies, our GRADE-CERQual assessment of some findings was downgraded in terms of relevance because the views described may not reflect those of people regarding vaccine trials for other pandemic or epidemic diseases. Adequacy relates to the degree of richness and quantity of data supporting a review finding. Moderate concerns about adequacy resulted in a downgrading of some review findings. Some factors were considered to be under the control of the trial team. These included how trial information was communicated and the inclusion of people in the community to help with trial information dissemination. Aspects of trial design were also considered under control of the trial team and included convenience of participation, provision of financial incentives and access to additional support services for those taking part in the trial. Other factors influencing people's decision to take part could be personal, from family, friends or wider society. From a personal perceptive, people had concerns about vaccine side effects, vaccine efficacy and possible impact on their daily lives (carer responsibilities, work, etc.). People were also influenced by their families, and the impact participation may have on relationships. The fear of stigma from society influenced the decision to take part. Also, from a societal perspective, the level of trust in governments' involvement in research and trial may influence a person's decision. Finally, the perceived rewards, both personal and societal, were influencing factors on the decision to participate. Personal rewards included access to a vaccine, improved health and improved disease knowledge, and a return to normality in the context of a pandemic or epidemic. Potential societal rewards included helping the community and contributing to science, often motivated by the memories of family and friends who had died from the disease. Authors' conclusions: This review identifies many of the factors that influence a person's decision to take part in a vaccine trial, and these reflect findings from reviews that examine trials more broadly. However, we also recognise some factors that become more important in connection with a vaccine trial in the context of a pandemic or epidemic. These factors include the potential stigma of taking part, the possible adverse effects of a vaccine, the added motivation for helping society, the role of community leaders in trial dissemination, and the level of trust placed in governments and companies developing vaccines. These specific influences need to be considered by trial teams when designing, and communicating about, vaccine trials in the context of a pandemic or epidemic.

Preclinical proof of concept of a tetravalent lentiviral T-cell vaccine against dengue viruses.

Nemirov K, Authié P, Souque P, Moncoq F, Noirat A, Blanc C, Bourgine M, Majlessi L, Charneau P.
15-08-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37654495/

Dengue virus (DENV) is responsible for approximately 100 million cases of dengue fever annually, including severe forms such as hemorrhagic dengue and dengue shock syndrome. Despite intensive vaccine research and development spanning several decades, a universally accepted and approved vaccine against dengue fever has not yet been developed. The major challenge associated with the development of such a vaccine is that it should induce simultaneous and equal protection against the four DENV serotypes, because past infection with one serotype may greatly increase the severity of secondary infection with a distinct serotype, a phenomenon known as antibody-dependent enhancement (ADE). Using a lentiviral vector platform that is particularly suitable for the induction of cellular immune responses, we designed a tetravalent T-cell vaccine candidate against DENV ("LV-DEN"). This vaccine candidate has a strong $CD8^+$ T-cell immunogenicity against the targeted non-structural DENV proteins, without inducing antibody response against surface antigens. Evaluation of its protective potential in the preclinical flavivirus infection model, i.e., mice knockout for the receptor to the type I IFN, demonstrated its significant protective effect against four distinct DENV serotypes, based on reduced weight loss, viremia, and viral loads in peripheral organs of the challenged mice. These results provide proof of concept for the use of lentiviral vectors for the development of efficient polyvalent T-cell vaccine candidates against all DENV serotypes.

Wolbachia wMel strain-mediated effects on dengue virus vertical transmission from Aedes aegypti to their offspring.

Duong Thi Hue K, da Silva Goncalves D, Tran Thuy V, Thi Vo L, Le Thi D, Vu Tuyet N, Nguyen Thi G, Huynh Thi Xuan T, Nguyen Minh N, Nguyen Thanh P, Yacoub S, Simmons CP.
31-08-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37653429/

Association of inhibitory NKG2A and activating NKG2D natural killer cell receptor genes with resistance to SARS-CoV-2 infection in a western Indian population.

Tripathy AS, Wagh P, Akolkar K, Walimbe AM, Potdar VA, Choudhary ML, Kadgi N, Nakate L, Abraham P.
31-08-2023
Arch Virol.
https://pubmed.ncbi.nlm.nih.gov/37653112/

Does ignoring transmission dynamics lead to underestimation of the impact of interventions against mosquito-borne disease?

Cavany S, Huber JH, Wieler A, Tran QM, Alkuzweny M, Elliott M, España G, Moore SM, Perkins TA.
Août-2023
BMJ Glob Health.
https://pubmed.ncbi.nlm.nih.gov/37652566/

New vector-control technologies to fight mosquito-borne diseases are urgently needed, the adoption of which depends on efficacy estimates from large-scale cluster-randomised trials (CRTs). The release of *Wolbachia*-infected mosquitoes is one promising strategy to curb dengue virus (DENV) transmission, and a recent CRT reported impressive reductions in dengue incidence following the release of these mosquitoes. Such trials can be affected by multiple sources of bias, however. We used mathematical models of DENV transmission during a CRT of *Wolbachia*-infected mosquitoes to explore three such biases: human movement, mosquito movement and coupled transmission dynamics between trial arms. We show that failure to account for each of these biases would lead to underestimated efficacy, and that the majority of this underestimation is due to a heretofore unrecognised bias caused by transmission coupling. Taken together, our findings suggest that *Wolbachia*-infected mosquitoes could be even more promising than the recent CRT suggested. By emphasising the importance of accounting for transmission coupling between arms, which requires a mathematical model, we highlight the key role that models can play in interpreting and extrapolating the results from trials of vector control interventions.

When does humoral memory enhance infection?

Nikas A, Ahmed H, Moore MR, Zarnitsyna VI, Antia R.
21-08-2023
PLoS Comput Biol.
https://pubmed.ncbi.nlm.nih.gov/37603552/

Antibodies and humoral memory are key components of the adaptive immune system. We consider and computationally model mechanisms by which humoral memory present at baseline might increase rather than decrease infection load; we refer to this effect as EI-HM (enhancement of infection by humoral memory). We first consider antibody dependent enhancement (ADE) in which antibody enhances the growth of the pathogen, typically a virus, and typically at intermediate 'Goldilocks' levels of antibody. Our ADE model reproduces ADE in vitro and enhancement of infection in vivo from passive antibody transfer. But notably the simplest implementation of our ADE model never results in EI-HM. Adding complexity, by making the cross-reactive antibody much less neutralizing than the de novo generated antibody or by including a sufficiently strong non-antibody immune response, allows for ADE-mediated EI-HM. We next consider the possibility that cross-reactive memory causes EI-HM by crowding out a possibly superior de novo immune response. We show that, even without ADE, EI-HM can occur when the cross-reactive response is both less potent and 'directly' (i.e. independently of infection load) suppressive with regard to the de novo response. In this case adding a non-antibody immune response to our computational model greatly reduces or completely eliminates EI-HM, which suggests that 'crowding out' is

unlikely to cause substantial EI-HM. Hence, our results provide examples in which simple models give qualitatively opposite results compared to models with plausible complexity. Our results may be helpful in interpreting and reconciling disparate experimental findings, especially from dengue, and for vaccination.

Language skills development in children with congenital Zika virus syndrome.

da Silva NC, Pinato L, Ribeiro EM, Giacheti CM.
Sept-2023
Early Hum Dev.
https://pubmed.ncbi.nlm.nih.gov/37595539/

Epigallocatechin Gallate: A Multifaceted Molecule for Neurological Disorders and Neurotropic Viral Infections.

Rani A, Saini V, Patra P, Prashar T, Pandey RK, Mishra A, Jha HC.
06-09-2023
ACS Chem Neurosci.
https://pubmed.ncbi.nlm.nih.gov/37590965/

Epigallocatechin-3-gallate (EGCG), a polyphenolic moiety found in green tea extracts, exhibits pleiotropic bioactivities to combat many diseases including neurological ailments. These neurological diseases include Alzheimer's disease, multiple sclerosis, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. For instance, in the case of Alzheimer's disease, the formation of a β-sheet in the region of the 10th-21st amino acids was significantly reduced in EGCG-induced oligomeric samples of Aβ40. Its interference induces the formation of Aβ structures with an increase in intercenter-of-mass distances, reduction in interchain/intrachain contacts, reduction in β-sheet propensity, and increase in α-helix. Besides, numerous neurotropic viruses are known to instigate or aggravate neurological ailments. It exerts an effect on the oxidative damage caused in neurodegenerative disorders by acting on GSK3-β, PI3K/Akt, and downstream signaling pathways via caspase-3 and cytochrome-c. EGCG also diminishes these viral-mediated effects, such as EGCG delayed HSV-1 infection by blocking the entry for virions, inhibitory effects on NS3/4A protease or NS5B polymerase of HCV and potent inhibitor of ZIKV NS2B-NS3pro/NS3 serine protease (NS3-SP). It showed a reduction in the neurotoxic properties of HIV-gp120 and Tat in the presence of IFN-γ. EGCG also involves numerous viral-mediated inflammatory cascades, such as JAK/STAT. Nonetheless, it also inhibits the Epstein-Barr virus replication protein (Zta and Rta). Moreover, it also impedes certain viruses (influenza A and B strains) by hijacking the endosomal and lysosomal compartments. Therefore, the current article aims to describe the importance of EGCG in numerous neurological diseases and its inhibitory effect against neurotropic viruses.

Co-Infection between Dengue Virus and SARS-CoV-2 in Cali, Colombia.

Agudelo-Rojas OL, Rebellón-Sánchez DE, Llanos Torres J, Zapata-Vásquez IL, Rodríguez S, Robles-Castillo S, Tejada Vega A, Parra-Lara LG, Rosso F.
14-08-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37580025/

Multifaceted contributions of Dicer2 to arbovirus transmission by Aedes aegypti.

Merkling SH, Crist AB, Henrion-Lacritick A, Frangeul L, Couderc E, Gausson V, Blanc H, Bergman A, Baidaliuk A, Romoli O, Saleh MC, Lambrechts L.
29-08-2023
Cell Rep.
https://pubmed.ncbi.nlm.nih.gov/37573505/

Exposure to ultraviolet-B radiation increases the susceptibility of mosquitoes to infection with dengue virus.

Alton LA, Novelo M, Beaman JE, Arnold PA, Bywater CL, Kerton EJ, Lombardi EJ, Koh C, McGraw EA.
Oct-2023
Glob Chang Biol.
https://pubmed.ncbi.nlm.nih.gov/37560790/

By 2100, greenhouse gases are predicted to reduce ozone and cloud cover over the tropics causing increased exposure of organisms to harmful ultraviolet-B radiation (UVBR). UVBR damages DNA and is an important modulator of immune function and disease susceptibility in humans and other vertebrates. The effect of UVBR on invertebrate immune function is largely unknown, but UVBR together with ultraviolet-A radiation impairs an insect immune response that utilizes melanin, a pigment that also protects against UVBR-induced DNA damage. If UVBR weakens insect immunity, then it may make insect disease vectors more susceptible to infection with pathogens of socioeconomic and public health importance. In the tropics, where UVBR is predicted to increase, the mosquito-borne dengue virus (DENV), is prevalent and a growing threat to humans. We therefore examined the effect of UVBR on the mosquito Aedes aegypti, the primary vector for DENV, to better understand the potential implications of increased tropical UVBR for mosquito-borne disease risk. We found that exposure to a UVBR dose that caused significant larval mortality approximately doubled the probability that surviving females would become infected with DENV, despite this UVBR dose having no effect on the expression of an effector gene involved in antiviral immunity. We also found that females exposed to a lower UVBR dose were more likely to have low fecundity even though this UVBR dose had no effect on larval size or activity, pupal cuticular melanin content, or adult mass, metabolic rate, or flight capacity. We conclude that future increases in tropical UVBR associated with anthropogenic global change may have the benefit of reducing mosquito-borne disease risk for humans by reducing mosquito fitness, but this benefit may be eroded if it also makes mosquitoes more likely to be infected with deadly pathogens.

Therapy for Chikungunya Arthritis: A Study of 133 Brazilian Patients.

Amaral JK, Bingham CO, Taylor PC, Vilá LM, Weinblatt ME, Schoen RT.
07-08-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37549898/

Chikungunya fever is a global vector-borne viral disease. Patients with acute chikungunya are usually treated symptomatically. The arthritic phase may be self-limiting. However, many patients develop extremely disabling arthritis that does not improve after months. The aim of this study was to describe the treatment of chikungunya arthritis (CHIKA) patients. A medical records review was conducted in 133 CHIKA patients seen at a rheumatology practice. Patients were diagnosed by clinical criteria and confirmed by the presence of anti-chikungunya IgM. Patients were treated with methotrexate (20 mg/week) and/or leflunomide (20 mg/day) and dexamethasone (0-4 mg/day) for 4 weeks. At baseline visit and 4 weeks after treatment, Disease Activity Score 28 (DAS28) and pain (using a visual analog scale) were ascertained. Five months after the end of treatment, patients were contacted to assess pain, tender joint count, and swollen joint count. The mean age of patients was 58.6 ± 13.7 years, and 119 (85%) were female. After 4 weeks of treatment, mean (SD) DAS28-erythrocyte sedimentation rate (6.0 [1.2] versus 2.7 [1.0], P < 0.001) and pain (81.8 [19.2] to 13.3 [22.9], P < 0.001) scores significantly decreased. A total of 123 patients were contacted 5 months after the end of treatment. Pain score, tender joint count, and swollen joint count significantly declined after 4 weeks of treatment, and the response was sustained for 5 months. In this group of patients with CHIKA, 4-week treatment induced a rapid clinical improvement that was maintained 5 months after the end of therapy; however, the contribution of treatment to these outcomes is uncertain.

SARS-CoV-2 variants, its recombinants and epigenomic exploitation of host defenses.

Saksena NK, Reddy SB, Miranda-Saksena M, Cardoso THS, Silva EMA, Ferreira JC, Rabeh WM.
Déc-2023
Biochim Biophys Acta Mol Basis Dis.
https://pubmed.ncbi.nlm.nih.gov/37549720/

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

Gu Z, Liu J, Qin L, Zhang Y, Cui W, Huang H, Liu L, Cao Y, Zhang H.
Août-2023
J Dermatol Sci.
https://pubmed.ncbi.nlm.nih.gov/37516644/

Imported and autochthonous dengue in Spain.

Herrero-Martínez JM, Sánchez-Ledesma M, Ramos-Rincón JM.
Oct-2023
Rev Clin Esp (Barc).
https://pubmed.ncbi.nlm.nih.gov/37507047/

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

Potential role of lncRNA in impairing cellular properties of human neural progenitor cells following exposure to Zika virus E protein.

Arora H, Prajapati B, Seth P.
Oct-2023
Exp Neurol.
https://pubmed.ncbi.nlm.nih.gov/37479020/

Zika virus (ZIKV) infection during the first trimester of the pregnancy may lead to Congenital zika syndrome in the neonates. The viral infection hampers foetal brain development and causes microcephaly. Human neural progenitor cells (hNPCs) play an important role in brain development, however they are highly susceptible to ZIKV infection. In this study, we elucidated the molecular mechanisms that lead to cellular alterations in hNPCs due to ZIKV E-protein. We investigated proliferation, differentiation, migration and inflammation in hNPCs, which may lead to microcephaly. In our study, we found that ZIKV E-protein causes cell cycle arrest, decrease in proliferation and increase in mitotic length of the dividing hNPCs. We observed CyclinD1 and upstream molecules (p21 and p53) of the pathway are dysregulated, and intracellular calcium at basal level as well as upon ATP stimulation were reduced following over expression of ZIKV E-protein. ZIKV E-protein transfected hNPCs exhibited pre-mature differentiation with pro-neural genes upregulated. Furthermore, ZIKV E-protein disrupted migrational properties of hNPCs and caused elevated levels of inflammatory chemokines and cytokines. To gain insights into molecular mechanisms of these effects on hNPCs, we explored the possible involvement of long non coding RNAs in ZIKV neuropathogenesis. We have shortlisted lncRNAs associated with differentially expressed genes from publicly available transcriptomic data and found some of those lncRNAs are differentially expressed upon E-protein transfection of hNPCs. Gene ontology analysis suggest these lncRNAs play an important role in regulation of viral life cycle, host's defence response and cell proliferation.

Mayaro virus detection by integrating sample preparation with isothermal amplification in portable devices.

Alipanah M, Manzanas C, Hai X, Lednicky JA, Paniz-Mondolfi A, Morris JG, Fan ZH.
Sept-2023
Anal Bioanal Chem.
https://pubmed.ncbi.nlm.nih.gov/37470813/

A novel approach for rapid and sensitive detection of Zika virus utilizing silver nanoislands as SERS platform.

Tripathi MN, Jangir P, Aakriti, Rai S, Gangwar M, Nath G, Saxena PS, Srivastava A.
05-12-2023
Spectrochim Acta A Mol Biomol Spectrosc.
https://pubmed.ncbi.nlm.nih.gov/37356391/

To control the spread of the disease, the Zika virus (ZIKV), a flavivirus infection spread by mosquitoes and common in across the world, needs to be accurately and promptly diagnosed. This endeavour gets challenging when early-stage illnesses have low viral loads. As a result, we have created a biosensor based on surface-enhanced Raman scattering (SERS) for the quick, accurate, and timely diagnosis of the Zika virus. In this study, a glass coverslip was coated with silver nanoislands, which were then utilized as the surface for creating the sensing platform. Silver nanoislands exhibit strong plasmonic activity and good conductive characteristics. It enhances the Raman signals as a result and gives the SERS platform an appropriate surface. The created platform has been applied to Zika virus detection. With a limit of detection (LOD) of 0.11 ng/mL, the constructed sensor exhibits a linear range from 5 ng/mL to 1000 ng/mL. Hence, even at the nanogram scale, this technique may be a major improvement over clinical diagnosis approaches for making proper, precise, and accurate Zika virus detection.

Serum ferritin level as a prognostic biomarker for predicting dengue disease severity: A systematic review and meta-analysis.

Shukla S, Jadhav SM, Gurav YK, Parashar D, Alagarasu K.
Sept-2023
Rev Med Virol.
https://pubmed.ncbi.nlm.nih.gov/37347209/

Dengue Uveitis - A Major Review.

Xie Cen A, Ng AWW, Rojas-Carabali W, Cifuentes-González C, de-la-Torre A, Mahendradas P, Agrawal R.
Sept-2023
Ocul Immunol Inflamm.
https://pubmed.ncbi.nlm.nih.gov/37315302/

Virus infection participates in the occurrence and development of human diseases through monoamine oxidase.

Sun Y, Liu W, Luo B.
Sept-2023
Rev Med Virol.
https://pubmed.ncbi.nlm.nih.gov/37294534/

Endometrial responses to bacterial and viral infection: a scoping review.

Lindsay CV, Potter JA, Grimshaw AA, Abrahams VM, Tong M.
05-09-2023
Hum Reprod Update.
https://pubmed.ncbi.nlm.nih.gov/37290428/

Background: The endometrium is a highly dynamic tissue that undergoes dramatic proliferation and differentiation monthly in order to prepare the uterus for implantation and pregnancy. Intrauterine infection and inflammation are being increasingly recognized as potential causes of implantation failure and miscarriage, as well as obstetric complications later in gestation. However, the mechanisms by which the cells of the endometrium respond to infection remain understudied and recent progress is slowed in part owing to similar overlapping studies being performed in different species. Objective and rationale: The aim of this scoping review is to systematically summarize all published studies in humans and laboratory animals that have investigated the innate immune sensing and response of the endometrium to bacteria and viruses, and the signaling mechanisms involved. This will enable gaps in our knowledge to be identified to inform future studies. Search methods: The Cochrane Library, Ovid Embase/Medline, PubMed, Scopus, Google Scholar, and Web of Science databases were searched using a combination of controlled and free text terms for uterus/endometrium, infections, and fertility to March 2022. All primary research papers that have reported on endometrial responses to bacterial and viral infections in the context of reproduction were included. To focus the scope of the current review, studies in domesticated animals, included bovine, porcine, caprine, feline, and canine species were excluded. Outcomes: This search identified 42 728 studies for screening and 766 full-text studies were assessed for eligibility. Data was extracted from 76 studies. The majority of studies focused on endometrial responses to Escherichia coli and Chlamydia trachomatis, with some studies of Neisseria gonorrhea, Staphylococcus aureus, and the Streptococcus family. Endometrial responses have only been studied in response to three groups of viruses thus far: HIV, Zika virus, and the herpesvirus family. For most infections, both cellular and animal models have been utilized in vitro and in vivo, focusing on endometrial production of cytokines, chemokines, and antiviral/antimicrobial factors, and the expression of innate immune signaling pathway mediators after infection. This review has identified gaps for future research in the field as well as highlighted some recent developments in organoid systems and immune cell co-cultures that offer new avenues for studying endometrial responses to infection in more physiologically relevant models that could accelerate future findings in this area. Wider implications: This scoping review provides an overarching summary and benchmark of the current state of research on endometrial innate immune responses to bacterial and viral infection. This review also highlights some exciting recent developments that enable future studies to be designed to deepen our understanding of the mechanisms utilized by the endometrium to respond to

infection and their downstream effects on uterine function.

Prescriptive, descriptive or predictive models: What approach should be taken when empirical data is limited? Reply to comments on "Mathematical models for Dengue fever epidemiology: A 10-year systematic review".

Aguiar M, Anam V, Blyuss KB, Estadilla CDS, Guerrero BV, Knopoff D, Kooi BW, Mateus L, Srivastav AK, Steindorf V, Stollenwerk N.
Sept-2023
Phys Life Rev.
https://pubmed.ncbi.nlm.nih.gov/37245453/

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

Lakshmanan C, Ranjit S, Natraj R, Venkatachalapathy P, Kumar VS, Lum LCS.
01-09-2023
Pediatr Crit Care Med.
https://pubmed.ncbi.nlm.nih.gov/37125796/

Neurological Disease Associated with Chikungunya in Indonesia.

Myint KSA, Mawuntu AHP, Haryanto S, Imran D, Dian S, Dewi YP, Ganiem AR, Anggreani R, Iskandar MM, Bernadus JBB, Maharani K, Susanto D, Estiasari R, Dewi H, Kristiani A, Gaghiwu L, Johar E, Yudhaputri FA, Antonjaya U, Ledermann JP, van Crevel R, Hamers RL, Powers AM.
13-06-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895435/

Phenotypic Variations of Aedes aegypti Populations and Egg Abundance According to Environmental Parameters in Two Dengue-Endemic Ecoregions in Paraguay.

Britos Molinas MB, Gayozo Melgarejo E, Rojas de Arias A.
20-06-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895428/

Dengue in Paraguay is an endemic disease of public health importance. Several studies suggest that an increased density of Aedes aegypti and the presence of dengue cases may be associated with climatic conditions. This study aimed to establish the phenotypic variations of Ae. aegypti from four cities (Asunción, Itauguá, Minga Guazú, and Ciudad del Este) and the potential association of environmental variables with the number of eggs in capture sites. Eleven morphometric phenotypic characters were evaluated, and environmental data were obtained from Earth Engine and local meteorological stations. An analysis was carried out using principal component analysis and linear discriminant analysis, and we estimated the correlation using [relative humidity, Normalized Difference Vegetation Index (NDVI) and Normalized Difference Water Index (NDWI)] between variables and the number of eggs in each site. Differences in mean NDVI and NDWI between cities and their relationship with the morphometric performance of individuals were also assessed. The study demonstrated morphometric variations between the populations of Ae. aegypti from two ecoregions, with the Litoral ecoregion populations presented a greater phenotypic variation than those observed in the Alto Paraná ecoregion. Significant statistical associations were registered between the number of eggs with relative humidity (r = -0.45) and the NDVI at 100 meters from the capture points (r = -0.61) for Minga Guazú, and with the NDWI at 100 meters (r = 0.54) for Ciudad del Este. Future studies on these Ae. aegypti populations, and its dispersion could contribute to improve vector control measures and foster future genetic studies.

Sensitive and Stable Molecular Detection of Dengue, Chikungunya, and Zika Viruses from Dried Blood Spots.

Cardona-Ospina JA, Stittleburg V, Millan-Benavidez N, Restrepo-Chica J, Key A, Rojas-Gallardo DM, Piantadosi A, Collins MH, Waggoner JJ.
05-07-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895398/

Standard molecular detection of many pathogens, in particular RNA viruses, requires appropriate handling in the field for preserving the quality of the sample until processing. This could be challenging in remote tropical areas. Dengue virus (DENV), chikungunya virus (CHIKV), and Zika virus (ZIKV) are RNA viruses, prominent among the causes of fever in the tropics. We aimed to test the stability of arboviral RNA in contrived dried blood spots prepared on Whatman 903 Protein saver cards as a means of sample collection and storage. We were able to detect DENV, CHIKV, and ZIKV by real-time RT-PCR up to 180 days after card inoculation with stable Ct values across the study period. Our study supports dried blood spots (DBS) on protein saver cards as a platform for stable detection of arboviral RNA of sufficient quality to be used in diagnostic RT-PCR assays and next generation sequencing.

COVID-19 Vaccination Intention in a Community Cohort in Ponce, Puerto Rico.

Sánchez-González L, Major CG, Rodriguez DM, Balajee A, Ryff KR, Lorenzi O, Linares M, Adams LE, Rivera-Amill V, Rolfes M, Paz-Bailey G.
11-07-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895388/

Therapeutic spectrum of piperine for clinical practice: a scoping review.

Yadav SS, Singh MK, Hussain S, Dwivedi P, Khattri S, Singh K.
2023

Crit Rev Food Sci Nutr.
https://pubmed.ncbi.nlm.nih.gov/34996326/

Leptospirosis among Dengue-Negative Febrile Patients in Selangor, Malaysia.

Loong SK, Abd-Majid MA, Teoh BT, Cheh MJ, Khor CS, Chao CC, Khoo JJ, AbuBakar S.
05-07-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895409/

In recent years, the number of leptospirosis cases, including the number of deaths, has exponentially increased in Malaysia. From June 2016 to February 2018, blood samples of 321 febrile patients with the presumptive diagnosis of dengue-like illness were examined for possible exposure to Leptospira. Two hundred fifty-five blood samples were tested as negative for dengue. Seminested polymerase chain reaction (PCR) and IgM ELISA for leptospirosis were performed. From the samples, an overall prevalence for leptospirosis based on PCR of 4.7% (12/255) was obtained. Eighteen percent (46/255) were positive for anti-Leptospira IgM antibodies. The genome sequences of six of 12 Leptospira PCR-positive samples showed > 97.0% similarity to Leptospira interrogans. One patient's sample consisted of Leptospira and chikungunya virus, suggesting a coinfection. Findings from the study suggest that leptospirosis is prevalent among dengue-negative febrile patients in Malaysia.

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

Carvalho T, Landim MG, Lima MLD, Bittar C, Faria BCAO, Rahal P, de Lima MCF, Junior VFDV, Joanitti GA, Calmon MF.
07-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37676868/

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

Selected phytochemicals of Momordica charantia L. as potential anti-DENV-2 through the docking, DFT and molecular dynamic simulation.

Huq AKMM, Roney M, Issahaku AR, Sapari S, Ilyana Abdul Razak F, Soliman MES, Mohd Aluwi MFF, Tajuddin SN.
07-09-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37676311/

Dengue in Timor-Leste during the COVID-19 phenomenon.

da Cruz ZV, Araujo AL, Ribas A, Nithikathkul C.
22-08-2023
Front Public Health.
https://pubmed.ncbi.nlm.nih.gov/37674687/

Projecting the future incidence and burden of dengue in Southeast Asia.

Colón-González FJ, Gibb R, Khan K, Watts A, Lowe R, Brady OJ.
06-09-2023
Nat Commun.
https://pubmed.ncbi.nlm.nih.gov/37673859/

Convergent trends and spatiotemporal patterns of Aedes-borne arboviruses in Mexico and Central America.

Gutierrez B, da Silva Candido D, Bajaj S, Rodriguez Maldonado AP, Ayala FG, Rodriguez MLT, Rodriguez AA, Arámbula CW, González ER, Martínez IL, Díaz-Quiñónez JA, Pichardo MV, Hill SC, Thézé J, Faria NR, Pybus OG, Preciado-Llanes L, Reyes-Sandoval A, Kraemer MUG, Escalera-Zamudio M.
06-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37672514/

Background: Aedes-borne arboviruses cause both seasonal epidemics and emerging outbreaks with a significant impact on global health. These viruses share mosquito vector species, often infecting the same host population within overlapping geographic regions. Thus, comparative analyses of the virus evolutionary and epidemiological dynamics across spatial and temporal scales could reveal convergent trends. Methodology/principal findings: Focusing on Mexico as a case study, we generated novel chikungunya and dengue (CHIKV, DENV-1 and DENV-2) virus genomes from an epidemiological surveillance-derived historical sample collection, and analysed them together with longitudinally-collected genome and epidemiological data

from the Americas. Aedes-borne arboviruses endemically circulating within the country were found to be introduced multiple times from lineages predominantly sampled from the Caribbean and Central America. For CHIKV, at least thirteen introductions were inferred over a year, with six of these leading to persistent transmission chains. For both DENV-1 and DENV-2, at least seven introductions were inferred over a decade. **Conclusions/significance:** Our results suggest that CHIKV, DENV-1 and DENV-2 in Mexico share evolutionary and epidemiological trajectories. The southwest region of the country was determined to be the most likely location for viral introductions from abroad, with a subsequent spread into the Pacific coast towards the north of Mexico. Virus diffusion patterns observed across the country are likely driven by multiple factors, including mobility linked to human migration from Central towards North America. Considering Mexico's geographic positioning displaying a high human mobility across borders, our results prompt the need to better understand the role of anthropogenic factors in the transmission dynamics of Aedes-borne arboviruses, particularly linked to land-based human migration.

Low-density hepatitis C virus infectious particles are protected from oxidation by secreted cellular proteins.

Granier C, Toesca J, Mialon C, Ritter M, Freitas N, Boson B, Pécheur EI, Cosset FL, Denolly S.
06-09-2023
mBio.
https://pubmed.ncbi.nlm.nih.gov/37671888/

Contexts motivating protective behaviours related to Aedes-borne infectious diseases in Curaçao.

Mulderij-Jansen V, Gerstenbluth I, Duits A, Tami A, Bailey A.
05-09-2023
BMC Public Health.
https://pubmed.ncbi.nlm.nih.gov/37670248/

Background: Aedes aegypti, the vector of arboviral diseases such as dengue and Zika virus infections, is difficult to control. Effective interventions must be practicable, comprehensive, and sustained. There is evidence that community participation can enhance mosquito control. Therefore, countries are encouraged to develop and integrate community-based approaches to mosquito control to mitigate Aedes-borne infectious diseases (ABIDs). Health professionals must understand the contexts motivating individuals' behaviour to improve community participation and promote behavioural change. Therefore, this study aimed to determine how contexts shaped individuals' protective behaviours related to ABIDs in Curaçao. **Methods:** From April 2019 to September 2020, a multi-method qualitative study applying seven (n = 54) focus group discussions and twenty-five in-depth interviews with locals was performed in Curaçao. The study was designed based on the Health Belief Model (HBM). Two cycles of inductive and deductive coding were employed, and Nvivo software was used to manage and analyse the data. **Results:** In this study, low media coverage (external cue to action) and limited experience with the symptoms of ABIDs (internal cue to action) were linked with a low perceived susceptibility and severity of ABIDs (low perceived threat). The low perceived threat was linked with reduced health-seeking behaviour (HSB) to prevent and control ABIDs. We also found that the perceived barriers outweigh the perceived benefits of ABID prevention and control interventions, obstructing HSB. On the one hand, insufficient knowledge reduced self-efficacy but contrary to expected, having good knowledge did not promote HSB. Lastly, we found that our participants believe that they are responsible for preventing ABIDs (internal locus of control) but at the same time indicated that their success depends on the efforts of the community and the health system (external locus of control). **Conclusions:** This study used the HBM to explain individual changes in HSB concerning ABIDs prevention and control in Curaçao. We can conclude that the perceived threat (perceived susceptibility and severity) and perceived barriers played an essential role in changing HSB. Health professionals must consider these two concepts' implications when designing a bottom-up approach for ABIDs control; otherwise, community participation will remain minimal.

Mimicking superinfection exclusion disrupts alphavirus infection and transmission in the yellow fever mosquito Aedes aegypti.

Reitmayer CM, Levitt E, Basu S, Atkinson B, Fragkoudis R, Merits A, Lumley S, Larner W, Diaz AV, Rooney S, Thomas CJE, von Wyschetzki K, Rausalu K, Alphey L.
12-09-2023
Proc Natl Acad Sci U S A.
https://pubmed.ncbi.nlm.nih.gov/37669371/

Multiple viruses, including pathogenic viruses, bacteriophages, and even plant viruses, cause a phenomenon termed superinfection exclusion whereby a currently infected cell is resistant to secondary infection by the same or a closely related virus. In alphaviruses, this process is thought to be mediated, at least in part, by the viral protease (nsP2) which is responsible for processing the nonstructural polyproteins (P123 and P1234) into individual proteins (nsP1-nsP4), forming the viral replication complex. Taking a synthetic biology approach, we mimicked this naturally occurring phenomenon by generating a superinfection exclusion-like state in *Aedes aegypti* mosquitoes, rendering them refractory to alphavirus infection. By artificially expressing Sindbis virus (SINV) and chikungunya virus (CHIKV) nsP2 in mosquito cells and transgenic mosquitoes, we demonstrated a reduction in both SINV and CHIKV viral replication rates in cells following viral infection as well as reduced infection prevalence, viral titers, and transmission potential in mosquitoes.

Jamestown Canyon virus is transmissible by Aedes aegypti and is only moderately blocked by Wolbachia co-infection.

Lau MJ, Dutra HLC, Jones MJ, McNulty BP, Diaz AM, Ware-Gilmore F, McGraw EA.
05-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37669272/

Behavioral Changes of Some Arboviral Vectors in Zika Forest: A Concern for Emerging and Re-Emerging Diseases in Uganda.

Lukindu M, Mukwaya LG, Masembe C, Birungi J.
05-09-2023
Vector Borne Zoonotic Dis.
https://pubmed.ncbi.nlm.nih.gov/37669008/

Zika virus screening during pregnancy: Results and lessons learned from a screening program and a post-delivery follow-up analysis (2016-2022).

Martínez-Arias A, Valerio L, Roure-Díez S, Fernández-Rivas G, Rivaya B, Pérez-Olmeda MT, Soldevila-Langa L, Parrón I, Clotet-Sala B, Vallès X, Rodrigo C.
05-09-2023
Birth Defects Res.
https://pubmed.ncbi.nlm.nih.gov/37668290/

Identification and molecular docking of novel chikungunya virus NSP4 inhibitory peptides from camel milk proteins.

Alguridi HI, Alzahrani F, Almalki S, Zamzami MA, Altayb HN.
05-09-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37668009/

The chikungunya (CHIK) virus is an arbovirus belonging to the alphavirus (*Togaviridae* family). Around 85% of infected individuals suffer from symptoms such as high fever and severe joint pain; about 30 to 40% will develop a chronic joint illness. The Nsp4 protease is the most conserved protein in the alphavirus family and serves as an RNA-dependent RNA polymerase (RdRp). Targeting this enzyme might inhibit the CHIKV replication cycle. This work aims to *in silico* study the CHIKV RdRp inhibitory effect of peptides derived from camel milk protein as antiviral peptides. Various bioinformatics tools were recruited to identify, screen, predict and assess peptides obtained from camel milk as antiviral peptides (AVPs). During this study, CHIKV Nsp4 (polymerase) was used as a target to be inhibited by interaction with peptides derived from camel milk protein. Among 91 putative bioactive peptides, the best predicted 5 were further evaluated. Molecular docking showed that the top 5 AVPs generated better docking scores and interacted well with active sites of Nsp4 by the formation of different hydrogen bonds as well as other bonds. AVP63 and AVP20 showed the best Molecular docking and MD simulation results. The residue 315ASP of the GDD motif (catalytic core) exhibited a favorable interaction with the AVPs. The findings of this study suggest that the AVP20 derived from camel milk protein can be a potential novel CHIKV polymerase inhibitor.

An intercellular bridge for chikungunya virus transmission.

Du Toit A.
04-09-2023
Nat Rev Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37667008/

Challenges encountered by natural repellents: Since obtaining until the final product.

Almeida AR, Oliveira ND, Pinheiro FASD, Morais WA, Ferreira LS.
Sept-2023
Pestic Biochem Physiol.
https://pubmed.ncbi.nlm.nih.gov/37666610/

Paris fights to halt spread of dengue mosquito.

Shepherd A.
04-09-2023
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37666518/

Social construction of risk and prevention practices related to Aedes mosquito-borne disease in an endemic municipality in Colombia.

Cortés García CM, Hormiga Sánchez CM, Ariza Abril JS, Becerra Fajardo YS.
Sept-2023
Rural Remote Health.
https://pubmed.ncbi.nlm.nih.gov/37666503/

A tale of 141 municipalities: the spatial distribution of dengue in Mato Grosso, Brazil.

Fernandes KAP, de Almeida Filho AR, Moura Alves TV, Bernardo CSS, Montibeller MJ, Mondini A, Bronzoni RVM.
04-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37665762/

Background: In recent years, the state of Mato Grosso has presented one of the highest dengue incidence rates in Brazil. The meeting of the Amazon, Cerrado and Pantanal biomes results in a large variation of rainfall and temperature across different regions of the state. In addition, Mato Grosso has been undergoing intense urban growth since the 1970s, mainly due to the colonization of the Mid-North and North regions. We analyzed factors involved in dengue incidence in Mato Grosso from 2008 to 2019. Methods: The Moran Global Index was used to assess spatial autocorrelation of dengue incidence using explanatory variables such as temperature, precipitation, deforestation, population density and municipal development index. Areas at risk of dengue were grouped by the Local Moran Indicator. Results: We noticed that areas at risk of dengue expanded from the Mid-North region to the North; the same pattern occurred from the

Southeast to the Northeast; the South region remained at low-risk levels. The increase in incidence was influenced by precipitation, deforestation and the municipal development index. **Conclusions:** The identification of risk areas for dengue in space and time enables public health authorities to focus their control and prevention efforts, reducing infestation and the potential impact of dengue in the human population.

Factors influencing the knowledge, attitude, and practices of police personnel toward dengue fever in Kathmandu, Nepal.

Paudel D, Kakchapati S, Lageju N, Karki S, Dhungana J, Regmi S, Chudal D, Sharma RP.
Jan-Déc 2023
J Occup Health.
https://pubmed.ncbi.nlm.nih.gov/37664983/

Objective: Dengue fever is a significant public health problem in Nepal, and police personnel are considered to play a crucial role in preventing and controlling dengue fever. This study aimed to assess the factors that influence the knowledge, attitudes, and practices of police personnel toward dengue in Kathmandu, Nepal. **Methods:** The study design was a descriptive cross-sectional study among 422 police personnel, where data were collected using self-administered questionnaires. Bi-variate analysis and multivariate analysis were used to examine the association between sociodemographic factors and environmental factors with knowledge, attitude, and practices of dengue. **Results:** The study found that the knowledge, attitude, and practice toward dengue prevention was 58%, 46%, and 75%, respectively. The study found that family history of dengue (AOR = 2.78, 95% CI = 1.38-5.6), owning bed nets (AOR = 2.13, 95% CI = 1.04-4.35) and having covered water storage containers (AOR = 2.99, 95% CI = 1.74-5.13) were associated with higher odds of knowledge on dengue. Having family history of dengue (AOR = 2.45, 95% CI = 1.24-4.87) and the presence of broken glasses or discarded plastic bottles in the house (AOR = 2.07, 95% CI = 1.93-5.36) were associated with attitude on dengue. Knowledge on dengue was associated with higher odds of attitude (AOR = 3.3, 95% CI = 2.09-5.36) and practices (AOR = 3.21, 95% CI = 1.93, 5.36). **Conclusion:** The study identified specific factors associated with knowledge, attitude, and practices toward dengue prevention. The study concluded that regular training and awareness-raising activities are needed to improve their knowledge, attitudes, and practices toward dengue.

A Case Report of Takotsubo Cardiomyopathy With Dengue.

Munasinghe KVP, Silva FHDS.
31-07-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37663978/

Larvicidal Potential of Caribbean Plants.

Layne-Yarde RNA, Sandiford SL.
26-08-2023
Biomed Res Int.
https://pubmed.ncbi.nlm.nih.gov/37663786/

Mosquitoes are vectors for numerous arboviruses such as dengue, chikungunya, and Zika which continue to negatively impact the health of Caribbean populations. Within the region, synthetic insecticides are primarily used to control mosquito populations. In many countries however, these compounds are becoming less effective due to resistance, and they may also be harmful to the environment. Thus, there is a significant need for the development of alternative agents to combat the mosquito threat in the Caribbean. Worldwide, botanical-based products are being increasingly investigated for vector control because they are environmentally friendly and are often highly effective mosquitocidal agents. Although the botanical diversity within the Caribbean is remarkable, work on plant biopesticides in the region remains limited. The aim of this review, therefore, is to discuss the use of Caribbean botanical extracts as larvicidal agents. Additionally, we highlight the need for future work in this area which may subsequently lead to the implementation of transformative public health policies.

The Effect of Age on Dengue Presentation and the Diagnostic Accuracy of the 2015 Pan American Health Organization Case Criteria in a Puerto Rican Cohort.

Odio CD, Sánchez-González L, Delorey M, Adams LE, Jones ES, Lorenzi O, Munoz-Jordan J, Rivera-Amill V, Paz-Bailey G.
19-07-2023
Open Forum Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37663092/

Antiviral activity of myricetin glycosylated compounds isolated from Marcetia taxifolia against chikungunya virus.

Muñoz AL, Cuéllar AF, Arévalo G, Santamaría BD, Rodríguez AK, Buendia-Atencio C, Reyes Chaparro A, Tenorio Barajas AY, Segura NA, Bello F, Suárez AI, Rangel HR, Losada-Barragán M.
27-07-2023
EXCLI J.
https://pubmed.ncbi.nlm.nih.gov/37662709/

Accuracy of smartphone camera urine photo colorimetry as indicators of dehydration.

Bustam A, Poh K, Shuin Soo S, Naseem FS, Md Yusuf MH, Hishamudin NU, Azhar MN.
30-08-2023
Digit Health.
https://pubmed.ncbi.nlm.nih.gov/37662675/

Objective: Direct urine color assessment has been shown to correlate with hydration status. However, this method is subject to inter- and intra-observer variability. Digital image colorimetry provides a more objective method. This study evaluated the diagnostic accuracy of urine photo colorimetry using different smartphones under different

lighting conditions, and determined the optimal cut-off value to predict clinical dehydration. Methods: The urine samples were photographed in a customized photo box, under five simulated lighting conditions, using five smartphones. The images were analyzed using Adobe Photoshop to obtain Red, Green, and Blue (RGB) values. The correlation between RGB values and urine laboratory parameters were determined. The optimal cut-off value to predict dehydration was determined using area under the receiver operating characteristic curve. Results: A total of 56 patients were included in the data analysis. Images captured using five different smartphones under five lighting conditions produced a dataset of 1400 images. The study found a statistically significant correlation between Blue and Green values with urine osmolality, sodium, urine specific gravity, protein, and ketones. The diagnostic accuracy of the Blue value for predicting dehydration were "good" to "excellent" across all phones under all lighting conditions with sensitivity >90% at cut-off Blue value of 170. Conclusions: Smartphone-based urine colorimetry is a highly sensitive tool in predicting dehydration.

N^4 -Hydroxycytidine/Molnupiravir Inhibits RNA-Virus Induced Encephalitis by Producing Mutated Viruses with Reduced Fitness.

Ojha D, Hill CS, Zhou S, Evans AB, Leung JM, Lewis CS, Amblard F, Schinazi RF, Baric RS, Peterson KE, Swanstrom R.
23-08-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37662274/

A diverse group of RNA viruses including Rabies, Polio, La Crosse, West Nile, Zika, Nipah, Eastern and Western equine encephalitis, Venezuelan equine encephalitis, Japanese encephalitis, and tick-borne encephalitis viruses have the ability to gain access to and replicate in the central nervous system (CNS), causing severe neurological disease. Current treatment for these patients is generally limited to supportive care. To address the need for a generalizable antiviral, we utilized a strategy of mutagenesis to limit virus replication. We evaluated ribavirin (RBV), favipiravir (FAV) and N^4 -hydroxycytidine (NHC) against La Crosse virus (LACV) which is the primary cause of pediatric arboviral encephalitis cases in North America. NHC was more potent than RBV or FAV in neuronal cells. Oral administration of molnupiravir (MOV), the 5'-isobutyryl prodrug of NHC, decreased neurological disease development by 32% following intraperitoneal (IP) infection of LACV. MOV also reduced disease by 23% when virus was administered intranasally (IN). NHC and MOV produced less fit viruses by incorporating predominantly G-to-A or C-to-U mutations. Furthermore, NHC also inhibited two other orthobunyaviruses, Jamestown Canyon virus and Cache Valley virus. Collectively, these studies indicate that NHC/MOV has therapeutic potential to inhibit virus replication and subsequent neurological disease caused by this neurotropic RNA virus.

Dengue Fever with Conjunctivitis Mimicking Zika Virus Infection.

Matono T, Yamate R.
2023
Intern Med.
https://pubmed.ncbi.nlm.nih.gov/37661417/

Dengue virus 3 genotype I (GI) lineage 1 (L1) isolates elicit differential cytopathic effect with syncytium formation in human glioblastoma cells (U251).

de Souza Andrade A, Oliveira Campos S, Dias J, Campos MA, Kroon EG.
03-09-2023
Virol J.
https://pubmed.ncbi.nlm.nih.gov/37661255/

Background: Dengue virus (DENV) is a Flaviviridae member classified into four antigenically distinct serotypes (DENV 1, 2, 3, and 4) and further subdivided genotypes. DENV3 is subdivided into four or five genotypes, depending on the classification adopted. Despite their high genetic proximity, as revealed by phylogenetic complete polyprotein analysis, DENV3 MG-20 and DENV3 PV_BR showed different neurovirulence in mice models. Our group identified six amino acid mutations in protein E, including the E62K and E123Q, which may affect interactions of hydrophobic clusters on domain II, thus leading to the observed differences in the studied viruses. Methods: Human glioblastoma cells (U251) derived from a malignant glioblastoma tumor by explant technique were infected by the DENV3 GIL1 isolates DENV3 MG-20 and DENV3 PV_BR and analyzed by plaque assays and titration, optical, immunofluorescence, and transmission electronic microscopy. Results: The two isolates showed different cytopathic effects (CPE) and fusogenic patterns, further confirmed by indirect immunofluorescence. Transmission electron microscopy revealed intense cytopathic effects in DENV3 MG-20 infected U251 cells, displaying endoplasmic reticulum hypertrophy and turgid vesicles with proteins and multiple viruses, distinct from DENV3 PV_BR infected cells. It is hypothesized that the different amino acids in the DENV3 MG-20 isolate are related to an increased membrane fusion ability in viral infection, thus facilitating immune system evasion and increased chances of central nervous system cell infection. Conclusion: These results emphasize the biological differences between the isolates, which could be a critical factor in host-virus interaction and severe dengue development. Our study presents comparative results of highly similar isolates with the potential to generate more subsidies for a deeper understanding of the DENV pathogenesis. The neurotropism of the isolate DENV3 MG-20 (belonging to the DENV3 GI L1 genotype) showing infection of nervous system cells (U251) could contribute to understanding neurological dengue disease.

Bangladesh's 2023 Dengue outbreak - age/gender-related disparity in morbidity and mortality and geographic variability of epidemic burdens.

Haider N, Asaduzzaman M, Hassan MN, Rahman M, Sharif AR, Ashrafi SAA, Lee SS, Zumla A.
01-09-2023

Int J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37660728/

Treatments for dengue: a Global Dengue Alliance to address unmet needs.

Dengue Alliance. Electronic address: gnmalavige@dndi.org.
31-08-2023
Lancet Glob Health.
https://pubmed.ncbi.nlm.nih.gov/37660714/
https://pubmed.ncbi.nlm.nih.gov/37660714/

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

Wong JM, Rivera A, Volkman HR, Torres-Velasquez B, Rodriguez DM, Paz-Bailey G, Adams LE.
Sept-2023
Am J Transplant.
https://pubmed.ncbi.nlm.nih.gov/37659833/

Production of a chimeric flavivirus that contains the major structural glycoprotein genes of T'Ho virus in the genetic background of Zika virus.

Tangudu CS, Hargett AM, Mitrisin BC, Laredo-Tiscareño SV, Blitvich BJ.
01-09-2023
Virol J.
https://pubmed.ncbi.nlm.nih.gov/37658438/

Effects of the source of information and knowledge of dengue fever on the mosquito control behavior of residents of border areas of Yunnan, China.

Lun X, Yang R, Lin L, Wang Y, Wang J, Guo Y, Xiu P, Zhu C, Liu Q, Xu L, Meng F.
01-09-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37658374/

Background: Strengthening the mosquito control measures undertaken by residents of an area where dengue fever is present can significantly decrease the spread of this disease. The aim of this study was to explore the effects of the source of information and knowledge of dengue fever on the mosquito control behavior of residents of areas at high risk of this disease to determine effective ways of enhancing this behavior. Methods: A survey was conducted via face-to-face interviews or questionnaires between March and May 2021 in three regions of the province of Yunnan, China. The survey included basic information about the respondents, the source(s) of their dengue fever information, the level of their dengue fever knowledge, and the measures they had implemented to control mosquitoes. Principal component analysis was used to extract the main components of the sources of information. Correlation analysis and structural equation analysis were used to explore the impact of the sources of information and residents' dengue fever knowledge on their mosquito control behavior. Results: Publicity achieved through mass media, including official WeChat accounts, magazines/newspapers, poster leaflets, television/radio and the Internet, had a direct effect on dengue fever knowledge and mosquito control behavior, and indirectly affected mosquito control behavior through dengue fever knowledge. Organized publicity campaigns, including information provided by medical staff and through community publicity, had a direct effect on dengue fever knowledge and indirectly affected mosquito control behavior through dengue fever knowledge. The residents' level of dengue fever knowledge had a significant, positive, direct effect on their mosquito control behavior. Conclusions: Mosquito control is an important measure for the prevention and control of outbreaks of dengue fever. An effective source of information can improve the level of dengue fever knowledge among residents and thus enhance their mosquito control behavior.

A Bayesian spatiotemporal approach to modelling arboviral diseases in Mexico.

Bukhari MH, Shad MY, Nguyen UDT, Treviño C JA, Jung W, Bajwa WU, Gallego-Hernández AL, Robinson R, Corral-Frías NS, Hamer GL, Wang P, Annan E, Ra CK, Keellings D, Haque U.
08-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37681342/

Physical virology: how physics is enabling a better understanding of recent viral invaders.

Cardoso-Lima R, Santos-Oliveira R, Souza PFN, Barbosa LRS, Wuite GJL, Alencar LMR.
17-06-2023
Biophys Rev.
https://pubmed.ncbi.nlm.nih.gov/37681101/

The world is frequently afflicted by several viral outbreaks that bring diseases and health crises. It is vital to comprehend how viral assemblies' fundamental components work to counteract them. Determining the ultrastructure and nanomechanical characteristics of viruses from a physical standpoint helps categorize their mechanical characteristics, offers insight into new treatment options, and/or shows weak spots that can clarify methods for medication targeting. This study compiles the findings from studies on the ultrastructure and nanomechanical behavior of SARS-CoV-2, ZIKV (Zika virus), and CHIKV (Chikungunya virus) viral particles. With results that uncovered aspects of the organization and the spatial distribution of the proteins on the surface of the viral particle as well as the deformation response of the particles when applied a recurring loading force, this review aims to provide further discussion on the mechanical properties of viral particles at the nanoscale, offering new prospects that could be employed for designing strategies for the prevention and treatment of viral diseases.

Thermodynamic and mechanistic analysis of the functional properties of dengue virus NS3 helicase.

Incicco JJ, Cababie LA, Sarto C, Adler NS, Amrein F, Mikkelsen E, Arrar M, Kaufman SB.
17-08-2023
Biophys Rev.
https://pubmed.ncbi.nlm.nih.gov/37681085/

Association of different blood groups in patients with Dengue fever and their relationship with the severity of the illness.

Iqbal N, Afridi MAR, Ali Z, Rafiq A.
Sept-Oct 2023
Pak J Med Sci.
https://pubmed.ncbi.nlm.nih.gov/37680846/

Real-World Study on Chai-Shi-Jie-Du Granules for the Treatment of Dengue Fever and the Possible Mechanisms Based on Network Pharmacology.

Yang H, Ma D, Li Q, Zhou W, Chen H, Shan X, Zheng H, Luo C, Ou Z, Xu J, Wang C, Zhao L, Su R, Chen Y, Liu Q, Tan X, Lin L, Jiang T, Zhang F.
30-08-2032
Evid Based Complement Alternat Med.
https://pubmed.ncbi.nlm.nih.gov/37680700/

Objectives: Traditional Chinese medicine (TCM) is a widely used method for treating dengue fever in China. TCM improves the symptoms of patients with dengue, but there is no standard TCM prescription for dengue fever. This real-world study aimed to evaluate the effects of Chai-Shi-Jie-Du (CSJD) granules for the treatment of dengue fever and the underlying mechanisms. Methods: We implemented a multicenter real-world study, an *in vitro* assay and network pharmacology analysis. Patients from 5 hospitals in mainland China who received supportive western treatment in the absence or presence of CSJD were assigned to the control and CSJD groups between 1 August and 31 December 2019. Propensity score matching (PSM) was performed to correct for biases between groups. The clinical data were compared and analyzed. The antidengue virus activity of CSJD was tested in Syrian baby hamster kidney (BHK) cells using the DENV2-NGC strain. Network pharmacological approaches along with active compound screening, target prediction, and GO and KEGG enrichment analyses were used to explore the underlying molecular mechanisms. Results: 137 pairs of patients were successfully matched according to age, sex, and the time from onset to presentation. The time to defervescence (1.7 days vs. 2.5 days, $P < 0.05$) and the disease course (4.1 days vs. 6.1 days, $P < 0.05$) were significantly shorter in the CSJD group than those in the control group. CSJD showed no anti-DENV2-NGC virus activity in BHK cells. Network pharmacology analysis revealed 108 potential therapeutic targets, and the top GO and KEGG terms were related to immunity, oxidative stress response, and the response to lipopolysaccharide. Conclusions: CSJD granules exhibit high potential for the treatment of dengue fever, and the therapeutic mechanisms involved could be related to regulating immunity, moderating the oxidative stress response, and the response to lipopolysaccharide.

Co-circulation of Chikungunya virus, Zika virus, and serotype 1 of Dengue virus in Western Bahia, Brazil.

de França Cirilo MV, Pour SZ, de Fatima Benedetti V, Farias JP, Fogaça MMC, da Conceição Simões R, Vidal PO, Birbrair A, de Andrade Zanotto PM, Luiz WB, Amorim JH.
23-08-2023
Front Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37680530/

Chikungunya, mayaro, dengue, zika, and yellow fever are mosquito-borne viral diseases caused, respectively, by *Chikungunya virus*, *Mayaro virus* (CHIKV and MAYV, respectively: *Togaviridae*: *Alphavirus*), *Dengue virus*, *Zika virus, and Yellow fever virus* (DENV, ZIKV, and YFV, respectively: *Flaviviridae*: *Flavivirus*). These viruses have an important epidemiological impact worldwide, especially in Brazil. Western Bahia is one of the less studied regions in that country regarding the circulation of these pathogens. In this study, we aimed to apply molecular biology assays to better know the mosquito-borne viruses circulating in Barreiras and Luís Eduardo Magalhães, two main cities of Western Bahia. From March to June 2021, we enrolled 98 patients with the clinical diagnosis of dengue. Personal information (gender and age) were retrieved at the moment of enrollment. Serum samples were obtained from volunteers and used in molecular detection of CHIKV, MAYV, DENV, ZIKV, and YFV by reverse transcription followed by real-time polymerase chain reaction as well as in genome sequencing aiming phylogenetic analysis. As the main result, we found that from the 98 patients 45 were infected by CHIKV, 32 were infected by serotype 1 of DENV (DENV-1) and six were infected by ZIKV, while 15 were negative for all arboviruses tested. In addition, phylogenetic analysis revealed that all CHIKV-positive samples were of the East/Central/South African (ECSA) genotype, while all DENV-1-positive samples were of the V genotype. These results clearly show that epidemiological surveillance cannot be based only on clinical evaluations. Laboratory diagnosis is important in arbovirus infection that are prevalent in a particular area. These findings also demonstrate the co-circulation of many arboviruses in Western Bahia in 2021.

Dense residential areas promote gene flow in dengue vector mosquito Aedes albopictus.

Yeo H, Tan HZ, Tang Q, Tan TRH, Puniamoorthy N, Rheindt FE.
09-08-2023
iScience.
https://pubmed.ncbi.nlm.nih.gov/37680477/

The Zika virus infection remodels the expression of the synaptotagmin-9 secretory protein.

Leiva S, Cantoia A, Fabbri C, Bugnon Valdano M, Luppo V, Morales MA, Rosano G, Gardiol D.
08-09-2023
Biol Chem.
https://pubmed.ncbi.nlm.nih.gov/37677740/

Adipokine levels and their association with clinical disease severity in patients with dengue.

Kuruppu H, Wickramanayake WPRH, Jeewandara C, Perananthara jah D, Colambage HS, Perera L, Gomes L, Wijewickrama A, Ogg GS, Malavige GN.
07-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37676889/

Adipokines have not been studied in acute dengue, despite their emerging role in inducing and regulating inflammation. Therefore, we sought to identify adipokine levels in patients with varying severities of acute dengue to understand their role in disease pathogenesis. We determined the levels of leptin, resistin, omentin, adiponectin, as well as IFNβ, and NS1 using quantitative ELISA in patients with dengue fever (DF = 49) and dengue haemorrhagic fever (DHF = 22) at admission (febrile phase) and at the time of discharge (recovery phase). The viral loads and serotypes of all samples were quantified using quantitative real-time RT-PCR. Resistin levels (p = 0.04) and omentin (p = 0.006) levels were significantly higher in patients who developed DHF. Omentin levels in the febrile phase also correlated with the AST (Spearman's r = 0.38, p = 0.001) and ALT levels (Spearman's r = 0.24, p = 0.04); as well as serum leptin levels with both AST (Spearman's r = 0.27, p = 0.02) and ALT (Spearman's r = 0.28, p = 0.02). Serum adiponectin levels in the febrile phase did not correlate with any of the other adipokines or with liver enzymes, but inversely correlated with CRP levels (Spearman's r = -0.31, p = 0.008). Although not significant (p = 0.14) serum IFNβ levels were lower in the febrile phase in those who progressed to develop DHF (median 0, IQR 0 to 39.4 pg/ml), compared to those who had DF (median 37.1, IQR 0 to 65.6 pg.ml). The data suggest that adipokines are likely to play a role in the pathogenesis of dengue, which should be further explored for the potential to be used as prognostic markers and as therapeutic targets.

Dracunculose

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

Zhou H, Zhang J, Kirbis BS, Mula Z, Zhang W, Kuang Y, Huang Q, Yin L.
07-09-2023
J Ethnobiol Ethnomed.
https://pubmed.ncbi.nlm.nih.gov/37679773/

Background: Despite the popularity of modern medicine, medicinal plants remain a cornerstone of treatment for numerous diseases, particularly among ethnic groups and tribal communities around the globe. Ethnomedicine offers advantages such as ease of use, convenience, and economic benefits. Medicinal plant knowledge within Bulang ethnic community of southwest China is a valuable complement to Chinese ethnomedicine systems. Accumulated medical knowledge is due to the extensive length of occupation by Bulang People, considered the earliest inhabitants of Xishuangbanna; this has resulted in the development of various traditional treatment methods with local characteristics and unique curative effects. Therefore, there is exceeding value in exploring the medical knowledge of Bulang. Methods: A total of 175 local informants participated in the interviews and distribution of questionnaires in 10 Bulang villages in Menghai County, Xishuangbanna Prefecture, Yunnan Province, China. We documented the community of Bulang's use of medicinal herbs, and we used both the informant consensus factor (ICF) and use value (UV) methodologies to analyze the data. Furthermore, we conducted a comparative study to explore the potential of Bulang traditional medicine by comparing it to traditional Dai medicine. Results: The study recorded 60 medicinal plant species belonging to 41 families and 59 genera, including 22 species of herb, 22 species of shrub, nine species of trees, and seven species of liana. Araceae, Compositae, Lamiaceae and Leguminosae were found to have the highest number of species. The affordability and cultural heritage of Bulang medicine make it advantageous, Investigated Informants report that increased usage of Western medicine (88%), less availability of herbal medicine (95.43%), and the reduction in medicinal plant resources (80.57%) pose significant threats to Bulang medicine. All Bulang medicinal plants are naturally grown, with only 22 per cent being cultivated. Camellia sinensis (0.94) and Zingiber officinale (0.89) showed the highest UV values, while the function of Phyllanthus emblica L. and Houttuynia cordata Thunb. were also noted. The ICF revealed digestive system related diseases were the most commonly treated, with conditions of the motor system using the highest number of plant species. Finally, a comparison with traditional Dai medicine determined that 22 plants (36.67%) of the 60 surveyed had higher medicinal value in Bulang medicine. Conclusion: Bulang communities primarily source medicinal plants from the wild. Should environmental damage lead to the extinction of these medicinal plants, it could result in a shift toward modern Western medicine as a preferred medical treatment. Bulang ethnomedicine is a vital supplement to China's traditional medicine, particularly aspects of ethnic medicine relevant to daily life. Future research should emphasize inter-ethnic medical studies to reveal the untapped potential of medicinal plants.

Surface albedo measurements and surface type classification from helicopter-based observations during MOSAiC.

Sperzel TR, Jäkel E, Pätzold F, Lampert A, Niehaus H, Spreen G, Rosenburg S, Birnbaum G, Neckel N, Wendisch M.
06-09-2023
Sci Data.
https://pubmed.ncbi.nlm.nih.gov/37673937/

Assessment of Colocasia esculenta leaf extract as a natural alternative for Sitophilus zeamais control: Toxicological, biochemical, and mechanistic insights.

Oriyomi VO, Fagbohun OF, Akinola FT, Adekola MB, Oyedeji TT.
Sept-2023
Pestic Biochem Physiol.
https://pubmed.ncbi.nlm.nih.gov/37666616/

The present study assessed the toxicological, biochemical, and mechanism of action of Colocasia esculenta leaf extract (CELE) on Wistar albino rat and on cholinergic, antioxidant, and antiinflammatory enzymes in Sitophilus zeamais. This was with a view to assessing the potential benefits and safety profile of CELE as a natural alternative for insect control. The bioactivity of the fraction was evaluated using insecticidal and repellent activities against colonies of Sitophilus zeamais to obtain a VLC-chromatographed fraction which was spectroscopically characterized and investigated for enzyme inhibition. The results revealed the ethyl acetate fraction (EAF) as the most potent one with LC_{50} 6.198 µg/ml and 6.6 ± 0.5 repellency. The EAF had an LD_{50} > 5000 mg/kg but repeated dose >800 mg/kgbw po administration caused significant ($p < 0.05$) increase in liver and kidney function biomarkers accompanied with elevated atherogenic and coronary indices. Also, renal and hepatomorphological lesions increased in a dose-dependent manner. The High-Performance Liquid Chromatography analysis profiled 7 unknown compounds while the GC-qMS revealed 103 compounds in the CC6 fraction allowing for their identification, quantification, and providing insights into the biological activities and its potentials application. The CC6 fraction inhibited glutathione S-transferase (IC_{50} = 2265.260.60 mg/ml), superoxide dismutase (IC_{50} = 1485.300.78 mg/ml), catalase (IC_{50} = 574.471.57 mg/ml), acetyl cholinesterase (IC_{50} = 838.280.51 mg/ml), butyryl cholinesterase (IC_{50} = 1641.76 ± 1.14 mg/ml) and upregulated cyclooxygenase-2 (IC_{50} = 37.89 ± 0.15 mg/ml). Based on the result of the study, it could be inferred that the unidentified compounds present in the EAF exhibit strong insecticidal properties. The study concluded that the acute toxicity of the potent fraction showed no abnormal clinical toxic symptoms while a repeated dose of the extract in sub-acute studies showed a toxic effect that is dose-dependent. The mechanism of action of the purified fraction could be said to be by inhibition of cholinergic and antioxidant enzymes. However, the potent fraction also upregulated the activity of anti-inflammatory enzymes. Hence, regulated amount of CELE at a repeated dose <800 mg/kgbw could be considered for use as an anti-pest agent in Integrated Pest Management of Sitophilus zeamais.

Effects of microplastics and cadmium on growth rate, photosynthetic pigment content and antioxidant enzymes of duckweed (Lemma minor).

Yang X, Liao HM, Tan AJ, Gan SX, Yang GL.
Sept-2023
Environ Sci Pollut Res Int.

Cadmium (Cd) and polyethylene (PE) seriously contaminate the aquatic environment and threaten human health. Many studies have reported the toxic effects of Cd and PE on plants, whereas few have reported the combined contamination of these two pollutants. In this study, duckweed (Lemma minor) was used as an indicator to explore the effect of PE microplastics (PE-MPs) at concentrations of 10, 50, 100, 200, and 500 mg/L on tolerance to 1 mg/L Cd. The results showed that different concentrations of PE-MPs inhibited the growth rate and chlorophyll content of duckweed to different degrees, both of which were minimal at 50 mg/L PE-MPs, 0.11 g/d, and 0.32 mg/g, respectively. The highest Cd enrichment (7.77 mg/kg) and bioaccumulation factors (94.22) of duckweed were detected when Cd was co-exposed with 50 mg/L of PE-MPs. Catalase and peroxidase activity first decreased and then increased with increasing PE-MPs concentrations, showing "hormesis effects", with minimum values of 11.47 U/g and 196.00 U/g, respectively. With increasing concentrations of PE-MPs, the effect on superoxide dismutase activity increased and then declined, peaking at 162.05 U/g, and displaying an "inverted V" trend. The amount of malondialdehyde rose with different PE-MPs concentrations. This research lay a foundation for using duckweed to purify water contaminated with MPs and heavy metals.

Effects of konjac glucan-nan/low-acyl gellan edible coatings loaded thymol-β-cyclodextrin microcapsules on postharvest blueberry.

Ding J, Liu C, Huang P, Li H, Liu Y, Sameen DE, Zhang Y, Liu Y, Qin W.
01-01-2024
Food Chem.
https://pubmed.ncbi.nlm.nih.gov/37549621/

Dracunculiasis Eradication: End-Stage Challenges.

Hopkins DR, Weiss AJ, Torres-Velez FJ, Sapp SGH, Ijaz K.
27-06-2022
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895421/

Echinococcose

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

He Y, Cui Q, Hu Z.
Juil-2023
Math Biosci Eng.
https://pubmed.ncbi.nlm.nih.gov/37679150/

A transmission dynamics model with the logistic growth of cystic echinococcus in sheep was formulated and analyzed. The basic reproduction number was derived and the results showed that the global dynamical behaviors were determined by its value. The disease-free equilibrium is globally asymptotically stable when the value of the basic reproduction number is less than one; otherwise, there exists a unique endemic equilibrium and it is globally asymptotically stable. Sensitivity analysis and uncertainty analysis of the basic reproduction number were also performed to screen the important factors that influence

the spread of cystic echinococcosis. Contour plots of the basic reproduction number versus these important factors are presented, too. The results showed that the higher the deworming rate of dogs, the lower the prevalence of echinococcosis in sheep and dogs. Similarly, the higher the slaughter rate of sheep, the lower the prevalence of echinococcosis in sheep and dogs. It also showed that the spread of echinococcosis has a close relationship with the maximum environmental capacity of sheep, and that they have a remarkable negative correlation. This reminds us that the risk of cystic echinococcosis may be underestimated if we ignore the increasing number of sheep in reality.

Primary cerebral cystic echinococcosis in a child from Roman countryside: Source attribution and scoping review of cases from the literature.

Casulli A, Pane S, Randi F, Scaramozzino P, Carvelli A, Marras CE, Carai A, Santoro A, Santolamazza F, Tamarozzi F, Putignani L.
05-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37669300/

Primary Hydatid Cyst of the Thigh: Atypical Location and Perioperative Strategies to Minimize Recurrence After Accidental Cyst Rupture.

Ahmed HA, Almasoudi EA, Hetaimish BM, Samargandi R.
03-08-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37664270/

Annual assessment of Echinococcus multilocularis surveillance reports submitted in 2023 in the context of commission delegated regulation (EU) 2018/772.

European Food Safety Authority (EFSA); Rusinà A, Zancanaro G.
31-08-2023
EFSA J.
https://pubmed.ncbi.nlm.nih.gov/37662482/

This report is part of the *Echinococcus multilocularis* surveillance scientific reports which are presented annually by EFSA to the European Commission and are intended to assess the sampling strategy, data collection and detection methods used by Finland, Ireland, United Kingdom (Northern Ireland) and Norway in their respective surveillance programmes. The surveillance programmes of these four countries were evaluated by checking the information submitted by each of them and verifying that the technical requirements were fulfilled as laid down in Commission Delegated Regulation (EU) 2018/772 of 21 November 2017 supplementing Regulation (EU) No 576/2013 of the European Parliament and of the Council with regard to preventive health measures for the control of *Echinococcus multilocularis* infection in dogs, and repealing Delegated Regulation (EU) No 1152/2011. The information was divided into four different categories for assessment: the type and sensitivity of the detection method, the selection of the target population, the sampling strategy and the methodology. For each category, the main aspects that need to be considered in order to accomplish the technical requirements of the legislation were checked against compliance of several criteria. The countries participating in this surveillance (Finland, Ireland, Norway and United Kingdom [Northern Ireland]) succeeded in the fulfilment of the technical legal requirements foreseen in Commission Delegated Regulation (EU) 2018/772 concerning these four different categories None of the four countries recorded positive samples in the 12-month reporting period.

Presence of Echinococcus granulosussensulato in the endoparasitic fauna of feral dogs in Tierra del Fuego, Argentina.

Zanini F, Di Salvo V, Pierangeli N, Lazzarini L, Curto E.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652635/

The feral dog population from Tierra del Fuego (Argentina) has affected provincial sheep production, and is responsible for the decrease of 43% of the sheep stock. In addition, feral dogs preys on the native fauna, especially the guanaco (Lama guanicoe), a species protected by law. Except for some data on the aforementioned impact, very little is known about feral dogs features in this region, such as distribution, abundance, diet, reproduction, health status, among others. Therefore, a descriptive observational study was carried out in the period 2018-2021 in Tierra del Fuego, with the aim to recognize the endoparasitic fauna of these dogs, with emphasis on Echinococcus granulosus sensu lato (s.l.). Feces samples were collected from 83 feral dogs captured in 15 farms, which were evaluated using flotation and sedimentation coproparasitological techniques, and optical microscope observation. These qualitative methods showed that 66.3% of the samples were positive. Nine parasitic forms were found, including eggs of taenids, Toxocara canis and Toxascaris leonina, and Sarcocystis spp. oocysts and Giardia spp. cysts. Samples with more than one parasitic form were also observed, among which the Taenia/Sarcocystis spp. association was the most frequent. For the diagnosis of canine echinococcosis, the detection of Echinococcus spp. antigens by Copro-ELISA and the molecular confirmation by Copro-PCR were performed. The Copro-ELISA test was positive in 10/80 (12.5%) of the samples processed, while 11 samples (13.8%) were positive by Copro-PCR. Their distribution showed that 9 (81.8%) corresponded to farms with sheep farming, and 2 (18.2%) with cattle farming. The presence of E. granulosus s.l. in feral dogs from Tierra del Fuego is the most relevant finding in this study. These results confirm that feral dogs have access to viscera infected with hydatid cysts. However, the intermediate hosts involved (sheep, cattle or guanacos) should be investigated. Its impact on the transmission of cystic echinococcosis in this region should be evaluated, as well as the adequacy of the disease prevention and control

actions implemented in Tierra del Fuego should be considered. Finally, the existence of a wild cycle of the disease should be evaluated, in which feral dogs would act as a source of infection for other animals and humans.

Case Report: Semi-Ex Vivo Hepatectomy Combined with Autologous Liver Transplantation for Alveolar Echinococcosis in Children.

Xia P, Wang XQ, Tian QS, Shang-Guan CL, Zhu HH.
07-08-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37549899/

A rare case of gallbladder cystic echinococcosis disease in western China.

Zheng Y, Xu L, Song X, Ding F, Li X.
Déc-2023
Parasitol Int.
https://pubmed.ncbi.nlm.nih.gov/37544640/

Hydatid disease, also known as echinococcosis, is an endemic zoonotic parasitic disease caused by larvae of the Echinococcus tapeworm.Humans as accidental intermediate hosts in the parasite life cycle, echinococcus usually parasitizes the liver, solitary cystic echinococcosis in the gallbladder is very rare. Here we report a rare case of cystic echinococcosis in the gallbladder without liver involvement. A female patient was admitted to the hospital primarily for "right upper abdominal pain with radiating pain in the back of the shoulder for 20 days", initially suspected to be gallbladder stones, and underwent laparoscopic cholecystectomy after completing the relevant investigations, and was diagnosed with primary cystic echinococcosis of the gallbladder based on the pathologic findings in the postoperative period. The patient recovered well after surgery and remained well without complications during the 6-month follow-up period. This case illustrates that echinococcus granulosus can also parasitize in the gallbladder only, although it is quite uncommon. In addition, it is difficult to distinguish it from gallbladder stones by conventional imaging. The diagnosis of some cases of gallbladder cystic echinococcosis is completed during surgery and confirmed by postoperative pathological results.

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

Luan H, Liu K, Tian Q, Chen Y, Peng C, Sun X, Song X.
31-07-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37524327/

Impact of Echinococcus granulosus Antigens on Monocyte Development and Dendritic Cell Differentiation.

Wang M, Qiao F, Li Z, Wang Q, Shang Z, Hei J, Ma X, Wang Y.
01-09-2023
Iran J Immunol.
https://pubmed.ncbi.nlm.nih.gov/37458144/

Leishmaniose

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

Dinesh RJ, Srividya A, Subramanian S, Krishnamoorthy K, Sabesan S, Raghorte MC, Kumar A, Jambulingam P.
07-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37676897/

Background: Triple drug regimen (IDA; Ivermectin, Diethylcarbamazine, Albendazole) recommended for accelerating elimination of lymphatic filariasis was launched in India in December 2018. Nagpur district in Maharashtra was one of the first five districts where this strategy was introduced. The National Vector Borne Disease Control Programme (NVBDCP) at the district reported ~85.0% treatment coverage in the first round of mass drug administration (MDA) with IDA implemented in EU-2 in Nagpur district in January 2019. As per the national guideline, a coverage evaluation survey was carried out and both quantitative and qualitative data were collected to assess the treatment coverage, the level of community preparation and identify the gaps, if any, for improvement. Methodology: A Coverage Evaluation Survey (CES) following the WHO recommended protocol was conducted in one of the two evaluation units (EU-2) in Nagpur district in March 2019. Coverage Sample Builder (CSB) V2.9 tool was used to calculate the sample size, select sites and estimate drug coverage. The CSB tool followed a two-stage cluster sampling procedure to select 30 primary sampling units (ward/village as a cluster) and a list of random numbers for selecting households (HHs) in each cluster. The results were analyzed for operational indicators. Stata ver. 14.0 software was used to construct the 95% confidence limits accounting for clustering. Results: A total of 1601 individuals aged 5-85 years of both gender from 328 HHs were surveyed from the 30 randomly selected clusters in EU-2. The mean age was 33.8±17.6 years. Among the surveyed population, 78.0% received the drugs (programme reach) and 66.1% consumed the drugs (survey coverage). Survey coverage was significantly higher in rural (82.6%) than in urban (59.4%) and peri-urban (58.6%) areas (P<0.001). Directly observed treatment (DOT) among the surveyed population was 51.6%. Adverse events were reported among 6.9% respondents who reported to have consumed the drugs. Conclusion: The IDA based MDA strategy could achieve just the required level of treatment coverage (~65%) in EU-2, Nagpur district, which had previously undergone several rounds of DA-MDAs (Diethylcarbamazine, Albendazole). Having achieved an effective treatment coverage of >80% in rural areas, the coverage in urban and peri-urban areas need to be improved in order to attain the impact of IDA-MDA. It is imperative to strengthen drug delivery and community preparation activities along with improved DOT especially in urban and peri-urban areas to achieve the required level

of treatment coverage. Addition of ivermectin did not have any additional perceived adverse events.

How correlations between treatment access and surveillance inclusion impact neglected tropical disease monitoring and evaluation-A simulated study.

Clark J, Davis EL, Prada JM, Gass K, Krentel A, Hollingsworth TD.
06-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37672518/

Neglected tropical diseases (NTDs) largely impact marginalised communities living in tropical and subtropical regions. Mass drug administration is the leading intervention method for five NTDs; however, it is known that there is lack of access to treatment for some populations and demographic groups. It is also likely that those individuals without access to treatment are excluded from surveillance. It is important to consider the impacts of this on the overall success, and monitoring and evaluation (M&E) of intervention programmes. We use a detailed individual-based model of the infection dynamics of lymphatic filariasis to investigate the impact of excluded, untreated, and therefore unobserved groups on the true versus observed infection dynamics and subsequent intervention success. We simulate surveillance in four groups-the whole population eligible to receive treatment, the whole eligible population with access to treatment, the TAS focus of six- and seven-year-olds, and finally in >20-year-olds. We show that the surveillance group under observation has a significant impact on perceived dynamics. Exclusion to treatment and surveillance negatively impacts the probability of reaching public health goals, though in populations that do reach these goals there are no signals to indicate excluded groups. Increasingly restricted surveillance groups over-estimate the efficacy of MDA. The presence of non-treated groups cannot be inferred when surveillance is only occurring in the group receiving treatment.

Chyluria: clearing the 'muddiness' with lipiodol lymphangiography.

Khera PS, Garg PK, Choudhary GR, Ghosh TS, Tiwari S, Choudhary B.
2023
Sudan J Paediatr.
https://pubmed.ncbi.nlm.nih.gov/37663099/

Comparison of collection methods for Phlebotomus argentipes sand flies to use in a molecular xenomonitoring system for the surveillance of visceral leishmaniasis.

McIntyre-Nolan S, Kumar V, Mark-Carew M, Kumar K, Nightingale ES, Dalla Libera Marchiori G, Rogers ME, Kristan M, Campino S, Medley GF, Das P, Cameron MM.
01-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37656745/

Pharmacokinetics of Moxidectin combined with Albendazole or Albendazole plus Diethylcarbamazine for Bancroftian Filariasis.

Chhonker YS, Bjerum C, Bala V, Ouattara AF, Koudou BG, Gabo TP, Alshehri A, Meïté A, Fischer PU, Weil GJ, King CL, Budge PJ, Murry DJ.
24-08-2032
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37616301/

Moxidectin (MOX) is a milbemycin endectocide recently approved by the U.S. FDA for the treatment of onchocerciasis in persons at least 12 years of age. MOX has been shown to have a good safety profile in recent clinical trials. The efficacy of MOX for the treatment of lymphatic filariasis (LF) and its potential use in mass drug administration protocols for the elimination of LF is currently under evaluation. In the context of a clinical trial, we investigated the pharmacokinetics and drug interactions of a combination of MOX plus albendazole (ALB) with or without diethylcarbamazine (DEC) compared to ivermectin (IVM) plus ALB with or without DEC in the following four different treatment arms: (I) IVM (0.2mg/kg) plus DEC (6 mg/kg) and ALB (400mg); (II) IVM plus ALB; (III) MOX (8 mg) plus DEC and ALB; and (IV) MOX plus ALB. Drug concentrations were determined using validated liquid chromatography-mass spectrometric methods. Pharmacokinetic parameters were determined using standard non-compartmental analysis methods. Statistical analysis was performed using JMP software. Fifty-eight of 164 study participants (53 men and five women) were included with ages ranging from 18 to 63 yrs (mean = 37). MOX apparent oral clearance (Cl/F) ranged from 0.7 to 10.8 L/hr with Cmax values ranging from 20.8 to 314.5 ng/mL. The mean (range) area under the curve (AUC)0-∞ for MOX, 3405 ng*hr/mL (742-11376), and IVM 1906 ng*hr/mL (692-5900), varied over a ~15.3 and ~8.5-fold range, respectively. The geometric mean ratio for Cmax, AUC0-t, and AUC0-∞ were within the no-drug interaction range of 80-125% for all drugs. This indicates that the addition of MOX to ALB alone or ALB plus DEC for LF therapy did not alter the drug exposure of co-administered drugs compared to IVM combinations. Clinical Trial Registration: NCT04410406, https://clinicaltrials.gov/.

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

Zhou Z, Sui X, Cao Z, Li X, Qing L, Tang J.
Oct-2023
Peptides.
https://pubmed.ncbi.nlm.nih.gov/37652635/

Secondary lymphedema often occurs after filariasis, trauma, lymph node dissection and radiation therapy, which is manifested by infiltration of inflammatory cells and fibrosis formation in pathologically. Substance P is a widely used neuropeptide in the field of tissue repair, while the regenerative potential of the substance P has not been proven in the secondary lymphedema. In this study,

animal model of secondary lymphedema was constructed by excising the skin and subcutaneous lymphatic network in the tail of mice, and the degree of swelling in the tail of mice was evaluated after 6 weeks under the treatment with substance P. Immunofluorescence staining was also performed to assess immune cell infiltration, subcutaneous fibrosis and lymphangiogenesis. The results revealed that substance P significantly alleviated post-surgical lymphedema in mice. Furthermore, we found that substance P promoted macrophages M2 polarization, a process associated with downregulation of the NF-kB/NLRP3 pathway. After application of disodium clodronate (macrophage scavenger, CLO), the positive effect of substance P in lymphedema is significantly inhibited. In vitro experiments, we further demonstrated the polarizing effect of substance P on bone marrow-derived macrophages (BMDMs), while substance P inhibited the activation of the NF-kB/NLRP3 pathway in BMDMs after the treatment of lipopolysaccharide (LPS). In addition, polarized macrophages were demonstrated to promote the proliferation, tube-forming and migratory functions of human lymphatic endothelial cells (hLEC). In conclusion, our study provides preliminary evidence that substance P alleviates secondary lymphedema by promoting macrophage M2 polarization, and this therapeutic effect may be associated with downregulation of the NF-kB/NLRP3 pathway.

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.
01-09-2023
Int Health.
https://pubmed.ncbi.nlm.nih.gov/37232124/

Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.

Geospatial modelling of lymphatic filariasis and malaria co-endemicity in Nigeria.

Eneanya OA, Reimer LJ, Fischer PU, Weil GJ.
01-09-2023
Int Health.
https://pubmed.ncbi.nlm.nih.gov/37096453/

Gale

Clinical and Epidemiological Characteristics of Patients Being Treated for Scabies in Spain: Opportunities for Improvement - A Multicenter Cross-Sectional CLINI-AEDV Study.

Casas CG, Villaverde RR, Carmona ÁP, Camporro ÁF, Angulo Menéndez AG, Buylla Puente MCÁ, Pasquali P, Vázquez ÁA, Masferrer E, González LR, Sánchez DR, Caballero-Linares CF, Vaquerizo AT, Pena NI, de Piérola SF, Seral CM, Carbó MA, Naranjo LA, Tornay RB, Novo TS, Tapia VF, Gorgojo AM, Mas JA, Parera Amer ME, Feal PP, Taberner R, Busquets MU, Sánchez IV, Aller LP, Gutiérrez IS, Bárcena TU, Manrique BA, Velázquez AS, García EM, Pérez MG, Doval IG; CLINI-AEDV.
05-09-2023
Actas Dermosifiliogr.
https://pubmed.ncbi.nlm.nih.gov/37678633/

Background and objective: The results of studies support the hypothesis that scabies is on the rise in Spain. There are also concerns about the possible development of resistance to treatment and an increase in atypical presentations. The aims of this study were to describe the demographic and clinical profile of patients with scabies seen by dermatologists in Spain, to identify the possible emergence of atypical forms of scabies, and to explore the frequency of treatment failures and associated risk factors. Methods: We conducted an observational, cross-sectional, multicenter study of data collected prospectively in April and May 2023 using the CLINI-AEDVp platform created by the Spanish Academy of Dermatology and Venereology (AEDV). Results: Participating dermatologists from 31 hospitals in 15 of Spain's autonomous communities recorded 186 cases of active scabies (51% in women) during the study period. A diagnostic certainty level of A, B or C as per the International Alliance for the Control of Scabies Consensus Criteria was required for diagnosis. Overall, 92% of patients had typical scabies and 66% had already been treated with a scabicide for the current episode. Of the treated patients, only 36% had received and completed adequate treatment (including the simultaneous treatment of all household members) and 50% had not received clear written recommendations. Conclusions: In a high proportion of the cases of scabies studied, the patient had already received treatment. In those cases, we observed several remediable shortcomings that could explain why some of these treatments had failed. Remedying these deficiencies should lead to better control of scabies and an improved assessment of the actual effectiveness of currently available scabicides.

[[Translated article]]Comment on «Epidemic Scabies: New Treatment Challenges in an Ancient Disease».

Suárez-Amor O, Monteagudo B, Cabanillas M.
05-09-2023
Actas Dermosifiliogr.
https://pubmed.ncbi.nlm.nih.gov/37678631/

No secondary impact of ivermectin mass drug administration for onchocerciasis elimination on the prevalence of scabies in northwestern Ethiopia.

Yirgu R, Middleton J, Fekadu A, Davey G, Bremner S, Jones CI, Cassell JA.
04-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37665766/

Background: Mass drug administration (MDA) is among the five major strategies that are currently in use to control, eliminate or eradicate Neglected Tropical Diseases (NTDs). Optimising MDA to control multiple NTDs maximises impact. The objective of this study is to estimate the secondary impact of ivermectin MDA for onchocerciasis on the prevalence of scabies. Methods: This quasi-experimental study was conducted in Ayu Guagusa district, northwestern Ethiopia. Scabies prevalence was estimated in surveys before the MDA, at 6 and 12 months afterwards. The sample size was 1437 people from a panel of 381 randomly selected study households. Multistage sampling was employed in randomly selecting six kebeles (the lowest administrative unit) with respective gotes (small villages) and households. All members of the selected households were invited to participate in the study and participants who were available in all three surveys formed a cohort. Results: Scabies prevalence was similar prior to the MDA (13.4%, 95% CI 11.7 to 15.2%) and 6 months after (11.7%, 95% CI 10.1 to 13.2%) but was substantially greater at 12 months (22.1%, 95% CI 20.1 to 24.1%). The 6-month incidence and disappearance rates were 10.8% (95% CI 8.8 to 13.2%) and 82.6% (95% CI 75.0 to 88.6%), respectively. Conclusions: Ivermectin MDA for onchocerciasis was not observed to have a secondary impact on the prevalence of scabies over the follow-up period of 12 months.

Evaluation of the scabicidal effect of a single dose of fluralaner in a rabbit model of crusted scabies.

Sharaf MS, Othman AA, Abd El Ghaffar AE, Ali DM, Eid MM.
01-09-2023
Parasitol Res.
https://pubmed.ncbi.nlm.nih.gov/37656230/

[Eczema and its treatment in older adults].

Harries L, Traidl S, Klespe KC, Werfel T.
Sept-2023
Dermatologie (Heidelb).
https://pubmed.ncbi.nlm.nih.gov/37638989/

Host, environment, and anthropogenic factors drive landscape dynamics of an environmentally transmitted pathogen: Sarcoptic mange in the bare-nosed wombat.

Ringwaldt EM, Brook BW, Buettel JC, Cunningham CX, Fuller C, Gardiner R, Hamer R, Jones M, Martin AM, Carver S.
Sept-2023
J Anim Ecol.
https://pubmed.ncbi.nlm.nih.gov/37221666/

Understanding the spatial dynamics and drivers of wildlife pathogens is constrained by sampling logistics, with implications for advancing the field of landscape epidemiology and targeted allocation of management resources. However, visually apparent wildlife diseases, when combined with remote-surveillance and distribution modelling technologies, present an opportunity to overcome this landscape-scale problem. Here, we investigated dynamics and drivers of landscape-scale wildlife disease, using clinical signs of sarcoptic mange (caused by Sarcoptes scabiei) in its bare-nosed wombat (BNW; Vombatus ursinus) host. We used 53,089 camera-trap observations from over 3261 locations across the 68,401 km^2 area of Tasmania, Australia, combined with landscape data and ensemble species distribution modelling (SDM). We investigated: (1) landscape variables predicted to drive habitat suitability of the host; (2) host and landscape variables associated with clinical signs of disease in the host; and (3) predicted locations and environmental conditions at greatest risk of disease occurrence, including some Bass Strait islands where BNW translocations are proposed. We showed that the Tasmanian landscape, and ecosystems therein, are nearly ubiquitously suited to BNWs. Only high mean annual precipitation reduced habitat suitability for the host. In contrast, clinical signs of sarcoptic mange disease in BNWs were widespread, but heterogeneously distributed across the landscape. Mange (which is environmentally transmitted in BNWs) was most likely to be observed in areas of increased host habitat suitability, lower annual precipitation, near sources of freshwater and where topographic roughness was minimal (e.g. human modified landscapes, such as farmland and intensive land-use areas, shrub and grass lands). Thus, a confluence of host, environmental and anthropogenic variables appear to influence the risk of environmental transmission of S. scabiei. We identified that the Bass Strait Islands are highly suitable for BNWs and predicted a mix of high and low suitability for the pathogen. This study is the largest spatial assessment of sarcoptic mange in any host species, and advances understanding of the landscape epidemiology of environmentally transmitted S. scabiei. This research illustrates how host-pathogen co-suitability can be useful for allocating management resources in the landscape.

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

Prevalence of intestinal parasites in street dogs (Canis lupus familiaris) with highlights on zoonosis in Lalitpur, Nepal.

Adhikari RB, Dhakal MA, Ghimire TR.
05-09-2023
Vet Med Sci.
https://pubmed.ncbi.nlm.nih.gov/37669424/

Progress from morbidity control to elimination as a public health problem of schistosomiasis and the status of soil-transmitted helminth infection in Togo: a second impact assessment after ten rounds of mass drug administration.

Dorkenoo AM, Phillips AE, Klein L, Lack F, Ataba E, Yakpa K, Tagba AE, Assoti BE, Sossou E, Tchalim M, Datagni G, Seim A, Milord MD, Kassankogno Y.
04-09-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37667301/

Background: Due to the burden of schistosomiasis (SCH) and soil-transmitted helminths (STH), Togo Ministry of Health launched a program for Preventive Chemotherapy Neglected Tropical Diseases (PC-NTDs) in 2009, initiating integrated mass drug administration (MDA) the following year for the three PC-NTDs: SCH, STH and onchocerciasis. Significant reduction of infection across the country was noted in 2015 during the first impact assessment, following 5 years of high-coverage MDA implemented at the sub-district level for SCH and district level for STH. After another 5 years of effective MDA, a second survey was conducted in 2021 to re-evaluate the situation of SCH and STH. Methods: A cross-section of school-aged children was taken across ten districts of Togo. A total of 302 schools in 92 sub-districts were sampled, with 24 school-aged children per school resulting in 7248 children surveyed. Urine samples were tested by haemastix® for Schistosoma haematobium, with urine filtration for the presence of eggs conducted on haematuria-positive samples. Stool samples were collected in a subset of 34 sub-districts in seven out of the ten surveyed districts, where STH and Schistosoma mansoni endemicity was high during the 2015 impact assessment. Duplicate (two) Kato-Katz analysis was performed for each stool sample. Sociodemographic and school-level water, sanitation and hygiene information was also collected. Results: Overall, SCH prevalence was 5.90% (95% CI: 5.4-6.5), with 5.09% (95% CI: 4.64-5.67) for S. haematobium and 2.56% (95% CI: 1.98-3.29) for S. mansoni. STH prevalence was 19.7% (95% CI: 18.2-21.4), with 19.6% (95% CI: 18.1-21.3) hookworm, 0.08% (95% CI: 2.2-5.8) Trichuris trichiura and 0.04% (95% CI: 0.01-0.33) Ascaris lumbricoides. Compared to baseline, a significant reduction in both SCH (22.2% to 5.90%) and STH (29.2% t0 19.7%) prevalence was observed. Children aged 5-9 years were less infected than older peers aged 10-14 years: 4.76% vs. 7.53% ($P < 0.01$) for SCH and 17.2% vs. 23.0% ($P < 0.01$) for STH. Conclusions: After 10 years of high coverage integrated MDA, Togo has achieved low prevalence SCH infection through the sub-district MDA implementation with considerable infection heterogeneity within sub-districts. As STH infection has not reached a level where the infections are not a public health problem, the sub-district treatment strategy could also be adopted in addition to improvement of treatment coverage among preschool age children and hygiene and sanitation practices.

Late relapse of cutaneous larva migrans.

Dam Larsen F, Larsen CS, Jespersen S.
23-08-2023
IDCases.
https://pubmed.ncbi.nlm.nih.gov/37663135/

Cutaneous larva migrans is a common disease in the tropics and among travelers. The itchy, serpentigious rash often appears within days to weeks after transmission. There are only few reported cases of late relapses. Here, we present a case of a relapse of cutaneous larva migrans more than one year after exposure.

High diversity and sharing of strongylid nematodes in humans and great apes co-habiting an unprotected area in Cameroon.

Ilík V, Kreisinger J, Modrý D, Schwarz EM, Tagg N, Mbohli D, Nkombou IC, Petrželková KJ, Pafčo B.
25-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37624869/

A case report and literature review of an aortoduodenal fistula complicated by intestinal Ascaris lumbricoides.

Hou XF, Liu LX, Zhao ZX, Yang JY.
Sept-2023
Asian J Surg.
https://pubmed.ncbi.nlm.nih.gov/37105813/

Leishmaniose

The application of MD simulation to lead identification, vaccine design, and structural studies in combat against leishmaniasis - A review.

Vijayakumar S, Laxman Kumar L, Borkotoky S, Murali A.
01-09-2023
Mini Rev Med Chem.
https://pubmed.ncbi.nlm.nih.gov/37680156/

Drug discovery, vaccine design, and protein interaction studies are rapidly moving toward the routine use of molecular dynamics simulations (MDS) and related methods. As a result of MDS, it is possible to gain insights into the dynamics and function of identified drug targets, antibody-antigen interactions, potential vaccine candidates, intrinsically disordered proteins, and essential proteins. The MDS appears to be used in all possible ways in combating diseases such as cancer, however, it has not been well documented as to how effectively it is applied to infectious diseases such as Leishmaniasis. As a result, this systematic review aims to survey the application of MDS in combating leishmaniasis. We have systematically collected articles that illustrate the implementation of MDS in drug discovery, vaccine development, and structural studies related to Leishmaniasis. Of all the

articles reviewed, we identified that only a limited number of studies focused on the development of vaccines against Leishmaniasis through MDS. Also, the PCA and FEL studies were not carried out in most of the studies. These two were globally accepted utilities to understand the conformational changes and hence it is recommended that this analysis should be taken up in similar approaches in the future.

Natural infection with Leishmania (Mundinia) martiniquensis supports Culicoides peregrinus (Diptera: Ceratopogonidae) as a potential vector of leishmaniasis and characterization of a Crithidia sp. isolated from the midges.

Kaewmee S, Mano C, Phanitchakun T, Ampol R, Yasanga T, Pattanawong U, Junkum A, Siriyasatien P, Bates PA, Jariyapan N.
22-08-2023
Front Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37675418/

Green SPIONs as a novel highly selective treatment for leishmaniasis: an in vitro study against Leishmania amazonensis intracellular amastigotes.

Verçoza BRF, Bernardo RR, de Oliveira LAS, Rodrigues JCF.
30-08-2023
Beilstein J Nanotechnol.
https://pubmed.ncbi.nlm.nih.gov/37674544/

Antileishmanial effects of Crotalaria spectabilis Roth aqueous extracts on Leishmania amazonensis.

Pacheco JS, Teixeira ÉMGF, Paschoal RG, Torres-Santos EC, Simone SG, Silva-López RED.
04-09-2023
An Acad Bras Cienc.
https://pubmed.ncbi.nlm.nih.gov/37672397/

Fifteen polar extracts from leaf, seed, pod, stem, flower and root of Crotalaria spectabilis were prepared using aqueous systems, based on the principles of green chemistry, and showed different protease inhibitor (PI) activities on trypsin, papain, pepsin and the extracellular L. amazonensis serine protease (LSPIII). The most pronounced inhibitory effect on LSPIII was observed in leaf (CS-P), root, stem, flower (CS-FPVPP) and pod (CS-VA) extracts. Crotalaria extracts exhibited low cytotoxicity on macrophages; however, they decreased the viability of L. amazonensis promastigotes and amastigotes, as observed in leaf (CS-AE, CS-P, CS-T and CS-PVPP), seed (CS-ST), flower and root (CS-RA) extracts. CS-P was chosen to study PI and secondary metabolites and a 10-12 kDa protein, analyzed by mass spectrometry, was identified as a serine PI homologous with papaya latex serine PI. Glycosylated flavonoids, such as quercetins, vitexin and tricin were the major secondary metabolites of CS-P. The presence of PIs in C. spectabilis is a new finding, especially in other organs than seeds since PIs have been reported only in seed legumes. Besides, this is the first report of antileishmanial activity of C. spectabilis extracts and the identification of serine polypeptide PI and glycosylated flavonoids from leaf.

Twitter trends in #Parasitology determined by text mining and topic modelling.

Ellis JT, Reichel MP.
12-08-2023
Curr Res Parasitol Vector Borne Dis.
https://pubmed.ncbi.nlm.nih.gov/37670843/

This study investigated the emergence and use of Twitter, as of July 2023 being rebranded as X, as the main forum for social media communication in parasitology. A dataset of tweets was constructed using a keyword search of Twitter with the search terms 'malaria', '*Plasmodium*', '*Leishmania*', '*Trypanosoma*', '*Toxoplasma*' and '*Schistosoma*' for the period from 2011 to 2020. Exploratory data analyses of tweet content were conducted, including language, usernames and hashtags. To identify parasitology topics of discussion, keywords and phrases were extracted using KeyBert and biterm topic modelling. The sentiment of tweets was analysed using VADER. The results show that the number of tweets including the keywords increased from 2011 (for malaria) and 2013 (for the others) to 2020, with the highest number of tweets being recorded in 2020. The maximum number of yearly tweets for *Plasmodium*, *Leishmania*, *Toxoplasma*, *Trypanosoma* and *Schistosoma* was recorded in 2020 (2804, 2161, 1570, 680 and 360 tweets, respectively). English was the most commonly used language for tweeting, although the percentage varied across the searches. In tweets mentioning *Leishmania*, only ~37% were in English, with Spanish being more common. Across all the searches, Portuguese was another common language found. Popular tweets on *Toxoplasma* contained keywords relating to mental health including depression, anxiety and schizophrenia. The *Trypanosoma* tweets referenced drugs (benznidazole, nifurtimox) and vectors (bugs, triatomines, tsetse), while the *Schistosoma* tweets referenced areas of biology including pathology, eggs and snails. A wide variety of individuals and organisations were shown to be associated with Twitter activity. Many journals in the parasitology arena regularly tweet about publications from their journal, and professional societies promote activity and events that are important to them. These represent examples of trusted sources of information, often by experts in their fields. Social media activity of influencers, however, who have large numbers of followers, might have little or no training in science. The existence of such tweeters does raise cause for concern to parasitology, as one may start to question the quality of information being disseminated.

Validation of a multiplex microsphere immunoassay for detection of antibodies to Trypanosoma cruzi in dogs.

Rodriguez CA, Busselman RE, Shen H, Saunders AB, Tarleton R, Hamer SA.
05-09-2023
J Vet Diagn Invest.

https://pubmed.ncbi.nlm.nih.gov/37670473/

'Self-stigma' of people with cutaneous leishmaniasis the unrecognized one: what do we think; what do we know; what can we prove?

Hagos B, Zerihun Z.
05-09-2023
Int J Equity Health.
https://pubmed.ncbi.nlm.nih.gov/37670383/

Cutaneous leishmaniasis (CL) refers to a group of parasitic infections caused by the protozoan parasite Leishmania spp. Lack of knowledge and awareness regarding this disease creates a burden for patients with CL to deal with self-stigma. The aim of this ethnographic study is to provide an analysis of self-stigma experienced by patients with CL through an in-depth understanding of the self-stigma experienced by patients with cutaneous leishmaniasis. A qualitative data analysis approach was used for this study. Semi-structured interviews and participant observation were conducted with 33 individuals with CL, and data were analyzed using a thematic analysis method. Interviews revealed that individuals with CL experience severe self-stigma. The participants spoke of their struggle to live with physical appearances that differed from societal norms. Furthermore, they also highlighted that people with CL are often viewed as unclean and contagious, which further adds to their self-stigma. Fear of social exclusion often forced individuals with CL to isolate themselves, leading to a detrimental impact on their mental health and quality of life. This study provides valuable insights into the experiences of patients with CL who are subjected to self-stigma. The findings suggest that the lack of knowledge and the considerable misconceptions surrounding CL create barriers for patients to deal with the condition and the self-stigma attached to it. To address this issue, there is a need for dedicated public health campaigns and health education that increase awareness about CL and provide appropriate support and care for those affected.

Histopathological, immunohistochemical and molecular analyses of foetuses from a female dog naturally infected by Leishmania (Leishmania) infantum - Case report.

Heil AC, de Melo Lima Waterloo M, Guerra JM, Ferreira AMR, da Silva Leite J.
05-09-2023
Vet Med Sci.
https://pubmed.ncbi.nlm.nih.gov/37669416/

Anti-Leishmania spp. antibody detection in domestic cats from a visceral leishmaniasis transmission area.

Hartmann G, Roman IJ, Lorenzetti DM, Herbichi AP, Mazaro RD, Dos Santos MY, Tonin AA, Vogel FSF, Fighera RA.
05-09-2023
Parasitol Res.
https://pubmed.ncbi.nlm.nih.gov/37669416/

LIMITATION OF PRIMERS USED IN PCR FOR THE CHARACTERIZATION OF LEISHMANIA INFANTUM.

de Araújo HK, de Oliveira Castro S, da Silva Valejo MJA, da Costa Lima Junior MS, Neitzke-Abreu HC.
01-10-2023
J Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37668295/

Conventional PCR provides Leishmania species characterization with even a small amount of biological material. Species-specific primers have been a widely used alternative; however, nonspecific amplifications are a reality, interfering with PCR efficiency. In endemic areas with multiple etiological agents for leishmaniasis, there is a requirement for higher specificity of primers. This study evaluates 3 pairs of primers described for the identification and characterization of Leishmania infantum. Primers RV1/RV2, LEISH1/LEISH2, and FLC2/RLC2 were used with the DNA of L. infantum, Leishmania amazonensis, and Leishmania braziliensis. An initial temperature curve was performed (52-62 C) to determine the optimal annealing temperature, followed by a dilution curve of Leishmania DNA (500 pg/µl, 50 pg/µl, 5 pg/µl, 500 fg/µl, 50 fg/µl, 5 fg/µl, and 0.5 fg/µl) to be used for analytical sensitivity. RV1/RV2 PCR amplified L. infantum and L. amazonensis at all analyzed temperatures; LEISH1/LEISH2 PCR amplified all 3 species of Leishmania, although at some temperatures L. infantum was specifically amplified, and, finally, FLC2/RLC2 PCR amplified only L. infantum at all temperatures analyzed. In terms of sensitivity, RV1/RV2 PCR detected 1 fg of L. infantum DNA and 100 pg of L. amazonensis DNA; LEISH1/LEISH2 PCR detected 1 fg of L. infantum DNA, 100 fg of L. amazonensis DNA, and 10 fg of L. braziliensis DNA; and FLC2/RLC2 PCR detected 10 fg of L. infantum DNA. Thus, PCR with FLC2/RLC2 primers is best suited for the molecular characterization of L. infantum, especially in areas where there is an incidence of more than 1 Leishmania species, such as South America.

Anti-leishmanial, immunomodulatory and additive potential effect of Piperine on Leishmania major: The in silico and in vitro study of Piperine and its combination.

Sharifi F, Mohamadi N, Afgar A, Oliaee RT.
02-09-2023
Exp Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37666407/

Background: Piperine (Pn), an indole alkaloid compound found in pepper, is an effective compound with anti-leishmanial medications that administered alone or in combination. This study aimed to use Pn for possible biochemical targets and to assess mechanisms of anti-leishmanial action and immunomodulatory roles. Methods: The ability of Pn to bind to interleukin-12P40 (IL-12P40) and interferon-γ (IFN-γ) was investigated using molecular docking. The leishmanicidal effect of Pn, meglumine antimoniate (Glucantime®; MA), and Pn plus MA was assessed on Leishmania major promastigotes and amastigotes. A real-time PCR was applied to quantify

cytokines gene expression in drug-treated murine macrophages. **Results:** The molecular docking findings indicated that Pn could bind to IL-12P40/IFN-γ. In silico analyses showed an affinity of Pn to IL-12P40/IFN-γ, with the MolDock score of -236.91 and -64.87 kcal/mol, respectively. Pn plus MA reduced the proliferation rate of promastigote and amastigote forms of L. major compared to each drug alone (IC_{50} = 43.22 and 19.41 µg/mL, respectively). Moreover, the combination drug demonstrated no cytotoxicity as the selectivity index (SI) was 14.81. Also, Th1-related cytokines were upregulated, while Th2-related cytokines were downregulated in Pn combination-treated murine macrophages. **Conclusions:** The superior effectiveness of combination therapy on L. major warrants further investigations on the clinical potential of this combination in the treatment of leishmaniasis.

Bcl-6 expression by $CD4^+$ T cells determines concomitant immunity and host resistance across distinct parasitic infections.

Meli AP, Russell GA, Swaminathan S, Weichselbaum L, MacMahon CA, Pernet E, Karo-Atar D, Rogers D, Rochette A, Fontes G, Mandl JN, Divangahi M, Klein OD, Gregorieff A, Stäger S, King IL.
31-08-2023
Mucosal Immunol.
https://pubmed.ncbi.nlm.nih.gov/37659724/

Safe Treatment With Secukinumab in a Patient With Axial Spondyloarthritis and a History of a Leishmania donovani Infection.

López-Medina C, Doblas A, Escudero-Contreras A, Collantes-Estévez E.
01-09-2023
J Rheumatol.
https://pubmed.ncbi.nlm.nih.gov/37657798/

Comparison of collection methods for Phlebotomus argentipes sand flies to use in a molecular xenomonitoring system for the surveillance of visceral leishmaniasis.

McIntyre-Nolan S, Kumar V, Mark-Carew M, Kumar K, Nightingale ES, Dalla Libera Marchiori G, Rogers ME, Kristan M, Campino S, Medley GF, Das P, Cameron MM.
01-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37656745/

Background: The kala-azar elimination programme has resulted in a significant reduction in visceral leishmaniasis (VL) cases across the Indian Subcontinent. To detect any resurgence of transmission, a sensitive cost-effective surveillance system is required. Molecular xenomonitoring (MX), detection of pathogen DNA/RNA in vectors, provides a proxy of human infection in the lymphatic filariasis elimination programme. To determine whether MX can be used for VL surveillance in a low transmission setting, large numbers of the sand fly vector Phlebotomus argentipes are required. This study will determine the best method for capturing P. argentipes females for MX. **Methodology/principal findings:** The field study was performed in two programmatic and two non-programmatic villages in Bihar, India. A total of 48 households (12/village) were recruited. Centers for Disease Control and Prevention light traps (CDC-LTs) were compared with Improved Prokopack (PKP) and mechanical vacuum aspirators (MVA) using standardised methods. Four 12x12 Latin squares, 576 collections, were attempted (12/house, 144/village,192/method). Molecular analyses of collections were conducted to confirm identification of P. argentipes and to detect human and Leishmania DNA. Operational factors, such as time burden, acceptance to householders and RNA preservation, were also considered. A total of 562 collections (97.7%) were completed with 6,809 sand flies captured. Females comprised 49.0% of captures, of which 1,934 (57.9%) were identified as P. argentipes. CDC-LTs collected 4.04 times more P. argentipes females than MVA and 3.62 times more than PKP ($p<0.0001$ for each). Of 21,735 mosquitoes in the same collections, no significant differences between collection methods were observed. CDC-LTs took less time to install and collect than to perform aspirations and their greater yield compensated for increased sorting time. No significant differences in Leishmania RNA detection and quantitation between methods were observed in experimentally infected sand flies maintained in conditions simulating field conditions. CDC-LTs were favoured by householders. **Conclusions/significance:** CDC-LTs are the most useful collection tool of those tested for MX surveillance since they collected higher numbers of P. argentipes females without compromising mosquito captures or the preservation of RNA. However, capture rates are still low.

In silico and immunoinformatics based multiepitope subunit vaccine design for protection against visceral leishmaniasis.

Bhowmik D, Bhuyan A, Gunalan S, Kothandan G, Kumar D.
01-09-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37655736/

Effects of host species on microbiota composition in Phlebotomus and Lutzomyia sand flies.

Tabbabi A, Mizushima D, Yamamoto DS, Kato H.
31-08-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37653518/

Exposure to Trypanosoma cruzi and Leishmania parasites in dogs from a rural locality of Yucatan, Mexico. A serological survey.

Reyes-Novelo E, Sauri-Arceo C, Panti-May A, Marín D, Canché-Pool EB, Chan-Espinoza DE, Marín C, Bolio-

González M, Rodríguez-Vivas RI, Torres-Castro M, Escobedo-Ortegón FJ.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652628/

Trypanosoma cruzi, the causal agent of American trypanosomiasis, and Leishmania spp., the causal agents of Leishmaniasis, are prevalent in more than 20 American countries, including Mexico. Dogs have been reported as incidental hosts for both parasites and may be helpful as transmission sentinels. We surveyed the dog population in a rural locality of the Merida municipality in Yucatan, Mexico, to evaluate the seroreactivity against T. cruzi and Leishmania spp. using two antigens, parasite homogenate (H) and iron superoxide dismutase extract (FeSODe), with two serological techniques (ELISA and Western Blot). Our study found that 3.33% of the tested dogs were seroreactive to T. cruzi using ELISA-H, and 29.5% were seroreactive to FeSODe antigen, with a 94.4% consistency between the two tests. Similarly, for L. mexicana, 1.6% were seroreactive using ELISA-H, and 9.8% were seroreactive using ELISA-FeSODe, with an 83.3% consistency between tests. For L. braziliensis, no dogs were seroreactive using ELISA-H, but 16.4% were seroreactive using ELISA-FeSODe, with a 90% consistency between tests. Finally, for L. infantum, 4.9% were seropositive using ELISA-H, and 6.6% were seropositive using ELISA-FeSODe, with a 75% consistency between tests. These results show noticeable evidence of exposure of dogs to trypanosomatid parasites and highlight the potential disease risk for the people and their companion animals in the region.

Canine Leishmania spp. infection in two distinct foci of visceral and cutaneous leishmaniasis in Tunisia.

Zribi L, El Houda Ben-Fayala N, Aissi W, Ben-Abid M, Souissi O, Hamdi N, Boulehmi N, Ghrab J, Jemni A, Jamel A, Handous M, Bouratbine A, Oliva G, Aoun K.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37672397/

Visceral leishmaniasis (VL) and zoonotic cutaneous leishmaniasis (ZCL) caused by Leishmania (L.) infantum and L. major, respectively, are endemic in Tunisia. The aim of the study was to assess canine Leishmania spp. infection prevalence as well as to identify the Leishmania species involved in two well-documented and geographically distinct VL and ZCL foci. One hundred seventy-six dogs were randomly recruited in the VL focus of Sbikha-Zaghouan (n = 100) and the ZCL focus of Echrarda-Nasrallah (n = 76). Physical examination and blood collection were systemically performed. Needle aspiration was done in case of lymph node (LN) enlargement. All sera were tested by ELISA. kDNA RT-PCR was performed on DNA extracts from (i) buffy coats of seropositive dogs and (ii) LN aspirates. Leishmania species identification was done by ITS1 PCR-sequencing. Thirty-three dogs (18.8%) were infected by Leishmania; 30 having anti-Leishmania antibodies and 3 were seronegative dogs with Leishmania DNA in LN aspirates. Prevalence of infection was significantly higher in VL foci than in ZCL foci (27% versus 7.9%, p = 0.002). Leishmania species was identified in 11 dogs and corresponded to L. infantum. Combination of serology and qPCR on LN aspirates seems to be the best option for canine leishmaniasis diagnosis. Infection is more frequent in VL foci and L. infantum is the only identified species.

NKG2D promotes CD8 T cell-mediated cytotoxicity and is associated with treatment failure in human cutaneous leishmaniasis.

Sacramento LA, Farias Amorim C, Campos TM, Saldanha M, Arruda S, Carvalho LP, Beiting DP, Carvalho EM, Novais FO, Scott P.
21-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37603573/

Cutaneous leishmaniasis exhibits a spectrum of clinical presentations dependent upon the parasites' persistence and host immunopathologic responses. Although cytolytic CD8 T cells cannot control the parasites, they significantly contribute to pathologic responses. In a murine model of cutaneous leishmaniasis, we previously found that NKG2D plays a role in the ability of cytolytic CD8 T cells to promote disease in leishmanial lesions. Here, we investigated whether NKG2D plays a role in human disease. We found that NKG2D and its ligands were expressed within lesions from L. braziliensis-infected patients and that IL-15 and IL-1β were factors driving NKG2D and NKG2D ligand expression, respectively. Blocking NKG2D reduced degranulation by CD8 T cells in a subset of patients. Additionally, our transcriptional analysis of patients' lesions found that patients who failed the first round of treatment exhibited higher expression of KLRK1, the gene coding for NKG2D, than those who responded to treatment. These findings suggest that NKG2D may be a promising therapeutic target for ameliorating disease severity in cutaneous leishmaniasis caused by L. braziliensis infection.

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

Li LQ, He Y, Liu T, Zhou J, Chen EQ.
Juil-2023
Future Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37522175/

Case Report: Extensive Facial Cutaneous Leishmaniasis in a Neonate.

Itzhaki Gabay S, Valdman-Grinshpoun Y, Ling G, Ben-Shimol S, Test G, Kaplan O, Horev A.
24-06-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37487561/

The adaptive roles of aneuploidy and polyclonality in Leishmania in response to environmental stress.

Negreira GH, de Groote R, Van Giel D, Monsieurs P, Maes I, de Muylder G, Van den Broeck F, Dujardin JC, Domagalska MA.
06-09-2023
EMBO Rep.
https://pubmed.ncbi.nlm.nih.gov/37470283/

Aneuploidy is generally considered harmful, but in some microorganisms, it can act as an adaptive mechanism against environmental stress. Here, we use Leishmania-a protozoan parasite with remarkable genome plasticity-to study the early steps of aneuploidy evolution under high drug pressure (using antimony or miltefosine as stressors). By combining single-cell genomics, lineage tracing with cellular barcodes, and longitudinal genome characterization, we reveal that aneuploidy changes under antimony pressure result from polyclonal selection of pre-existing karyotypes, complemented by further and rapid de novo alterations in chromosome copy number along evolution. In the case of miltefosine, early parasite adaptation is associated with independent point mutations in a miltefosine transporter gene, while aneuploidy changes only emerge later, upon exposure to increased drug levels. Therefore, polyclonality and genome plasticity are hallmarks of parasite adaptation, but the scenario of aneuploidy dynamics depends on the nature and strength of the environmental stress as well as on the existence of other pre-adaptive mechanisms.

Morphology does not allow differentiating the species of the Phlebotomus perniciosus complex: Molecular characterization and investigation of their natural infection by Leishmania infantum in Morocco.

Gijón-Robles P, Gómez-Mateos M, Corpas-López E, Abattouy N, Merino-Espinosa G, Morillas-Márquez F, Corpas-López V, Díaz-Sáez V, Riyad M, Martín-Sánchez J.
Sept-2023
Zoonoses Public Health.
https://pubmed.ncbi.nlm.nih.gov/37337345/

Morphological and DNA-based complemented approaches were applied for characterization of sympatric populations of Phlebotomus longicuspis and Phlebotomus perniciosus in Morocco. Both sand fly species are generally recorded in sympatry in North Africa but on few occasions have been molecularly characterized. The diagnostic confusion of these species has led to errors in their geographical distribution and probably, in the assignment of their role in the transmission of L. infantum. Sand flies were caught inside households in El Borouj, central Morocco, in 2014-2015. For female sand flies, detection of L. infantum natural infection and blood meal identification were carried out. According to morphological identification, Phlebotomus longicuspis s.l. (34.7%) was the second most abundant Phlebotomus species after P. sergenti, followed by atypical Phlebotomus perniciosus (7.1%); 11.6% of the male specimens of P. longicuspis s.l. were identified as P. longicuspis LCx according to the number of coxite setae. The density of Larroussius species was very high (31 Larroussius/light trap/night) in the peripheral neighbourhood of Oulad Bouchair (p = 0.001) where the first case of cutaneous leishmaniasis due to Leishmania infantum was detected in 2017. Phylogenetic trees based on three independent genes highlighted three well-supported clusters within P. perniciosus complex that could be interpreted as corresponding to P. perniciosus, P. longicuspis s.s. and an undescribed species, all coexisting in sympatry. Some females with typical morphology of P. longicuspis were genetically homologous to P. perniciosus. The taxa cannot be differentiated by morphological methods but characterized by a distinctive genetic lineage for which the synapomorphic characters are described. Leishmania infantum was detected in females of all clusters with a low parasite load. Population genetics will help to assess the threat of the geographical spread of L. infantum in Morocco by determining the density, abundance and vector role of the species of the P. perniciosus complex identified correctly.

A neglected among the neglected: a review of cutaneous leishmaniasis in Guatemala.

Lopez Y, Arana B, Rizzo N, Duran E, Acosta-Serrano Á, Mendizabal-Cabrera R.
01-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37103337/

Evaluation of the susceptibility of Tritrichomonas foetus to extracts of Lantana camara (Verbenaceae) by flow cytometry.

López LA, Luque ME, Rivero MB, Abdala ME, Carranza PG, Luna BE, Di Lullo D, Volta BJ, Rodriguez SA, Rivero FD.
Sept-2023
Vet Res Commun.
https://pubmed.ncbi.nlm.nih.gov/37100969/

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

Álvarez L, Marín-García PJ, Llobat L.
Sept-2023
Vet Res Commun.
https://pubmed.ncbi.nlm.nih.gov/37059873/

Case Report: The First Case Report of Visceral Leishmaniasis in Cambodia.

Lyvannak S, Sreynich K, Heng S, Thyl M, Chandna A, Chanpheaktra N, Pises N, Farrilend P, Jarzembowski J, Leventaki V, Davick J, Neunert C, Keller F, Kean LS, Camitta B, Tarlock K, Watkins B.
13-06-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895585/

Leishmaniasis is considered a neglected tropical disease that is commonly found in Asia, Africa, South America, and

Mediterranean countries. Visceral leishmaniasis (VL) is the most severe form of the disease and is almost universally fatal if left untreated. The symptoms of VL overlap with many infectious diseases, malignancies, and other blood disorders. The most common findings include fever, cytopenias, and splenomegaly. Given the nonspecific symptoms, the diagnosis requires detailed laboratory investigations, including bone marrow examination, that can be challenging in low- and middle-income countries. Diagnostic limitations likely lead to the underdiagnosis or delay in diagnosis of VL. We describe, to our knowledge, the first case report of VL in Cambodia in a child presenting with fever, anemia, and thrombocytopenia. The diagnosis required a liver biopsy and multiple bone marrow biopsies to visualize intracellular Leishmania spp. Our case illustrates the diagnostic challenges and the importance of timely diagnosis. This case also highlights the need for heightened awareness of the diagnostic findings of VL and improved reporting of tropical diseases.

Case Report: Leishmaniasis in a 33-Year-Old Man with Multiple Sclerosis.

Guerra-Amor A, Lopez-Gonzalez A, Bosch-Nicolau P, Rodriguez-Acevedo B, Zabalza A, Sulleiro E, Espinosa-Pereiro J, Aznar ML, Salvador F, Sánchez-Montalvá A, Molina I.
05-07-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/35895413/

Lèpre

Association of diabetes, smoking, and alcohol use with subclinical-to-symptomatic spectrum of tuberculosis in 16 countries: an individual participant data meta-analysis of national tuberculosis prevalence surveys.

Hamada Y, Quartagno M, Law I, Malik F, Bonsu FA, Adetifa IMO, Adusi-Poku Y, D'Alessandro U, Bashorun AO, Begum V, Lolong DB, Boldoo T, Dlamini T, Donkor S, Dwihardiani B, Egwaga S, Farid MN, Celina G Garfin AM, Mae G Gaviola D, Husain MM, Ismail F, Kaggwa M, Kamara DV, Kasozi S, Kaswaswa K, Kirenga B, Klinkenberg E, Kondo Z, Lawanson A, Macheque D, Manhiça I, Maama-Maime LB, Mfinanga S, Moyo S, Mpunga J, Mthiyane T, Mustikawati DE, Mvusi L, Nguyen HB, Nguyen HV, Pangaribuan L, Patrobas P, Rahman M, Rahman M, Rahman MS, Raleting T, Riono P, Ruswa N, Rutebemberwa E, Rwabinumi MF, Senkoro M, Sharif AR, Sikhondze W, Sismanidis C, Sovd T, Stavia T, Sultana S, Suriani O, Thomas AM, Tobing K, Van der Walt M, Walusimbi S, Zaman MM, Floyd K, Copas A, Abubakar I, Rangaka MX.
30-08-2023
EClinicalMedicine.
https://pubmed.ncbi.nlm.nih.gov/37680950/

Background: Non-communicable diseases (NCDs) and NCD risk factors, such as smoking, increase the risk for tuberculosis (TB). Data are scarce on the risk of prevalent TB associated with these factors in the context of population-wide systematic screening and on the association between NCDs and NCD risk factors with different manifestations of TB, where ~50% being asymptomatic but bacteriologically positive (subclinical). We did an individual participant data (IPD) meta-analysis of national and sub-national TB prevalence surveys to synthesise the evidence on the risk of symptomatic and subclinical TB in people with NCDs or risk factors, which could help countries to plan screening activities. Methods: In this systematic review and IPD meta-analysis, we identified eligible prevalence surveys in low-income and middle-income countries that reported at least one NCD (e.g., diabetes) or NCD risk factor (e.g., smoking, alcohol use) through the archive maintained by the World Health Organization and by searching in Medline and Embase from January 1, 2000 to August 10, 2021. The search was updated on March 23, 2023. We performed a one-stage meta-analysis using multivariable multinomial models. We estimated the proportion of and the odds ratio for subclinical and symptomatic TB compared to people without TB for current smoking, alcohol use, and self-reported diabetes, adjusted for age and gender. Subclinical TB was defined as microbiologically confirmed TB without symptoms of current cough, fever, night sweats, or weight loss and symptomatic TB with at least one of these symptoms. We assessed heterogeneity using forest plots and I^2 statistic. Missing variables were imputed through multi-level multiple imputation. This study is registered with PROSPERO (CRD42021272679). Findings: We obtained IPD from 16 national surveys out of 21 national and five sub-national surveys identified (five in Asia and 11 in Africa, N = 740,815). Across surveys, 15.1%-56.7% of TB were subclinical (median: 38.1%). In the multivariable model, current smoking was associated with both subclinical (OR 1.67, 95% CI 1.27-2.40) and symptomatic TB (OR 1.49, 95% CI 1.34-1.66). Self-reported diabetes was associated with symptomatic TB (OR 1.67, 95% CI 1.17-2.40) but not with subclinical TB (OR 0.92, 95% CI 0.55-1.55). For alcohol drinking ≥ twice per week vs no alcohol drinking, the estimates were imprecise (OR 1.59, 95% CI 0.70-3.62) for subclinical TB and OR 1.43, 95% CI 0.59-3.46 for symptomatic TB). For the association between current smoking and symptomatic TB, I^2 was high (76.5% (95% CI 62.0-85.4), while the direction of the point estimates was consistent except for three surveys with wide CIs. Interpretation: Our findings suggest that current smokers are more likely to have both symptomatic and subclinical TB. These individuals can, therefore, be prioritised for intensified screening, such as the use of chest X-ray in the context of community-based screening. People with self-reported diabetes are also more likely to have symptomatic TB, but the association is unclear for subclinical TB. Funding: None.

Elucidating anti-aging and antioxidant activity of Hydnocarpus anthelmintica on skin aging and cosmeceutical potentials: in silico and in vitro study.

Kim M, Lee E, Kim YB.
01-09-2023
Comb Chem High Throughput Screen.
https://pubmed.ncbi.nlm.nih.gov/37680148/

Introduction: Hydnocarpus anthelmintica (HA) has been traditionally used for treating leprosy and is known for its antioxidant and anti-inflammatory activities. The aim of this study was to investigate the active compounds and targets of HA extracts, involved in oxidative stress and skin aging. The active compounds and targets of HA extracts were identified using network pharmacology. **Method:** The pathway study was conducted using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. HA semen was measured for its in-vitro antioxidant activity using 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay and anti-aging activities using collagenase, elastase, and tyrosinase assays. A total of 21 intersecting core targets were identified from 8 compounds, 51 action targets, and 1810 skin aging and oxidative stress-associated target genes. **Result:** A compound-target network was constructed, and 3 compounds (luteolin, beta-carotene and genkwanin), and 4 hub genes (TP53, HSP90AA1, JUN, and MAPK1) were identified. The KEGG pathway study revealed that the compounds were correlated with PI3K-Akt, p53, HIF-1, and MAPK signaling. **Conclusion:** The results of in-vitro experiments showed the effect of HA extract on oxidative stress reduction and collagenase inhibition. We discovered two main active compounds, luteolin and β-carotene, that may be involved in p53 and MAPK signaling, and showed HA extract activity against oxidative stress and collagenase.

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

Tok PSK, Wong LP, Liew SM, Razali A, Mahmood MI, Chinnayah T, Kawatsu L, Toha HR, Mohd Yusof K, Abd Rahman R, Che Mat Din SNA, Loganathan T.
07-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37676902/

Implementation of targeted next-generation sequencing for the diagnosis of drug-resistant tuberculosis in low-resource settings: a programmatic model, challenges, and initial outcomes.

de Araujo L, Cabibbe AM, Mhuulu L, Ruswa N, Dreyer V, Diergaardt A, Günther G, Claassens M, Gerlach C, Utpatel C, Cirillo DM, Nepolo E, Niemann S.
03-08-2023
Front Public Health.
https://pubmed.ncbi.nlm.nih.gov/37674674/

More on Autochthonous Leprosy in the United States. Reply.

Adler BL, Ochoa MT.
07-09-2023
N Engl J Med.
https://pubmed.ncbi.nlm.nih.gov/37672709/

More on Autochthonous Leprosy in the United States.

Pieters T, Meredith AL, Braig HR.
07-09-2023
N Engl J Med.
https://pubmed.ncbi.nlm.nih.gov/37672708/

[The plans of Ernesto Ottoni to Combat the "affliction of lepers:" lazarettos, treatments, and endeavors to tackle leprosy in nineteenth century São Paulo].

Abreu JLN, Quadros LS.
04-09-2023
Hist Cienc Saude Manguinhos.
https://pubmed.ncbi.nlm.nih.gov/37672430/

This article presents the plans for a lazaretto in the city of São Paulo in the mid-nineteenth century. It consists of the transcription and analysis of an opinion prepared by the physician Ernesto Benedicto Ottoni, addressed to the president of the province of São Paulo. The article includes an analysis of the plans for the building, bearing in mind the prevailing miasma theory; the contemporary conceptions of leprosy treatment, especially beliefs regarding the transmissibility of the disease; and the physician's idealization of the routines for the treatment, work, leisure, and recovery of patients.

A history of thalidomide in India.

Wimmelbücker L, Kar A.
Juil-2023
Med Hist.
https://pubmed.ncbi.nlm.nih.gov/37668377/

A Rare Case of Hansen's Disease Complicated by G6PD Deficiency.

Yerke Hansen P, Myers E, Rajalingam K, Labanowski M.
01-08-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37664264/

Exploration of Neurofilament Light Chain and Nerve Ultrasound in Leprotic Neuropathy.

Nasr-Eldin YK, Cartwright MS, Hamed A, Ali LH, Abdel-Nasser AM.
04-09-2023
J Ultrasound Med.
https://pubmed.ncbi.nlm.nih.gov/37661825/

Coleus vettiveroides ethanolic root extract induces cytotoxicity by intrinsic apoptosis in HepG2 cells.

Mohamed Azar KAH, Ezhilarasan D, Shree Harini K.
03-09-2023
J Appl Toxicol.
https://pubmed.ncbi.nlm.nih.gov/37661188/

Hepatocellular carcinoma (HCC) contributes to more than 80% of all primary cancers globally and ranks fourth in cancer-related deaths, due to the lack of an effective, definite therapeutic drug. Coleus vettiveroides (CV) has been used in Indian traditional medicine to treat diabetes,

liver ailments, skin diseases, leukoderma, and leprosy. This study investigates the anticancer effect of CV ethanolic root extract in HepG2 cells. HepG2 cells were treated with CV extract, and its cytotoxicity was analyzed by MTT assay. AO/EB staining, propidium iodide staining, DCFH-DA assay, phalloidine staining, flow cytometry, and qPCR studies were performed for ROS expression, apoptosis and cell cycle analysis. The phytochemical analysis confirmed the presence of quercetin and galangin in CV root extract. The results showed that CV inhibited the proliferation of HepG2 cells, with altered cellular and nuclear morphology. CV was also found to increase intracellular ROS levels and oxidative stress markers in HepG2 cells. CV significantly altered the actin microfilament distribution in HepG2 cells and caused cell cycle arrest at the sub G_0 -G_1 phase. CV also induced mitochondria-mediated apoptosis, as evidenced by increased expression of p53, Bax, cytochrome C, Apaf-1, PARP, caspase-3 and caspase-9, and downregulated Bcl-2 expression. Therefore, CV exerts its anticancer effect by inducing mitochondrial dysfunction, oxidative stress, cytoskeletal disorganization, cell cycle arrest, and mitochondria-mediated apoptosis, and it could be a potent therapeutic option for HCC.

Systemic lupus erythematosus mimicking leprosy: A challenge to early diagnosis.

Nunes Brito P, Pereira Barros D, Nunes Brito B, Brito Silva R, Costa Maciel ME, Camilo Nunes de Sousa M.
Août-Sept 2023
Reumatol Clin (Engl Ed).
https://pubmed.ncbi.nlm.nih.gov/37661118/

Efficiency and equity of bed utilization in China's health institutions: based on the rank-sum ratio method.

Zhang H, Shi L, Yang J, Sun G.
02-09-2023
Int J Equity Health.
https://pubmed.ncbi.nlm.nih.gov/37660026/

Alice Ball: chemist who developed a treatment for leprosy.

Ferry G.
02-09-2023
Lancet.
https://pubmed.ncbi.nlm.nih.gov/37659772/

Cardiovascular events associated with thalidomide and prednisone in leprosy type 2 reaction.

Alfredo MAC, Schmitt JV, Miola AC, Milagres SP, Lastoria JC.
Août-2023
An Bras Dermatol.
https://pubmed.ncbi.nlm.nih.gov/37657956/

Background: Thalidomide is the drug of choice for the treatment of type 2 leprosy reactions and is often associated with corticosteroids. The use of these drugs in multiple myeloma is associated with the risk of cardiovascular events, but there have been few studies assessing this risk in leprosy patients. Objective: To evaluate the occurrence of cardiovascular events in patients with multibacillary leprosy and their correlation with the use of thalidomide and prednisone. Methods: Analytical cross-sectional study of all patients diagnosed with multibacillary leprosy treated at the Dermatology Service between 2012 and 2022, using electronic medical records. Thromboembolic vascular events, both arterial and venous, including acute myocardial infarction, were considered. The main independent variable was the concomitant use of thalidomide and prednisone during follow-up. Results: A total of 89 patients were included, of which 19 used thalidomide and prednisone concomitantly. There were five cardiovascular events (26.3%), three of which of deep venous thrombosis. The combined use of medications was associated with the events (PR=6.46 [3.92 to 10.65]; p<0.01). Study limitations: Small number of events, single-center retrospective study. Conclusion: The hypothesis of an association between cardiovascular events and the concomitant use of thalidomide and prednisone is supported, but more robust prospective studies are required for a better assessment.

Role of cytopathology in diagnosing phaeohyphomycosis masquerading as nerve abscess in a lepromatous leprosy patient: A case report.

Yadav SK, Chandana BK, Panwar H, Chaurasia JK, Jayashankar E, Asati D.
29-08-2023
Int J Surg Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37657385/

Clofazimine nanoclusters show high efficacy in experimental TB with amelioration in paradoxical lung inflammation.

Jadhav K, Jhilta A, Singh R, Ray E, Sharma N, Shukla R, Singh AK, Verma RK.
21-08-2023
Biomater Adv.
https://pubmed.ncbi.nlm.nih.gov/37657277/

Mounting Evidence Suggests Leprosy Is Endemic in Florida.

Harris E.
05-09-2032
JAMA.
https://pubmed.ncbi.nlm.nih.gov/37585214/

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, 01-09-2032Diassy L, Conde M, Touré A, Delamou A.
01-09-2023

Int Health.
https://pubmed.ncbi.nlm.nih.gov/37232124/

Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.

Morsures de serpent

Kounis syndrome after anti-snake venom intradermal skin test: A case report.

Elgendy MM, Madkour SA, El-Moneim Sheta AA, Hamouda EH, Ghitani SA.
05-09-2023
Toxicon.
https://pubmed.ncbi.nlm.nih.gov/37678580/

The Royal Armoury: Venomics and antivenomics of king cobra (Ophiophagus hannah) from the Indian Western Ghats.

Jaglan A, Bhatia S, Martin G, Sunagar K.
04-09-2023
Int J Biol Macromol.
https://pubmed.ncbi.nlm.nih.gov/37673142/

Despite being famous as 'the king' of the snake world, the king cobra (Ophiophagus hannah) has remained a mysterious species, particularly with respect to its venom ecology. In contrast, venom research has largely focussed on the 'big four' snakes that are greatly responsible for the burden of snakebite in the Indian subcontinent. This study aims to bridge the current void in our understanding of the O. hannah venom by investigating its proteomic, biochemical, pharmacological, and toxinological profiles via interdisciplinary approaches. Considering their physical resemblance, the king cobra is often compared to the spectacled cobra (Naja naja). Comparative venomics of O. hannah and N. naja in this study provided interesting insights into their venom compositions, activities, and potencies. Our findings suggest that the O. hannah venom, despite being relatively less complex than the N. naja venom, is equally potent. Finally, our in vitro and in vivo assays revealed that both Indian polyvalent and Thai Red Cross monovalent antivenoms completely fail to neutralise the O. hannah venom. Our findings provide guidelines for the management of bites from this clinically important yet neglected snake species in India.

Harm due to the use of pressure bandage immobilisation in patients bitten by snakes in Australia.

Little M.
05-0-2023
Clin Toxicol (Phila).
https://pubmed.ncbi.nlm.nih.gov/37668172/

[A case of poisoning caused by head and face bite of Deinagkistrodon acutus].

Liu MJ, Liu WJ, Lai LJ, Xie LT, Chen SR, Lan P.
20-08-2023
Zhonghua Lao Dong Wei Sheng Zhi Ye Bing Za Zhi.
https://pubmed.ncbi.nlm.nih.gov/37667162/

Successful management of late stage of acute compartment syndrome after 72 h snake bite in 8-year-old female. A case report.

Brimo Alsaman MZ, Toutounji Z, Arab R, Al Sam SO, Alhaj Akil MA, Kenno MF, Al Ballan MA, Roumiah D, Alhamad Q, Muqayyd MS, Remmo KR.
22-08-2023
Trauma Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37663375/

One of the most serious complications of snakebite is compartment syndrome (CS), Signs of CS include paresthesia in the distal part and pain that is out of proportion to the severity of the injury, Management involves improving the general condition, and fasciotomy has been found to be effective. An 8-year-old girl was referred to the internal emergency department in our hospital 72 h after a snake bite. She was unconscious, in poor general condition, and had a high fever. Edema was present throughout the right lower limb, extending to the abdomen, with signs of cellular necrosis (blackening with bubbles) on the right foot. The diagnosis of CS was made, and the patient underwent fasciotomy after improving the general condition. Although snake bites are rare, surgeons should be concerned about life-threatening and limb-threatening complications. CS can be effectively treated with fasciotomy. Additionally, it is important to emphasize the significance of daily dressing and regular follow-up for achieving the best results.

Considerations for the development of a field-based medical device for the administration of adjunctive therapies for snakebite envenoming.

Werner RM, Soffa AN.
19-08-2032
Toxicon X.
https://pubmed.ncbi.nlm.nih.gov/37661997/

The timely administration of antivenom is the most effective method currently available to reduce the burden of snakebite envenoming (SBE), a neglected tropical disease that most often affects rural agricultural global populations. There is increasing interest in the development of adjunctive small molecule and biologic therapeutics that target the most problematic venom

components to bridge the time-gap between initial SBE and the administration antivenom. Unique combinations of these therapeutics could provide relief from the toxic effects of regional groupings of medically relevant snake species. The application a PRISMA/PICO literature search methodology demonstrated an increasing interest in the rapid administration of therapies to improve patient symptoms and outcomes after SBE. Advice from expert interviews and considerations regarding the potential routes of therapy administration, anatomical bite location, and species-specific venom delivery have provided a framework to identify ideal metrics and potential hurdles for the development of a field-based medical device that could be used immediately after SBE to deliver adjunctive therapies. The use of subcutaneous (SC) or intramuscular (IM) injection were identified as potential routes of administration of both small molecule and biologic therapies. The development of a field-based medical device for the delivery of adjunctive SBE therapies presents unique challenges that will require a collaborative and transdisciplinary approach to be successful.

Factors associated with mortality after snakebite envenoming in children: a scoping review.

Guile L, Lee A, Gutiérrez JM.
01-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37264929/

Therapeutic spectrum of piperine for clinical practice: a scoping review.

Yadav SS, Singh MK, Hussain S, Dwivedi P, Khattri S, Singh K.
2023
Crit Rev Food Sci Nutr.
https://pubmed.ncbi.nlm.nih.gov/34996326/

Mycétome

The unraveling of Sudan's health system: catastrophic consequences of ongoing conflict.

Alfadul ESA, Alrawa SS, Eltigani HF, Ahmed A, Siddig EE.
06-09-2023
Med Confl Surviv.
https://pubmed.ncbi.nlm.nih.gov/37674343/

Case report: The dot in circle sign: A pathognomonic MRI sign of Madura foot.

Oueriagli Nabih O, El Bouardi N, Haloua M, Alami B, Lamrani Y, Boubbou M, Maaroufi M.
25-08-2023
Radiol Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37670911/

Mycetoma or Madura's foot is a rare condition in Morocco. It is a chronic infection that affects deep subcutaneous tissues and may eventually spread to deep tissues, muscles, and bones. It is caused by fungi or bacteria and most often affects the foot. Biopsy and microbiological examination help to establish a definitive diagnosis, but may delay it. Imaging plays a crucial role in early diagnosis, particularly MRI findings that show a pathognomonic sign of mycetoma which is the dot-in-the-circle sign. Computed tomography provides a better analysis of bone changes than plain radiography. Treatment is very difficult, especially if the diagnosis is delayed, and may even lead to amputation. We present here a case of mycetoma of the foot with some MRI features.

Online image: Mycetoma- a neglected tropical disease in West Texas.

Songtanin B, Nugent K, Nath S.
31-08-2023
Am J Med Sci.
https://pubmed.ncbi.nlm.nih.gov/37659468/

Onchocercose

First report of filarial nematodes in the genus Onchocerca infecting black flies (Diptera: Simuliidae) in Iran.

Khanzadeh F, Maleki-Ravasan N, Adler PH, Karimian F, Kudela M.
04-09-2023
Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37666968/

Black flies are blood-sucking insects of public health importance, and they are effective vectors of pathogens and parasites, such as filarial nematodes of the genus Onchocerca. Our previous surveys have shown that individuals of Simulium turgaicum are annoying pests of humans and livestock in the Aras River Basin of Iran. In the present study, adult black flies of S. turgaicum were trapped from different ecotopes of five villages in Khoda-Afarin County, Iran. By using a sensitive nested PCR assay and targeting the nuclear 18S rDNA-ITS1 marker, filarial infections were found in 38 (1.89%) of 2005 black flies. Homology exploration of 360 bp of the sequences indicated that the filarial worms are members of the family Onchocercidae, with maximum alignment scores of 93-95%. Phylogenetic analysis showed that two Iranian Onchocerca isolates were clustered in the O. fasciata-O. volvulus lineage and were well separated from other filarial nematodes. Both the entomological evidence (empty abdomen of the specimens) and climatologic data (adequate accumulated degree days for development) suggest that the filarial DNA was probably that of infective larvae of vertebrates. This is the first report of an infection by Onchocerca species in S. turgaicum and the first record of onchocercids in black flies in Iran; however, more research is required to demonstrate transmission of these filarial worms by black flies in nature.

Rage

Benefit-cost analysis of coordinated strategies for control of rabies in Africa.

Bucher A, Dimov A, Fink G, Chitnis N, Bonfoh B, Zinsstag J.
07-09-2023
Nat Commun.
https://pubmed.ncbi.nlm.nih.gov/37679314/

Previous research suggests that dog mass vaccination campaigns can eliminate rabies locally, resulting in large human and animal life gains. Despite these demonstrated benefits, dog vaccination programs remain scarce on the African continent. We conducted a benefit-cost analysis to demonstrate that engaging into vaccination campaigns is the dominant strategy for most countries even in the absence of coordinated action between them. And quantify how coordinated policy measures across countries in Africa could impact rabies incidence and associated costs. We show that coordinated dog mass vaccination between countries and PEP would lead to the elimination of dog rabies in Africa with total welfare gains of USD 9.5 billion (95% CI: 8.1 - 11.4 billion) between 2024 and 2054 (30 years). Coordinated disease control between African countries can lead to more socially and ecologically equitable outcomes by reducing the number of lost human lives to almost zero and possibly eliminating rabies.

Whole Genome Sequencing for Rapid Characterization of Rabies Virus Using Nanopore Technology.

Bautista C, Jaswant G, French H, Campbell K, Durrant R, Gifford R, Kia GSN, Ogoti B, Hampson K, Brunker K.
18-08-2023
J Vis Exp.
https://pubmed.ncbi.nlm.nih.gov/37677046/

Genomic data can be used to track the transmission and geographic spread of infectious diseases. However, the sequencing capacity required for genomic surveillance remains limited in many low- and middle-income countries (LMICs), where dog-mediated rabies and/or rabies transmitted by wildlife such as vampire bats pose major public health and economic concerns. We present here a rapid and affordable sample-to-sequence-to-interpretation workflow using nanopore technology. Protocols for sample collection and the diagnosis of rabies are briefly described, followed by details of the optimized whole genome sequencing workflow, including primer design and optimization for multiplex polymerase chain reaction (PCR), a modified, low-cost sequencing library preparation, sequencing with live and offline base calling, genetic lineage designation, and phylogenetic analysis. Implementation of the workflow is demonstrated, and critical steps are highlighted for local deployment, such as pipeline validation, primer optimization, inclusion of negative controls, and the use of publicly available data and genomic tools (GLUE, MADDOG) for classification and placement within regional and global phylogenies. The turnaround time for the workflow is 2-3 days, and the cost ranges from $25 per sample for a 96 sample run to $80 per sample for a 12 sample run. We conclude that setting up rabies virus genomic surveillance in LMICs is feasible and can support progress toward the global goal of zero dog-mediated human rabies deaths by 2030, as well as enhanced monitoring of wildlife rabies spread. Moreover, the platform can be adapted for other pathogens, helping to build a versatile genomic capacity that contributes to epidemic and pandemic preparedness.

Assessment of knowledge, attitude, and practice of dog owners to rabies disease in Kahama town council, Shinyanga region, Tanzania.

Iddi S, Mlenga F, Hamasaki K, Mwita S, Konje E.
06-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37672544/

Prevalence of Brucella species in stray cattle, dogs and cats: A systematic review.

Sharma V, Sharma R, Aulakh RS, Singh BB.
01-09-2023
Prev Vet Med.
https://pubmed.ncbi.nlm.nih.gov/37669604/

Evolution and distribution of rabies viruses from a panorama view.

Li G, Zhang Y, He HL, Chen CY, Li X, Xiao Y, Yan ZB, Chu Y, Luo J, Guo XF.
05-09-2023
Microbiol Spectr.
https://pubmed.ncbi.nlm.nih.gov/37668395/

Rabies kills more than 59,000 people annually, mainly in developing countries. Previous studies on the evolution and distribution of rabies viruses (RABVs) were scattered. Here, we explore the evolution and distribution of this deadly virus from a novel panorama view. Multiple bioinformatic software tools were employed to analyze the phylogenetic diversity, evolution, spatiotemporal, and distribution of RABVs. The analyses were based on 1,202 qualified full-length genomes of RABVs and numerous literatures. Of the 10 distinct phylogenetic clades of RABV that we identified, more frequent intra- and inter-clade recombination occurs in the sequences of Asian-SEA, Arctic, and Cosmopolitan clades isolated from China, while according to existing sequence information, RABV might originate from bats (posterior probability, PP = 0.75, PP = 0.60 inferred from N and L genes, separately) in North America (PP = 0.57, PP = 0.62 inferred from N and L genes, separately). Due to the difference in evolutionary rate of N (2.22×10^{-4} subs/site/year, 95% HPD $1.99\text{-}2.47 \times 10^{-4}$ subs/site/year) and L genes (1.67×10^{-4} subs/site/year, 95% HPD $1.59\text{-}1.74 \times 10^{-4}$ subs/site/year), the root age was 1,406.6 (95% HPD 1,291.2-1,518.2) and 1,122.7 (95% HPD 1,052.4-1,193.9) inferred from N and L genes, separately. Among other findings, Mephitidae plays an important role in the interspecific transmission and communication of RABV, which we found tends to spread to populations genetically proximate to the host. We also identified amino acids under positive selection in different genes of

different clades as well as single nucleotide variation sites important for different lineages. IMPORTANCE Rabies virus is widely distributed all over the world, and wild animals are its largest potential reservoir. Our study offers a panorama view about evolution and distribution of rabies viruses and emphasizes the need to monitor the transmission dynamics of animal rabies.

Immunogenicity evaluation of a novel virus-like particle vaccine candidate against SARS-CoV-2 in BALB/c.

Bahramali G, Mashhadi Abolghasem Shirazi M, Hannan M, Aghasadeghi MR, Khosravy MS, Arjmand S, Sadat SM.
04-09-2023
Pathog Dis.
https://pubmed.ncbi.nlm.nih.gov/37667486/

Case of human rabies despite post-exposure prophylaxis (PEP) and complete recovery after intrathecal rabies immunoglobulin (RIG).

Ing SK, Ng Han Sim B, Lee YH, Ling TY.
04-09-2023
BMJ Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37666566/

Rabies, a fatal viral zoonotic disease, has become a public health concern in Sarawak, Malaysia. Despite pre-exposure and post-exposure prophylaxis being available, there has been limited progress in developing treatments for rabies, emphasising the pressing need for productive solutions. We present a laboratory-confirmed human rabies case in which the patient survived without neurological sequelae after receiving intrathecal rabies immunoglobulin.

Impact of the COVID-19 pandemic on routine vaccination services in Shaanxi province, Northwest China: Non-pharmaceutical intervention period and mass COVID-19 vaccination period.

Zhang C, Hu W, Li Y, Lv Y, Zhang S.
01-08-2023
Hum Vaccin Immunother.
https://pubmed.ncbi.nlm.nih.gov/37665634/

Efficacy of heat-inactivated Mycobacterium bovis vaccine delivered to European badgers (Meles meles) through edible bait.

Juste RA, Blanco-Vázquez C, Barral M, Prieto JM, Varela-Castro L, Lesellier S, Dave D, Sevilla IA, Martín Ezquerra AB, Adriaensen H, Herrero-García G, Garrido JM, Casais R, Balseiro A.
21-08-2023
Heliyon.
https://pubmed.ncbi.nlm.nih.gov/37662827/

N^4-Hydroxycytidine/Molnupiravir Inhibits RNA-Virus Induced Encephalitis by Producing Mutated Viruses with Reduced Fitness.

Ojha D, Hill CS, Zhou S, Evans AB, Leung JM, Lewis CS, Amblard F, Schinazi RF, Baric RS, Peterson KE, Swanstrom R.
23-08-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37662274/

A diverse group of RNA viruses including Rabies, Polio, La Crosse, West Nile, Zika, Nipah, Eastern and Western equine encephalitis, Venezuelan equine encephalitis, Japanese encephalitis, and tick-borne encephalitis viruses have the ability to gain access to and replicate in the central nervous system (CNS), causing severe neurological disease. Current treatment for these patients is generally limited to supportive care. To address the need for a generalizable antiviral, we utilized a strategy of mutagenesis to limit virus replication. We evaluated ribavirin (RBV), favipiravir (FAV) and N^4-hydroxycytidine (NHC) against La Crosse virus (LACV) which is the primary cause of pediatric arboviral encephalitis cases in North America. NHC was more potent than RBV or FAV in neuronal cells. Oral administration of molnupiravir (MOV), the 5'-isobutyryl prodrug of NHC, decreased neurological disease development by 32% following intraperitoneal (IP) infection of LACV. MOV also reduced disease by 23% when virus was administered intranasally (IN). NHC and MOV produced less fit viruses by incorporating predominantly G-to-A or C-to-U mutations. Furthermore, NHC also inhibited two other orthobunyaviruses, Jamestown Canyon virus and Cache Valley virus. Collectively, these studies indicate that NHC/MOV has therapeutic potential to inhibit virus replication and subsequent neurological disease caused by this neurotropic RNA virus.

Communicating the risks of handling bats: analysing approaches used by Australian stakeholders in the context of Australian bat lyssavirus.

Liang BP, Wingett K, Bosward KL, Taylor MR.
04-09-2023
Aust Vet J.
https://pubmed.ncbi.nlm.nih.gov/37661860/

Australian bat lyssavirus (ABLV) is a member of the Lyssavirus genus of the Rhabdoviridae family and is found in Australian bat species. It is of public health concern because of the rabies-like syndrome it causes in humans, resulting in government health and wildlife agencies using varied communication approaches to inform targeted audiences about zoonotic risks associated with handling bats. Despite these warnings, the number of reports of human-bat interactions remains high. This paper details a survey conducted to analyse the approaches utilised by a range of stakeholders to educate and communicate warnings to their target audiences. The survey focused on identifying the target audiences, communication methods used, along with the message frequency, content, and perceived effectiveness. Analysis of the top three messages delivered by stakeholders revealed that over half were information-focused messages and over a third, instruction-focused. Stakeholders identified the need to

balance messaging about bat handling risks with information regarding the vulnerable status of bats and their environmental significance. Whilst the most common and (perceived) effective method of communication was one-on-one discussions, it was also identified to be ineffective for targeting mass audiences leading stakeholders to recognise the need to adapt to more efficient means of communication. The outcomes of this study may be useful to improve risk communication strategies regarding ABLV in Australia.

Canine Leishmania spp. infection in two distinct foci of visceral and cutaneous leishmaniasis in Tunisia.

Zribi L, El Houda Ben-Fayala N, Aissi W, Ben-Abid M, Souissi O, Hamdi N, Boulehmi N, Ghrab J, Jemni A, Jamel A, Handous M, Bouratbine A, Oliva G, Aoun K.
Sepot-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652625/

Schistosomiase

Corrigendum: Dynamics of host immune response development during Schistosoma mansoni infection.

Costain AH, Phythian-Adams AT, Colombo SAP, Marley AK, Owusu C, Cook PC, Brown SL, Webb LM, Lundie RJ, Borger JG, Smits HH, Berriman M, MacDonald AS.
10-08-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37675098/

Discovery of new Schistosoma mansoni aspartyl protease inhibitors by structure-based virtual screening.

Gomes BF, Senger MR, Moreira-Filho JT, Vasconcellos Junior FJ, Dantas RF, Owens R, Andrade CH, Neves BJ, Silva-Junior FP.
01-09-2023
Mem Inst Oswaldo Cruz.
https://pubmed.ncbi.nlm.nih.gov/37672425/

Background: Schistosomiasis is a neglected tropical disease caused by trematodes of the genus Schistosoma, with a limited treatment, mainly based on the use of praziquantel (PZQ). Currently, several aspartic proteases genes have already been identified within the genome of Schistosoma species. At least one enzyme encoded from this gene family (SmAP), named SmCD1, has been validated for the development of schistosomicidal drugs, since it has a key role in haemoglobin digestion by worms. Objective: In this work, we integrated a structure-based virtual screening campaign, enzymatic assays and adult worms ex vivo experiments aiming to discover the first classes of SmCD1 inhibitors. Methods: Initially, the 3D-structures of SmCD1, SmCD2 and SmCD3 were generated using homology modelling approach. Using these models, we prioritised 50 compounds from 20,000 compounds from ChemBridge database for further testing in adult worm aqueous extract (AWAE) and recombinant SmCD1 using enzymatic assays. Findings: Seven compounds were confirmed as hits and among them, two compounds representing new chemical scaffolds, named 5 and 19, had IC50 values against SmCD1 close to 100 µM while presenting binding efficiency indexes comparable to or even higher than pepstatin, a classical tight-binding peptide inhibitor of aspartyl proteases. Upon activity comparison against mammalian enzymes, compound 50 was selective and the most potent against the AWAE aspartic protease activity (IC50 = 77.7 µM). Combination of computational and experimental results indicate that compound 50 is a selective inhibitor of SmCD2. Compounds 5, 19 and 50 tested at low concentrations (10 uM) were neither cytotoxic against WSS-1 cells (48 h) nor could kill adult worms ex-vivo, although compounds 5 and 50 presented a slight decrease on female worms motility on late incubations times (48 or 72 h). Main conclusion: Overall, the inhibitors identified in this work represent promising hits for further hit-to-lead optimisation.

Twitter trends in #Parasitology determined by text mining and topic modelling.

Ellis JT, Reichel MP.
12-08-2023
Curr Res Parasitol Vector Borne Dis.
https://pubmed.ncbi.nlm.nih.gov/37670843/

Gall bladder schistosomiasis diagnosed incidentally post laparoscopic cholecystectomy: A case report.

Kyejo W, Panjwani S, Ismail A, Mathew B, Ngimba C, Mwanga A.
02-09-2023
Int J Surg Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37669608/

Introduction and importance: Schistosomiasis is a neglected tropical disease caused by parasitic worms of the genus Schistosoma. It primarily affects the intestines, liver, and urinary tract however, rare cases have been reported where the parasite invades other organs. This case report presents an incidental finding of schistosomiasis, upon histopathology evaluation, in a patient who underwent laparoscopic cholecystectomy for symptomatic gallstone disease with recurrent attacks of cholecystitis. Case presentation: We present the case of a 42-year-old female patient who presented to the emergency department with symptoms and signs suggestive of acute cholecystitis. She underwent conservative management with interval laparoscopic cholecystectomy with histopathology findings of Schistosoma eggs within the walls of the gallbladder. Underwent eradication therapy with praziquantel. Clinical discussion: The finding of Schistosoma eggs in the gallbladder wall during routine histopathological examination highlights the importance of considering schistosomiasis, and other parasites, in cases of recurrent bouts of cholecystitis. The case challenges the conventional understanding of the transmission patterns of this parasitic infection and raises questions about

potential atypical life cycle routes within the human body. It also emphasizes the importance of routine histopathology analysis of specimen removed from the body. **Conclusion:** This case report presents a rare occurrence of schistosomiasis cholecystitis in a 42-year-old female patient underscoring the importance of considering parasitic infections. Thorough histopathological examination in routine surgeries is crucial for early detection and targeted treatment. The patient's positive response to praziquantel therapy highlights its effectiveness in managing schistosomiasis, which is a neglected tropical disease.

Progress from morbidity control to elimination as a public health problem of schistosomiasis and the status of soil-transmitted helminth infection in Togo: a second impact assessment after ten rounds of mass drug administration.

Dorkenoo AM, Phillips AE, Klein L, Lack F, Ataba E, Yakpa K, Tagba AE, Assoti BE, Sossou E, Tchalim M, Datagni G, Seim A, Milord MD, Kassankogno Y.
04-09-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37667301/

Background: Due to the burden of schistosomiasis (SCH) and soil-transmitted helminths (STH), Togo Ministry of Health launched a program for Preventive Chemotherapy Neglected Tropical Diseases (PC-NTDs) in 2009, initiating integrated mass drug administration (MDA) the following year for the three PC-NTDs: SCH, STH and onchocerciasis. Significant reduction of infection across the country was noted in 2015 during the first impact assessment, following 5 years of high-coverage MDA implemented at the sub-district level for SCH and district level for STH. After another 5 years of effective MDA, a second survey was conducted in 2021 to re-evaluate the situation of SCH and STH. **Methods:** A cross-section of school-aged children was taken across ten districts of Togo. A total of 302 schools in 92 sub-districts were sampled, with 24 school-aged children per school resulting in 7248 children surveyed. Urine samples were tested by haemastix® for Schistosoma haematobium, with urine filtration for the presence of eggs conducted on haematuria-positive samples. Stool samples were collected in a subset of 34 sub-districts in seven out of the ten surveyed districts, where STH and Schistosoma mansoni endemicity was high during the 2015 impact assessment. Duplicate (two) Kato-Katz analysis was performed for each stool sample. Sociodemographic and school-level water, sanitation and hygiene information was also collected. **Results:** Overall, SCH prevalence was 5.90% (95% CI: 5.4-6.5), with 5.09% (95% CI: 4.64-5.67) for S. haematobium and 2.56% (95% CI: 1.98-3.29) for S. mansoni. STH prevalence was 19.7% (95% CI: 18.2-21.4), with 19.6% (95% CI: 18.1-21.3) hookworm, 0.08% (95% CI: 2.2-5.8) Trichuris trichiura and 0.04% (95% CI: 0.01-0.33) Ascaris lumbricoides. Compared to baseline, a significant reduction in both SCH (22.2% to 5.90%) and STH (29.2% t0 19.7%) prevalence was observed. Children aged 5-9 years were less infected than older peers aged 10-14 years: 4.76% vs. 7.53% ($P < 0.01$) for SCH and 17.2% vs. 23.0% ($P < 0.01$) for STH. **Conclusions:** After 10 years of high coverage integrated MDA, Togo has achieved low prevalence SCH infection through the sub-district MDA implementation with considerable infection heterogeneity within sub-districts. As STH infection has not reached a level where the infections are not a public health problem, the sub-district treatment strategy could also be adopted in addition to improvement of treatment coverage among preschool age children and hygiene and sanitation practices.

H19/Mir-130b-3p/Cyp4a14 potentiate the effect of praziquantel on liver in the treatment of Schistosoma japonicum infection.

Ma R, Liu Q, Liu Z, Sun X, Jiang X, Hou J, Zhang Y, Wu Y, Cheng M, Dong Z.
31-08-2023
Acta Trop.
https://pubmed.ncbi.nlm.nih.gov/37659685/

The long road to schistosomiasis elimination in Zanzibar: A systematic review covering 100 years of research, interventions and control milestones.

Trippler L, Knopp S, Welsche S, Webster BL, Stothard JR, Blair L, Allan F, Ame SM, Juma S, Kabole F, Ali SM, Rollinson D, Pennance T.
2023
Adv Parasitol.

Prevalence of Soil-Transmitted Helminths and Schistosoma mansoni among Schoolchildren across Altitudinal Gradients in Amhara National Regional State, Ethiopia.

Abie A, Hailu T, Alemu G, Nibret E, Amor A, Munshea A.
14-08-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37580029/

Soil-transmitted helminths (STHs) and Schistosoma mansoni infections are common parasitic infections in sub-Saharan Africa. Their distributions vary across altitudes in Ethiopia. Hence, ongoing updates of infection risk factors and prevalence data are necessary for successful intervention. A school-based, cross-sectional study was conducted from October to December 2019 involving 530 schoolchildren who were recruited by systematic random sampling from Amhara Regional State. A structured questionnaire was used to collect data on sociodemographic, geographical and environmental factors. Stool samples were collected and processed by Ritchie's and Kato Katz techniques. Data were entered into EpiData and analyzed using SPSS. Descriptive statistics were used to compute prevalence, and logistic regression was used to assess factors associated with STHs and S. mansoni infections. Variables with $P < 0.05$ were considered statistically significant. Among 530 schoolchildren, 169 (31.9%) and 78 (14.7%) were infected

with STHs and S. mansoni, respectively. The prevalence of STHs (40.2%) in the semi-highlands and S. mansoni (30.4%) in the lowlands was high. Infrequent shoes wearing, exposure to soil, not washing vegetables before eating, and living outside in lowland areas were significantly associated with STHs infections ($P < 0.05$). Schoolchildren who fetched water to irrigate fields, swam in rivers, and lived in lowland areas were significantly associated with S. mansoni infection ($P < 0.05$). In conclusion, prevalence rates of STHs and S. mansoni infections differed across altitudes in Amhara Regional State. Therefore, current control strategies including deworming and provision of clean water and education on sanitation and hygiene should be intensified and adapted to the local context.

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.
Sept-2023
Infect Dis Now.
https://pubmed.ncbi.nlm.nih.gov/37142230/

Objectives: Little is known about the burden of urogenital schistosomiasis (UGS) outside endemic areas. This study was aimed at describing urinary complications of UGS detected among African migrants in French primary care facilities. Patients and methods: A retrospective cohort study included patients with UGS diagnosed from 2004 to 2018 in 5 primary health centers in Paris. Cases were defined by the presence of typical Schistosoma haematobium eggs at urine microscopy. Demographic, clinical, biological and imaging data were collected. Ultrasonography (U-S) findings were classified in accordance with the WHO guidelines. Results: U-S was prescribed for all patients and performed in 100/118. Sex ratio (F/M) was 2/98, and mean age 24.4 years. Patients were from West Africa (73% from Mali) and consulted 8 months (median) after their arrival. Among the 95 patients with interpretable findings, 32 (33.7%) had abnormalities related to UGS, considered as major in 6 cases (6.3%), and mostly localized at the bladder (31/32) without detection of cancer. No sociodemographic, clinical, or biological factors were found to be associated with U-S abnormalities. All 100 patients were treated by praziquantel (PZQ). Among those with abnormalities, 20/32 received two to four doses at various time intervals. Post-cure imaging control performed in 19/32 showed persistent abnormalities in 6 patients, on average 5 months after the last PZQ uptake. Conclusion: Urinary tract abnormalities associated with UGS were common and predominated at the bladder. U-S should be prescribed to any patient with positive urine microscopy. Schedules for PZQ uptake and U-S monitoring for patients with complications remain to be determined.

A 14-year follow-up of ultrasound-detected urinary tract pathology associated with urogenital schistosomiasis in women living in the Msambweni region of coastal Kenya.

Joekes E, McMonnies K, Blanshard A, Mutuku FM, Ireri E, Mungai P, Stothard JR, Bustinduy AL, King CH.
01-09-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37042291/

Trachome

Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

Cherif MS, Keita M, Dahal P, Guilavogui T, Beavogui AH, Diassy L, Conde M, Touré A, Delamou A.
01-09-2023
Int Health.
https://pubmed.ncbi.nlm.nih.gov/37232124/

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

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

Environmental risk factors that have an impact on the ocular surface were reviewed and associations with age and sex, race/ethnicity, geographical area, seasonality, prevalence and possible interactions between risk factors are reviewed. Environmental factors can be (a) climate-related: temperature, humidity, wind speed, altitude, dew point, ultraviolet light, and allergen or (b) outdoor and indoor pollution: gases, particulate matter, and other sources of airborne pollutants. Temperature affects ocular surface homeostasis directly and indirectly, precipitating ocular surface diseases and/or symptoms, including trachoma. Humidity is negatively associated with dry eye disease. There is little data on wind speed and dewpoint. High altitude and ultraviolet light exposure are associated with pterygium, ocular surface degenerations and neoplastic disease. Pollution is associated with dry eye disease and conjunctivitis. Primary Sjögren syndrome is associated with exposure to chemical solvents. Living within a potential zone of active volcanic eruption is associated with eye irritation. Indoor pollution, "sick" building or house can also be associated with eye irritation. Most ocular surface conditions are multifactorial, and several environmental factors may contribute to specific diseases. A systematic review was conducted to answer the following research question: "What are the associations between outdoor environment pollution and signs or symptoms of dry eye disease in humans?" Dry eye disease is associated with air pollution (from NO_2) and soil pollution (from chromium), but not from air pollution from CO or PM_{10}. Future research should adequately account for confounders, follow up over time,

and report results separately for ocular surface findings, including signs and symptoms.

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

Roaming behavior of the owned domestic cats (Felis catus) with possible roles in the transmission of Opisthorchis viverrini in the endemic area in Khon Kaen, Thailand.

Sakamoto M, Upontain S, Sota P, Mariner J, Tangkawattana P, Tangkawattana S.
01-09-2023
Acta Trop.
https://pubmed.ncbi.nlm.nih.gov/37660777/

The Hallmarks of Liver Fluke Related Cholangiocarcinoma: Insight into Drug Target Possibility.

Loilome W, Namwat N, Jusakul A, Techasen A, Klanrit P, Phetcharaburanin J, Wangwiwatsin A.
2023
Recent Results Cancer Res.
https://pubmed.ncbi.nlm.nih.gov/37660331/

Epidemiology and Control of Opisthorchis viverrini Infection: Implications for Cholangiocarcinoma Prevention.

Khuntikeo N, Thinkhamrop B, Crellen T, Eamudomkarn C, Petney TN, Andrews RH, Sithithaworn P.
2023
Recent Results Cancer Res.
https://pubmed.ncbi.nlm.nih.gov/37660330/

It is known that Opisthorchis viverrini (OV) is the most significant risk factor for the development of cholangiocarcinoma (CCA); hence, it is also known as carcinogenic parasite. Effective control and elimination of OV infection should significantly reduce O. viverrini-related CCA. This chapter includes details of the three recently developed innovative tools, namely the Isan cohort database software, an OV-RDT for screening of O. viverrini, and an ultrasound telecommunication system. Past and current control programs, i.e., education, medication, and sanitation were discussed and stressed the need for a comprehensive control program which encompasses primary, secondary, and tertiary patient care programs for confirmation and management of suspected CCA cases. The approach of mathematical modeling for control of OV and CCA was also briefly described. Additionally, we highlighted the current progress toward control of OV and CCA in Thailand and potential for expansion into nearby countries in Southeast Asia.

Opisthorchis viverrini Life Cycle, Distribution, Systematics, and Population Genetics.

Saijuntha W, Andrews RH, Sithithaworn P, Petney TN.
2023
Recent Results Cancer Res.
https://pubmed.ncbi.nlm.nih.gov/37660329/

Opisthorchis viverrini plays a key role as the carcinogenic liver fluke causing bile duct cancer in Southeast Asia. A comprehensive understanding of its life cycle, distribution, systematics, and population genetics is critically important as they underpin the effective development and establishment of future prevention and control programs that center on opisthorchiasis and cholangiocarcinoma. This chapter provides detailed information concerning the basic biology and updated information of O. viverrini related to its host life cycle, transmission route via raw, partially cooked or fermented freshwater cyprinid fish, endemic areas, and the discovery of new foci. Previous sequential studies over the last two decades on the phylogenetic and systematic relationships, genetic variation, and population genetics of O. viverrini as well as its snail intermediate host Bithynia spp. are presented and discussed, which have led to the currently known complex species level systematics and population genetics framework of this host-parasite system. Additionally, further directions for comprehensive research are suggested to provide a more complete understanding of liver fluke, O. viverrini-related cholangiocarcinoma.

Introduction.

Khuntikeo N, Andrews RH, Petney TN, Khan SA.
2023
Recent Results Cancer Res.
https://pubmed.ncbi.nlm.nih.gov/37660328/

Development of a novel method for diagnosis of fasciolosis based on cathepsin L7 in ruminants.

Gong JZ, Fan YM, Yuan W, Pan M, Liu D, Tao JP, Huang SY.
29-08-2023
Vet Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37657153/

Genetic characterization and regional distribution of lymnaeid snails in northern Patagonia, Argentina.

Soler P, Abdala AM, Larroza M.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652637/

Gastrointestinal parasites of domestic sheep from Patagonia throughout

historical times: A paleoparasitological approach.

Beltrame MO, Moviglia GS, De Tommaso D, Quintana S.
Sept-2023
Vet Parasitol Reg Stud Reports.
https://pubmed.ncbi.nlm.nih.gov/37652634/

Diversity, prevalence and risk factors associated to gastrointestinal tract parasites in wild and domestic animals from Pakistan.

Khattak I, Akhtar A, Shams S, Usman T, Haider J, Nasreen N, Khan A, Ben Said M.
Déc-2023
Parasitol Int.
https://pubmed.ncbi.nlm.nih.gov/37442336/

The gastrointestinal tract (GIT) of animals contains various helminth parasites, responsible for subclinical and clinical parasitism. The health situation of animals is seriously affected by these parasites and leads massive financial losses for the livestock trade. The present study was conducted to determine the prevalence and associated risk factors of GIT parasites in small and large ruminants of Mardan district and zoo animals of Golden Life Safari Park Khyber Pakhtunkhwa. A total of 419 fecal samples were collected including 117 from goats, 110 from cattle, 80 from sheep, 66 from buffaloes, 40 from birds, four from deer, and two from leopards. The fecal samples were subjected to sedimentation and floatation to identify parasite eggs. Of a total of 419 fecal samples, 215 (51.31%) were found positive for GIT parasites eggs. The prevalence of GIT parasites was high in sheep (65%), followed by goats (62.39%), cattle (42.70%), and buffaloes (37.87%). In birds, GIT parasite eggs were identified in 11 (45.83%) and 7 (43.75%) fecal samples of Pheasant and Peacock, respectively. However, an absence of infection was noted in fecal samples from deer and leopards. Eggs of GIT Parasites belonging to one superfamily and four different genera were recognized in fecal samples of domestic animals and buffaloes, which were Trichostrongyloidea (19.81%), Strongyloides (9.31%), Trichuris (7.77%), Monezia (6.44%), and Fasciola (4.53%). For bird, the coccidia group comprises the highest representation of parasites (2.63%), followed by the Trichuris genus (1.67%). Settlement, management system, anthelminthic medications and body condition score were significantly associated with the occurrence of GIT parasites in feces ($P < 0.05$). Animals from rural settlements, rearing under poor management systems, with thin (poor) body condition and under warmed were more affected by GIT parasites. The diversity and the high prevalence of GIT parasites reported in this study highlights the urgent need for intervention through treatment and modification of management practices in the investigated areas of Pakistan.

Plasma lipopolysaccharide elevations in cattle associated with early-stage infection by Fasciola hepatica.

Marendy D, Gabor L, George SD, Parker A, Doyle E.
Sept-2023
Aust Vet J.
https://pubmed.ncbi.nlm.nih.gov/37317661/

Fasciolosis is an endemic zoonotic parasitic disease with significant impacts on human health and both animal health and production. Early post-infection impacts on the host remain unclear. The objective of this study was to determine the changes, if any, to levels of endotoxin in cattle plasma in response to early-stage infection with Fasciola hepatica. Thirty-six (36) commercial bred cattle were experimentally infected with approximately 400 viable metacercariae. Plasma lipopolysaccharide (endotoxin) levels were examined on 24 occasions from 0 h before infection to 336 h after infection using the Limulus Amoebocyte Lysate chromogenic end point assay and compared with that of six (6) uninfected control animals. Peak lipopolysaccharide levels in infected animals were reached at 52 h after infection and returned to pre-infection levels at time 144 h after infection. Infected animals had significantly elevated lipopolysaccharide levels between 24 and 120 h after infection when compared to uninfected animals. The mean change in endotoxin units (EU)/mL over time after infection was statistically significant in infected animals. Elevations of lipopolysaccharide occurred in all infected animals suggesting a possible repeatable and titratable endotoxemia conducive to therapeutic agent model development.

Trypanosomes (trypanosomiase et maladie de Chagas)

The Power of Molecular Dynamics Simulations and Their Applications to Discover Cysteine Protease Inhibitors.

Dos Santos Nascimento IJ, Santana Gomes JN, de Oliveira Viana J, de Medeiros E Silva YMS, Barbosa EG, de Moura RO.
01-09-2023
Mini Rev Med Chem.
https://pubmed.ncbi.nlm.nih.gov/37680157/

A large family of enzymes with the function of hydrolyzing peptide bonds, called peptidases or cysteine proteases (CPs), are divided into three categories according to the peptide chain involved. CPs catalyze the hydrolysis of amide, ester, thiol ester, and thioester peptide bonds. They can be divided into several groups, such as papain-like (CA), viral chymotrypsin-like CPs (CB), papain-like endopeptidases of RNA viruses (CC), legumain-type caspases (CD), and showing active residues of His, Glu/Asp, Gln, Cys (CE). The catalytic mechanism of CPs is the essential cysteine residue present in the active site. These mechanisms are often studied through computational methods that provide new information about the catalytic mechanism and identify inhibitors. The role of computational methods during drug design and development stages is increasing. Methods in Computer-Aided Drug Design (CADD) accelerate the discovery process, increase the chances of selecting more promising molecules for experimental studies, and can identify

critical mechanisms involved in the pathophysiology and molecular pathways of action. Molecular dynamics (MD) simulations are essential in any drug discovery program due to their high capacity for simulating a physiological environment capable of unveiling significant inhibition mechanisms of new compounds against target proteins, especially CPs. Here, a brief approach will be shown on MD simulations and how the studies were applied to identify inhibitors or critical information against cysteine protease from several microorganisms, such as Trypanosoma cruzi (cruzain), Trypanosoma brucei (rhodesain), Plasmodium spp. (falcipain), and SARS-CoV-2 (Mpro). We hope the readers will gain new insights and use our study as a guide for potential compound identifications using MD simulations.

Trypanosomes as a magnifying glass for cell and molecular biology.

Lukeš J, Speijer D, Zíková A, Alfonzo JD, Hashimi H, Field MC.
05-09-2023
Trends Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37679284/

A nuclear orthologue of the dNTP triphosphohydrolase SAMHD1 controls dNTP homeostasis and genomic stability in Trypanosoma brucei.

Antequera-Parrilla P, Castillo-Acosta VM, Bosch-Navarrete C, Ruiz-Pérez LM, González-Pacanowska D.
22-08-2023
Front Cell Infect Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37674581/

Identification of natural lead molecules as potential Trypanosoma cruzi cruzipain inhibitors and decoding the interaction mechanism for the treatment of Chagas disease: a computational biology analysis.

Tripathi RKP, Dey R, Das N.
07-09-2023
Nat Prod Res.
https://pubmed.ncbi.nlm.nih.gov/37674430/

Twitter trends in #Parasitology determined by text mining and topic modelling.

Ellis JT, Reichel MP.
12-08-2023
Curr Res Parasitol Vector Borne Dis.
https://pubmed.ncbi.nlm.nih.gov/37670843/

This study investigated the emergence and use of Twitter, as of July 2023 being rebranded as X, as the main forum for social media communication in parasitology. A dataset of tweets was constructed using a keyword search of Twitter with the search terms 'malaria', '*Plasmodium*', '*Leishmania*', '*Trypanosoma*', '*Toxoplasma*' and '*Schistosoma*' for the period from 2011 to 2020. Exploratory data analyses of tweet content were conducted, including language, usernames and hashtags. To identify parasitology topics of discussion, keywords and phrases were extracted using KeyBert and biterm topic modelling. The sentiment of tweets was analysed using VADER. The results show that the number of tweets including the keywords increased from 2011 (for malaria) and 2013 (for the others) to 2020, with the highest number of tweets being recorded in 2020. The maximum number of yearly tweets for *Plasmodium*, *Leishmania*, *Toxoplasma*, *Trypanosoma* and *Schistosoma* was recorded in 2020 (2804, 2161, 1570, 680 and 360 tweets, respectively). English was the most commonly used language for tweeting, although the percentage varied across the searches. In tweets mentioning *Leishmania*, only ~37% were in English, with Spanish being more common. Across all the searches, Portuguese was another common language found. Popular tweets on *Toxoplasma* contained keywords relating to mental health including depression, anxiety and schizophrenia. The *Trypanosoma* tweets referenced drugs (benznidazole, nifurtimox) and vectors (bugs, triatomines, tsetse), while the *Schistosoma* tweets referenced areas of biology including pathology, eggs and snails. A wide variety of individuals and organisations were shown to be associated with Twitter activity. Many journals in the parasitology arena regularly tweet about publications from their journal, and professional societies promote activity and events that are important to them. These represent examples of trusted sources of information, often by experts in their fields. Social media activity of influencers, however, who have large numbers of followers, might have little or no training in science. The existence of such tweeters does raise cause for concern to parasitology, as one may start to question the quality of information being disseminated.

Validation of a multiplex microsphere immunoassay for detection of antibodies to Trypanosoma cruzi in dogs.

Rodriguez CA, Busselman RE, Shen H, Saunders AB, Tarleton R, Hamer SA.
05-09-2023
J Vet Diagn Invest.
https://pubmed.ncbi.nlm.nih.gov/37670473/

Neutrophil metalloproteinase driven spleen damage hampers infection control of trypanosomiasis.

Pham HTT, Magez S, Choi B, Baatar B, Jung J, Radwanska M.
05-09-2023
Nat Commun.
https://pubmed.ncbi.nlm.nih.gov/37669943/

Recent blood transcriptomic analysis of rhodesiense sleeping sickness patients has revealed that neutrophil signature genes and activation markers constitute the top indicators of trypanosomiasis-associated inflammation. Here, we show that Trypanosoma brucei infection results in expansion and differentiation of four splenic neutrophil subpopulations, including Mki67^{+}Birc5^{+}Gfi1^{+}Cebpe^{+} proliferation-competent precursors, two intermediate

immature subpopulations and Cebpb^{+}Spi1^{+}Irf7^{+}Mcl1^{+}Csf3r^{+} inflammation reprogrammed mature neutrophils. Transcriptomic scRNA-seq profiling identified the largest immature subpopulation by Mmp8/9 positive tertiary granule markers. We confirmed the presence of both metalloproteinases in extracellular spleen homogenates and plasma. During infection, these enzymes digest extracellular matrix components in the absence of sufficient TIMP inhibitory activity, driving remodeling of the spleen follicular architecture. Neutrophil depletion prevents the occurrence of organ damage, resulting in increased plasma cell numbers and prolonged host survival. We conclude that trypanosomiasis-associated neutrophil activation is a major contributor to the destruction of the secondary lymphoid architecture, required for maintaining an efficient adaptive immune response.

Comprehensive sub-mitochondrial protein map of the parasitic protist Trypanosoma brucei defines critical features of organellar biology.

Pyrih J, Hammond M, Alves A, Dean S, Sunter JD, Wheeler RJ, Gull K, Lukeš J.
04-09-2023
Cell Rep.
https://pubmed.ncbi.nlm.nih.gov/37669165/

Intra-host Trypanosoma cruzi strain dynamics shape disease progression: the missing link in Chagas disease pathogenesis.

Dumonteil E, Desale H, Tu W, Hernandez-Cuevas N, Shroyer M, Goff K, Marx PA, Herrera C.
05-09-2023
Microbiol Spectr.
https://pubmed.ncbi.nlm.nih.gov/37668388/

Identification of the ATPase alpha subunit of Trypanosoma cruzi as a potential biomarker for the diagnosis of Chagas disease.

Morales-Velásquez M, Barón-Vera JP, Pulgarín-Osorio MI, Sánchez-Jiménez MM, Ospina-Villa JD.
05-09-2023
Biomarkers.
https://pubmed.ncbi.nlm.nih.gov/37667642/

Population structure and migration in Triatoma infestans (Hemiptera: Reduviidae) from the Argentine Chaco: an integration of genetic and morphometric data.

Piccinali RV, Gaspe MS, Nattero J, Gürtler RE.
02-09-2023
Acta Trop.
https://pubmed.ncbi.nlm.nih.gov/37666351/

Molecular basis of the glycosomal targeting of PEX11 and its mislocalization to mitochondrion in trypanosomes.

Krishna CK, Schmidt N, Tippler BG, Schliebs W, Jung M, Winklhofer KF, Erdmann R, Kalel VC.
17-08-2023
Front Cell Dev Biol.
https://pubmed.ncbi.nlm.nih.gov/37664461/

PEX19 binding sites are essential parts of the targeting signals of peroxisomal membrane proteins (mPTS). In this study, we characterized PEX19 binding sites of PEX11, the most abundant peroxisomal and glycosomal membrane protein from *Trypanosoma brucei* and *Saccharomyces cerevisiae*. *Tb*PEX11 contains two PEX19 binding sites, one close to the N-terminus (BS1) and a second in proximity to the first transmembrane domain (BS2). The N-terminal BS1 is highly conserved across different organisms and is required for maintenance of the steady-state concentration and efficient targeting to peroxisomes and glycosomes in both baker's yeast and *Trypanosoma brucei*. The second PEX19 binding site in *Tb*PEX11 is essential for its glycosomal localization. Deletion or mutations of the PEX19 binding sites in *Tb*PEX11 or *Sc*PEX11 results in mislocalization of the proteins to mitochondria. Bioinformatic analysis indicates that the N-terminal region of *Tb*PEX11 contains an amphiphilic helix and several putative TOM20 recognition motifs. We show that the extreme N-terminal region of *Tb*PEX11 contains a cryptic N-terminal signal that directs PEX11 to the mitochondrion if its glycosomal transport is blocked.

Immunopathogenesis in Trypanosoma cruzi infection: a role for suppressed macrophages and apoptotic cells.

Vellozo NS, Matos-Silva TC, Lopes MF.
17-08-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37662946/

During *Trypanosoma cruzi* infection, macrophages phagocytose parasites and remove apoptotic cells through efferocytosis. While macrophage 1 (M1) produces proinflammatory cytokines and NO and fights infection, M2 macrophages are permissive host cells that express arginase 1 and play a role in tissue repair. The regulation of M1 and M2 phenotypes might either induce or impair macrophage-mediated immunity towards parasite control or persistence in chronic Chagas disease. Here, we highlight a key role of macrophage activation in early immune responses to *T. cruzi* that prevent escalating parasitemia, heart parasitism, and mortality during acute infection. We will discuss the mechanisms of macrophage activation and deactivation, such as T cell cytokines and efferocytosis, and how to improve macrophage-mediated immunity to prevent parasite persistence, inflammation, and the development of chagasic cardiomyopathy. Potential vaccines or therapy must enhance early T cell-macrophage crosstalk and parasite control to restrain the pathogenic outcomes of parasite-induced inflammation in the heart.

Topoisomerase II inhibitor cures trypanosome infections.

Crunkhorn S.
Sept-2023
Nat Rev Drug Discov.
https://pubmed.ncbi.nlm.nih.gov/37468690/

Ulcère de Buruli

Is BCG vaccination of possums the solution to the Buruli ulcer epidemic in south-eastern Australia?

O'Brien DP, Blasdell K, Muhi S, Marais BJ, Buddle B, McNamara B, Athan E.
07-09-2023
Med J Aust.
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Neglected tropical diseases in Republic of Guinea: disease endemicity, case burden and the road towards the 2030 target.

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Neglected tropical diseases (NTDs) predominantly affect vulnerable and marginalized populations in tropical and subtropical areas and globally affect more than one billion people. In Guinea, the burden of NTDs is estimated to be >7.5 disability-adjusted life years per million inhabitants. Currently the Guinea NTDs master plan (2017-2020) has identified eight diseases as public health problems: onchocerciasis, lymphatic filariasis, trachoma, schistosomiasis and soil-transmitted helminthiasis, leprosy, human African trypanosomiasis and Buruli ulcer. In this review we discuss the past and the current case burden of the priority NTDs in Guinea, highlight the major milestones and discuss current and future areas of focus for achieving the 2030 target outlined by the World Health Organization.