Réseau MTN Francophone

Veille scientifique
Maladies tropicales négligées

Semaine 32
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Cysticercose

Community knowledge, attitudes and practices related to Taenia solium taeniosis and cysticercosis in Zambia.

Zulu G, Mwape KE, Welte TM, Simuunza MC, Hachangu A, Mutale W, Chembensofu M, Sikasunge CS, Phiri IK, Winkler AS.
10-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37561784/

Cysticercus pisiformis-derived novel-miR1 targets TLR2 to inhibit the immune response in rabbits.

Chen G, Pu G, Wang L, Li Y, Liu T, Li H, Zhang S, Wang X, Liu X, Luo X.
25-07-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37559722/

Cysticercosis pisiformis, a highly prevalent parasitic disease worldwide, causes significant economic losses in the rabbit breeding industry. Previous investigations have identified a novel microRNA, designated as novel-miR1, within the serum of rabbit infected with *Cysticercus pisiformis*. In the present study, we found that *C. pisiformis*-derived novel-miR1 was released into the rabbit serum via exosomes. Through computational analysis using TargetScan, miRanda, and PITA, a total of 634 target genes of novel-miR1 were predicted. To elucidate the functional role of novel-miR1, a dual-luciferase reporter assay was utilized and demonstrated that novel-miR1 targets rabbit Toll-like receptor 2 (TLR2). Rabbit peripheral blood lymphocytes (PBLCs) were transfected with novel-miR1 mimic and mimic NC, and the *in vitro* experiments confirmed that novel-miR1 suppressed the expression of pro-inflammatory cytokines such as TNF-α, IL-1β, and IL-6 through the nuclear factor kappa B (NF-κB) pathway. *In vivo* experiments demonstrated that novel-miR1 was significantly upregulated during the 1-3 months following infection with *C. pisiformis in* rabbits. Notably, this upregulation coincided with a downregulation of TLR2, P65, pP65, TNF-α, IL-1β, and IL-6 in PBLCs. Collectively, these results indicate that the novel-miR1 derived from *C. pisiformis* inhibited the rabbits' immune response by suppressing the NF-κB-mediated immune response. This immune modulation facilitates parasite invasion, survival, and establishment of a persistent infection.

Dengue, chikungunya et maladie à virus Zika

Alignment of multiple metabolomics LC-MS datasets from disparate diseases to reveal fever-associated metabolites.

Năstase AM, Barrett MP, Cárdenas WB, Cordeiro FB, Zambrano M, Andrade J, Chang J, Regato M, Carrillo E, Botana L, Moreno J, Regnault C, Milne K, Spence PJ, Rowe JA, Rogers S.
24-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37486920/

Acute febrile illnesses are still a major cause of mortality and morbidity globally, particularly in low to middle income countries. The aim of this study was to determine any possible metabolic commonalities of patients infected with disparate pathogens that cause fever. Three liquid chromatography-mass spectrometry (LC-MS) datasets investigating the metabolic effects of malaria, leishmaniasis and Zika virus infection were used. The retention time (RT) drift between the datasets was determined using landmarks obtained from the internal standards generally used in the quality control of the LC-MS experiments. Fitted Gaussian Process models (GPs) were used to perform a high level correction of the RT drift between the experiments, which was followed by standard peakset alignment between the samples with corrected RTs of the three LC-MS datasets. Statistical analysis, annotation and pathway analysis of the integrated peaksets were subsequently performed. Metabolic dysregulation patterns common across the datasets were identified, with kynurenine pathway being the most affected pathway between all three fever-associated datasets.

Structures of dengue virus RNA replicase complexes.

Osawa T, Aoki M, Ehara H, Sekine SI.
03-08-2023
Mol Cell.
https://pubmed.ncbi.nlm.nih.gov/37478848/

The reemergence of dengue virus in Sudan.

Mustafa MI, Makhawi AM.
Sept-2023
J Infect Public Health.
https://pubmed.ncbi.nlm.nih.gov/37473544/

Dengue fever (DF) is a mosquito-transmitted arboviral disease caused by 1 of 4 closely related but antigenically distinct serotypes of dengue virus (DENV), DENV-1-4. The primary vector of DENV is Aedes aegypti and Aedes albopictus mosquitoes. Humans are the main carrier of the virus and the amplifying host with non-human primates plays a considerable role in sylvatic cycle. On November 8, 2022, an outbreak of dengue fever has killed at least five people in North Kordofan State. On 23 Nov 2022, the Sudanese Ministry of Health reported 3326 cases of dengue fever across 8 Sudanese States; while 23 patients died from the fever. Sudan is witnessing its worst outbreak of dengue fever in over a decade, especially in North and South Kordofan and Red Sea State are hit hard. In this review, we will focus on the recent outbreak of dengue fever in many Sudanese states.

Exclusion of pregnant people from emergency vaccine clinical trials: A systematic review of clinical trial protocols and reporting from 2009 to 2019.

Minchin J, Harris GH, Baumann S, Smith ER.
07-08-2023
Vaccine.
https://pubmed.ncbi.nlm.nih.gov/37442686/

Background: Existing ethics guidance and regulatory requirements emphasize the need for pregnancy-specific safety and efficacy data during the development of vaccines in health emergencies. Our objective was to conduct a systematic review of vaccine clinical trials during active epidemic periods. Methods: We searched for Phase II and Phase III vaccine clinical trials initiated during the H1N1 influenza, Middle East Respiratory Syndrome Coronavirus (MERS-CoV), Zika, and Ebola virus disease (EVD) outbreaks from 2009 to 2019. Data were extracted from clinical trial protocols identified in the following registries: ClinicalTrials.gov, Pan African Clinical Trial Registry (PACTR), and all primary registries indicated by the World Health Organization's International Clinical Trials Registry Platform (ICTRP). Published studies from registered clinical trials were located through PubMed. Data was extracted on eligibility criteria and pregnancy outcomes. Data from this study is available in the Center for Open Science Data Repository: https://osf.io/nfk2p/?view_only=47deb3b206724af9b46c9c0c0083a267. Results: We identified 96 vaccine clinical trial protocols and included 84 in analysis. 5 records were excluded in screening for irrelevant abstracts, 7 were excluded in full-text assessment (1 for a therapeutic drug trial, 3 for enrolling elderly adults only, 3 for enrolling children/adolescents only). There were no eligible trials for MERS-CoV or Zika virus vaccines. Overall, 8 protocols explicitly included pregnant people; of these, 3 were completed trials with published results. Incidental pregnancies and outcomes of pregnant participants were reported in 2 studies, 10 studies reported serious adverse events related to pregnancy without mentioning total incidental pregnancies. A total of 411 recorded pregnancy outcomes were reported, with 293 from the 3 pregnancy-eligible studies with results. 71 serious adverse events pertaining to pregnancy were reported from all clinical trials with results. Conclusion: Pregnant people are underrepresented in vaccine clinical trials conducted during outbreaks, resulting in underreporting of pregnancy-related outcomes and a lack of protection for pregnant people and neonates from infectious diseases.

Detection of dengue virus serotype 1 from gadfly in China.

Qi NS, Zhang X, Liao SQ, Li J, Liu JM, Shao JW, Sun MF.
Sept-2023
J Infect.
https://pubmed.ncbi.nlm.nih.gov/37442374/

Human exposure risk assessment for infectious diseases due to temperature and air pollution: an overview of reviews.

Song X, Guo X, Hu X, Zhang Y, Wei D, Hu Y, Jiang L, Zhang Y.
Août-2023
Environ Sci Pollut Res Int.
https://pubmed.ncbi.nlm.nih.gov/37440140/

Air pollution and global temperature change are expected to affect infectious diseases. Air pollution usually causes inflammatory response and disrupts immune defense system, while temperature mainly exacerbates the effect of vectors on humans. Yet to date overview of systematic reviews assessing the exposure risk of air pollutants and temperature on infectious diseases is unavailable. This article aims to fill this research gap. PubMed, Embase, the Cochrane Library, Web of Science, and the Cumulative Index to Nursing and Allied Health Literature were searched. Systematic reviews and meta-analyses investigated the exposure risk of pollutants or temperature on infectious diseases were included. Two investigators screened literature, extracted data and performed the risk of bias assessments independently. A total of 23 articles met the inclusion criteria, which 3 (13%) were "low" quality and 20 (87%) were "critically low" quality. COVID-19 morbidity was associated with long-term exposure $PM_{2.5}$ (RR = 1.056 per 1 [Formula: see text], 95% CI: 1.039-1.072) and NO_2 (RR = 1.042 per 1 [Formula: see text], 95% CI: 1.017-1.068). In addition, for each 1 °C increase in temperature, the morbidity risk of dengue increased 13% (RR = 1.130 per 1 °C, 95% CI: 1.120-1.150), infectious diarrhea increased 8% (RR = 1.080 per 1 °C, 95% CI: 1.050-1.200), and hand, foot and mouth disease (HFMD) increased 5% (RR = 1.050 per 1 °C, 95% CI: 1.020-1.080). In conclusion, $PM_{2.5}$ and NO_2 increased the risk of COVID-19 and temperatures were associated with dengue, infectious diarrhoea and HFMD morbidity. Moreover, the exposure risk of temperature on COVID-19 was recommended to be further explored.

Development of a thermochromic lateral flow assay to improve sensitivity for dengue virus serotype 2 NS1 detection.

Trakoolwilaiwan T, Takeuchi Y, Leung TS, Sebek M, Storozhuk L, Nguyen L, Tung LD, Thanh NTK.
10-08-2023
Nanoscale.
https://pubmed.ncbi.nlm.nih.gov/37427537/

ZIKV infection differentially affects the transcriptional profiles in HTR8 and U251 cells.

Chen Q, Li N, Zeng S, Wu S, Luo X, Zhang S, Zhu L, Wu J, Xie T, Bai S, Zhang H, Jiang Z, Lin S, Wu N, Jiang Y, Fang S, Wang X, Shu Y, Luo H.
Sept-2023
Virus Res.
https://pubmed.ncbi.nlm.nih.gov/37390859/

A new cluster of chikungunya virus West Africa genotype isolated from Aedes albopictus in China.

Li N, Peng C, Yuan Y, Hao Y, Ma W, Xiao P.
Sept-2023
J Infect.
https://pubmed.ncbi.nlm.nih.gov/37331428/

Prepandemic cross-reactive humoral immunity to SARS-CoV-2 in Africa: Systematic review and meta-analysis.

Ioannidis JPA, Contopoulos-Ioannidis DG.
Sept-2023
Int J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37327857/

Global and local evolutionary dynamics of Dengue virus serotypes 1, 3, and 4.

Islam A, Deeba F, Tarai B, Gupta E, Naqvi IH, Abdullah M, Dohare R, Ahmed A, Almajhdi FN, Hussain T, Parveen S.
09-06-2023
Epidemiol Infect.
https://pubmed.ncbi.nlm.nih.gov/37293986/

Evolutionary studies on Dengue virus (DENV) in endemic regions are necessary since naturally occurring mutations may lead to genotypic variations or shifts in serotypes, which may lead to future outbreaks. Our study comprehends the evolutionary dynamics of DENV, using phylogenetic, molecular clock, skyline plots, network, selection pressure, and entropy analyses based on partial CprM gene sequences. We have collected 250 samples, 161 in 2017 and 89 in 2018. Details for the 2017 samples were published in our previous article and that of 2018 are presented in this study. Further evolutionary analysis was carried out using 800 sequences, which incorporate the study and global sequences from GenBank: DENV-1 (*n* = 240), DENV-3 (*n* = 374), and DENV-4 (*n* = 186), identified during 1944-2020, 1956-2020, and 1956-2021, respectively. Genotypes V, III, and I were identified as the predominant genotypes of the DENV-1, DENV-3, and DENV-4 serotypes, respectively. The rate of nucleotide substitution was found highest in DENV-3 (7.90×10^{-4} s/s/y), followed by DENV-4 (6.23×10^{-4} s/s/y) and DENV-1 (5.99×10^{-4} s/s/y). The Bayesian skyline plots of the Indian strains revealed dissimilar patterns amongst the population size of the three serotypes. Network analyses showed the presence of different clusters within the prevalent genotypes. The data presented in this study will assist in supplementing the measures for vaccine development against DENV.

Neutralizing antibodies against Omicron BA.5 among children with infection alone, vaccination alone, and hybrid immunity.

Suntronwong N, Kanokudom S, Assawakosri S, Vichaiwattana P, Klinfueng S, Phowatthanasathian H, Chansaenroj J, Srimuan D, Thatsanathorn T, Duangchinda T, Chantima W, Pakchotanon P, Sudhinaraset N, Wanlapakorn N, Poovorawan Y.
Sept-2023
Int J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37207716/

Objectives: To assess the binding antibody response and strength of neutralization against Omicron BA.5 in serum samples from children with different antigen exposures (infection/vaccination) and hybrid immunity. Methods: This study recruited children aged 5-7 years. All samples were tested for anti-nucleocapsid immunoglobulin (Ig)G, anti-receptor binding domain (RBD) IgG, and total anti-RBD Ig. Neutralizing antibodies (nAbs) against Omicron BA.5 were determined using a focus reduction neutralization test. Results: A total of 196 serum samples from unvaccinated children with infection (n = 57), vaccination alone (n = 71), and hybrid immunity (n = 68). Our results showed that 90% of the samples from children with hybrid immunity, 62.2% from two-dose vaccination, and 48% from Omicron infection alone had detectable nAbs against Omicron BA.5. The highest neutralizing titer was observed in infection plus two-dose vaccination, which reached 6.3-fold increase, whereas nAb titers in two-dose vaccination was comparable to Omicron-infected sera. However, sera from pre-Omicron infection and single-dose vaccination failed to neutralize Omicron BA.5; although, the total anti-RBD Ig were comparable with Omicron-infected sera. Conclusion: This result highlights that hybrid immunity provided cross-reactive antibodies to neutralize Omicron BA.5 compared with either vaccination or infection alone. The finding emphasizes the importance of vaccination in unvaccinated children who are infected with pre-Omicron or Omicron variants.

Climate and visitors as the influencing factors of dengue fever in Badung District of Bali, Indonesia.

Maulana MR, Yudhastuti R, Lusno MFD, Mirasa YA, Haksama S, Husnina Z.
Sept-2023
Int J Environ Health Res.
https://pubmed.ncbi.nlm.nih.gov/35435067/

Badung district has recorded the highest dengue fever (DF) in Bali Province. This research presents the distribution of DF in Badung district and analyses its association with climate and visitors. The monthly data of DF, climate and number of visitors during January 2013 to December 2017 were analysed using Poisson Regression. A total of 10,689 new DF cases were notified from January 2013 to December 2017. DF in 2016 was recorded as the heaviest incidence. Monthly DF cases have positive association with average temperature (0.59 (95% CI: 0.56-.62)), precipitation (5.7×10^{-4} (95% CI: 3.8×10^{-4} - 7.6×10^{-4})), humidity (.014 (95% CI: 0.003-.025)) and local visitors (7.40×10^{-6} 95% CI: 5.88×10^{-6} : 8.91×10^{-6}). Negative association was shown between DF cases with foreign visitors (-2.18×10^{-6} (95% CI: -2.50×10^{-6} : -1.87×10^{-6})). This study underlines the urgency to integrate climate and tourism for DF surveillance.

Ex vivo gut cultures of Aedes aegypti are efficiently infected by mosquito-borne alpha- and flaviviruses.

Rosales Rosas AL, Wang L, Goossens S, Cuvry A, Li LH, Santos-Ferreira N, Soto A, Dallmeier K, Rocha-Pereira J, Delang L.
04-08-2023
Microbiol Spectr.
https://pubmed.ncbi.nlm.nih.gov/37540021/

Erste Impfung gegen Dengue-Fieber.

Blume T.
Août-2023
MMW Fortschr Med.
https://pubmed.ncbi.nlm.nih.gov/37537467/

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

Noval MG, Spector SN, Bartnicki E, Izzo F, Narula N, Yeung ST, Damani-Yokota P, Dewan MZ, Mezzano V, Rodriguez-Rodriguez BA, Loomis C, Khanna KM, Stapleford KA.
03-08-2023
Nat Commun.
https://pubmed.ncbi.nlm.nih.gov/37537212

How climate change is changing dengue fever.

Bashir A.
03-08-2023
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37536724/

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

Ngwe Tun MM, Raini SK, Fernando L, Gunawardene Y, Inoue S, Takamatsu Y, Urano T, Muthugala R, Hapugoda M, Morita K.
Sept-2023
J Infect Public Health.

Background: Zika Virus (ZIKV) is a re-emerging, arthropod-borne flavivirus transmitted by Aedes mosquitoes (Ae. aegypti and Ae. albopictus). The coexistence of dengue virus (DENV) and ZIKV concurrently has been associated with a wide array of neurological complications, which may influence the clinical outcomes of infections. Sri Lanka witnessed a severe dengue epidemic in 2017, characterized by extraordinary and severe disease manifestations with considerable morbidity. Therefore, this study assessed the potential occurrence of ZIKV infection during DENV outbreak in Sri Lanka from 2017 to 2019, which could bear substantial implications for public health. Methods: Five hundred ninety-five serum samples were procured from individuals suspected of dengue and admitted to Kandy National Hospital between 2017 and 2018 and the Negombo District General Hospital between 2018 and 2019. These samples underwent quantitative real-time RT-PCR (qRT-PCR) to identify the presence of the ZIKV gene, while enzyme-linked immunosorbent assay was employed to detect ZIKV-specific IgM and IgG antibodies. Focus reduction neutralization tests were subsequently conducted to confirm ZIKV infection. Results: Among the 595 serum samples, 6 (1.0%) tested positive for ZIKV using qRT-PCR. Anti-ZIKV IgM and IgG were identified in 18.0% and 38.6% patients. Sixty-six (11.0%) samples demonstrated the presence of anti-ZIKV IgM and IgG. Within ZIKV IgM-positive samples, 2.2% exhibited neutralizing antibodies against ZIKV. Through the implementation of qRT-PCR, ZIKV IgM detection, and neutralization testing, 2% and 3.7% cases of ZIKV infections were confirmed in the Kandy and Negombo regions, respectively. Conclusion: This study is the inaugural endeavor to substantiate the existence of ZIKV infection in Sri Lanka utilizing molecular and serological analysis. The findings of this investigation imply that ZIKV was circulating throughout the 2017-2019 DENV outbreak. These results underscore the necessity for improved preparedness for future outbreaks, fortifying governmental policies on public health, and establishing effective early warning systems regarding the emergence of these viruses.

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

Ashraf-Uz-Zaman M, Li X, Yao Y, Mishra CB, Moku BK, Song Y.
10-08-2023
J Med Chem.
https://pubmed.ncbi.nlm.nih.gov/37506506/

Genetic differentiation among Aedes aegypti populations from different eco-geographical zones of India.

Sumitha MK, Kalimuthu M, Kumar MS, Paramasivan R, Kumar NP, Sunish IP, Balaji T, Sarma DK, Kumar D, Suman DS, Srivastava H, Bhowmick IP, Vaishnav K, Singh OP, Patil PB, Tyagi S, Mohanty SS, Barik TK, Uragayala S, Kumar A, Gupta B.
27-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37498944/

The present study explicitly evaluated the genetic structure of Aedes aegypti Linn, the vector of dengue, chikungunya, and Zika viruses, across different geo-climatic zones of India and also elucidated the impact of ecological and topographic factors. After data quality checks and removal of samples with excess null alleles, the final analysis was performed on 589 individual samples using 10 microsatellite markers. Overall findings of this study suggested that, Ae. aegypti populations are highly diverse with moderate genetic differentiation between them. Around half of the populations (13 out of 22) formed two genetic clusters roughly associated with geographical regions. The remaining nine populations shared genetic ancestries with either one or both of the clusters. A significant relationship between genetic and geographic distance was observed, indicating isolation by distance. However, spatial autocorrelation analysis predicted the signs of long-distance admixture. Post-hoc environmental association analysis showed that 52.7% of genetic variations were explained by a combination of climatic and topographic factors, with latitude and temperature being the best predictors. This study indicated that though overall genetic differentiation among Ae. aegypti populations across India is moderate (Fst = 0.099), the differences between the populations are developing due to the factors associated with geographic

locations. This study improves the understanding of the Ae. aegypti population structure in India that may assist in predicting mosquito movements across the geo-climatic zones, enabling effective control strategies and assessing the risk of disease transmission.

Reinvestigation of the risk of stroke after dengue virus infection: A population-based cohort study.

Chien YW, Wang YP, Chi CY, Shih HI.
Sept-2023
J Infect Public Health.
https://pubmed.ncbi.nlm.nih.gov/37494777/

Experimental infection of Artibeus lituratus bats and no detection of Zika virus in neotropical bats from French Guiana, Peru, and Costa Rica suggests a limited role of bats in Zika transmission.

Aguilar-Setién A, Salas-Rojas M, Gálvez-Romero G, Almazán-Marín C, Moreira-Soto A, Alfonso-Toledo J, Obregón-Morales C, García-Flores M, García-Baltazar A, Serra-Cobo J, López-Roig M, Reyes-Puma N, Piche-Ovares M, Romero-Vega M, Barrantes Murillo DF, Soto-Garita C, Alfaro-Alarcón A, Corrales-Aguilar E, López-Díaz O, Pontier D, Filippi-Codaccioni O, Pons JB, Duhayer J, Drexler JF.
24-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37486923/

Study of the Aetiology and Clinical Manifestations of Thrombocytopenia in a Tertiary Care Centre.

Choudhary MK, Mishra AK, Kumar P, Jamal I, Ahmad A, Prasad G, Prasad D.
07-07-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37551236/

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, Fereira JC, Rabeh WM.
05-08-2023
Biochim Biophys Acta Mol Basis Dis.
https://pubmed.ncbi.nlm.nih.gov/37549720/

Since 2003, we have seen the emergence of novel viruses, such as SARS-CoV-1, MERS, ZIKA, swine flu virus H1N1, Marburg, Monkeypox, Ebola, and SARS-CoV-2, but none of them gained pandemic proportions similar to SARS-CoV-2. This could be attributed to unique viral traits, allowing its rapid global dissemination following its emergence in October 2019 in Wuhan, China, which appears to be primarily driven by the emergence of highly transmissible and virulent variants that also associate, in some cases, with severe disease and considerable mortality caused by fatal pneumonia, acute respiratory distress syndrome (ARDS) in infected individuals. Mechanistically, several factors are involved in viral pathogenesis, and epigenetic alterations take the front seat in host-virus interactions. The molecular basis of all viral infections, including SARS-CoV-2, tightly hinges on the transitory silencing of the host gene machinery via epigenetic modulation. SARS-CoV-2 also hijacks and subdues the host gene machinery, leading to epigenetic modulation of the critical host elements responsible for antiviral immunity. Epigenomics is a powerful, unexplored avenue that can provide a profound understanding of virus-host interactions and lead to the development of epigenome-based therapies and vaccines to counter viruses. This review discusses current developments in SARS-CoV-2 variation and its role in epigenetic modulation in infected hosts. This review provides an overview, especially in the context of emerging viral strains, their recombinants, and their possible roles in the epigenetic exploitation of host defense and viral pathogenesis. It provides insights into host-virus interactions at the molecular, genomic, and immunological levels and sheds light on the future of epigenomics-based therapies for SARS-CoV-2 infection.

Application of medical information system to identify dengue outbreak

factors: Insights from a hyperendemic city in Malaysia.

Keat-Chuan Ng C, Linus-Lojikip S, Mohamed K, Hss AS.
Sept-2023
Int J Med Inform.
https://pubmed.ncbi.nlm.nih.gov/37549500/

Vertical transmission of African-lineage Zika virus through the fetal membranes in a rhesus macaque (Macaca mulatta) model.

Koenig MR, Mitzey AM, Zeng X, Reyes L, Simmons HA, Morgan TK, Bohm EK, Pritchard JC, Schmidt JA, Ren E, Leyva Jaimes FB, Winston E, Basu P, Weiler AM, Friedrich TC, Aliota MT, Mohr EL, Golos TG.
07-08-2023
PLoS Pathog.
https://pubmed.ncbi.nlm.nih.gov/37549143/

Zika virus (ZIKV) can be transmitted vertically from mother to fetus during pregnancy, resulting in a range of outcomes including severe birth defects and fetal/infant death. Potential pathways of vertical transmission in utero have been proposed but remain undefined. Identifying the timing and routes of vertical transmission of ZIKV may help us identify when interventions would be most effective. Furthermore, understanding what barriers ZIKV overcomes to effect vertical transmission may help improve models for evaluating infection by other pathogens during pregnancy. To determine the pathways of vertical transmission, we inoculated 12 pregnant rhesus macaques with an African-lineage ZIKV at gestational day 30 (term is 165 days). Eight pregnancies were surgically terminated at either seven or 14 days post-maternal infection. Maternal-fetal interface and fetal tissues and fluids were collected and evaluated for ZIKV using RT-qPCR, in situ hybridization, immunohistochemistry, and plaque assays. Four additional pregnant macaques were inoculated and terminally perfused with 4% paraformaldehyde at three, six, nine, or ten days post-maternal inoculation. For these four cases, the entire fixed pregnant uterus was evaluated with in situ hybridization for ZIKV RNA. We determined that ZIKV can reach the MFI by six days after infection and infect the fetus by ten days. Infection of the chorionic membrane and the extraembryonic coelomic fluid preceded infection of the fetus and the mesenchymal tissue of the placental villi. We did not find evidence to support a transplacental route of ZIKV vertical transmission via infection of syncytiotrophoblasts or villous cytotrophoblasts. The pattern of infection observed in the maternal-fetal interface provides evidence of paraplacental vertical ZIKV transmission through the chorionic membrane, the outer layer of the fetal membranes.

Complexity in the dengue spreading: A network analysis approach.

Lima LL, Atman APF.
07-08-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37549129/

Missing Cells-A Rare Case of Persisting Thrombocytopenia in Pregnancy With Dengue and Role of Romiplostim in These Cases.

Sinha R, Datta MR, Singh V.
Juin-2023
J Family Reprod Health.
https://pubmed.ncbi.nlm.nih.gov/37547782/

Dengue Myocarditis: A Case Report and Major Review.

Cristodulo R, Luoma-Overstreet G, Leite F, Vaca M, Navia M, Durán G, Molina F, Zonneveld B, Perrone SV, Barbagelata A, Kaplinsky E.
04-08-2023
Glob Heart.
https://pubmed.ncbi.nlm.nih.gov/37547170/

Activation of ATF3 via the Integrated Stress Response Pathway Regulates Innate Immune and Autophagy Processes to Restrict Zika Virus.

Badu P, Pager CT.
27-07-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37546954/

Zika virus (ZIKV) is a re-emerging mosquito-borne flavivirus that can have devastating health consequences. The developmental and neurological effects from a ZIKV infection arise in part from the virus triggering cellular stress pathways and perturbing transcriptional programs. To date, the underlying mechanisms of transcriptional control directing viral restriction and virus-host interaction are understudied. Activating Transcription Factor 3 (ATF3) is a stress-induced transcriptional effector that modulates the expression of genes involved in a myriad of cellular processes, including inflammation and antiviral responses, to restore cellular homeostasis. While ATF3 is known to be upregulated during ZIKV infection, the mode by which ATF3 is activated and the specific role of ATF3 during ZIKV infection is unknown. In this study, we show via inhibitor and RNA interference approaches that ZIKV infection initiates the integrated stress response pathway to activate ATF4 which in turn induces ATF3 expression. Additionally, by using a CRISPR-Cas9 system to deplete ATF3, we found that ATF3 acts to limit ZIKV gene expression in A549 cells. In particular, the ATF3-dependent anti-ZIKV response occurred through regulation of innate immunity and autophagy pathways. We show that ATF3 differentially regulates the expression of innate immune response genes and suppresses the transcription of autophagy related genes to influence autophagic flux. Our study therefore highlights an important role for the integrated stress response pathway and ATF3 in establishing an antiviral effect during ZIKV infection. Importance: ZIKV is a re-emerging mosquito-borne flavivirus associated with congenital Zika syndrome in infants and Guillain Barré syndrome in adults. As a cytoplasmic virus, ZIKV co-opts host cellular mechanisms to support viral processes and consequently, reprograms the host transcriptional profile. Such viral-directed

transcriptional changes and their proor anti-viral significance remain understudied. We previously showed that ATF3, a stress-induced transcription factor, is significantly upregulated in ZIKV infected mammalian cells, along with other cellular and immune response genes. Here, we specifically define the intracellular pathway responsible for ATF3 activation and elucidate the impact of ATF3 expression on ZIKV infection. Our data provides novel insights into the role of the integrated stress response pathway in stimulating ATF3 which differentially regulates the innate immune response and autophagy at the transcript level to antagonize ZIKV gene expression. This study establishes a framework that links viral-induced stress response to transcriptional regulation of host defense pathways and thus expands the depth of knowledge on virus-mediated transcriptional mechanisms during ZIKV infection which in turn will inform future therapeutic strategies.

wMel replacement of dengue-competent mosquitoes is robust to near-term change.

Vásquez VN, Kueppers LM, Rašić G, Marshall JM.
2023
Nat Clim Chang.
https://pubmed.ncbi.nlm.nih.gov/37546688/

Zika virus E protein modulates functions of human brain microvascular endothelial cells and astrocytes: implications on blood-brain barrier properties.

Kaur G, Pant P, Bhagat R, Seth P.
20-07-2023
Front Cell Neurosci.
https://pubmed.ncbi.nlm.nih.gov/37545876/

A novel colorimetric biosensor for rapid detection of dengue virus upon acid-induced aggregation of colloidal gold.

Cam Duyen VT, Van Toi V, Van Hoi T, Truong PL.
07-08-2023
Anal Methods.
https://pubmed.ncbi.nlm.nih.gov/37545366/

The dengue virus, once transmitted to people through a mosquito bite, causes an infectious disease called dengue fever. Dengue fever can develop into two fatal syndromes, namely dengue shock syndrome and dengue hemorrhagic fever. The existing strategies for detecting dengue infection mainly employ serological immunoassays and a real time PCR technique. Along with the positive features of efficiency, accuracy, and reproducibility, these procedures are limited by being time-consuming, costly, requiring special equipment for analysis, and unable to be carried out at the point-of-care level. Herein, we developed a colorimetric nanosensor for detecting dengue virus in clinical samples that is rapid, accurate, sensitive, and less expensive. The sensing platform relies on the specific binding between the DNA-conjugated AuNPs and genomic RNA of dengue, which results in the DNA-RNA heteroduplex structure formation that turns the gold colloid's ruby red color to blue due to the nano-aggregation in an acidic environment, which can be detected by the naked eye or measuring the absorbance. The DNA probe was designed to bind to a genomic RNA conserved region recognized in all four dengue serotypes. Dengue virus serotype 1 was utilized as a framework for virus detection; the designed nanosensor exhibited great specificity and selectivity, with the detection limit of ~1 pg μL^{-1} (~1.66 × 10^6 RNA copies per reaction) and time of analysis of about 1 h including the RNA extraction step. The proposed colorimetric nanosensor offers an alternative tool for specific and highly sensitive detection of dengue that eliminates the requirement for thermal cycling and primer sets in PCR-based assays.

Dengue virus serotype 2 genotype III evolution during the 2019 outbreak in Mato Grosso, Midwestern Brazil.

Dos Santos MAM, Pavon JAR, Dias LS, Viniski AE, Souza CLC, de Oliveira EC, de Azevedo VC, da Silva SP, Cruz ACR, Medeiros DBA, Nunes MRT, Slhessarenko RD.
05-08-2023
Infect Genet Evol.
https://pubmed.ncbi.nlm.nih.gov/37544570/

DENV-2 was the main responsible for a 70% increase in dengue incidence in Brazil during 2019. That year, our metagenomic study by Illumina NextSeq on serum samples from acute febrile patients (n = 92) with suspected arbovirus infection, sampled in 22 cities of the state of Mato Grosso (MT), in the middle west of Brazil, revealed eight complete genomes and two near-complete sequences of DENV-2 genotype III, one Human parvovirus B19 genotype I (5,391 nt) and one Coxsackievirus A6 lineage D (4,514 nt). These DENV-2 sequences share the aminoacidic identities of BR4 lineage on E protein domains I, II and III, and were included in a clade with sequences of the same lineage circulating in the southeast of Brazil in the same year. Nevertheless, 11/34 non-synonymous mutations are unique to three strains inthis study, distributed in the E (n = 6), NS3 (n = 2) and NS5 (n = 3) proteins. Other 14 aa changes on C (n = 1), E (n = 3), NS1 (n = 2), NS2A (n = 1) and NS5 (n = 7) were first reported in a genotype III lineage, having been already reported only in other DENV-2 genotypes. All 10 sequences have mutations in the NS5 protein (14 different aa changes). Nine E protein aa changes found in two sequences, six of which are unique, are in the ectodomain; where the E:M272T change is on the hinge of the E protein at domain II, in a region critical for the anchoring to the host cell receptor. The NS5:G81R mutation, in the methyltransferase domain, was found in one strain of this study. Altogether, these data points to an important evolution of DENV-2 genotype III lineage BR4 during this outbreak in 2019 in MT. Genomic surveillance is essential to detect virus etiology and evolution, possibly related to immune evasion and viral fitness changes leading to future novel outbreaks.

Bangladesh faces record dengue outbreak.

Burki T.

05-08-2023
Lancet.
https://pubmed.ncbi.nlm.nih.gov/37544320/

Neutrophil infiltration leads to fetal growth restriction by impairing the placental vasculature in DENV-infected pregnant mice.

Zhang Y, Sheng Z, Chen Q, Zhou A, Cao J, Xue F, Ye Y, Wu N, Gao N, Fan D, Liu L, Li Y, Wang P, Liang L, Zhou D, Zhang F, Li F, An J.
04-08-2023
EBioMedicine.
https://pubmed.ncbi.nlm.nih.gov/37544202/

Background: Dengue virus (DENV) infection during pregnancy increases the risk of adverse fetal outcomes, which has become a new clinical challenge. However, the underlying mechanism remains unknown. Methods: The effect of DENV-2 infection on fetuses was investigated using pregnant interferon α/β receptor-deficient (Ifnar1$^{-/-}$) mice. The histopathological changes in the placentas were analyzed by morphological techniques. A mouse inflammation array was used to detect the cytokine and chemokine profiles in the serum and placenta. The infiltration characteristics of inflammatory cells in the placentas were evaluated by single-cell RNA sequencing. Findings: Fetal growth restriction observed in DENV-2 infection was mainly caused by the destruction of the placental vasculature rather than direct damage from the virus in our mouse model. After infection, neutrophil infiltration into the placenta disrupts the expression profile of matrix metalloproteinases, which leads to placental dysvascularization and insufficiency. Notably, similar histopathological changes were observed in the placentas from DENV-infected puerperae. Interpretation: Neutrophils play key roles in placental histopathological damage during DENV infection, which indicates that interfering with aberrant neutrophil infiltration into the placenta may be an important therapeutic target for adverse pregnancy outcomes in DENV infection. Funding: The National Key Research and Development Plans of China (2021YFC2300200-02 to J.A., 2019YFC0121905 to Q.Z.C.), the National Natural Science Foundation of China (NSFC) (U1902210 and 81972979 to J. A., 81902048 to Z. Y. S., and 82172266 to P.G.W.), and the Support Project of High-level Teachers in Beijing Municipal Universities in the Period of 13th Five-year Plan, China (IDHT20190510 to J. A.).

Large-scale reference-free analysis of flavivirus sequences in Aedes aegypti whole genome DNA sequencing data.

Spadar A, Phelan JE, Clark TG, Campino S.
05-08-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37543604/

Serotype-associated immune response and network immunoclusters in children and adults during acute Dengue virus infection.

Henrique Ferreira Sucupira P, Silveira Ferreira M, Santos Coutinho-da-Silva M, Alves Bicalho K, Carolina Campi-Azevedo A, Pedro Brito-de-Sousa J, Peruhype-Magalhães V, Rios M, Konduru K, Teixeira-Carvalho A, Grazziela Alves Coelho-Dos-Reis J, Ribeiro do Valle Antonelli L, Bortolo de Rezende V, Ludolf Ribeiro de Melo F, Couto Garcia C, Carla Silva-Andrade J, Artur da Costa-Rocha I, Alves da Rocha L, Aprigio Silva V, Damasceno Pinto S, Araújo de Melo S, Guimarães Costa A, de Souza Gomes M, Rodrigues Amaral L, Luiz Lima Bertarini P, Cristina da Silva Furtado E, Vieira Pinto da Silva E, Alves Ramos B, Barros Dos Santos É, Nazaré Oliveira Freitas M, Maria Caetano Faria A, Fernando da Costa Vasconcelos P, de Souza Bastos M, Carício Martins L, Assis Martins-Filho O, Sobreira Silva Araújo M.
Sept-2023
Cytokine.
https://pubmed.ncbi.nlm.nih.gov/37542834/

Zika-specific neutralizing antibodies targeting inter-dimer envelope epitopes.

Sankhala RS, Dussupt V, Donofrio G, Gromowski GD, De La Barrera RA, Larocca RA, Mendez-Rivera L, Lee A, Choe M, Zaky W, Mantus G, Jensen JL, Chen WH, Gohain N, Bai H, McCracken MK, Mason RD, Leggat D, Slike BM, Tran U, Jian N, Abbink P, Peterson R, Mendes EA, Freitas de Oliveira Franca R, Calvet GA, Bispo de Filippis AM, McDermott A, Roederer M, Hernandez M, Albertus A, Davidson E, Doranz BJ, Rolland M, Robb ML, Lynch RM, Barouch DH, Jarman RG, Thomas SJ, Modjarrad K, Michael NL, Krebs SJ, Joyce MG.
09-08-2023
Cell Rep.
https://pubmed.ncbi.nlm.nih.gov/37561630/

Zika virus (ZIKV) is an emerging pathogen that causes devastating congenital defects. The overlapping epidemiology and immunologic cross-reactivity between ZIKV and dengue virus (DENV) pose complex challenges to vaccine design, given the potential for antibody-dependent enhancement of disease. Therefore, classification of ZIKV-specific antibody targets is of notable value. From a ZIKV-infected rhesus macaque, we identify ZIKV-reactive B cells and isolate potent neutralizing monoclonal antibodies (mAbs) with no cross-reactivity to DENV. We group these mAbs into four distinct antigenic groups targeting ZIKV-specific cross-protomer epitopes on the envelope glycoprotein. Co-crystal structures of representative mAbs in complex with ZIKV envelope glycoprotein reveal envelope-dimer epitope and unique dimer-dimer epitope targeting. All four specificities are serologically identified in convalescent humans following ZIKV infection, and representative mAbs from all four groups protect against ZIKV replication in mice. These results provide key insights into ZIKV-specific antigenicity and have implications for ZIKV vaccine, diagnostic, and therapeutic development.

Sequence data from a travel-associated case of microcephaly highlight a persisting risk due to Zika virus circulation in Thailand.

Marquine S, Durand GA, Modenesi G, Khouadhria S, Piorkowski G, Badaut C, Canivez T, De Lamballerie X, Grard G, Klitting R.
10-08-2023
J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37561039/

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.
10-08-2023
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.

Clinical features and transmission risk analysis of dengue virus infections in Shenzhen, During 2014-2019.

Ye G, Xu Z, Yang M, Wang J, Liang J, Yin J, Yang Y, Xia H, Liu Y.
08-07-2023
Comput Struct Biotechnol J.
https://pubmed.ncbi.nlm.nih.gov/37560123/

Dengue fever (DF) and dengue hemorrhagic fever (DHF) are among the most common tropical diseases affecting humans. To analyze the risk of clinical and transmission of DF/DHF in Shenzhen, the surveillance on patients of all-age patients with dengue virus (DENV) infections was conducted. Our findings revealed that the majority of DENV-infected patients are young to middle-aged males, and the development of the disease is accompanied by abnormal changes in the percentages of neutrophils, lymphocytes, and basophils. Demographic analysis revealed that these patients is concentrated in areas such as Futian District, which may be due to the higher mosquito density and temperature than that in other area. Subsequent, mosquito infection experiments confirmed that the effect of temperature shift on DENV proliferation and transmission. Not only that, constant temperatures can enhance the spread of DENV, even increase the risk of epidemic. Thus, the role of innate immune response should be highlighted in the prediction of severe severity of DENV-infected patients, and temperature should be taken into account in the prevention and control of DENV. Introduction: Dengue fever (DF) and dengue hemorrhagic fever (DHF) are among the most common tropical diseases affecting humans, and which caused by the four dengue virus serotypes (DENV 1-4). Objectives: To analyze the risk of clinical and transmission of DF/DHF in Shenzhen. Methods: The surveillance on patients of all-age patients with dengue virus (DENV) infections was conducted. Results: Our findings revealed that the majority of DENV-infected patients are young to middle-aged males, and the development of the disease is accompanied by abnormal changes in the percentages of neutrophils, lymphocytes, and basophils. Demographic analysis revealed that these patients is concentrated in areas such as Futian District, which may be due to the higher mosquito density and temperature than that in other area. Subsequent, mosquito infection experiments confirmed that the effect of temperature shift on DENV proliferation and transmission. Not only that, constant temperatures can enhance the spread of DENV, even increase the risk of epidemic. Conclusion: 1. Elevated levels of neutrophils, lymphocytes, basophils, and temperature are all significant risk factors for dengue transmission and pathogenesis; 2. Temperature increasing is associated with a higher risk of dengue transmission; 3. Fluctuations in temperature around 28 °C (28 ± 5 °C) would increase dengue transmission.

Neurological Manifestations of Perinatal Dengue.

Singh S, Alallah J, Amrit A, Maheshwari A, Boppana S.
2023
Newborn (Clarksville).
https://pubmed.ncbi.nlm.nih.gov/37559696/

Dengue viruses (DENVs) are single-stranded RNA viruses belonging to the family Flaviviridae. There are four distinct antigenically related serotypes, DENVs types 1, 2, 3, and 4. These are all mosquito-borne human pathogens. Congenital dengue disease occurs when there is mother-to-fetus transmission of the virus and should be suspected in endemic regions in neonates presenting with fever, maculopapular rash, and thrombocytopenia. Although

most of the infected infants remain asymptomatic, some can develop clinical manifestations such as sepsis-like illness, gastric bleeding, circulatory failure, and death. Neurological manifestations include intracerebral hemorrhages, neurological malformations, and acute focal/disseminated encephalitis/encephalomyelitis. Dengue NS1Ag, a highly conserved glycoprotein, can help the detection of cases in the viremic stage. We do not have proven specific therapies yet; management is largely supportive and is focused on close monitoring and maintaining adequate intravascular volume.

Direct and indirect effects of age on dengue severity: The mediating role of secondary infection.

Annan E, Treviño J, Zhao B, Rodriguez-Morales AJ, Haque U.
09-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37556473/

Dengue virus serotypic replacement of NS3 protease or helicase domain causes chimeric viral attenuation but can be recovered by a compensated mutation at helicase domain or NS2B, respectively.

Teramoto T.
09-08-2023
J Virol.
https://pubmed.ncbi.nlm.nih.gov/37555662/

Mosquito-borne dengue viruses (DENVs) have evolved to four serotypes with 69%-78% amino acid identities, resulting in incomplete immunity, where one serotype's infection does not cross-protect against secondary infections by other serotypes. Despite the amino acid differences, structural and nonstructural (NS) proteins among serotypes play similar functions. NS3 is an enzyme complex: NS3 has N-terminal protease (PRO) and C-terminal helicase (HEL) activities in addition to 5' RNA triphosphatase (5'RTP), which is involved in the RNA capping process. In this study, the effects of NS3 replacements among serotypes were tested. The replacement of NS3 full-length (FULL), PRO or HEL region suppressed viral replication in BHK-21 mammalian cells, while the single compensatory mutation improved the viral replications; P364S mutation in HEL revived PRO (DENV3)-replaced DENV1, while S68T alteration in NS2B recovered HEL (DENV1)-replaced DENV2. The results suggest that the interactions between PRO and HEL as well as HEL and NS2B are required for replication competence. Lower-frequency mutations also appeared at various locations in viral proteins, although after infecting C6/36 mosquito cells, the mutations' frequencies changed, and/or new mutations appeared. In contrast, the inter-domain region (INT, 12 amino acids)-replaced chimera quickly replicated without mutation in BHK-21 cells, although extended cell culture accumulated various mutations. These results suggest that NS3 variously interacts with DENV proteins, in which the chimeric NS3 domain replacements induced amino acid mutations, irrespective of replication efficiency. However, the viral sequences are further adjusted for replication efficiency, to fit in both mammalian cells and mosquito cells. IMPORTANCE Enzyme activities for replicating DENV 5' cap positive (+) sense RNA have been shown to reside in NS3 and NS5. However, it remains unknown how these enzymes coordinately synthesize negative (-) sense RNA, from which abundant 5' cap (+) sense RNA is produced. We previously revealed that NS5 dimerization and NS5 methyltransferase(MT)-NS3HEL interaction are important for DENV replication. Here, we found that replication incompetence due to NS3PRO or HEL replacement was compensated by a mutation at HEL or NS2B, respectively, suggesting that the interactions among NS2B, NS3PRO, and HEL are critical for DENV replication.

Marburg virus disease outbreak in Tanzania: current efforts and recommendations - a short communication.

Bulimbe DB, Masunga DS, Paul IK, Kassim GH, Bahati PB, Thomas JA, Mwakisole C, Nazir A, Uwishema O.
08-07-2023
Ann Med Surg (Lond).
https://pubmed.ncbi.nlm.nih.gov/37554886/

Identification of prior dengue-naïve Dengvaxia recipients with an increased risk for symptomatic dengue during fever surveillance in the Philippines.

Dai YC, Sy AK, Jiz M, Tsai JJ, Bato J, Quinoñes MA, Reyes MAJ, Wang WK.
24-07-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37554332/

Introduction: Dengue virus (DENV) is the leading cause of mosquito-borne viral diseases in humans. Dengvaxia, the first licensed dengue vaccine, is recommended for DENV-seropositive individuals aged 9-45 years. In the Philippines, Dengvaxia was administered to more than 830,000 children without prior serological testing in 2016-2017. Subsequently, it was revealed that DENV-seronegative children who received Dengvaxia developed severe disease following breakthrough DENV infection. As a result, thousands of children participating in the mass vaccination campaign were at higher risk of severe dengue disease. It is vital that an assay that identifies baseline DENV-naïve Dengvaxia recipients be developed and validated. This would permit more frequent and extensive assessments and timely treatment of breakthrough DENV infections. Methods: We evaluated the performance of a candidate assay, the DENV1-4 nonstructural protein 1 (NS1) IgG enzyme-linked immunosorbent assay (ELISA), developed by the University of Hawaii (UH), using well-documented serum/plasma samples including those >20 years post-DENV infection, and tested samples from 199 study participants including 100 Dengvaxia recipients from the fever surveillance programs in the Philippines. Results: The sensitivity and specificity of the assay were 96.6% and 99.4%, respectively, which are higher than those reported for pre-vaccination screening. A significantly higher rate of symptomatic breakthrough DENV infection was found

among children that were DENV-naïve (10/23) than among those that were DENV-immune (7/53) when vaccinated with Dengvaxia (p=0.004, Fisher's exact test), demonstrating the feasibility of the assay and algorithms in clinical practice. Conclusion: The UH DENV1-4 NS1 IgG ELISA can determine baseline DENV serostatus among Dengvaxia recipients not only during non-acute dengue but also during breakthrough DENV infection, and has implications for assessing the long-term safety and effectiveness of Dengvaxia in the post-licensure period.

Analytical and diagnostic performance characteristics of reverse-transcriptase loop-mediated isothermal amplification assays for dengue virus serotypes 1-4: A scoping review to inform potential use in portable molecular diagnostic devices.

Arkell P, Mairiang D, Songjaeng A, Malpartida-Cardenas K, Hill-Cawthorne K, Avirutnan P, Georgiou P, Holmes A, Rodriguez-Manzano J.
08-08-2023
PLOS Glob Public Health.
https://pubmed.ncbi.nlm.nih.gov/37552632/

Detection of dengue virus serotype 4 in Sudan.

Desogi M, Ali M, Gindeel N, Khalid F, Abdelraheem M, Alnaby A, Saad M, Elamin E, Kheir M, Mukhtar M.
27-06-2023
East Mediterr Health J.
https://pubmed.ncbi.nlm.nih.gov/37551755/

Background: Dengue virus infection is spreading globally and most parts of Sudan have witnessed repeated dengue outbreaks, with the detection of DENV-1, DENV-2 and DENV-3 serotypes. Aims: In this report we describe the dengue fever outbreaks that occurred in eastern Sudan (Kassala and Port Sudan cities) from August to November 2019. Methods: We enrolled 79 (29.8%) suspected cases from Kassala and 186 (70.2%) from Port Sudan who presented with fever. The participants were medically examined and their clinical signs recorded. Blood samples were collected for complete blood count, detection of anti-dengue virus IgM, detection of NS1 dengue antigen and identification of the virus serotype using RT-PCR.

Results: The main clinical presentations were fever, abdominal pain, joint pain and vomiting, and thrombocytopenia was the main laboratory finding. One hundred and twenty-five blood samples tested positive for the anti-dengue IgM antibody, and 145 were positive for the NS1 antigen. Using RT-PCR, we identified 35 (24%) infections with DENV-2, 100 (69%) with DENV-3 and 10 (7%) with DENV-4 serotypes. Conclusions: We identified multiple serotypes - DENV-2, DENV-3 and DENV-4 - as the causes of the outbreak. The presence of DENV-4 serotype was documented for the first time in Sudan.

Global prevalence of asymptomatic dengue infections - a systematic review and meta-analysis.

Asish PR, Dasgupta S, Rachel G, Bagepally BS, Girish Kumar CP.
Sept-2023
Int J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37463631/

Objectives: The burden of asymptomatic dengue infections is understudied. Therefore, we systematically reviewed the literature to estimate the global prevalence of asymptomatic dengue infections. Methods: We searched cross-sectional studies reporting the prevalence of asymptomatic dengue infections from PubMed, Scopus, and Embase. Prevalence of asymptomatic dengue infections was pooled and reported as proportions with a 95% confidence interval (CI). This systematic review protocol was a priori registered in The International Prospective Register of Systematic Reviews (Reg: No. CRD42020218446). Results: We included 41 studies with 131,953 cases in our analysis. The overall pooled prevalence of asymptomatic dengue infections was 59.26% (95% CI: 43.76-74.75, I^2 = 99.93%), with 65.52% (95% CI: 38.73-92.32, I^2 = 99.95%) during outbreaks and 30.78% (95% CI: 21.39-40.16, I^2 = 98.78%) during non-outbreak periods. The pooled prevalence among the acutely infected individuals was 54.52% (95% CI: 17.73-46.76, I^2 = 99.91%), whereas, among primary and secondary asymptomatic dengue infections, it was 65.36% (95% CI: 45.76-84.96, I^2 = 98.82) and 48.99% (95% CI: 27.85-70.13, I^2 = 99.08%) respectively. Conclusion: The majority of dengue cases are asymptomatic and may play a significant role in disease transmission. Public health strategies aimed at dengue outbreak response and mitigation of disease burden should include early detection of asymptomatic cases.

Dracunculose

Transcriptome analysis reveals important regulatory genes and pathways for tuber color variation in Pinellia ternata (Thunb.) Breit.

Yin C, Tang D, Liu X, Li Z, Xiang Y, Gao K, Li H, Yuan L, Huang B, Li J.
Sept-2023
Protoplasma.
https://pubmed.ncbi.nlm.nih.gov/36918417/

Echinococcose

Infection of sheep by Echinococcus multilocularis in Gansu, China: evidence from mitochondrial and nuclear DNA analysis.

Shumuye NA, Li L, Li WH, Zhang NZ, Wu YT, Wu YD, Tian WJ, Zhang LS, Nian XF, Dai GD, Chen WG, Gao SZ, Tian XQ, Liu JS, Li B, Kebede N, Fu BQ, Yan HB, Jia WZ.
10-08-2023
Infect Dis Poverty.
https://pubmed.ncbi.nlm.nih.gov/37563679/

Background: In the normal life cycle of the parasite (Echinococcus multilocularis) that causes alveolar echinococcosis, domestic and wild carnivores act as definitive hosts, and rodents act as intermediate hosts. The presented study contributes to the research on the distribution and transmission pattern of E. multilocularis in China having identified sheep as an unusual intermediate host taking part in the domestic transmission of alveolar echinococcosis in Gansu Province, China. **Methods:** From 2020 to 2021, nine whitish different cyst-like were collected from the liver of sheep in Gansu Province for examination. A near complete mitochondrial (mt) genome and selected nuclear genes were amplified from the cyst-like lesion for identification. To confirm the status of the specimen, comparative analysis with reference sequences, phylogenetic analysis, and network analysis were performed. **Results:** The isolates displayed ≥ 98.87% similarity to E. multilocularis NADH dehydrogenase sub-unit 1 (nad1) (894 bp) reference sequences deposited in GenBank. Furthermore, amplification of the nad4 and nad2 genes also confirmed all nine samples as E. multilocularis with > 99.30% similarity. Additionally, three nuclear genes, pepck (1545 bp), elp-exons VII and VIII (566 bp), and elp-exon IX (256 bp), were successfully amplified and sequenced for one of the isolates with 98.42% similarity, confirming the isolates were correctly identified as E. multilocularis. Network analysis also correctly placed the isolates with other E. multilocularis. **Conclusions:** As a result of the discovery of E. multilocularis in an unusual intermediate host, which is considered to have the highest zoonotic potential, the result clearly demonstrated the necessity for expanded surveillance in the area.

Cystic echinococcosis microRnas as potential non-invasive biomarkers: current insights and upcoming perspective.

Habibi B, Gholami S, Bagheri A, Fakhar M, Moradi A, Khazeei Tabari MA.
08-08-2023
Expert Rev Mol Diagn.
https://pubmed.ncbi.nlm.nih.gov/37553726/

Introduction: Echinococcosis, also known as hydatidosis, is a zoonotic foodborne disease occurred by infection with the larvae of Echinococcus spp. which can lead to the development of hydatid cysts in various organs of the host. The diagnosis of echinococcosis remains challenging due to limited diagnostic tools. **Areas covered:** In recent years, microRNAs (miRNAs) have emerged as a promising biomarker for various infectious diseases, including those caused by helminths. Recent studies have identified several novel miRNAs in Echinococcus spp. shedding light on their essential roles in hydatid cyst host-parasite interactions. In this regard, several studies have shown that Echinococcus-derived miRNAs are present in biofluids such as serum and plasma of infected hosts. The detection of these miRNAs in the early stages of infection can serve as an early prognostic and diagnostic biomarker for echinococcosis. **Expert opinion:** The miRNAs specific to *Echinococcus* spp. show great potential as early diagnostic biomarkers for echinococcosis and can also provide insights into the pathogenesis of this disease. This review attempts to provide a comprehensive overview of *Echinococcus*-specific miRNAs, their use as early diagnostic biomarkers, and their function in host-parasite interactions.

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/

Climate determines transmission hotspots of Polycystic Echinococcosis, a life-threatening zoonotic disease, across Pan-Amazonia.

San-José A, Mayor P, Carvalho B, El Bizri HR, Antunes AP, Antunez Correa M, Aquino R, Bodmer RE, Boubli JP, Carvalho EAR Jr, Campos-Silva JV, Constantino PAL, de Paula MJ, Desbiez ALJ, Fang T, Gómez-Puerta LA, Knoop SB, Longin G, Morcatty TQ, Maranhão L, Massocato GF, Munari DP, Nunes AV, Puertas P, Oliveira MA, Pezzuti JCB, Richard-Hansen C, Santos G, Valsecchi J, von Mühlen EM, Bosmediano J, Rodó X.
15-08-2023
Proc Natl Acad Sci U S A.
https://pubmed.ncbi.nlm.nih.gov/37549288/

Polycystic Echinococcosis (PE), a neglected life-threatening zoonotic disease caused by the cestode *Echinococcus vogeli,* is endemic in the Amazon. Despite being treatable, PE reaches a case fatality rate of around 29% due to late or missed diagnosis. PE is sustained in Pan-Amazonia by a complex sylvatic cycle. The hunting of its infected intermediate hosts (especially the lowland paca *Cuniculus paca*) enables the disease to further transmit to humans, when their viscera are improperly handled. In this study, we compiled a unique dataset of host occurrences (~86000 records) and disease infections (~400 cases) covering the entire Pan-Amazonia and employed different modeling and statistical tools to unveil the spatial distribution of PE's key animal hosts. Subsequently, we derived a set of ecological, environmental, climatic, and hunting covariates that potentially act as transmission risk factors and used them as predictors of two independent Maximum Entropy models, one for animal infections and one for human infections. Our findings indicate that temperature stability promotes the sylvatic circulation of the disease. Additionally, we show how El Niño-Southern Oscillation (ENSO) extreme events disrupt hunting patterns throughout Pan-Amazonia, ultimately affecting the probability of spillover. In a scenario where climate extremes are projected to intensify, climate change at regional level appears to be indirectly driving the spillover of *E. vogeli*. These results hold substantial implications for a wide range of zoonoses acquired at the wildlife-human interface for which transmission is related to the manipulation and consumption of wild meat, underscoring the pressing need for enhanced awareness and intervention strategies.

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

Yan Z, Lingcong X, Xiaojing S, Fanghui D, Xun L.
04-08-2023
Parasitol Int.
https://pubmed.ncbi.nlm.nih.gov/37544640/

A novel multiplex real-time PCR for the molecular diagnosis of metacestode infections in human patients.

Oberli A, Furrer L, Skoko L, Müller N, Gottstein B, Bittel P.
04-08-2023
Clin Microbiol Infect.
https://pubmed.ncbi.nlm.nih.gov/37544608/

IgG glycomic profiling identifies potential biomarkers for diagnosis of echinococcosis.

Feng X, BaiMaYangJin, Mo X, Zhang F, Hu W, Feng Z, Zhang T, Wei L, Lu H.
25-07-2023
J Chromatogr B Analyt Technol Biomed Life Sci.
https://pubmed.ncbi.nlm.nih.gov/37540936/

Establishment and application of unbiased in vitro drug screening assays for the identification of compounds against Echinococcus granulosus sensu stricto.

Kaethner M, Preza M, Kaempfer T, Zumstein P, Tamponi C, Varcasia A, Hemphill A, Brehm K, Lundström-Stadelmann B.
04-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37540716/

Echinococcus multilocularis and E. granulosus s.l. are the causative agents of alveolar and cystic echinococcosis, respectively. Drug treatment options for these severe and neglected diseases are limited to benzimidazoles, which are not always efficacious, and adverse side effects are reported. Thus, novel and improved treatments are needed. In this study, the previously established platform for E. multilocularis in vitro drug assessment was adapted to E. granulosus s.s. In a first step, in vitro culture protocols for E. granulosus s.s. were established. This resulted in the generation of large amounts of E. granulosus s.s. metacestode vesicles as well as germinal layer (GL) cells. In vitro culture of these cells formed metacestode vesicles displaying structural characteristics of metacestode cysts generated in vivo. Next, drug susceptibilities of E. multilocularis and E. granulosus s.s. protoscoleces, metacestode vesicles and GL cells were comparatively assessed employing established assays including (i) metacestode vesicle damage marker release assay, (ii) metacestode vesicle viability assay, (iii) GL cell viability assay, and (iv) protoscolex motility assay. The standard drugs albendazole, buparvaquone, mefloquine, MMV665807, monepantel, niclosamide and nitazoxanide were included. MMV665807, niclosamide and nitazoxanide were active against the parasite in all four assays against both species. MMV665807 and monepantel were significantly more active against E. multilocularis metacestode vesicles, while albendazole and nitazoxanide were significantly more active against E. multilocularis GL cells. Albendazole displayed activity against E. multilocularis GL cells, but no effects were seen in albendazole-treated E. granulosus s.s. GL cells within five days. Treatment of protoscoleces with albendazole and monepantel had no impact on motility. Similar results were observed for both species with praziquantel and its enantiomers against protoscoleces. In conclusion, in vitro culture techniques and drug screening methods previously established for E. multilocularis were successfully implemented for E. granulosus s.s., allowing comparisons of drug efficacy between the two species. This study provides in vitro culture techniques for the reliable generation of E. granulosus s.s. metacestode vesicles and GL cell cultures and describes the validation of standardized in vitro drug screening methods for E. granulosus s.s.

mmu-miRNA-342-3p promotes hepatic stellate cell activation and hepatic fibrosis induced by Echinococcus multilocularis infection via targeting Zbtb7a.

Cao S, Wang D, Wu Y, Zhang J, Pu L, Luo X, Zhang X, Sun X, Zheng Y, Wang S, Guo X.
25-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37490505/

Liver fibrosis is one of the histopathological characters during Echinococcus multilocularis infection. The activation of hepatic stellate cells (HSCs) is a key event in the development of liver fibrosis. However, the molecular mechanism of HSC activation in the E. multilocularis infection-induced liver fibrosis remains largely unclear. Here, we reported that mmu-miR-342-3p was most dominantly expressed in HSCs and was upregulated in the HSCs in response to E. multilocularis infection. We further showed that mmu-miR-342-3p was able to bind to the 3' UTR of the Zbtb7a gene and regulated its expression. Moreover, mmu-miR-342-3p expression was negatively correlated with its target gene Zbtb7a in HSCs during E. multilocularis infection. Knockdown of mmu-miR-342-3p promoted the expression of Gfap in the activated HSCs in vitro. In the E. multilocularis-infected mice, knockdown of mmu-miR-342-3p suppressed the expression of α-Sma, Col1α1, and TGF-β but promoted the expression of Gfap. Therefore, mmu-miR-342-3p is a key regulator for activation of HSCs, and inhibiting mmu-miR-342-3p to suppressed Zbtb7a-mediated TGF-β signaling in activated HSCs could be a novel strategy to treat liver fibrosis induced by E. multilocularis.

Complete mitochondrial exploration of Echinococcus multilocularis from French alveolar echinococcosis patients.

Bohard L, Lallemand S, Borne R, Courquet S, Bresson-Hadni S, Richou C, Millon L, Bellanger AP, Knapp J.

Sept-2023
Int J Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37148987/

Filariose lymphatique

Soil-transmitted helminths: A critical review of the impact of co-infections and implications for control and elimination.

Lebu S, Kibone W, Muoghalu CC, Ochaya S, Salzberg A, Bongomin F, Manga M.
10-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37561673/

Comparative Safety Surveillance of Triple (IDA) Versus Dual Therapy (DA) in Mass Drug Administration for Elimination of Lymphatic Filariasis in Kenya: A Cohort Event Monitoring Study.

Khaemba C, Barry A, Omondi WP, Kirui E, Oluka M, Parthasarathi G, Njenga SM, Guantai A, Aklillu E.
08-08-2023
Drug Saf.
https://pubmed.ncbi.nlm.nih.gov/37552438/

Introduction: Dual diethylcarbamazine and albendazole (DA) therapy is the standard mass drug administration (MDA) regimen for lymphatic filariasis in Kenya. Following the recent World Health Organization recommendation, Kenya piloted triple therapy with ivermectin, diethylcarbamazine, and albendazole (IDA) in MDA. Objective: We conducted a community-based, observational, cohort event monitoring study to compare the types, frequency, severity, and predictors of adverse events following dual versus triple therapy in 20,421 eligible residents. Methods: Residents in Kilifi (n = 10,010) and Mombasa counties (n = 10,411) received DA and IDA through MDA campaigns, respectively. Adverse events were actively monitored through house-to-house visits on days 1, 2, and 7 after MDA. Any clinical events reported before and after MDA were cross-checked and verified to differentiate pre-existing events from MDA-associated adverse events. Results: Overall, 5807 and 3102 adverse events were reported by 2839 and 1621 individuals in the IDA and DA groups, respectively. The incidence of experiencing one or more adverse events was significantly higher ($p < 0.0001$) in the IDA group (27.3%; 95% confidence interval [CI] 26.4-28.2) than in the DA group (16.2%; 95% CI 15.5-16.9). Dizziness (15.9% vs 5.9%) and drowsiness (10.1% vs 2.6%) were the most common adverse events and significantly higher in the IDA group compared with the DA group ($p < 0.0001$). Most adverse events were mild or moderate with a few severe cases (IDA = 0.05%; 95% CI 0.35-0.78, DA = 0.03%; 95% CI 0.14-0.60). Female sex, obesity, taking three or more diethylcarbamazine or ivermectin tablets, and having pre-existing clinical symptoms were significant predictors of adverse events following IDA treatment. Conclusions: Ivermectin, diethylcarbamazine, and albendazole as a combination is as safe and well tolerated as DA to use in MDA campaigns with no serious life-threatening adverse events. Systemic mild-to-moderate adverse events with a few severe cases and transient adverse events are more common with IDA treatment than with DA treatment. Hence, integrating pharmacovigilance into a MDA program is recommended for the timely detection and management of adverse events.

Spatial predictive risk mapping of lymphatic filariasis residual hotspots in American Samoa using demographic and environmental factors.

Cadavid Restrepo AM, Martin BM, Fuimaono S, Clements ACA, Graves PM, Lau CL.
24-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37486947/

Gale

Bullous scabies, the light shed on etiopathogenesis and treatment: report of five paediatric cases.

Arslan H, Gündüz Ö.
Juin-2023
Postepy Dermatol Alergol.
https://pubmed.ncbi.nlm.nih.gov/37545831/

Introduction: Bullous scabies (BS) is an infrequent and atypical presentation of scabies, with a predilection for elderly males. The mechanism of BS is not fully understood; superinfection, friction due to pruritus, autoeczemation, direct injury from mite's lytic enzymes, cross-reactivity of scabies protein with basal membrane zone antigens are considered to be possible reasons. Aim: To define clinical features of paediatric BS cases, which is an extremely rare subtype of scabies. Material and methods: This is a retrospective study of paediatric BS cases seen at two tertiary care centres. Previously described bacterial culture, antibiogram and follow-up records were investigated retrospectively. Confirmed scabies cases, according to the "International Alliance for the Control of Scabies (IACS)" with bullae were included. All cases were treated with 10% sulfur ointment for 3 consecutive days, two cycles. Households of cases were also treated simultaneously. Systemic antibiotics were added to patients with elevated acute phase reactants according to the antibiogram results. Informed consent was obtained from patients' parents. Results: Five BS cases were included. Three cases were male, two cases were female. Four cases had staphylococcus aureus, one had group-A beta haemolytic streptococcus positive bullae culture. All cases achieved a rapid complete resolution of symptoms after topical 10% sulfur ointment. Conclusions: Paediatric BS is an extremely rare entity of scabies. Bacterial superinfection plays a key role in bullae formation. 10% sulfur ointment is a highly effective treatment option for paediatric BS.

Genital nodular scabies: An uncommon presentation.

Cardiel Herranz G, Sánchez Malo MJ, Miranda Mairal L, Hidalgo Sanz J.
03-08-2023
Med Clin (Barc).
https://pubmed.ncbi.nlm.nih.gov/37543461/

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

Abdolrasouli A, Cousins CD, Basu TN, Trotman D, Hay RJ.
04-08-2023
Clin Exp Dermatol.
https://pubmed.ncbi.nlm.nih.gov/37539683/

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

Gallbladder Perforation with Choledochogastric Fistula Due to Ascaris Infestation, a Case Report.

Amsalu A, Molla Y.
02-08-2023
Int Med Case Rep J.
https://pubmed.ncbi.nlm.nih.gov/37551359/

We present a case of a 35-year-old Ethiopian female patient presented with right upper quadrant abdominal pain. Studies suspected gallbladder disease, for which she operated. Intraoperatively, gallbladder perforation with choledochogastric fistula was identified, with *Ascaris lumbricoides* (AL) worm in the common bile duct. Cholecystectomy was performed; common bile was repaired with T-tube and gastric repair. Patient was discharged 11 days after. On subsequent follow-up at the surgical referral clinic, the patient had no complaints.

Molecular variability of the Ancylostoma secreted Protein-2 (Aca-asp-2) gene from Ancylostoma caninum contributes to expand information on population genetic studies of hookworms.

Furtado LFV, de Miranda RRC, Tennessen JA, Blouin MS, Rabelo ÉML.
05-08-2023
Exp Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37544398/

Giardia duodenalis and dysentery in Iron Age Jerusalem (7th-6th century BCE).

Mitchell PD, Wang T, Billig Y, Gadot Y, Warnock P, Langgut D.
Juil-2023
Parasitology.
https://pubmed.ncbi.nlm.nih.gov/37231841/

The aim of this study was to determine if the protozoa that cause dysentery might have been present in Jerusalem, the capital of the Kingdom of Judah, during the Iron Age. Sediments from 2 latrines pertaining to this time period were obtained, 1 dating from the 7th century BCE and another from the 7th to early 6th century BCE. Microscopic investigations have previously shown that the users were infected by whipworm (*Trichuris trichiura*), roundworm (*Ascaris lumbricoides*), *Taenia* sp. tapeworm and pinworm (*Enterobius vermicularis*). However, the protozoa that cause dysentery are fragile and do not survive well in ancient samples in a form recognizable using light microscopy. Enzyme-linked immunosorbent assay kits designed to detect the antigens of *Entamoeba histolytica*, *Cryptosporidium* sp. and *Giardia duodenalis* were used. Results for *Entamoeba* and *Cryptosporidium* were negative, while *Giardia* was positive for both latrine sediments when the analysis was repeated three times. This provides our first microbiological evidence for infective diarrhoeal illnesses that would have affected the populations of the ancient near east. When we integrate descriptions from 2nd and 1st millennium BCE Mesopotamian medical texts, it seems likely that outbreaks of dysentery due to giardiasis may have caused ill health throughout early towns across the region.

Zoonotic helminths of dogs and risk factors associated with polyparasitism in Grenada, West Indies.

Macpherson MLA, Zendejas-Heredia PA, Sylvester W, Gasser RB, Traub RJ, Colella V, Macpherson CNL.
Juil-2023
Parasitology.
https://pubmed.ncbi.nlm.nih.gov/37184089/

Canine soil-transmitted helminths (STHs) cause important zoonoses in the tropics, with varying degrees of intensity of infection in humans and dogs. This study aimed to investigate the prevalence and associated risk factors for STHs in community dogs residing in Grenada, West Indies. In May 2021, 232 canine fecal samples were examined for zoonotic helminths by microscopy (following flotation), and genomic DNA from a subset of 211 of these samples were subjected to multiplex qPCR for the detection and specific identification of hookworms, *Toxocara* spp. and *Strongyloides*. Microscopic examination revealed that 46.5% (108/232, 95% CI 40–52.9), 9% (21/232, 95% CI 5.35–12.7) and 5.2% (12/232, 95% CI 2.3–8) of the samples contained eggs of *Ancylostoma* spp., *Toxocara* spp. and *Trichuris vulpis*, respectively. Multiplex qPCR revealed that, 42.2% (89/211, 95% CI 35.5–48.8) were positive for at least 1 zoonotic parasite. Of these, 40.8% (86/211, 95% CI 34.1–47.3) of samples tested positive for *Ancylostoma* spp., 36% (76/211, 95% CI 29.5–42.9) were positive for *A. caninum,* 13.3% (28/211, 95% CI 9–18.6) for *A. ceylanicum*, 5.7% for *T. canis* (12/211, 95% CI 2.97–8.81) and 1% (2/211, 95% CI 0–2.26) for *Strongyloides* spp. (identified as *S. stercoralis* and *S. papillosus* by conventional PCR-based Sanger sequencing). Using a multiple logistic regression model, a low body score and free-roaming behaviour were significant predictors of test-positivity for these parasitic nematodes in dogs ($P < 0.05$). Further studies of zoonotic STHs in humans should help

elucidate the public health relevance of these parasites in Grenada.

Leishmaniose

Clinical Profile and Diagnosis of Recurrent Cutaneous Leishmaniasis.

Arruda S, Agra-Duarte G, Lago J, Oliveira L, Zacarias E, Carvalho LP, Machado PRL, de Oliveira CI, Carvalho EM.
22-07-2023
Open Forum Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37564745/

TLR-2 agonist Pam3CSK4 has no therapeutic effect on visceral leishmaniasis in BALB/c mice and may enhance the pathogenesis of the disease.

Liao X, He J, Wang R, Zhang J, Wei S, Xiao Y, Zhou Q, Zheng X, Zhu Z, Zheng Z, Li J, Zeng Z, Chen D, Chen J.
06-08-2023
Immunobiology.
https://pubmed.ncbi.nlm.nih.gov/37562277/

Self-application of aminoglycoside-based creams to treat cutaneous leishmaniasis in travelers.

Mouri O, Melenotte C, Guéry R, Cotteret C, Schweitzer-Chaput A, Perignon A, Thellier M, Bourrat E, Kaguelidou F, Siriez JY, Malvy D, Gangneux JP, Duvignaud A, Ravel C, Cisternino S, Ransom J, Caumes E, Lortholary O, Grogl M, Buffet P.
10-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37561802/

Background: In endemic foci, the use of an aquaphilic cream containing paromomycin with/without gentamicin to treat cutaneous leishmaniasis (CL) is safe, painless and cures 78-82% of patients with New and Old World CL. Self-application in travelers requires evaluation. Methods: Travelers with 1-10 lesions of confirmed CL were prospectively treated with the paromomycin-gentamicin formulation (WR279396, 2012-2017, Group 1) and carefully follow up, or treated with a locally produced paromomycin-only cream (2018-2022, Group 2). The cream was applied once under supervision, then self-applied daily for 20-30 days. A cured lesion was defined as 100% re-epithelialization at day 42 without relapse at three months. Results: Medical features were similar in Group 1 (17 patients), and Group 2 (23 patients). Patients were infected with either Leishmania major, L. infantum, L. killicki, L. guyanensis, L. braziliensis, or L. naiffi. Intention-to-treat and per-protocol cure rates were 82% (95% confidence interval (CI) [64.23;100.00]) and 87% (95% CI [71,29;100.00]) in Group 1, and 69% (95% CI [50.76; 88.37]) and 76% (95% CI [57.97; 94.41]) in Group 2. In the pooled Group 1&2, 75% (95% CI [61.58;88.42]) (30/40) and 81% (95% CI [68,46;93.6]) (30/37) of patients were cured in intention-to-treat and per-protocol, respectively. There were no significant differences observed in the success rates between Old World and New World CL (83.3% vs. 60%, p = 0.14). Prospective observations in Group 1 showed that adverse events were mainly pruritus (24%) and pain (18%) on lesions (all mild or moderate). No mucosal involvement was observed in either group. Discussion: In this representative population of travelers who acquired CL either in the Old or New World, the 81% per-protocol cure rate of a self-applied aminoglycoside cream was similar to that observed in clinical trials.

Recurrent mucosal leishmaniasis of the epiglottis in an immunosuppressed patient.

Lopes SB, Aleixo RV, Silva JM, Cruz G, Ferreira E, Rabadão E.
25-07-2023
IDCases.
https://pubmed.ncbi.nlm.nih.gov/37554428/

Leishmaniasis is a disease caused by the intracellular protozoan parasite *Leishmania* and are known more than 20 species(1) harmful for men. A 74-year-old man, with sarcoidosis treated with methotrexate and corticoid, was assessed, in 2021, by an ENT specialist due to dysphagia, dysphonia, and odynophagia with a 5-year evolution and progressive worsening. A biopsy of the right vocal cord and epiglottis was performed, and the histology demonstrated the presence of amastigotes in the tissues coloured by Giemsa making the diagnosis of Leishmaniasis. The patient was referred to the Infectious Diseases Department, with the diagnosis of mucosal leishmaniasis, and hospitalized for treatment with Liposomal Amphotericin B. The dysphagia and odynophagia improved and was discharged to Infectious Diseases Day hospital to continue treatment. He completed a total of 10 days of treatment and continued follow up in Infectious Diseases, Pneumology and ENT departments. During this time the patient stopped treatment with methotrexate but maintained deflazacort 6 mg per day. In 2023, the patient presented with worsening dysphonia and dysphagia. A new biopsy of the epiglottis was performed in the ENT department. *Leishmania* DNA was detected, and histology was compatible with Leishmaniasis of the left larynx. He was hospitalized in Infectious Diseases department and started treatment with Liposomal Amphotericin B. The patient completed a total of 10 days of treatment, and, by this time, the medical team decided to maintain suppressive therapy once a month with Liposomal Amphotericin B, until the patient present with a CD4 leucocyte count superior to 350/mm^3 . By the time of this article, the patient maintained follow up in the Infectious Disease department with monthly sessions of therapy.

Visceral leishmaniasis-human immunodeficiency virus coinfection in a 52-year-old male in southwest Iran: a case report.

Moogahi S, Tadi Beni F, Tavalla M, Fasihi-Karami M, Kazemi F.
09-08-2023
J Med Case Rep.

https://pubmed.ncbi.nlm.nih.gov/37553714/

Leishmania (L.) amazonensis LaLRR17 increases parasite entry in macrophage by a mechanism dependent on GRP78.

Peña MS, Tang FHF, Franco FAL, Rodrigues AT, Carrara GMP, Araujo TLS, Giordano RJ, Palmisano G, de Camargo MM, Uliana SRB, Stolf BS.
09-08-2023
Parasitology.
https://pubmed.ncbi.nlm.nih.gov/37553284/

Thiadiazine thione derivatives as anti-leishmanial agents: synthesis, biological evaluation, structure activity relationship, ADMET, molecular docking and molecular dyanamics simulation studies.

Tamanna, Fu C, Qadir M, Shah MIA, Shtaiwi A, Khan R, Khan SU, Htar TT, Zada A, Lodhi MA, Ateeq M, Ali A, Naeem M, Ibrahim M, Khan SW.
07-08-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37551015/

During last decades, 3,5-disubstituted-tetrahydro-*2H*-thiadiazine-2-thione scaffold remains the center of interest due to their ease of preparation, diverse range substituents at N-3 and N-5 positions, and profound biological activities. In the current study, a series of 3,5-disubstituted-tetrahydro-*2H*-thiadiazine-2-thiones were synthesized in good to excellent yield, and the structure of the compounds were confirmed by various spectroscopic techniques such as FTIR, ^{1}H-NMR, ^{13}C-NMR and Mass spectrometry, and finally evaluated against *Leishmania major*. Whereas, all the evaluated compounds (1-33), demonstrate potential leishmanicidal activities with IC_{50} values in the range of (1.30- 149.98 uM). Among the evaluated compounds such as 3, 4, 6, and 10 exhibited excellent leishmanicidal activities with IC_{50} values of (2.17 µM), (2.39 µM), (2.00 µM), and (1.39 µM), respectively even better than the standard amphotericin B (IC_{50} = 0.50) and pentamidine (IC_{50} = 7.52). In order to investigate binding interaction of the most active compounds, molecular docking study was conducted with *Leishmania major*. Further molecular dynamic simulation study was also carried out to assess the stability and correct binding of the most active compound 10, within active site of the *Leishamania major*. Likewise, the physiochemical properties, drug likeness, and ADMET of the most active compounds were investigated, it was found that none of the compounds violate Lipiniski's rule of five, which show that this class of compounds had enough potential to be used as drug candidate in near future.Communicated by Ramaswamy H. Sarma.

CYP5122A1 encodes an essential sterol C4-methyl oxidase in Leishmania donovani and determines the antileishmanial activity of antifungal azoles.

Wang M, Jin Y, Basu S, Feng M, Ning Y, Munasinghe I, Joachim A, Li J, Madden R, Burks H, Gao P, Perera C, Werbovetz K, Zhang K.
27-07-2023
Res Sq.
https://pubmed.ncbi.nlm.nih.gov/37546914/

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

Mirzaei R, Karampoor S, Korotkova NL.
27-07-2023
Pathol Res Pract.
https://pubmed.ncbi.nlm.nih.gov/37544130/

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

Binding profile of quinonoid-dihydrobiopterin to quinonoid-dihydropteridine reductase examined by in silico and in vitro analyses.

Kono H, Hara S, Furuta T, Ichinose H.
04-08-2023
J Biochem.
https://pubmed.ncbi.nlm.nih.gov/37540845/

Immunogenic mapping of rDyn-1 and rKDDR-plus proteins and selection of oligopeptides by immunoblotting for the diagnosis of Leishmania infantum-infected dogs.

Siqueira WF, Cardoso MS, Fraga VG, Ottino J, Ribeiro VM, Gondim CN, de Paiva Barçante JM, Amado Gomes AC, Galdino AS, Eersels K, van Grinsven B, Bartholomeu DC, Bueno LL, Cleij T, Fujiwara RT.
04-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37540724/

Host preference and human blood index of Phlebotomus orientalis, an exophilic sand fly vector of visceral leishmaniasis in eastern Sudan.

Jibreel T, Khogali A, Jiménez M, Raiyed A, Dakein O, Alsharif B, Khalid NM, Osman OF, Nour BYM, Mohamed GH, Molina R, Vidal-

López A, Díaz-Regañón R, den Boer M, Alvar J, Courtenay O, Elnaiem DE.
04-08-2023
Med Vet Entomol.
https://pubmed.ncbi.nlm.nih.gov/37540228/

Visceral leishmaniasis (VL, kala azar), caused by Leishmania donovani, transmitted by Phlebotomus orientalis, is a serious systemic disease that causes high morbidity and mortality rates in Sudan and other parts of East Africa and the world. Despite progress in understanding the epidemiology of the disease in East Africa, little is known about the host preference of P. orientalis in kala azar endemic villages of Sudan, which have some of the highest VL incidence rates in the world. The present study used host choice experiments and blood-meal identification approaches to determine the host preference of P. orientalis in kala azar endemic villages in Gedarif state, eastern Sudan. In the host choice experiment, tent traps were used to compare the attractiveness of cows, donkeys, sheep and goats for host-seeking P. orientalis. In the blood-meal identification study, blood-fed P. orientalis females, captured inside houses and peri-domestic habitats, were subjected to molecular typing using cytochrome b gene (cyt b) amplification and sequence analysis. Cows and donkeys were the most attractive to blood-seeking P. orientalis, followed by goats. Similarly, the blood-meal analysis of P. orientalis showed that the vector preferentially feeds on cows, followed by donkeys, humans and goats. The human blood index of P. orientalis was 19.4% (42/216), indicating a high zoophilic habit of the vector, both inside and outside the houses. Although the order of host preference varied by location, it was clear that cows are the most preferred host of P. orientalis in the area. Results are discussed in relation to the role of domestic/livestock animals in VL zoopotentiation and zooprophylaxis. Inference is made on the potential impact of insecticide treatment of cows in control of the vector and the transmission of VL in Sudan and other parts of East Africa.

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

Sherafati J, Dayer MS, Ghaffarifar F, Akbarzadeh K, Pirestani M.
03-08-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37535629/

Leishmaniasis is a zoonotic disease caused by an intracellular parasite from the genus Leishmania. Lack of safe and effective drugs has increasingly promoted researches into new drugs of natural origin to cure the disease. The study, therefore, aimed to investigate the anti-leishmanial effects of Lucilia sericata larval excretion/secretion (ES) in combination with Apis mellifera honey as a synergist on Leishmania major using an in vitro model. Various concentrations of honey and larval ES fractions were tested against promastigotes and intracellular amastigotes of L. major using macrophage J774A.1 cell line. The inhibitory effects and cytotoxicity of ES plus honey were evaluated using direct counting method and MTT assay. To assess the effects of larval ES plus honey on the amastigote form, the rate of macrophage infection and the number of amastigotes per infected macrophage cell were estimated. The 50% inhibitory concentration (IC50) values were 21.66 µg/ml, 43.25 60 µg/ml, 52.58 µg/ml, and 70.38 µg/ml for crude ES plus honey, ES >10 kDa plus honey, ES <10 kDa plus honey, and honey alone, respectively. The IC50 for positive control (glucantime) was 27.03 µg/ml. There was a significant difference between viability percentages of promastigotes exposed to different doses of applied treatments compared to the negative control ($p \leq 0.0001$). Microscopic examination of amastigote forms revealed that dosages applied at 150 to 300 µg/ml significantly reduced the rate of macrophage infection and the number of amastigotes per infected macrophage cell. Different doses of larval products plus honey did not show a significant toxic effect agaist macrophage J774 cells. The larval ES fractions of L. sericata in combination with A. mellifera honey acted synergistically against L. major.

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

Srivastava A, Nair A, Pandey SP, Kluck GEG, Mesquita I, Ghosh T, Bose A, Baral R, Silvestre R, Bodhale N, Saha B.
Sept-2023
Cytokine.
https://pubmed.ncbi.nlm.nih.gov/37515982/

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

Thomas MG, McGonagle K, Rowland P, Robinson DA, Dodd PG, Camino-Díaz I, Campbell L, Cantizani J, Castañeda P, Conn D, Craggs PD, Edwards D, Ferguson L, Fosberry A, Frame L, Goswami P, Hu X, Korczynska J, MacLean L, Martin J, Mutter N, Osuna-Cabello M, Paterson C, Peña I, Pinto EG, Pont C, Riley J, Shishikura

Y, Simeons FRC, Stojanovski L, Thomas J, Wrobel K, Young RJ, Zmuda F, Zuccotto F, Read KD, Gilbert IH, Marco M, Miles TJ, Manzano P, De Rycker M.
10-08-2023
J Med Chem.
https://pubmed.ncbi.nlm.nih.gov/37506194/

There is an urgent need for new treatments for Chagas disease, a parasitic infection which mostly impacts South and Central America. We previously reported on the discovery of GSK3494245/DDD01305143, a preclinical candidate for visceral leishmaniasis which acted through inhibition of the *Leishmania* proteasome. A related analogue, active against *Trypanosoma cruzi*, showed suboptimal efficacy in an animal model of Chagas disease, so alternative proteasome inhibitors were investigated. Screening a library of phenotypically active analogues against the *T. cruzi* proteasome identified an active, selective pyridazinone, the development of which is described herein. We obtained a cryo-EM co-structure of proteasome and a key inhibitor and used this to drive optimization of the compounds. Alongside this, optimization of the absorption, distribution, metabolism, and excretion (ADME) properties afforded a suitable compound for mouse efficacy studies. The outcome of these studies is discussed, alongside future plans to further understand the series and its potential to deliver a new treatment for Chagas disease.

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

Basu S, Pawlowic MC, Hsu FF, Thomas G, Zhang K.
28-07-2023
PLoS Pathog.
https://pubmed.ncbi.nlm.nih.gov/37506172/

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

Novel mutations in genes of the IL-12/IFN-γ axis cause susceptibility to tuberculosis.

Ahmad S, Ahmed J, Khalifa EH, Khattak FA, Khan AS, Farooq SU, Osman SMA, Salih MM, Ullah N, Khan TA.
Sept-2023
J Infect Public Health.
https://pubmed.ncbi.nlm.nih.gov/37437430/

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

Marmo VLM, Ambrósio JAR, Gonçalves EP, Raniero LJ, Beltrame Junior M, Pinto JG, Ferreira-Strixino J, Simioni AR.
Août-2023
Photochem Photobiol Sci.
https://pubmed.ncbi.nlm.nih.gov/37115408/

Lèpre

Prediction of the occurrence of leprosy reactions based on Bayesian networks.

de Andrade Rodrigues RS, Heise EFJ, Hartmann LF, Rocha GE, Olandoski M, de Araújo Stefani MM, Latini ACP, Soares CT, Belone A, Rosa PS, de Andrade Pontes MA, de Sá Gonçalves H, Cruz R, Penna MLF, Carvalho DR, Fava VM, Bührer-Sékula S, Penna GO, Moro CMC, Nievola JC, Mira MT.
26-07-2023
Front Med (Lausanne).
https://pubmed.ncbi.nlm.nih.gov/37564037/

Introduction: Leprosy reactions (LR) are severe episodes of intense activation of the host inflammatory response of uncertain etiology, today the leading cause of permanent nerve damage in leprosy patients. Several genetic and non-genetic risk factors for LR have been described; however, there are limited attempts to combine this information to estimate the risk of a leprosy patient developing LR. Here we present an artificial intelligence (AI)-based system that can assess LR risk using clinical, demographic, and genetic data. Methods: The study includes four datasets from different regions of Brazil, totalizing 1,450 leprosy patients followed prospectively for at least 2 years to assess the occurrence of LR. Data mining using WEKA software was performed following a two-step protocol to select the variables included in the AI system, based on Bayesian Networks, and developed using the NETICA software. Results: Analysis of the complete database resulted in a system able to estimate LR risk with 82.7% accuracy, 79.3% sensitivity, and 86.2% specificity. When using only databases for which host genetic

information associated with LR was included, the performance increased to 87.7% accuracy, 85.7% sensitivity, and 89.4% specificity. Conclusion: We produced an easy-to-use, online, free-access system that identifies leprosy patients at risk of developing LR. Risk assessment of LR for individual patients may detect candidates for close monitoring, with a potentially positive impact on the prevention of permanent disabilities, the quality of life of the patients, and upon leprosy control programs.

Elimination of tuberculosis requires prior control of silicosis including sub-radiological silicosis.

Singh D, Sarkar B, Sarkar K.
Juil-2023
Indian J Tuberc.
https://pubmed.ncbi.nlm.nih.gov/37562900/

Study of Cutaneous Manifestations in Alcohol Dependence Syndrome Patients in a Rural Tertiary Care Center in India.

Rao SK, Srinivas RT, Reddy M, Ashraf A.
Jan-2023
Addict Health.
https://pubmed.ncbi.nlm.nih.gov/37560076/

Background: Chronic alcoholism is a multifactorial condition predisposed by environmental, social, and psychological factors. Alcohol dependence syndrome (ADS) can present with varied cutaneous and systemic manifestations. The effects of alcohol use include cutaneous infections, infestations, features of malnutrition, exacerbation of pre-existing dermatoses, and alcohol-related dermatoses. This study aimed to analyze and document cutaneous manifestations secondary to infections, infestations, malnutrition, and modifications of pre-existing dermatoses in ADS patients and investigate the correlation between the presence of cutaneous manifestations and duration and quantity of alcohol intake. Methods: The present observational study was carried out in the Department of Dermatology for a period of one year. A total of 172 male patients with ADS presenting with skin manifestations were included in the study. Detailed analysis of history, clinical examination, and relevant investigations were conducted. Findings: Out of 172 male patients with ADS, the most common dermatoses noted were infections (166, 96.5%) and features of malnutrition (161, 93.6%). Exacerbation of pre-existing dermatoses (101, 58.7%) and alcohol-related dermatoses (85, 49.4%) were also observed. Conclusion: Most of the dermatoses were significantly correlated with the quantity of alcohol intake than with its duration, implying that higher quantity of alcohol intake has more impact on cutaneous and systemic manifestations. Identifying the cutaneous manifestations in ADS patients plays an important role in recognizing the underlying systemic disorders which in turn facilitates early intervention and thereby prevents complications.

Rescue treatment with intravenous immunoglobulin and amniotic membrane dressing in refractory paediatric pemphigus vulgaris with sepsis.

Akham R, Bhatia R, Paonam R, Hazarika N.
09-08-2023
BMJ Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37558274/

Cyclophosphamide in a Recalcitrant Case of Nekam's Disease.

Muddebihal A, Khurana A, Sardana K.
01-07-2023
Dermatol Pract Concept.
https://pubmed.ncbi.nlm.nih.gov/37557153/

Extragenital Lichen Sclerosus et Atrophicus-Morphea Overlap Masquerading as Lupus Vulgaris: Histopathology to the Rescue.

Prasanna S, Haridas NS, Kharkar V, Khade P.
01-07-2023
Dermatol Pract Concept.
https://pubmed.ncbi.nlm.nih.gov/37557133/

Erdheim Chester Disease: A Rare Entity from North India.

Swarnkar B, Anand GRP, Gupta S, Agarwal S.
01-07-2023
Dermatol Pract Concept.
https://pubmed.ncbi.nlm.nih.gov/37557124/

From Passos the Indian to Doctor Chernoviz: experiments to cure leprosy in nineteenth-century Pará.

Henrique MC.
04-08-2023
Hist Cienc Saude Manguinhos.
https://pubmed.ncbi.nlm.nih.gov/37556716/

A Comparative Study on Therapeutic Efficacy of Autologous Platelet-rich Plasma, Autologous Platelet-rich Fibrin Matrix, Recombinant Human Epidermal Growth Factor, and Collagen Particles in Nonhealing Leg Ulcers.

Gehlawat T, Karia UK, Shah SR, Vyas HR, Parghi MB, Doshi YJ, Shah BJ.
Avr-Juin 2023
J Cutan Aesthet Surg.
https://pubmed.ncbi.nlm.nih.gov/37554680/

Background: Nonhealing leg ulcers are challenging to manage and cause significant patient morbidity. To promote healing, newer techniques focus on delivering/enhancing dermal matrix components. Aim: The aim of this study was to compare the therapeutic efficacy of autologous platelet-rich plasma (PRP), autologous platelet-rich fibrin matrix (PRFM), recombinant human epidermal growth factor (rhEGF), and

collagen particles in treating nonhealing leg ulcers. **Materials and methods:** Open, randomized prospective study was conducted in a single tertiary center over 2 years where after fulfilling the criteria, randomization was done into four groups. Group A: Autologous PRP (double spin, manual method, weekly); Group B: Autologous PRFM (weekly); Group C: rhEGF (daily application); and Group D: Collagen particles (weekly) along with cleansing, debris removal, and wound dressing. Treatment endpoints were complete healing/6 months of treatment, whichever was earlier. Follow-up was done two weekly by clinical assessment, photographs, and measurement of the ulcer area. Epi info 7 software was used for statistical analysis. **Results:** A total of 48 patients completed the study, 12 in each group, with mean age: 42.37 ± 4.56 years and male-to-female ratio 2.6:1. Underlying etiology was varicosities (43.75%), traumatic (25%), diabetes (22.91%), and leprosy (8.34%). At baseline, all groups were comparable in terms of patient and ulcer characteristics. Complete healing was seen in 79.17% at the end of 12 weeks: 91.67% of patients from Groups A and B each, and 66.67% from Groups C and D each. The mean time to complete healing was 6.9 ± 2.5 weeks, the least in Group B (4.73 ± 2.3 weeks). Differences between excellent (≥75%) ulcer healing across all groups were statistically significant at the end of 8 weeks where Group B showed maximum improvement. No major adverse events were seen. **Conclusion:** PRFM resulted in relatively faster ulcer healing compared with other modalities.

Dressing Materials: A Comprehensive Review.

Bhoyar SD, Malhotra K, Madke B.
Avr-Juin 2023
J Cutan Aesthet Surg.
https://pubmed.ncbi.nlm.nih.gov/37554675/

A Randomized Controlled Study Comparing the Efficacy of Autologous Smashed Follicular Dermal Graft and Epidermal Cell Suspension versus Normal Saline Dressing in the Treatment of Chronic Nonhealing Trophic Ulcers in Patients with Hansen's Disease.

Dheemant M, Harikishan KY, Naveen S, Belliappa PR.
Avr-Juin 2023
J Cutan Aesthet Surg.
https://pubmed.ncbi.nlm.nih.gov/37554673/

Background: Trophic ulcers remain the most common reason for hospitalization in patients with Hansen's disease. With the introduction of new therapeutic regimens, leprosy can now be cured. However, complications of the disease, such as sensory loss, muscle palsy, absorption of extremities, and recurrent ulcers, still lead to substantial morbidity. The management of patients with trophic ulcers and their consequences is difficult, because it is a recurrent and recalcitrant problem. **Aims:** To evaluate the efficacy of autologous smashed follicular dermal graft and epidermal cell suspension (ECS) in the treatment of chronic nonhealing trophic ulcers in patients with Hansen's disease and to compare its efficacy with normal saline dressing. **Materials and methods:** A total of 46 chronic nonhealing trophic ulcers were randomized into two groups (23 ulcers in each): Ulcers in Group A were treated with autologous smashed follicular dermal graft and ECS; ulcers in Group B were treated with normal saline dressings. Ulcers were assessed based on the rate of ulcer size reduction at every week till 12 weeks and then once a month till the sixth month. **Results:** All 23 (100%) ulcers in Group A had healed within the study period of six months, whereas only 14 (60.9%) ulcers had healed in Group B. Nine (39.1%) ulcers in Group B had not healed even at the end of six months. All 23 (100%) ulcers in Group A had healed within eight weeks, which was statistically significant, *P* value <0.05. **Conclusion:** Trophic ulcers heal faster by autologous smashed follicular dermal graft and ECS, with good results of re-epithelialization of the ulcer bed than by normal saline dressing.

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

Shakya R, Maharjan SK.
31-07-2023
Asian J Anesthesiol.
https://pubmed.ncbi.nlm.nih.gov/37553724/

Background: Dexmedetomidine is a potent α_2 agonist which has been used for blunting the stress responses during critical events such as laryngoscopy, endotracheal intubation, pneumoperitoneum creation, and extubation. The purpose of this study was to see the efficacy of intravenously administered dexmedetomidine at a dose of 0.5 mcg/kg in attenuating the hemodynamic responses due to pneumoperitoneum during laparoscopic cholecystectomy under general anesthesia. **Methods:** Sixty patients, ASA-PS class I (American Society of Anesthesiologist physical status class I), aged between 18 and 60 years, of either sex with weight ranging from 50 to 80 kg, scheduled for laparoscopic cholecystectomy were randomized into two groups (groups A and B) in a double-blinded fashion. Both groups were pre-medicated with an injection glycopyrrolate. Group A received 100 mL normal saline (NS) over 10 minutes while group B received dexmedetomidine 0.5 mcg/kg diluted in 100 mL NS over 10 minutes before induction of general anesthesia. Heart rate, systolic, diastolic, and mean arterial pressures were noted. **Results:** Following pneumoperitoneum, there was no statistically significant difference in the hemodynamic parameters between the two groups (P > 0.05).

Clinicopathologic Spectrum of Lysozyme-Associated Nephropathy.

Kudose S, Cossey LN, Canetta PA, Sekulic M, Vanbeek CA, Huls FB, Gupta I, Bu L, Alexander MP, Cornell LD, Fidler ME, Markowitz GS, Larsen CP, D'Agati VD, Nasr SH, Santoriello D.
15-05-2023
Kidney Int Rep.
https://pubmed.ncbi.nlm.nih.gov/37547521/

Rituximab in Patients With Primary Membranous Nephropathy With High Immunologic Risk.

Naik S, Pal D, Shukla S, Kumar V, Kumar A, Jha V, Minz R, Sethi J, Bharati J, Divyaveer S, Kumar V, Rathi M, Kohli HS, Ramachandran R.
16-05-2023
Kidney Int Rep.
https://pubmed.ncbi.nlm.nih.gov/37547518/

A Survey-Based Assessment of Awareness Regarding Parthenium hysterophorus in a Rural Population of North India.

Sharma SK, Dash S, Shukla P, Gupta R, Sami U.
06-07-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37546154/

Spatial factors for COVID-19 associated community deaths in an urban area of Lusaka, Zambia: an observational study.

Hamukale A, Imamura T, Kapina M, Borkovska O, Musuka CA, Tembo E, Xie Y, Tedesco C, Zulu PM, Sakubita P, Kapaya F, Hamoonga R, Mazaba ML, Nagata C, Ishiguro A, Kapata N, Mukonka V, Sinyange N.
15-05-2023
Pan Afr Med J.
https://pubmed.ncbi.nlm.nih.gov/37545603/

Implementing community based inclusive development for people with disability in Latin America: a mixed methods perspective on prioritized needs and lessons learned.

Bachfischer A, Barbosa MC, Rojas AAR, Bechler R, Schwienhorst-Stich EM, Kasang C, Simmenroth A, Parisi S.
04-08-2023
Int J Equity Health.
https://pubmed.ncbi.nlm.nih.gov/37542266/

Background: Research on the needs of people with disability is scarce, which promotes inadequate programs. Community Based Inclusive Development interventions aim to promote rights but demand a high level of community participation. This study aimed to identify prioritized needs as well as lessons learned for successful project implementation in different Latin American communities. Methods: This study was based on a Community Based Inclusive Development project conducted from 2018 to 2021 led by a Columbian team in Columbia, Brazil and Bolivia. Within a sequential mixed methods design, we first retrospectively analyzed the project baseline data and then conducted Focus Group Discussions, together with ratings of community participation levels. Quantitative descriptive and between group analysis of the baseline survey were used to identify and compare sociodemographic characteristics and prioritized needs of participating communities. We conducted qualitative thematic analysis on Focus Group Discussions, using deductive main categories for triangulation: 1) prioritized needs and 2) lessons learned, with subcategories project impact, facilitators, barriers and community participation. Community participation was assessed via spidergrams. Key findings were compared with triangulation protocols. Results: A total of 348 people with disability from 6 urban settings participated in the baseline survey, with a mean age of 37.6 years (SD 23.8). Out of these, 18 participated within the four Focus Group Discussions. Less than half of the survey participants were able to read and calculate (42.0%) and reported knowledge on health care routes (46.0%). Unemployment (87.9%) and inadequate housing (57.8%) were other prioritized needs across countries. Focus Group Discussions revealed needs within health, education, livelihood, social and empowerment domains. Participants highlighted positive project impact in work inclusion, self-esteem and ability for self-advocacy. Facilitators included individual leadership, community networks and previous reputation of participating organizations. Barriers against successful project implementation were inadequate contextualization, lack of resources and on-site support, mostly due to the COVID-19 pandemic. The overall level of community participation was high (mean score 4.0/5) with lower levels in Brazil (3.8/5) and Bolivia (3.2/5). Conclusion: People with disability still face significant needs. Community Based Inclusive Development can initiate positive changes, but adequate contextualization and on-site support should be assured.

Antibodies against native proteins of Mycobacterium tuberculosis can detect pulmonary tuberculosis patients.

Dewi DNSS, Mertaniasih NM, Soedarsono, Hagino K, Yamazaki T, Ozeki Y, Artama WT, Kobayashi H, Inouchi E, Yoshida Y, Ishikawa S, Shaban AK, Tateishi Y, Nishiyama A, Ato M, Matsumoto S.
04-08-2023
Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37542102/

COVID-19 vaccination and leprosy-A UK hospital-based retrospective cohort study.

de Barros B, Pierce R, Sprenger C, Ong ELH, Walker SL.
04-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37540711/

Background: Individuals with leprosy are at risk of leprosy reactions, T-cell mediated immunological complications, which lead to nerve function impairment. Leprosy reactions require systemic immunosuppression which is a risk factor for severe COVID-19. Vaccination for SARS-CoV-2 infection is recommended in the UK and became widely available in 2021 with individuals at increased risk of severe disease, including the immunosuppressed, prioritised. Vaccines for SARS-CoV-2 may provoke a T cell response. The latter poses a theoretical risk of provoking an immunological response to latent Mycobacterium leprae infection leading to clinical disease or in those with

clinical disease triggering a leprosy reaction. BCG vaccination is associated with the development of leprosy in a small proportion of healthy contacts of people with leprosy within twelve weeks of administration. BCG causes a Th1 immune response. Methodology/principal findings: We performed a retrospective cohort study to determine the SARS-CoV-2 vaccination status of individuals diagnosed with leprosy attending the Leprosy Clinic in 2021 and whether any had developed leprosy or experienced a new leprosy reaction within twelve weeks of receiving a dose of a SARS-CoV-2 vaccine. The electronic patient records were used to retrieve data. Fifty-two individuals with leprosy attended the clinic in 2021 of which five people were newly diagnosed with leprosy. Thirty-seven (71%) were male and the median age was 48.5 years old (Range 27-85 years). Eight (15.4%) individuals were taking multi-drug therapy (MDT) and eight (15.4%) had completed MDT within three years of the study. Twenty-two (41.5%) individuals were prescribed a systemic immunosuppressant drug during 2021. Ten (18.9%) individuals have one or more risk factors for severe COVID-19. The SARS-CoV-2 vaccination status of fifty (96%) were recorded of which forty-nine were vaccinated (98%). One individual had declined vaccination. One individual was diagnosed with borderline tuberculoid (BT) leprosy having developed red skin lesions with reduced sensation (which increased in size and number) and thickened peripheral nerves one week after a second dose of BNT162b2 vaccine. Another individual who had completed MDT more than three years earlier developed red plaques and tender thickened nerves consistent with a leprosy Type 1 reaction eight weeks after a single dose of BNT162b2 vaccine (having received two doses of CoronaVac vaccine three months earlier). Conclusions/significance: The development of BT leprosy and a Type 1 reaction in another individual shortly after a dose of BNT162b2 vaccine may be associated with vaccine mediated T cell responses. The benefits of vaccination to reduce the risk of severe COVID-19 outweigh these unwanted events but data from leprosy endemic countries may provide further information about potential adverse effects of augmented T cell responses in individuals with leprosy or latent M. leprae infection.

Leprosy may now be endemic in Florida, clinicians warn.

Mahase E.
03-08-2032
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37536721/

Dimitrios Zambakis' Scientific Hypothesis on the Transmission of Leprosy.

Chen K, Talbot C, Mammis A.
Août-2023
J Med Biogr.
https://pubmed.ncbi.nlm.nih.gov/35139681/

Morsures de serpent

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

Das K, Das S, Mohakud NK, Pradhan SK, Sahu SK.
07-08-2023
Trop Doct.
https://pubmed.ncbi.nlm.nih.gov/37545383/

Our study evaluates the risk factors of acute kidney injury (AKI) in children with snake envenomation. Out of 145 cases, 54 (37%) developed AKI. Unsurprisingly, the mortality increased with oliguria and higher levels of creatinine. Bleeding manifestations were also more common among the AKI group.

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

Deikumah JP, Biney RP, Awoonor-Williams JK, Gyakobo MK.
28-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37506181/

A long-term observational study of paediatric snakebite in Kilifi County, south-east Kenya.

Abouyannis M, Boga M, Amadi D, Ouma N, Nyaguara A, Mturi N, Berkley JA, Adetifa IM, Casewell NR, Lalloo DG, Hamaluba M.
17-07-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37459350/

Characterisation of two snake toxin-targeting human monoclonal immunoglobulin G antibodies expressed in tobacco plants.

Moore CM, Ljungars A, Paul MJ, Dahl CH, Ahmadi S, Adams AC, Grav LM, Schoffelen S, Voldborg BG, Laustsen AH, Ma JK.
15-08-2023
Toxicon.
https://pubmed.ncbi.nlm.nih.gov/37442299/

Current snakebite antivenoms are based on polyclonal animal-derived antibodies, which can neutralize snake venom toxins in envenomed victims, but which are also associated with adverse reactions. Therefore, several efforts within antivenom research aim to explore the utility of recombinant monoclonal antibodies, such as human immunoglobulin G (IgG) antibodies, which are routinely used in the clinic for other indications. In this study, the feasibility of using tobacco plants as bioreactors for expressing full-length human monoclonal IgG antibodies against snake toxins was investigated. We show that the plant-produced antibodies perform similarly to their mammalian cell-expressed equivalents in terms of in vitro antigen binding. Complete neutralization was

achieved by both the plant and mammalian cell-produced anti-α-cobratoxin antibody. The feasibility of using plant-based expression systems may potentially make it easier for laboratories in resource-poor settings to work with human monoclonal IgG antibodies.

Exotic (non-native) snakebite envenomation in Japan: A review of the literature between 2000 and 2022.

Aoki Y, Yoshimura K, Sakai A, Tachikawa A, Tsukamoto Y, Takahashi K, Yamano S, Smith C, Hayakawa K, Tasaki O, Ariyoshi K, Warrell DA.
15-08-2023
Toxicon.
https://pubmed.ncbi.nlm.nih.gov/37442298/

A limited number of studies have investigated the clinical characteristics of snakebite envenomation by exotic (non-native) snakes in Japan. This study reviewed the literature to determine the status and risk of bites by exotic pet snakes in Japan. We reviewed reports of snakebite due to exotic snakes in Japan published between 2000 and 2022, excluding reports of bites by snakes native to Japan, such as Gloydius blomhoffii, Rhabdophis tigrinus, and Protobothrops flavoviridis. During the study period, 11 exotic snakebites were recorded, involving 11 species. The majority of those bitten (10/11 cases) were male, all cases were hand injuries, and there were no fatalities. The snakes responsible belonged to the Colubridae (4/11 cases), Viperidae (4/11 cases), and Elapidae (3/11 cases) families. Cases of envenomation by G. brevicaudus, Bungarus candidus, and Dendroaspis angusticeps were of particular interest. Ten of the eleven patients developed local cytotoxic signs, and three developed "compartment syndrome," in which the surgeons performed decompressive incisions. Two bites from elapid snakes and one from a viperid snake resulted in respiratory failure. Antivenom was given in two cases. Complications were observed, such as acute kidney injury, rhabdomyolysis, coagulopathy, and residual dysfunction of the affected finger. Emergency rooms should be prepared to manage patients who have been bitten by exotic snakes, even though the number of reported cases is not high in Japan. Initial stabilization of patients is crucial, before a definitive diagnosis is made, as with native snakebite envenomation. Finger bites are reported in most cases, which may result in functional impairment of the fingers. In order to collect more comprehensive patient data in Japan, a reporting system for all snakebite envenomations should be considered.

A prospective observational phase IV study on effectiveness of animal derived polyclonal antibody antivenoms against West African carpet viper (Echis romani) induced coagulopathy and mortality.

Dajel TB, Abubakar SB, Dan-Amarya NM, Azi NA, Mu'azu S, Hamza M, Iliyasu G, Gwarzo MY, Habib AG.
15-08-2023
Toxicon.
https://pubmed.ncbi.nlm.nih.gov/37393958/

Global parameter optimisation and sensitivity analysis of antivenom pharmacokinetics and pharmacodynamics.

M Morris N, A Blee J, Hauert S.
15-08-2023
Toxicon.
https://pubmed.ncbi.nlm.nih.gov/37356552/

Mycétome

Hemoptysis as the presenting manifestation of bronchiectasis-associated hospitalization in Korea.

Seo H, Cha SI, Park J, Lim JK, Park JE, Choi SH, Lee YH, Yoo SS, Lee SY, Lee J, Kim CH, Park JY.
31-07-2023
J Thorac Dis.
https://pubmed.ncbi.nlm.nih.gov/37559598/

Background: Patients with bronchiectasis commonly experience disease exacerbations, which cause significant morbidity and mortality. However, data regarding the clinical features of bronchiectasis patients hospitalized with hemoptysis are scarce. Methods: We retrospectively collected the data of patients with bronchiectasis-associated hospitalization at a tertiary referral center in Korea, and classified them into the hemoptysis and infective exacerbation (IE) groups. The presence of hemoptysis was defined as a volume of expectorated blood larger than 10 mL per 24 hours. The clinical, radiological, and laboratory parameters were compared between the two groups. Results: Patients were classified into the hemoptysis [267 (54.5%)] and IE [223 (45.5%)] groups. Among the 44 patients of the hemoptysis group, 37 (84.1%) presented with hemoptysis than with IE at the recurrent episode. The hemoptysis group had a significantly lower 30-day mortality than that of the IE group. Previous pulmonary tuberculosis (TB), mycetoma, and bronchial artery hypertrophy were independently associated with the hemoptysis group. In contrast, male sex, poor performance status, colonization of *Pseudomonas aeruginosa*, ≥3 involved lobes, cystic bronchiectasis, and emphysema were inversely associated with the hemoptysis group. The absence of hemoptysis was one of the independent predictors of 30-day mortality in patients with bronchiectasis-associated hospitalization. Conclusions: In Korea, bronchiectasis patients hospitalized with hemoptysis exhibit a distinct phenotype, and are more likely to have previous pulmonary TB, mycetoma, and bronchial artery hypertrophy. Hemoptysis is associated with a lower risk of short-term mortality compared to IE in bronchiectasis-associated hospitalization.

Urgent call to protect children and their health in Sudan.

Siddig EE, Eltigani HF, Ahmed A.
09-08-2023
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37558248/

Pulmonary Tuberculosis with Concomitant Aspergillus Fungal Ball in a Diabetic Indian Male: A Rare Case Report.

Yadav S.
06-07-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37546067/

Pulmonary tuberculosis is rampant in some countries. The disease is an outcome of infection by *Mycobacterium tuberculosis* and is more common in immunocompromised individuals. Furthermore, mycetoma or a fungal ball can develop in cavitary lesions of tuberculosis. The present case is a rare presentation of pulmonary tuberculosis with concomitant *Aspergillus* fungal ball in a diabetic Indian male. A clinical examination with a strong laboratory and radiological workup helped establish the final diagnosis. The patient was initiated on anti-tubercular chemotherapy and advised lobectomy.

Rage

Rabies in Chozna "Potus flavus": a warning of a potential threat to public and animal health.

Concha-Velasco F, Aguirre E, Ortiz-Cam L, Quispe-Jihuallancca H, Bernable-Villasante L, Bascope R, Arizabal M, Vargas-Luna E, Espinoza-Culupú A, Mantari C, Lopez-Ingunza R.
10-08-2023
Vet Q.
https://pubmed.ncbi.nlm.nih.gov/37560894/

Animal bites management in Northern Iran: Challenges and solutions.

Bay V, Shirzadi MR, Jafari Sirizi M, Asl IM.
27-07-2023
Heliyon.
https://pubmed.ncbi.nlm.nih.gov/37554820/

Objectives: Animal bite is considered a serious social, economic, and health risk for societies with poor animal bites and population management. The objective of this study was to propose a model for animal bites management in Golestan Province. Methods: The present study is a multi-method study conducted quantitatively and qualitatively. First, as a cross-sectional study, the animal bites in Golestan Province and the country were calculated and their trend was predicted. Secondly, in the qualitative study (content analysis), the challenges, barriers, and methods of animal bite control were extracted through conducting semi-structured interviews and focused group discussion meetings. Finally, the model of animal bite management was developed and it was confirmed by Round Delphi. The data were analyzed via content analysis using MAXQDA18. The participants in this study consisted of university professors, managers, and executive officers involved in animal bite and rabies control plans. Results: This study revealed that the animal bite in Golestan Province had an upward trend, as in the country, and dogs were the main cause of bites (90%). The obstacles and challenges of current animal bites control program in eight areas were expressed by the participants. Also, the animal bite management model, which was obtained from the data of different stages of this study, included nine fields and 41 sub-fields. The fields of the animal bite management model included: providing a cultural package, resolving barriers to animal population control plans, wide coverage of dog vaccination, passing and enacting preventive laws, attracting financial support, constructing standard equipment, providing proper medical services, enhancing inter-departmental coordination, and controlling rabies in the wild. This model was confirmed in a Delphi round. Conclusion: Our study indicated that Golestan Province with an average bite higher than twice the country's average is one of the leading provinces in this regard. Thus, revising the animal bite and animal population control plans in this province is necessary. The model designed in this study can be used as a practical guide by policy makers and officials to manage animal bite and related consequences in this province.

Enhancing rabies prevention in tourist destinations such as Indonesia.

Wirawan IMA, Matsee W, Astuti PAS, Sutarsa IN.
08-08-2023
J Travel Med.
https://pubmed.ncbi.nlm.nih.gov/37552057/

No evidence from complementary data sources of a direct glutamatergic projection from the mouse anterior cingulate area to the hippocampal formation.

Andrianova L, Yanakieva S, Margetts-Smith G, Kohli S, Brady ES, Aggleton JP, Craig MT.
07-08-2023
Elife.
https://pubmed.ncbi.nlm.nih.gov/37545394/

The connectivity and interplay between the prefrontal cortex and hippocampus underpin various key cognitive processes, with changes in these interactions being implicated in both neurodevelopmental and neurodegenerative conditions. Understanding the precise cellular connections through which this circuit is organised is, therefore, vital for understanding these same processes. Overturning earlier findings, a recent study described a novel excitatory projection from anterior cingulate area to dorsal hippocampus. We sought to validate this unexpected finding using multiple, complementary methods: anterograde and retrograde anatomical tracing, using anterograde and retrograde adeno-associated viral vectors, monosynaptic rabies tracing, and the Fast Blue classical tracer. Additionally, an extensive data search of the Allen Projection Brain Atlas database was conducted to find the stated projection within any of the deposited anatomical studies as an independent verification of our own results. However, we failed to find any evidence of a direct, monosynaptic glutamatergic projection from mouse anterior cingulate cortex to the hippocampus proper.

Fecal microbiota of the synanthropic golden jackal (Canis aureus).

Lapid R, Motro Y, Craddock H, Khalfin B, King R, Bar-Gal GK, Moran-Gilad J.
05-08-2023
Anim Microbiome.
https://pubmed.ncbi.nlm.nih.gov/37542305/

The golden jackal (Canis aureus), is a medium canid carnivore widespread throughout the Mediterranean region and expanding into Europe. This species thrives near human settlements and is implicated in zoonoses such as rabies. This study explores for the first time, the golden jackal fecal microbiota. We analyzed 111 fecal samples of wild golden jackals using 16S rRNA amplicon sequencing the connection of the microbiome to animal characteristics, burden of pathogens and geographic and climate characteristics. We further compared the fecal microbiota of the golden jackal to the black-backed jackal and domestic dog. We found that the golden jackal fecal microbiota is dominated by the phyla Bacteroidota, Fusobacteriota and Firmicutes. The golden jackal fecal microbiota was associated with different variables, including geographic region, age-class, exposure to rabies oral vaccine, fecal parasites and toxoplasmosis. A remarkable variation in the relative abundance of different taxa was also found associated with different variables, such as age-class. Linear discriminant analysis effect size (LEfSe) analysis found abundance of specific taxons in each region, Megasphaera genus in group 1, Megamonas genus in group 2 and Bacteroides coprocola species in group 3. We also found a different composition between the fecal microbiota of the golden jackal, blacked-backed jackal and the domestic dog. Furthermore, LEfSe analysis found abundance of Fusobacterium and Bacteroides genera in the golden jackal, Clostridia class in blacked-backed jackal and Megamonas genus in domestic dog. The golden jackal fecal microbiota is influenced by multiple factors including host traits and pathogen burden. The characterization of the microbiota of this thriving species may aid in mapping its spread and proximity to human settlements. Moreover, understanding the jackal microbiota could inform the study of potential animal and human health risks and inform control measures.

Uncovering the endemic circulation of rabies in Cambodia.

Layan M, Dacheux L, Lemey P, Brunker K, Ma L, Troupin C, Dussart P, Chevalier V, Wood JLN, Ly S, Duong V, Bourhy H, Dellicour S.
04-08-2023
Mol Ecol.
https://pubmed.ncbi.nlm.nih.gov/37540190/

Schistosomiase

Schistosomiasis (Schistosoma mansoni)-a rare cause of complex liver cysts.

Chmielewski J, Probst P, Muller MK, Antony P, Kovacevic D.
04-08-2023
J Surg Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37560609/

Characteristics of peripheral lymphocyte subsets in patients with different stages of schistosomiasis japonica.

Zhou Z, Li J, Jiang J, Luo Y, Yingzi M.
07-08-2023
Parasite Immunol.
https://pubmed.ncbi.nlm.nih.gov/37551055/

Immune cells are important for the development of schistosomiasis japonica and are also critical for the treatment of schistosomiasis. The immune cells in the peripheral blood help assess the immune state. The peripheral lymphocytes in schistosomiasis mansoni were well studied; however, immune cells in patients with different stages of schistosomiasis japonica are not well analysed. Here, we performed a preliminary study to explore characteristics of peripheral lymphocyte subsets in patients with different stages of schistosomiasis japonica. 135 patients with Schistosoma japonicum infection and 25 healthy volunteers were included in this study, including 84 patients with chronic S. japonicum infection and 51 patients with advanced S. japonicum infection. Flow cytometry analysis was performed to evaluate peripheral lymphocytes including T cells, B cells, and natural killer (NK) cells. Blood routine and liver function test data were analysed. Ultrasound examination was used to access liver fibrosis according to the World Health Organization standard about ultrasound in schistosomiasis. Demographic data analysis suggested there was no difference in age and gender in patients with S. japonicum infection and health control group. Liver function tests showed that patients with advanced schistosomiasis had a higher incidence of liver function abnormality and blood lipid than those with chronic schistosomiasis. Blood routine results reflected that haemoglobin, red blood cells, platelets, as well as lymphocytes in the advanced group were significantly less than that in the chronic group. Furthermore, flow cytometry analysis indicated that the percentage of $CD4^+$ T cells was lower in the advanced group, but the percentage of $CD19^+$ B cells was higher in the advanced group. In addition, the number of $CD3^+$ T cells, $CD3^+$ $CD4^+$ T cells, $CD3^+$ $CD8^+$ T cells, and NK cells was less in the advanced group when compared with those in the chronic group. In addition, there was a correlation between the decrease in $CD4^+$ T cells and more severe fibrosis on ultrasound images. Our results indicated that the immune state in the peripheral is different in different stages of S. japonicum infection. Lymphocyte subset analysis has potential to facilitate differential diagnosis of different stages of schistosomiasis japonica and even to be a prognostic factor.

Optimisation of the DNA dipstick as a rapid extraction method for Schistosoma japonicum in infected mice samples and spiked human clinical samples.

Aula OP, McManus DP, Jones MK, You H, Cai P, Gordon CA.
07-08-2023
Infect Dis Poverty.
https://pubmed.ncbi.nlm.nih.gov/37550723/

Genetic profiles of Schistosoma haematobium parasites from Malian transmission hotspot areas.

Privat A, Jérôme B, Bakary S, Laurent D, Assitan D, Niaré DS, Ahristode A, Hassim G, Manon B, Sarah D, Moudachirou I, Thomas S, Abdoulaye D.
04-08-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37542265/

Divide, conquer and reconstruct: How to solve the 3D structure of recalcitrant Micro-Exon Gene (MEG) protein from Schistosoma mansoni.

Nedvedova S, Guillière F, Miele AE, Cantrelle FX, Dvorak J, Walker O, Hologne M.
03-08-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37535563/

Micro-Exon Genes are a widespread class of genes known for their high variability, widespread in the genome of parasitic trematodes such as Schistosoma mansoni. In this study, we present a strategy that allowed us to solve the structures of three alternatively spliced isoforms from the Schistoma mansoni MEG 2.1 family for the first time. All isoforms are hydrophobic, intrinsically disordered, and recalcitrant to be expressed in high yield in heterologous hosts. We resorted to the chemical synthesis of shorter pieces, before reconstructing the entire sequence. Here, we show that isoform 1 partially folds in a-helix in the presence of trifluoroethanol while isoform 2 features two rigid elbows, that maintain the peptide as disordered, preventing any structuring. Finally, isoform 3 is dominated by the signal peptide, which folds into a-helix. We demonstrated that combining biophysical techniques, like circular dichroism and nuclear magnetic resonance at natural abundance, with in silico molecular dynamics simulation for isoform 1 only, was the key to solve the structure of MEG 2.1. Our results provide a crucial piece to the puzzle of this elusive and highly variable class of proteins.

Influence of a chronic Schistosoma mansoni infection on the outcomes of a SARS-CoV-2 infection in the hamster model.

Rissmann M, Veldhuis Kroeze EJB, Tielens AGM, Rockx B, van Hellemond JJ.
Sept-2023
J Infect.
https://pubmed.ncbi.nlm.nih.gov/37419283/

Trachome

Soil-transmitted helminths: A critical review of the impact of co-infections and implications for control and elimination.

Lebu S, Kibone W, Muoghalu CC, Ochaya S, Salzberg A, Bongomin F, Manga M.
10-08-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37561673/

Prevalence of active trachoma infection and associated factors post-war resettled population in raya kobo districts, North East Ethiopia: A community-based cross-sectional study in 2022.

Kebede F, Jamal M.
06-08-2023
Health Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37554953/

Background: Active trachoma infection poses a serious threat to public health, particularly for those who live in an unprivileged area and has practiced open-field defecation. This study aimed to estimate the prevalence of active trachoma infection and associated factors in the post-war resettled population in Raya Kobo district, North East Ethiopia: a community-based cross-sectional study in 2022. Methods: A community-based cross-sectional study was conducted among 602 participants randomly selected in 14 slum villages in Raya Kobo from February 16th to March 30th, 2023. After the data was collected using a semi-structured questionnaire and entered into Epi-data version 3.2. The study participants were chosen using a two-stage sampling process. Binary logistic regression was used to identify factors for active trachoma infection. Adjusted odds ratios (AORs) with 95% confidence intervals (CIs) were claimed for the strength of association at $p < 0.05$. Results: Overall, 602 (99.9%) study participants were included in the final analysis. At the end of the study period, 126 (20.9) participants developed active trachoma infection. On multivariable analysis, were aged ≥45 years (AOR = 7.9, 95% CI = 2.4-25.3), history of eye infection (AOR = 3.7, 95% CI = 2.4-10.4, $p = 0.001$), were poor wealth index (AOR = 9.2, 95% CI = 2.7-23.7), having separated kitchen (AOR = 4.05, 95% CI = 1.86-8.86), living with animals (AOR = 5.92, 95% CI = 2.31-14.7) and having got administration of mass-drug (AOR = 8.9, 95% CI = 2.36-33.6) were significant risk factors for active trachoma infection. Whereas, face washing practice regularly (AOR = 0.23, 95% CI = 0.127-0.43), and toilet availability (AOR = 0.35, 95% CI = 0.20-0.97) were preventive factors for active trachoma infection. Conclusion: A significant prevalence of active trachoma infection was reported in the area as compared with previous findings and urgent clinical intervention, and the WHO critical SAFE strategies (surgery, antibiotics, facial cleanliness, and environmental improvement) implementation is highly needed in the area. In addition, healthcare providers should focus on information dissemination on proper latrine utilization, and washing the face regularly to prevent active trachoma infection is highly recommended.

Prevalence of trachoma in the non-indigenous Baixo Jaguaribe micro-region, Ceara State, Northeast Brazil.

Maciel AMS, Ramos Junior AN, Ferreira AF, de Almeida NMGS, de Almeida PC, Szwarcwald CL, Favacho JDFR, Franco Filho LC, Gomes VDS, Damasceno LS, Maciel MMS, Delerino AL, Pires Neto RDJ.
08-08-2023
Trans R Soc Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37551629/

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

How do parasitic worms prevent diabetes? An exploration of their influence on macrophage and β-cell crosstalk.

Camaya I, O'Brien B, Donnelly S.
26-07-2023
Front Endocrinol (Lausanne).
https://pubmed.ncbi.nlm.nih.gov/37564976/

Rapid Detection and Identification of Fasciola spp. and Dicrocoelium spp. Isolated from the Ruminant Livestock of Northwest Iran Using High-Resolution Melting Analysis (HRM).

Hajialilo E, Hosseini-Safa A, Spotin A, Saraei M, Ghanbari Johkool M, Piri H, Heydarian P.
Avr-2023
Iran J Public Health.
https://pubmed.ncbi.nlm.nih.gov/37551192/

Recurrent Loculated Pleural Effusions Due to Pleuropulmonary Paragonimus westermani Infection.

Sarwar S, Kipp AJ, Vaughan SD.
07-08-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37549895/

Neutrophils form extracellular traps in response to Opisthorchis viverrini crude antigens, which are elevated in neutrophils from opisthorchiasis patients with hepatobiliary abnormalities.

Watakulsin K, Chuenchom C, Thapphan C, Thai TD, Chareonsudjai S, Faksri K, Suttiprapa S, Tangkawatana S, Sripa B, Edwards SW, Salao K.
15-08-2023
Biol Open.
https://pubmed.ncbi.nlm.nih.gov/37493409/

Opisthorchis viverrini (Ov) infection can cause several disease conditions of the bile duct including hepatobiliary abnormalities (HBAs) and the most severe, cholangiocarcinoma (CCA). Fibrosis occurs when tissues are damaged and normal wound-healing responses are dysregulated. Neutrophils are the first cells to migrate to an infection site to protect the host from intruding extracellular pathogens through a wide range of effector mechanisms such as phagocytosis, production of reactive oxygen species, proteases, or release of neutrophil extracellular traps (NETs). In this work, we used confocal microscopy to assess whether Ov crude antigens can cause release of NETs from neutrophils from Ov-free individuals. We demonstrated for the first time that these antigens could induce release of NETs ex vivo in a dose-dependent manner from neutrophils isolated from Ov-free individuals. Intriguingly, when we measured NETs from neutrophils isolated from Ov-infected patients, we found increased spontaneous production of NETs in patients with HBAs. Interestingly, exposure to Ov crude antigens lowered the level of NETs released by neutrophils from patients with active Ov infection regardless of HBA status. We propose that in the case of acute Ov infection, even when concentration of Ov antigens is relatively low, neutrophils can form NETs. However, when this infection becomes chronic, manifesting as a definite HBA, the levels of NET production are reduced when treated with Ov crude antigens. Excessive production of proinflammatory mediators from these NETs might have effects on the parasites, but may also lead to excessive injury of surrounding tissues resulting in HBAs and may lead eventually to the most severe complications such as CCA.

Distinct antibody response in susceptible and non-susceptible hosts of the carcinogenic liver fluke Opisthorchis viverrini infection.

Watakulsin K, Surapaitoon A, Ulag LH, Kaing S, Suyapoh W, Saichua P, Salao K, Tangkawatana S, Suttiprapa S.
Juil-2023
Parasitology.
https://pubmed.ncbi.nlm.nih.gov/37288733/

Trypanosomes (trypanosomiase et maladie de Chagas)

Deep serological profiling of the Trypanosoma cruzi TSSA antigen reveals different epitopes and modes of recognition by Chagas disease patients.

Romer G, Bracco LA, Ricci AD, Balouz V, Berná L, Villar JC, Ramsey JM, Nolan MS, Torrico F, Kesper N, Altcheh J, Robello C, Buscaglia CA, Agüero F.
09-08-2023
PLoS Negl Trop Dis.

https://pubmed.ncbi.nlm.nih.gov/37556493/

Background: Trypanosoma cruzi, the agent of Chagas disease, displays a highly structured population, with multiple strains that can be grouped into 6-7 evolutionary lineages showing variable eco-epidemiological traits and likely also distinct disease-associated features. Previous works have shown that antibody responses to 'isoforms' of the polymorphic parasite antigen TSSA enable robust and sensitive identification of the infecting strain with near lineage-level resolution. To optimize the serotyping performance of this molecule, we herein used a combination of immunosignaturing approaches based on peptide microarrays and serum samples from Chagas disease patients to establish a deep linear B-cell epitope profiling of TSSA. Methods/principle findings: Our assays revealed variations in the seroprevalence of TSSA isoforms among Chagas disease populations from different settings, hence strongly supporting the differential distribution of parasite lineages in domestic cycles across the Americas. Alanine scanning mutagenesis and the use of peptides of different lengths allowed us to identify key residues involved in antibody pairing and the presence of three discrete B-cell linear epitopes in TSSAII, the isoform with highest seroprevalence in human infections. Comprehensive screening of parasite genomic repositories led to the discovery of 9 novel T. cruzi TSSA variants and one TSSA sequence from the phylogenetically related bat parasite T. cruzi marinkellei. Further residue permutation analyses enabled the identification of diagnostically relevant or non-relevant substitutions among TSSA natural polymorphisms. Interestingly, T. cruzi marinkellei TSSA displayed specific serorecognition by one chronic Chagas disease patient from Colombia, which warrant further investigations on the diagnostic impact of such atypical TSSA. Conclusions/significance: Overall, our findings shed new light into TSSA evolution, epitope landscape and modes of recognition by Chagas disease patients; and have practical implications for the design and/or evaluation of T. cruzi serotyping strategies.

Molecular Characterization of Trypanosoma cruzi Reactivation and Follow-up in a Case Series of People With HIV.

Fernandez ML, Albizu CL, Nicita D, Besuschio S, Giomi C, Biondi ML, Leguizamón MS, Garcia J, Corti M, Schijman A, Burgos JM.
10-07-2023
Open Forum Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37555130/

AAK1-like: A putative pseudokinase with potential roles in cargo uptake in bloodstream form Trypanosoma brucei parasites.

Black JA, Klinger CM, Lemgruber L, Dacks JB, Mottram JC, McCulloch R.
07-08-2023
J Eukaryot Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37548427/

Whole Genome Assembly of a Hybrid Trypanosoma cruzi Strain Assembled with Nanopore Sequencing Alone.

Hakim JMC, Gutierrez Guarnizo SA, Machaca EM, Gilman RH, Mugnier MR.
27-07-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37546813/

Trypanosoma cruzi is the causative agent of Chagas disease, which causes 10,000 deaths per year. Despite the high mortality caused by the pathogen, relatively few parasite genomes have been assembled to date; even some commonly used laboratory strains do not have publicly available genome assemblies. This is at least partially due to *T. cruzi*' s highly complex and highly repetitive genome: while describing the variation in genome content and structure is critical to better understanding *T. cruzi* biology and the mechanisms that underlie Chagas disease, the complexity of the genome defies investigation using traditional short read sequencing methods. Here, we have generated a high-quality whole genome assembly of the hybrid Tulahuen strain, a commercially available Type VI strain, using long read Nanopore sequencing without short read scaffolding. Using automated tools and manual curation for annotation, we report a genome with 25% repeat regions, 17% variable multigene family members, and 27% transposable elements. Notably, we find that regions with transposable elements are significantly enriched for surface proteins, and that on average surface proteins are closer to transposable elements compared to other coding regions. This finding supports a possible mechanism for diversification of surface proteins in which mobile genetic elements such as transposons facilitate recombination within the gene family. This work demonstrates the feasibility of nanopore sequencing to resolve complex regions of *T. cruzi* genomes, and with these resolved regions, provides support for a possible mechanism for genomic diversification.

An epidemiological survey of vector-borne pathogens infecting cattle in Kyrgyzstan.

Zhyldyz A, Aitakin K, Atabek B, Elmurat J, Rysbek N, Jailobek O, Ahedor B, Otgonsuren D, Mumbi NNM, Guswanto A, Sivakumar T, Yokoyama N.
04-08-2023
Parasitol Int.
https://pubmed.ncbi.nlm.nih.gov/37544641/

Cattle production is a major contributor to the national economy of Kyrgyzstan. Most cattle in Kyrgyzstan are managed via extensive systems and graze in communal pastures. As a result, infestations with ectoparasites are widespread, implying that various vector-borne diseases might be common in cattle. However, methods to control such infectious diseases are not available in Kyrgyzstan because the epidemiology of vector-borne pathogens (VBPs) infecting cattle remains unclear. The present study was therefore designed to survey Kyrgyz cattle for VBPs. We prepared blood DNA samples from 319 cattle in Kyrgyzstan and screened them with specific PCR assays for

detecting Babesia bovis, Babesia bigemina, Babesia naoakii, Theileria annulata, Theileria orientalis, Trypanosoma evansi, Trypanosoma theileri, and Anaplasma marginale infections. Our findings indicated that the surveyed cattle were infected with six of the eight pathogens targeted, with the exceptions being B. naoakii and Try. evansi. The most common pathogen was T. orientalis (84.3%), followed by B. bigemina (47.6%), T. annulata (16.6%), A. marginale (11.6%), Try. theileri (7.2%), and B. bovis (2.5%). Additional screening of the B. bovis- and B. bigemina-negative samples with a Babesia genus-specific 18S rRNA PCR identified two positive samples, and sequencing analysis confirmed that each of them was infected with either Babesia major or Babesia occultans. To the best of our knowledge, this is the first report of B. bovis, B. bigemina, B. occultans, Try. theileri, and A. marginale infections in cattle in Kyrgyzstan. Our findings suggest that cattle in Kyrgyzstan are at high risk of infectious diseases caused by VBPs.

Binding profile of quinonoid-dihydrobiopterin to quinonoid-dihydropteridine reductase examined by in silico and in vitro analyses.

Kono H, Hara S, Furuta T, Ichinose H.
04-08-2023
J Biochem.
https://pubmed.ncbi.nlm.nih.gov/37540845/

Complementation Assays for Co-chaperone Function.

Edkins AL, Blatch GL.
2023
Methods Mol Biol.
https://pubmed.ncbi.nlm.nih.gov/37540430/

The development of mutant microorganisms lacking J domain proteins (JDPs; formerly called Hsp40s) has enabled the development of complementation assays for testing the co-chaperone function of JDPs. In these assays, an exogenously expressed novel JDP is tested for its ability to functionally substitute for a non-expressed or nonfunctional endogenous JDP(s) by reversing a stress phenotype. For example, the in vivo functionality of prokaryotic JDPs can be tested on the basis of their ability to reverse the thermosensitivity of a dnaJ cbpA mutant strain of the bacterium Escherichia coli (OD259). Similarly, the in vivo functionality of eukaryotic JDPs can be assessed in a thermosensitive ydj1 mutant strain of the yeast Saccharomyces cerevisiae (JJ160). Here we outline the use of these thermosensitive microorganisms in complementation assays to functionally characterize a JDP from the bacterium, Agrobacterium tumefaciens (AgtDnaJ), and a JDP from the trypanosomal parasite, Trypanosoma cruzi (TcJ2).

Ulcère de Buruli

Behavioral interplay between mosquito and mycolactone produced by Mycobacterium ulcerans and bacterial gene expression induced by mosquito proximity.

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Mycolactone is a cytotoxic lipid metabolite produced by Mycobacterium ulcerans, the environmental pathogen responsible for Buruli ulcer, a neglected tropical disease. Mycobacterium ulcerans is prevalent in West Africa, particularly found in lentic environments, where mosquitoes also occur. Researchers hypothesize mosquitoes could serve as a transmission mechanism resulting in infection by M. ulcerans when mosquitoes pierce skin contaminated with M. ulcerans. The interplay between the pathogen, mycolactone, and mosquito is only just beginning to be explored. A triple-choice assay was conducted to determine the host-seeking preference of Aedes aegypti between M. ulcerans wildtype (MU, mycolactone active) and mutant (MUlac-, mycolactone inactive). Both qualitative and quantitative differences in volatile organic compounds' (VOCs) profiles of MU and MUlac- were determined by GC-MS. Additionally, we evaluated the interplay between Ae. aegypti proximity and M. ulcerans mRNA expression. The results showed that mosquito attraction was significantly greater (126.0%) to an artificial host treated with MU than MUlac-. We found that MU and MUlac produced differential profiles of VOCs associated with a wide range of biological importance from quorum sensing (QS) to human odor components. RT-qPCR assays showed that mycolactone upregulation was 24-fold greater for MU exposed to Ae. aegypti in direct proximity. Transcriptome data indicated significant induction of ten chromosomal genes of MU involved in stress responses and membrane protein, compared to MUlac- when directly having access to or in near mosquito proximity. Our study provides evidence of possible interkingdom interactions between unicellular and multicellular species that MU present on human skin is capable of interreacting with unrelated species (i.e., mosquitoes), altering its gene expression when mosquitoes are in direct contact or proximity, potentially impacting the production of its VOCs, and consequently leading to the stronger attraction of mosquitoes toward human hosts. This study elucidates interkingdom interactions between viable M. ulcerans bacteria and Ae. aegypti mosquitoes, which rarely have been explored in the past. Our finding opens new doors for future research in terms of disease ecology, prevalence, and pathogen dispersal outside of the M. ulcerans system.