Réseau MTN Francophone

Veille scientifique
Maladies tropicales négligées

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25 septembre au 01 octobre 2023

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Cysticercose

Editorial: Host-pathogen interaction in cestodes infection.

Tharmalingam J, Brehm K, Kundu S, Młocicki D, Paredes R.
11-09-2023
Front Cell Infect Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37767200/

A Case of Neurocysticercosis in Rural South Dakota.

Merrill L, Hurd A, Hohn L, Reynen P.
Août-2023
S D Med.
https://pubmed.ncbi.nlm.nih.gov/37734078/

Dengue, chikungunya et maladie à virus Zika

Phylodynamics of dengue virus 2 in Nicaragua leading up to the 2019 epidemic reveals a role for lineage turnover.

Thongsripong P, Edgerton SV, Bos S, Saborío S, Kuan G, Balmaseda A, Harris E, Bennett SN.
28-09-2023
BMC Ecol Evol.
https://pubmed.ncbi.nlm.nih.gov/37770825/

Epidemiological and genomic investigation of chikungunya virus in Rio de Janeiro state, Brazil, between 2015 and 2018.

Moreira FRR, Menezes MT, Salgado-Benvindo C, Whittaker C, Cox V, Chandradeva N, Paula HHS, Martins AF, Chagas RRD, Brasil RDV, Cândido DDS, Herlinger AL, Ribeiro MO, Arruda MB, Alvarez P, Tôrres MCP, Dorigatti I, Brady O, Voloch CM, Tanuri A, Iani F, Souza WM, Cardozo SV, Faria NR, Aguiar RS.
28-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37769008/

Since 2014, Brazil has experienced an unprecedented epidemic caused by chikungunya virus (CHIKV), with several waves of East-Central-South-African (ECSA) lineage transmission reported across the country. In 2018, Rio de Janeiro state, the third most populous state in Brazil, reported 41% of all chikungunya cases in the country. Here we use evolutionary and epidemiological analysis to estimate the timescale of CHIKV-ECSA-American lineage and its epidemiological patterns in Rio de Janeiro. We show that the CHIKV-ECSA outbreak in Rio de Janeiro derived from two distinct clades introduced from the Northeast region in mid-2015 (clade RJ1, n = 63/67 genomes from Rio de Janeiro) and mid-2017 (clade RJ2, n = 4/67). We detected evidence for positive selection in non-structural proteins linked with viral replication in the RJ1 clade (clade-defining: nsP4-A481D) and the RJ2 clade (nsP1-D531G). Finally, we estimate the CHIKV-ECSA's basic reproduction number (R0) to be between 1.2 to 1.6 and show that its instantaneous reproduction number (Rt) displays a strong seasonal pattern with peaks in transmission coinciding with periods of high Aedes aegypti transmission potential. Our results highlight the need for continued genomic and epidemiological surveillance of CHIKV in Brazil, particularly during periods of high ecological suitability, and show that selective pressures underline the emergence and evolution of the large urban CHIKV-ECSA outbreak in Rio de Janeiro.

Philippine immunization coverage and dengvaxia: An infodemiological study.

Jamora RDG, Lim MAR, Espiritu AI.
Jan-Déc 2023
Pediatr Int.
https://pubmed.ncbi.nlm.nih.gov/37767858/

Background: A dengue vaccine, dengvaxia, was licensed for the first time in 2015. It was approved for use in 11 countries where dengue infection is endemic, including the Philippines. In November 2017, controversy arose in the Philippines regarding the dengvaxia vaccine. We hypothesized that the dengvaxia controversy might be correlated with immunization coverage in the Philippines. Methods: We performed an analytical and infodemiological study on web-based interest in dengvaxia, both globally and in 18 dengue endemic countries, from 2015 to 2020 using Google Trends™. Comparisons were made with search trends for the components of the National Immunization Program (NIP) and vaccine coverage by computing the Pearson product-moment correlation coefficient (r) between each variable. Results: Among the 18 countries included, the Philippines had the highest search volume index for dengvaxia, with peaks in searches coinciding with that of worldwide search trends. There was no correlation between the relative search volume for dengvaxia with that of vaccines included in the NIP in the Philippines from 2015 to 2020. There was no significant correlation between web-based interest in dengvaxia and the estimated immunization coverage from 2015 to 2019. Conclusion: There was no significant correlation between web-based interest in dengvaxia, the vaccines in the NIP, and national immunization coverage.

Seroprevalence and incidence of primary dengue infection and its correlation with fetomaternal prognosis in Western Rajasthan.

Prakash P, Gupta E, Nareda P, Gupta E, Agarwal R, Ashopa V, Beelwal A.
Août-2023
J Family Med Prim Care.
https://pubmed.ncbi.nlm.nih.gov/37767431/

A Birth Cohort Follow-Up Study on Congenital Zika Virus Infection in Vietnam.

Toizumi M, Vu CN, Huynh HT, Uematsu M, Tran VT, Vo HM, Nguyen HAT, Ngwe Tun MM, Bui MX, Dang DA, Moriuchi H, Yoshida LM.
15-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766334/

Associations between Dengue Incidence, Ecological Factors, and Anthropogenic Factors in Singapore.

Tewari P, Guo P, Dickens B, Ma P, Bansal S, Lim JT.
13-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766323/

Singapore experiences endemic dengue. Vector control remains the primary means to reduce transmission due to the lack of available therapeutics. Resource limitations mean that vector-control tools need to be optimized, which can be achieved by studying risk factors related to disease transmission. We developed a statistical modelling framework which can account for a high-resolution and high-dimensional set of covariates to delineate spatio-temporal characteristics that are associated with dengue transmission from 2014 to 2020 in Singapore. We applied the proposed framework to two distinct datasets, stratified based on the primary type of housing within each spatial unit. Generalized additive models reveal non-linear exposure responses between a large range of ecological and anthropogenic factors as well as dengue incidence rates. At values below their mean, lesser mean total daily rainfall (Incidence rate ratio (IRR): 3.75, 95% CI: 1.00-14.05, Mean: 4.40 mm), decreased mean windspeed (IRR: 3.65, 95% CI: 1.87-7.10, Mean: 4.53 km/h), and lower building heights (IRR: 2.62, 95% CI: 1.44-4.77, Mean: 6.5 m) displayed positive associations, while higher than average annual NO_2 concentrations (IRR: 0.35, 95% CI: 0.18-0.66, Mean: 13.8 ppb) were estimated to be negatively associated with dengue incidence rates. Our study provides an understanding of associations between ecological and anthropogenic characteristics with dengue transmission. These findings help us understand high-risk areas of dengue transmission, and allows for land-use planning and formulation of vector control policies.

Ecological Niche Modeling of Aedes and Culex Mosquitoes: A Risk Map for Chikungunya and West Nile Viruses in Zambia.

Velu RM, Kwenda G, Bosomprah S, Chisola MN, Simunyandi M, Chisenga CC, Bumbangi FN, Sande NC, Simubali L, Mburu MM, Tembo J, Bates M, Simuunza MC, Chilengi R, Orba Y, Sawa H, Simulundu E.
08-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766306/

Advanced Detection Method for Dengue NS1 Protein Using Ultrasensitive ELISA with Thio-NAD Cycling.

Chen PK, Chang JH, Ke LY, Kao JK, Chen CH, Yang RC, Yoshimura T, Ito E, Tsai JJ.
08-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766300/

Dengue fever, a mosquito-borne disease in tropical and subtropical climates caused by the dengue virus (DENV), has become a major social and economic burden in recent years. However, current primary detection methods are inadequate for early diagnosis of DENV because they are either time-consuming, expensive, or require training. Non-structural protein 1 (NS1) is secreted during DENV infection and is thus considered a suitable biomarker for the development of an early detection method. In the present study, we developed a detection method for the NS1 protein based on a previously reported thio-NAD cycling ELISA (i.e., ultrasensitive ELISA) and successfully achieved a LOD of 1.152 pg/mL. The clinical diagnosis potential of the detection system was also evaluated by using 85 patient specimens, inclusive of 60 DENV-positive and 25 DENV-negative specimens confirmed by the NAAT method. The results revealed 98.3% (59/60) sensitivity and 100% (25/25) specificity, which was in almost perfect agreement with the NAAT data with a kappa coefficient of 0.972. The present study demonstrates the diagnostic potential of using an ultrasensitive ELISA as a low-cost, easy-to-use method for the detection of DENV compared with NAAT and could be of great benefit in low-income countries.

The Innate Immune Response in DENV- and CHIKV-Infected Placentas and the Consequences for the Fetuses: A Minireview.

de Andrade Vieira Alves F, Nunes PCG, Arruda LV, Salomão NG, Rabelo K.
06-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766291/

Dengue virus (DENV) and chikungunya (CHIKV) are arthropod-borne viruses belonging to the *Flaviviridae* and *Togaviridae* families, respectively. Infection by both viruses can lead to a mild indistinct fever or even lead to more severe forms of the diseases, which are characterized by a generalized inflammatory state and multiorgan involvement. Infected mothers are considered a high-risk group due to their immunosuppressed state and the possibility of vertical transmission. Thereby, infection by arboviruses during pregnancy portrays a major public health concern, especially in countries where epidemics of both diseases are regular and public health policies are left aside. Placental involvement during both infections has been already described and the presence of either DENV or CHIKV has been observed in constituent cells of the placenta. In spite of that, there is little knowledge regarding the intrinsic earlier immunological mechanisms that are developed by placental cells in response to infection by both arboviruses. Here, we approach some of the current information available in the literature about the exacerbated presence of cells involved in the innate immune defense of the placenta during DENV and CHIKV infections.

Broad-Spectrum Antiviral Activity of Influenza A Defective Interfering Particles against Respiratory Syncytial, Yellow Fever, and Zika Virus Replication In Vitro.

Pelz L, Piagnani E, Marsall P, Wynserski N, Hein MD, Marichal-Gallardo P, Kupke SY, Reichl U.
04-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766278/

Immune Response to Chikungunya Virus: Sex as a Biological Variable and Implications for Natural Delivery via the Mosquito.

Taylor M, Rayner JO.
03-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766276/

Chikungunya virus (CHIKV) is a mosquito-borne virus with significant public health implications around the world. Climate change, as well as rapid urbanization, threatens to expand the population range of *Aedes* vector mosquitoes globally, increasing CHIKV cases worldwide in return. Epidemiological data suggests a sex-dependent response to CHIKV infection. In this review, we draw attention to the importance of studying sex as a biological variable by introducing epidemiological studies from previous CHIKV outbreaks. While the female sex appears to be a risk factor for chronic CHIKV disease, the male sex has recently been suggested as a risk factor for CHIKV-associated death; however, the underlying mechanisms for this phenotype are unknown. Additionally, we emphasize the importance of including mosquito salivary components when studying the immune response to CHIKV. As with other vector-transmitted pathogens, CHIKV has evolved to use these salivary components to replicate more extensively in mammalian hosts; however, the response to natural transmission of CHIKV has not been fully elucidated.

Comprehensive Characterization of Viral Diversity of Female Mosquitoes in Madagascar.

Bennouna A, Tantely ML, Raharinosy V, Andriamandimby SF, Bigot T, Chrétien D, Jacquemet E, Volant S, Temmam S, Dussart P, Lacoste V, Girod R, Eloit M.
31-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766259/

Longitudinal Study of Viral Diversity Associated with Mosquito Species Circulating in Cambodia.

Mohamed Ali S, Rakotonirina A, Heng K, Jacquemet E, Volant S, Temmam S, Boyer S, Eloit M.
29-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766237/

Metavirome Analysis and Identification of Midge-Borne Viruses from Yunnan Province, China, in 2021.

Li C, Wang W, Zhang X, Xiao P, Li Z, Wang P, Shi N, Zhou H, Lu H, Gao X, Zhang H, Jin N.
26-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766224/

Midges are widely distributed globally and can transmit various human and animal diseases through blood-sucking. As part of this study, 259,300 midges were collected from four districts in Yunnan province, China, to detect the viral richness and diversity using metavirome analysis techniques. As many as 26 virus families were detected, and the partial sequences of bluetongue virus (BTV), dengue virus (DENV), and Getah virus (GETV) were identified by phylogenetic analysis and PCR amplification. Two BTV gene fragments, 866 bps for the VP2 gene of BTV type 16 and 655 bps for the VP5 gene of BTV type 21, were amplified. The nucleotide sequence identities of the two amplified BTV fragments were 94.46% and 98.81%, respectively, with two classical BTV-16 (GenBank: JN671907) and BTV-21 strains (GenBank: MK250961) isolated in Yunnan province. Furthermore, the BTV-16 DH2021 strain was successfully isolated in C6/36 cells, and the peak value of the copy number reached 3.13×10^7 copies/μL after five consecutive BHK-21 cell passages. Moreover, two 2054 bps fragments including the E gene of DENV genotype Asia II were amplified and shared the highest identity with the DENV strain isolated in New Guinea in 1944. A length of 656 bps GETV gene sequence encoded the partial capsid protein, and it shared the highest identity of 99.68% with the GETV isolated from Shandong province, China, in 2017. Overall, this study emphasizes the importance of implementing prevention and control strategies for viral diseases transmitted by midges in China.

Dengue Fever Surveillance in Mato Grosso do Sul: Insights from Genomic Analysis and Implications for Public Health Strategies.

Castilho de Arruda LD, Giovanetti M, Fonseca V, Zardin MCSU, Lichs GGC, Asato S, Esposito AOP, Tokeshi Müller M, Xavier J, Fritsch H, Lima M, de Oliveira C, Santos EV, Maziero LMA, Frias DFR, Ahad das Neves D, Ferreira da Silva L, Rodrigues Barretos EC, Tsuha Oshiro PE, Modafari Goday B, Lemos Dos Santos JK, Kashima S, Albuquerque CFC, Said RFDC, Rosewell A, Demarchi LHF, Croda J, Alcantara LCJ, Cavalheiro Maymone Gonçalves C.
23-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766197/

Since its discovery in early 1916, dengue fever, a common vector-borne illness in Brazil, has resulted in extensive urban outbreaks and poses a serious threat to the public's health. Understanding the dynamics of Dengue Virus (DENV) serotypes circulating in different regions of Brazil is essential for implementing effective disease control and prevention measures. In response to this urgent need, we

conducted an on-site training program in genomic surveillance in collaboration with the Central Laboratory of Health and the Secretary of Health of the Mato Grosso do Sul state. This initiative resulted in the generation of 177 DENV genome sequences collected between May 2021 and May 2022, a period during which over 11,391 dengue fever cases were reported in the state. Through this approach, we were able to identify the co-circulation of two different dengue serotypes (DENV1 and DENV2) as well as the existence of diverse viral lineages within each genotype, suggesting that multiple introduction events of different viral strains occurred in the region. By integrating epidemiological data, our findings unveiled temporal fluctuations in the relative abundance of different serotypes throughout various epidemic seasons, highlighting the complex and changing dynamics of DENV transmission throughout time. These findings demonstrate the value of ongoing surveillance activities in tracking viral transmission patterns, monitoring viral evolution, and informing public health actions.

Evaluating Known Zika Virus NS2B-NS3 Protease Inhibitor Scaffolds via In Silico Screening and Biochemical Assays.

Santos LH, Rocha REO, Dias DL, Ribeiro BMRM, Serafim MSM, Abrahão JS, Ferreira RS.
19-09-2023
Pharmaceuticals (Basel).
https://pubmed.ncbi.nlm.nih.gov/37765127/

Phylogenetic Investigations of Dengue 2019-2021 Outbreak in Guadeloupe and Martinique Caribbean Islands.

Garcia-Van Smévoorde M, Piorkowski G, Emboulé L, Dos Santos G, Loraux C, Guyomard-Rabenirina S, Joannes MO, Fagour L, Najioullah F, Cabié A, de Lamballerie X, Vega-Rúa A, Césaire R, Calvez E.
20-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764990/

Dengue fever has been a public health problem in the Caribbean region since 1981, when it first reappeared in Cuba. In 1989, it was reported in Martinique and Guadeloupe (two French islands 200 km apart); since then, DENV has caused several epidemics locally. In 2019-2021, DENV-1, DENV-2, and DENV-3 were detected. Serotype distribution was differentiated, with DENV-2 and DENV-3 predominating in Guadeloupe and Martinique, respectively. Complete genome sequencing was carried out on 32 specimens, and phylogenic analysis identified the circulation of genotype V for DENV-1, cosmopolitan genotype for DENV-2, and genotype III for DENV-3. However, two distinct circulating groups were identified for DENV-1 and DENV-3, suggesting independent introductions. Overall, despite the context of the COVID-19 pandemic and the associated travel restrictions, these results confirm the active circulation of DENV and specific epidemiological features on each of the two islands. Such differences may be linked to the founder effect of the various introduction events, and to local factors such as the population immunity and the transmission capacity of the vectors. Further genomic and epidemiological characterization of DENV strains remains essential to understand how dengue spreads in each specific geographical context and to prevent future epidemics.

Impact of Treatment with Ustekinumab on Severe Infections in a Patient with Uncontrolled Psoriasis and Late-Onset Combined Primary Immunodeficiency: Case Report.

Prestes-Carneiro LE, de Abreu MAMM, Roncada EVM, Muchon DG, Caliani FM, Vasconcelos DM.
12-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764964/

Characterization of Viral Interference in Aedes albopictus C6/36 Cells Persistently Infected with Dengue Virus 2.

González-Flores AM, Salas-Benito M, Rosales-García VH, Zárate-Segura PB, Del Ángel RM, De Nova-Ocampo MA, Salas-Benito JS.
06-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764943/

Arboviruses are an important group of pathogens that cause diseases of medical and veterinary concern worldwide. The interactions of these viruses with their host cells are complex, and frequently, the coexistence of two different viruses in the same cell results in the inhibition of replication in one of the viruses, which is a phenomenon called viral interference. This phenomenon can be exploited to develop antiviral strategies. Insect cell lines persistently infected with arboviruses are useful models with which to study viral interference. In this work, a model of C6/36-HT cells (from *Aedes albopictus* mosquitoes) persistently infected with Dengue virus, serotype 2, was used. Viral interference was evaluated via plaque and flow cytometry assays. The presence of heterotypic interference against the other serotypes of the same virus and homologous interference against yellow fever virus was determined; however, this cell line did not display heterologous viral interference against Sindbis virus. The mechanisms responsible for viral interference have not been fully elucidated, but small RNAs could be involved. However, the silencing of Ago3, a key protein in the genome-derived P-element-induced wimpy testis pathway, did not alter the viral interference process, suggesting that viral interference occurs independent of this pathway.

Current Status of Vector-Borne Diseases in Croatia: Challenges and Future Prospects.

Vilibic-Cavlek T, Janev-Holcer N, Bogdanic M, Ferenc T, Vujica Ferenc M, Krcmar S, Savic V, Stevanovic V, Ilic M, Barbic L.
01-09-2023
Life (Basel).
https://pubmed.ncbi.nlm.nih.gov/37763260/

Different vector-borne pathogens are present or have (re-)emerged in Croatia. Flaviviruses tick-borne encephalitis (TBEV), West Nile (WNV), and Usutu (USUV) are widely distributed in continental regions, while Toscana virus (TOSV) and sandfly fever viruses are detected at the Croatian littoral. Recently, sporadic clinical cases of Tahyna orthobunyavirus (TAHV) and Bhanja bandavirus infection and seropositive individuals have been reported in continental Croatia. Acute infections and serologic evidence of WNV, TBEV, USUV, and TAHV were also confirmed in sentinel animals and vectors. Autochthonous dengue was reported in 2010 at the Croatian littoral. Lyme borreliosis is the most widely distributed vector-borne bacterial infection. The incidence is very high in northwestern and eastern regions, which correlates with numerous records of *Ixodes ricinus* ticks. Acute human *Anaplasma phagocytophilum* infections are reported sporadically, but there are many records of serologic evidence of anaplasmosis in animals. Mediterranean spotted fever (*Rickettsia conorii*) and murine typhus (*Rickettsia typhi*) are the main rickettsial infections in Croatia. Human leishmaniasis is notified sporadically, while serologic evidence of leishmaniasis was found in 11.4% of the Croatian population. After the official eradication of malaria in 1964, only imported cases were reported in Croatia. Since vector-borne diseases show a growing trend, continuous monitoring of vectors is required to protect the population from these infections.

Production of Recombinant Zika Virus Envelope Protein by Airlift Bioreactor as a New Subunit Vaccine Platform.

da Costa HHM, Bielavsky M, Orts DJB, Araujo S, Adriani PP, Nogueira JS, Astray RM, Pandey RP, Lancellotti M, Cunha-Junior JP, Prudencio CR.
11-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762254/

Loss of MXRA8 Delays Mammary Tumor Development and Impairs Metastasis.

Simpson KE, Staikos CA, Watson KL, Moorehead RA.
06-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762032/

Matrix-remodeling-associated protein 8 or MXRA8 is a transmembrane protein that can bind arthritogenic alpha viruses like the Chikungunya virus and provide viral entry into cells. MXRA8 can also interact with integrin β3 and thus possibly regulate cell-cell interactions and binding to the extracellular matrix. While *MXRA8* has been associated with reduced survival in patients with colorectal and renal clear cell cancers, the role of *MXRA8* in breast cancer remains largely unexplored. Therefore, the aim of this research was to determine the role of *MXRA8* in breast cancer by knocking out *MXRA8* in the human triple-negative breast cancer cell line MDA-MB-231. The loss of *MXRA8* reduced cell proliferation in vitro but had no effect on apoptosis or migration in cultured cells. However, the loss of *MXRA8* significantly delayed tumor development and reduced metastatic dissemination to the lungs in a xenograft model. RNA sequencing identified three genes, *ADMATS1*, *TIE1*, and *BMP2*, whose expression were significantly reduced in *MXRA8*-knockout tumors compared to control tumors. *MXRA8* staining of a human breast cancer tissue array revealed higher levels of *MXRA8* in primary tumors and metastases of aggressive tumor subtypes (TNBC and $HER2^+$) compared to less aggressive, ER^+ breast cancers. Our findings demonstrate for the first time that *MXRA8* regulates the progression of human TNBC possibly through influencing the interaction of tumor cells with their microenvironment.

Bayesian Analysis Used to Identify Clinical and Laboratory Variables Capable of Predicting Progression to Severe Dengue among Infected Pediatric Patients.

Corzo-Gómez J, Guzmán-Aquino S, Vargas-De-León C, Megchún-Hernández M, Briones-Aranda A.
05-09-2023
Children (Basel).
https://pubmed.ncbi.nlm.nih.gov/37761469/

Enhanced broad spectrum in vitro antiviral efficacy of 3-F-4-MeO-Bn, 3-CN, and 4-CN derivatives of lipid remdesivir nucleoside monophosphate prodrugs.

McMillan RE, Lo MK, Zhang XQ, Beadle JR, Valiaeva N, Garretson AF, Clark AE, Freshman J, Murphy J, Montgomery JM, Spiropoulou CF, Schooley RT, Hostetler KY, Carlin AF.
25-09-2023
Antiviral Res.
https://pubmed.ncbi.nlm.nih.gov/37758067/

Broad spectrum oral antivirals are urgently needed for the early treatment of many RNA viruses of clinical concern. We previously described the synthesis of 1-O-octadecyl-2-O-benzyl-glycero-3-phospho-RVn (V2043), an orally bioavailable lipid prodrug of remdesivir nucleoside (RVn, GS-441524) with broad spectrum antiviral activity against viruses with pandemic potential. Here we compared the relative activity of V2043 with new RVn lipid prodrugs containing sn-1 alkyl ether or sn-2 glycerol modifications. We found that 3-F-4-MeO-Bn, 3-CN-Bn, and 4-CN-Bn sn-2 glycerol modifications improved antiviral activity compared to V2043 when tested in vitro against clinically important RNA viruses from 5 virus families. These results support the continued development of V2043 and sn-2 glycerol modified RVn lipid prodrugs for the treatment of a broad range of RNA viruses for which there are limited therapies.

Activity of domain III-specific antibodies in early convalescence: A case study.

Medina-Carrasco D, Pupo D, González-Lodeiro LG, García LE, Martin AM, Huerta V.
15-09-2023
Virology.
https://pubmed.ncbi.nlm.nih.gov/37757730/

The Dengue virus complex (DENV), formed by four serotypes, constitutes the most important arbovirus affecting humans. The structural domain III of their envelope protein (DIII) elicits strongly neutralizing serotype-specific antibodies. Contrasting results have been obtained regarding their role in the serum neutralizing activity of infected patients. We used a DENV immune serum from a secondary infection to examine the impact of characterizing the anti-DIII antibody response after affinity purification with recombinant DIII proteins to eliminate potential interferences from the interactions with human plasma proteins and other anti-DENV antibodies. Total anti-DENV IgG repertoire and anti-DIIIE antibodies were compared in functionality. In early convalescence, reactivity of anti-DIII antibodies is serotype specific and exhibits the strongest reactivity with infecting serotypes. Purification of anti-DIII antibodies emphasizes the reactivity profile as compared to total IgG fraction and serum. Serotype-specificity of the virus neutralization activity correlated with the apparent kD of the binding to recombinant DIIIs.

Disentangling local and global climate drivers in the population dynamics of mosquito-borne infections.

Cazelles B, Cazelles K, Tian H, Chavez M, Pascual M.
29-09-2023
Sci Adv.
https://pubmed.ncbi.nlm.nih.gov/37756402/

Identifying climate drivers is essential to understand and predict epidemics of mosquito-borne infections whose population dynamics typically exhibit seasonality and multiannual cycles. Which climate covariates to consider varies across studies, from local factors such as temperature to remote drivers such as the El Niño-Southern Oscillation. With partial wavelet coherence, we present a systematic investigation of nonstationary associations between mosquito-borne disease incidence and a given climate factor while controlling for another. Analysis of almost 200 time series of dengue and malaria around the globe at different geographical scales shows a systematic effect of global climate drivers on interannual variability and of local ones on seasonality. This clear separation of time scales of action enhances detection of climate drivers and indicates those best suited for building early-warning systems.

Correction: Srisuphanunt et al. Molecular Mechanisms of Antibiotic Resistance and Novel Treatment Strategies for Helicobacter pylori Infections. Trop. Med. Infect. Dis. 2023, 8, 163.

Srisuphanunt M, Wilairatana P, Kooltheat N, Duangchan T, Katzenmeier G, Rose JB.
29-08-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755917/

Study on Morphological Changes and Interference in the Development of Aedes aegypti Caused by Some Essential Oil Constituents.

Serdeiro MT, Dias TD, de Lima NTR, Barbosa-Filho JM, Belato RS, Santos-Mallet JRD, Maleck M.
07-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755901/

Transfluthrin and Metofluthrin as Effective Repellents against Pyrethroid-Susceptible and Pyrethroid-Resistant Aedes aegypti (L.) (Diptera: Culicidae).

Kim DY, Hii J, Chareonviriyaphap T.
14-09-2023
Insects.
https://pubmed.ncbi.nlm.nih.gov/37754735/

Biotechnological Potential of Microorganisms for Mosquito Population Control and Reduction in Vector Competence.

Katak RM, Cintra AM, Burini BC, Marinotti O, Souza-Neto JA, Rocha EM.
22-08-2023
Insects.
https://pubmed.ncbi.nlm.nih.gov/37754686/

Nanomedicine as a potential novel therapeutic approach against the dengue virus.

Zohra T, Saeed F, Ikram A, Khan T, Alam S, Adil M, Gul A, Almawash S, Ayaz M.
27-09-2023
Nanomedicine (Lond).
https://pubmed.ncbi.nlm.nih.gov/37753727/

Acute Hemorrhagic Pancreatitis as a Rare Complication of Dengue Fever.

Khataniar H, Vellankal S.
23-09-2023
ACG Case Rep J.
https://pubmed.ncbi.nlm.nih.gov/37753103/

Dengue fever can lead to a range of symptoms, including severe manifestations such as dengue hemorrhagic fever. We report a rare case of severe dengue with hemorrhagic pancreatitis and pseudocyst formation in a 28-year-old woman. Initially presenting with fever, abdominal pain, and gastrointestinal symptoms, the patient developed worsening pain, vomiting, and an abdominal mass. Imaging revealed a pancreatic mass, and elevated amylase and lipase confirmed pancreatitis. Interventional radiology drained the hemorrhagic fluid from the suspected pseudocyst, leading to patient improvement and eventual discharge. This uncommon complication of acute hemorrhagic pancreatitis in dengue fever has not been previously documented.

DENV-1 genotype V linked to the 2022 dengue epidemic in Southern Brazil.

Gularte JS, Sacchetto L, Demoliner M, Girardi V, da Silva MS, Filippi M, Pereira VMAG, Hansen AW, da Silva LL, Fleck JD, de Almeida PR, Nogueira ML, Spilki FR.
21-09-2023
J Clin Virol.
https://pubmed.ncbi.nlm.nih.gov/37751628/

Knowledge, attitude and practice (KAP) and risk factors on dengue fever among children in Brazil, Fortaleza: A cross-sectional study.

Zhang Y, Zahreddine M, Abreu K, Dantas MA, Charland K, Pierce L, Ridde V, Zinszer K.
25-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37747907/

Computer-aided identification of dengue virus NS2B/NS3 protease inhibitors: an integrated molecular modelling approach for screening of phytochemicals.

Mufti IU, Sufyan M, Shahid I, Alzahrani AR, Shahzad N, M Alanazi IM, Ibrahim IAA, Rehman S.
25-09-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37747078/

Globally, dengue (DENV) fever has appeared as the most widespread vector-borne disease, affecting more than 100 million individuals annually. No approved anti-DENV therapy or preventive vaccine is available yet. DENV NS3 protein is associated with protease activity and is essential for viral replication process within the host cell. NS2B is linked with NS3 protein as a cofactor. Hence, NS3/NS2B is a potential druggable target for developing inhibitors against dengue virus. In the present study, a dataset of *Beta vulgaris* L.-based natural compounds was developed. Virtual ligand screening of 30 phytochemicals was carried out to find novel inhibitors against the NS2B/NS3 protein. Spatial affinity, drug-likeness, and binding behaviors of selected phytochemicals were analyzed. Post-simulation analysis, including Principal Component Analysis (PCA), MMGBSA, and Co-relation analysis, was also performed to provide deep insight for elucidating protein-ligand complexes. This computer-aided screening scrutinized four potent phytochemicals, including betavulgaroside II, vitexin xyloside, epicatechin, and isovitexin2-O-xyloside inhibitors exhibiting optimal binding with viral NS3/NS2B protein. Our study brings novel scaffolds against DENV NS2B/NS3 of serotype-2 to act as lead molecules for further biological optimization. In future, this study will prompt the exploration and development of adjuvant anti-DENV therapy based on natural compounds.Communicated by Ramaswamy H. Sarma.

Repurposing of antiparasitic drugs against the NS2B-NS3 protease of the Zika virus.

Pant S, Jena NR.
25-09-2023
J Biomol Struct Dyn.
https://pubmed.ncbi.nlm.nih.gov/37747074/

Asian Zika virus can acquire generic African-lineage mutations during in utero infection.

Sabi AJ, Singh PP, Trus I, Khanh Le NP, Karniychuk U.
25-09-2023
Emerg Microbes Infect.
https://pubmed.ncbi.nlm.nih.gov/37747060/

Once Forgotten Now Re-emerging: Scrub Typhus Infection in Pediatric Patients From North West India.

Mukhopadhyay S, Gupta R, Shukla S, Bhattacharjee P, Bhatnagar R, Yadav S, Kamal SF, Virk A, Imran S, Liyakath A.
24-08-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37746469/

Background Scrub typhus is an important cause of acute febrile illness in children. It is one of the re-emerging infections in the Asia Pacific region. It is caused by the gram-negative bacteria *Orientia tsutsugamushi* and is spread by the bite of trombiculid mites. The initial symptomatology is nonspecific with fever, headache, vomiting, etc. The presence of eschar is said to be pathognomic. It is a systemic illness, and vasculitis is the basic pathogenic mechanism. Materials and methods A retrospective observational study was conducted in two medical colleges and associated hospitals of western Uttar Pradesh (UP) and Rajasthan, India. Case files of 21 confirmed cases of scrub typhus admitted from April 2021 to October 2022 were reviewed. Scrub typhus was suspected in children with acute undifferentiated fever, and suggestive signs and symptoms were confirmed serologically with IgM enzyme-linked immunoassay (ELISA). Demographic and clinical details were noted. Results During the study period, a total of 335 cases of acute undifferentiated fever were seen, and 6.2% of them were diagnosed as having scrub typhus infection on detailed investigation. The most common symptom was fever in 100% of them, vomiting in 57.1%, abdomen pain in 42.8%, and diarrhea in 19%. Maculopapular, erythematous rash was present in 19% of cases. None of the patients had eschar. Microvascular leakage was the main complication in 28.5%. Unusual complications seen were empyema and valvulitis in 4.7% of patients. Conclusion Scrub typhus is also seen in urban setups and in dry arid areas like Rajasthan and North West UP. So, relevant investigations should be a part of the evaluation in pediatric patients with acute undifferentiated fever. Eschar can be absent, and empyema and valvulitis are some uncommon complications. A high degree of suspicion and early diagnosis are essential as an undiagnosed infection is rapidly fatal.

Falciparum Malaria, Leptospirosis, and Vibrio mimicus Encephalitis in a Resilient Patient: A Remarkable Case of Triple Infection Survival.

Saboo K, Gemnani R, Kumar S, Acharya S, Mishra P.

21-08-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37746455/

Malaria is referred to as a "rainy season disease" and is brought on by *Plasmodium* species. *Leptospira interrogans*, a spirochete, cause zoonosis leptospirosis. It is pretty uncommon for both diseases to coinfect one another. Before assuming a fever is caused by a vector-borne disease, it is essential to first rule out other possible causes, regardless of the patient's risk factors. This case report demonstrates an unusual coinfection and how it manifests. The patient can avoid many deadly consequences with early detection and prompt treatment. There have been reports of coinfections between malaria and various infectious diseases, including dengue, hantavirus, and filariasis. Recently, a few case reports of coinfection with leptospirosis and malaria have also been published. Leptospirosis and malaria are both spreadable diseases that are prevalent throughout the world, particularly in the tropics. We discuss a case of coinfection with meningoencephalitis, leptospirosis, and malaria in a young male who required intensive care unit (ICU) care. It is difficult to distinguish between single infections and coinfections due to the wide variability in presentation, which may further confound the clinical features. Furthermore, when a coinfection is present but has not yet been identified, the clinical course may worsen because there is no effective treatment. This case report demonstrates the uncommon coinfection appearance and related symptoms. The case study also examined the management of patients with leptospirosis, meningoencephalitis, and life-threatening malaria coinfections as well as the clinical course of such coinfections. A meningeal infection or inflammation that resembles both meningitis and encephalitis is referred to as meningoencephalitis.

Multi-epitope Antigen for Specific Serological Detection of Dengue Viruses.

Pereira SS, Andreata-Santos R, de Castro-Amarante MF, Venceslau-Carvalho AA, Sales NS, Silva MO, Alves RPDS, Jungmann P, Ferreira LCS.
16-09-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766342/

Dengue is an infectious disease of global health concern that continues to require surveillance. Serological testing has been used to investigate dengue-infected patients, but specificity is affected by the co-circulation of ZIKA virus (ZIKV), which shares extensive antigen similarities. The goal of this study was the development of a specific dengue virus (DENV) IgG ELISA based on a multi-epitope NS1-based antigen for antibody detection. The multi-epitope protein (T-ΔNS1), derived from a fragment of the NS1-protein of the four DENV serotypes, was expressed in *Escherichia coli* and purified via affinity chromatography. The antigenicity and specificity were evaluated with sera of mice infected with DENV-1-4 or ZIKV or after immunization with the recombinant ΔNS1 proteins. The performance of the T-ΔNS1-based IgG ELISA was also determined with human serum samples. The results demonstrate that the DENV T-ΔNS1 was specifically recognized by the serum IgG of dengue-infected mice or humans but showed no or reduced reactivity with ZIKV-infected subjects. Based on the available set of clinical samples, the ELISA based on the DENV T-ΔNS1 achieved 77.42% sensitivity and 88.57% specificity. The results indicate that the T-ΔNS1 antigen is a promising candidate for the development of specific serological analysis.

Arboviral Risk Associated with Solid Organ and Hematopoietic Stem Cell Grafts: The Prophylactic Answers Proposed by the French High Council of Public Health in a National Context.

Pozzetto B, Grard G, Durand G, Paty MC, Gallian P, Lucas-Samuel S, Diéterlé S, Fromage M, Durand M, Lepelletier D, Chidiac C, Hoen B, Nicolas de Lamballerie X.
22-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766192/

Low CCL2 and CXCL8 Production and High Prevalence of Allergies in Children with Microcephaly Due to Congenital Zika Syndrome.

Bezerra WP, Salmeron ACA, Branco ACCC, Morais IC, de Farias Sales VS, Machado PRL, Souto JT, de Araújo JMG, Guedes PMDM, Sato MN, Nascimento MSL.
29-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766239/

Evaluation of remote radiologist-interpreted point-of-care ultrasound for suspected dengue patients in a primary health care facility in Colombia.

Osorio L, Prieto I, Zuluaga D, Ropero D, Dewan N, Kirsch JD.
28-09-2023
Infect Dis Poverty.
https://pubmed.ncbi.nlm.nih.gov/37759280/

Background: Early identification of plasma leakage may guide treatment decisions in dengue patients. This study evaluated the value of point-of-care ultrasound (POCUS) to detect plasma leakage and predict hospitalization or referral to a higher level of care in suspected dengue patients under routine conditions at a primary care facility in Colombia. Methods: We conducted a cohort study between April 2019 and March 2020 in a primary care hospital in Cali, Colombia. We prospectively included and followed 178 patients who were at least 2 years old with fever of less than 10 days and clinician-suspected dengue. A trained general practitioner performed a standardized POCUS protocol. Images were quality-rated and overread by an expert radiologist, and her results and those of the general practitioner were compared using the Kappa index. Logistic regression was used to identify factors associated with plasma leakage at enrollment and explore its prognostic value regarding hospital admission or referral to a higher level of care. Results: Half (49.6%) POCUS images were of suitable quality to be interpreted. The proportion of plasma leakage reported by the

radiologist was 85.1% (95% CI: 78.6-90.2%) and 47.2% by the study physician (Kappa = 0.25, 95% CI: 0.15-0.35). The most frequent ultrasound findings were ascites (hepatorenal 87.2%, splenorenal 64%, or pelvic 21.8%) and gallbladder wall thickening (10.5%). Plasma leakage was higher in subjects with thrombocytopenia (aOR = 4, 95% CI: 1.3-12.1) and lower in patients 30-59 years old (aOR = 0.1, 95% CI: 0.0-0.4) than in those 18 years old or younger. POCUS evidence of plasma leakage (aOR = 8.2, 95% CI: 2.2-29.9), thrombocytopenia (aOR = 6.3, 95% CI: 2.4-16.0) and pulse pressure (aOR = 1.1, 95% CI: 1.07-1.2) were associated with hospital admission or referral to a higher level of care. Conclusions: Ultrasound is useful to detect plasma leakage in primary care and, challenges remain to guarantee high-quality images and diagnostic accuracy, for which a standardized dengue POCUS protocol and training program is needed.

Age and socio-economic status affect dengue and COVID-19 incidence: spatio-temporal analysis of the 2020 syndemic in Buenos Aires City.

Carbajo AE, Cardo MV, Pesce M, Iummato LE, Bárcena Barbeira P, Santini MS, Utgés ME.
22-09-2023
PeerJ.
https://pubmed.ncbi.nlm.nih.gov/37753173/

Live-Attenuated CHIKV Vaccine with Rearranged Genome Replicates in vitro and Induces Immune Response in Mice.

Tretyakova I, Joh J, Lukashevich IS, Alejandro B, Gearon M, Chung D, Pushko P.
16-09-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37745520/

Chikungunya fever virus (CHIKV) is a mosquito-borne alphavirus that causes wide-spread human infections and epidemics in Asia, Africa and recently, in the Americas. There is no approved vaccine and CHIKV is considered a priority pathogen by CEPI and WHO. Previously, we developed immunization DNA (iDNA) plasmid capable of launching live-attenuated CHIKV vaccine in vivo . Here we report the use of CHIKV iDNA plasmid to prepare a novel, live-attenuated CHIKV vaccine V5040 with rearranged RNA genome for improved safety. In V5040, genomic RNA was rearranged to encode capsid gene downstream from the glycoprotein genes. To secure safety profile, attenuated mutations derived from experimental CHIKV 181/25 vaccine were also engineered into E2 gene of V5040. The DNA copy of rearranged CHIKV genomic RNA with attenuated mutations was cloned into iDNA plasmid pMG5040 downstream from the CMV promoter. After transfection in vitro, pMG5040 launched replication of V5040 virus with rearranged genome and attenuating E2 mutations. Furthermore, V5040 virus was evaluated in experimental murine models for safety and immunogenicity. Vaccination with V5040 virus subcutaneously resulted in elicitation of CHIKV-specific, virus-neutralizing antibodies. The results warrant further evaluation of V5040 virus with rearranged genome as a novel live-attenuated vaccine for CHIKV.

Genome evolution of dengue virus serotype 1 under selection by Wolbachia pipientis in Aedes aegypti mosquitoes.

Thi Hue Kien D, Edenborough K, da Silva Goncalves D, Thuy Vi T, Casagrande E, Thi Le Duyen H, Thi Long V, Thi Dui L, Thi Tuyet Nhu V, Thi Giang N, Thi Xuan Trang H, Lee E, Donovan-Banfield I, Thi Thuy Van H, Minh Nguyet N, Thanh Phong N, Van Vinh Chau N, Wills B, Yacoub S, Flores H, Simmons C.
03-03-2023
Virus Evol.
https://pubmed.ncbi.nlm.nih.gov/37744653/

The introgression of antiviral strains of *Wolbachia* into *Aedes aegypti* mosquito populations is a public health intervention for the control of dengue. Plausibly, dengue virus (DENV) could evolve to bypass the antiviral effects of *Wolbachia* and undermine this approach. Here, we established a serial-passage system to investigate the evolution of DENV in *Ae. aegypti* mosquitoes infected with the *w*Mel strain of *Wolbachia*. Using this system, we report on virus genetic outcomes after twenty passages of serotype 1 of DENV (DENV-1). An amino acid substitution, E203K, in the DENV-1 envelope protein was more frequently detected in the consensus sequence of virus populations passaged in *w*Mel-infected *Ae. aegypti* than wild-type counterparts. Positive selection at residue 203 was reproducible; it occurred in passaged virus populations from independent DENV-1-infected patients and also in a second, independent experimental system. In wild-type mosquitoes and human cells, the 203K variant was rapidly replaced by the progenitor sequence. These findings provide proof of concept that *w*Mel-associated selection of virus populations can occur in experimental conditions. Field-based studies are needed to explore whether *w*Mel imparts selective pressure on DENV evolution in locations where *w*Mel is established.

Daily dataset of precipitation and temperature in the Department of Cauca, Colombia.

Blanco K, Villamizar SR, Avila-Diaz A, Marceló-Díaz C, Santamaría E, Lesmes MC.
03-09-2023
Data Brief.
https://pubmed.ncbi.nlm.nih.gov/37743883/

Validation of the use of dried blood spots in a chikungunya virus IgG serological assay.

Magalhaes T, Portilho MM, Moreira PSS, Marinho ML, Dias WP, Gonçalves NM, Rodrigues OAS, Montes J, Reis L, Jesus DF, Silva TO, Dultra LS, Nery JS, Ribeiro GS.
22-09-2023
J Immunol Methods.
https://pubmed.ncbi.nlm.nih.gov/37742825/

Dried blood spot (DBS) sampling is a simple, fast, and minimally invasive blood collection method that is

particularly useful for diagnostic or epidemiological studies in hard-to-reach populations. Nevertheless, the use of DBS in assays that have been optimized with gold-standard samples (serum or plasma) must be optimized to yield reliable results. Here, we describe the validation of DBS in a commercial assay to measure IgG against chikungunya virus (CHIKV IgG ELISA; Euroimmun, Lübeck, Germany). During a health survey of people experiencing homelessness in Salvador, Brazil, between September 2021 and February 2022, a subset (75/523; 14.3%) of the study participants had paired capillary (for DBS preparation) and venous (for serum separation) blood samples collected. A pilot optimization test was initially performed with 17 paired samples to compare the CHIKV IgG ELISA absorbance values between serum and three different dilutions of DBS. Based on the preliminary results, the best DBS dilution was selected for a final evaluation comparing paired serum and DBS samples from 58 participants. The sensitivity and specificity of the CHIKV ELISA of DBS compared to sera were 100% (95% C.I.: 85.8-100%) and 100% (95% C.I.: 93-100%), respectively. In the linear regression analysis, a coefficient of determination (R^2) value of 0.98 indicated the excellent performance of DBS in predicting the serum levels of IgG CHIKV antibodies. Our findings suggest that DBS at an optimized dilution is reliable for investigating the prevalence of CHIKV IgG antibodies during population surveys in the commercial assay tested here.

Refocusing on Zika virus in Brazil.

Alves L.
23-09-2023
Lancet.
https://pubmed.ncbi.nlm.nih.gov/37742694/

Seroprevalence of dengue virus infection in Pune City in India, 2019: A decadal change.

Alagarasu K, Tomar S, Patil J, Bachal R, More R, Bote M, Kakade M, Venkatesh V, Parashar D, Tandale BV.
28-08-2023
J Infect Public Health.
https://pubmed.ncbi.nlm.nih.gov/37742447/

Dengue vaccine acceptance and willingness to pay: a systematic review and meta-analysis.

Orellano P, Reynoso J, Salomón OD, Vezzani D.
21-09-2023
Public Health.
https://pubmed.ncbi.nlm.nih.gov/37741155/

Objective: Dengue is the most important human vector-borne disease in terms of disease burden. A first dengue vaccine has recently been licenced, and others are in advanced stages of development. However, to date, none of these vaccines has achieved balanced efficacy and safety for all dengue serotypes. The aim of this systematic review and meta-analysis was to assess the global acceptance and willingness to pay for unspecified dengue vaccines. Methods: This systematic review and meta-analysis included cross-sectional and cohort studies that reported values for vaccine acceptance (percentage) and willingness to pay for currently available or hypothetical vaccines. These values were pooled using random-effects models for the acceptance, while weighted linear regression was chosen for willingness to pay. Heterogeneity between studies was assessed using prediction intervals (PIs), and a domain-based tool was used to assess the risk of bias. Subgroup and sensitivity analyses were performed where appropriate. This study was registered with PROSPERO (CRD42021255784). Results: We included 19 studies from the Americas and Asia in the quantitative meta-analysis. The risk of bias was mainly related to the selection of participants and to the assumptions about the safety and efficacy of the vaccines. The percentage of vaccine acceptance was 88.3% (95% CI: 81.0%-93.0%), with some heterogeneity between studies (80% PI: 52.9%-98.1%). Willingness to pay was US$ 46.7 (95% CI: 25.9-67.5) per vaccine recipient. There were differences between continents, with higher acceptance in the Americas. Conclusions: We were able to obtain global estimates of vaccine acceptance and willingness to pay and identify the associated factors that influence these values. This knowledge is relevant for the planning of future vaccination strategies.

Insecticide susceptibility status on Aedes aegypti (Linn) and Aedes albopictus (Skuse) of Chittorgarh district, Rajasthan, India.

Jangir PK, Prasad A.
20-09-2023
Exp Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37739025/

Vector-borne diseases are a major burden to human health. It accounts for more than 17% of the total infectious diseases and causes more than 0.7 million deaths annually. Mosquitoes are potential vectors for many vector-borne diseases that cause illness to public health, globally. Vector species of the genus Aedes i.e., Aedes aegypti and Aedes albopictus are the vector for many arboviruses such as dengue, chikungunya, yellow fever, and Zika in India. Dengue is one of the most prevalent viral infections causing a high number of cases throughout the world and resistance to insecticides can be a reason for the failure of vector control strategies. This study was carried out to check the degree of resistance among these vectors in the Chittorgarh district of Rajasthan, India through standard World Health Organization protocol. The resistance was monitored to pyrethroids i.e., deltamethrin (0.05%), permethrin (0.75%), alphacypermethrin (0.05%); organochlorine i.e., DDT (4%), and an organophosphate larvicide i.e., temephos (0.02 mg/L) in both vector species. Complete resistance to DDT was observed among all tested populations of both species. All tested populations of Aedes albopictus were found susceptible to pyrethroids. Aedes aegypti was found resistant in the Mangalwad population, unconfirmed resistant in Bhopalsagar and Rashmi populations while the remaining are susceptible to permethrin. The Mangalwad population was also found unconfirmed resistant to deltamethrin and

alphacypermethrin. Larvae of both species were found susceptible to temephos. Decreasing the use of DDT will help to reduce the impact on human health and environmental contamination. However, temephos as a larvicide, deltamethrin, and alphacypermethrin as an adulticide can be used in critical disease outbreaks at a minimum concentration as mosquitoes are found susceptible in the study area.

Myocarditis manifestations in dengue cases: A systematic review and meta-analysis.

Sandeep M, Padhi BK, Yella SST, Sruthi KG, Venkatesan RG, Krishna Sasanka KBS, Satapathy P, Mohanty A, Al-Tawfiq JA, Iqhrammullah M, Rabaan AA, Kabi A, Sah S, Rustagi S, Al-Qaim ZH, Barboza JJ, Waheed Y, Harapan H, Sah R.
14-08-2023
J Infect Public Health.
https://pubmed.ncbi.nlm.nih.gov/37738692/

Mitochondrial DNA variation in Aedes aegypti (Diptera: Culicidae) mosquitoes from Jeddah, Saudi Arabia.

Thia JA, Endersby-Harshman N, Collier S, Nassar MS, Tawfik EA, Alfageeh MB, Elfekih S, Hoffmann AA.
20-09-2023
J Med Entomol.
https://pubmed.ncbi.nlm.nih.gov/37738428/

Economic Evaluation of Novel Models of Care for Patients With Acute Medical Problems.

Goh OQM, Xin X, Lim WT, Tan MWJ, Kan JYL, Osman HB, Kee W, Teo TY, Tan WB, Kang ML, Graves N.
05-09-2023
JAMA Netw Open.
https://pubmed.ncbi.nlm.nih.gov/37738050/

Wulfenioidins D-N, Structurally Diverse Diterpenoids with Anti-Zika Virus Activity Isolated from Orthosiphon wulfenioides.

Tu WC, Huang YX, Li B, Jiang YJ, Yang QY, Zeb MA, Yang PY, Wang HJ, Li XL, Xiao WL, Zheng CB, Liu MF.
22-09-2023
J Nat Prod.
https://pubmed.ncbi.nlm.nih.gov/37737089/

Eleven diterpenoids, wulfenioidins D-N (**1**-**11**), classified into five distinct carbon skeletons with one unreported framework, and four modified abietane diterpenoids were isolated from the whole plant of *Orthosiphon wulfenioides*. The structures and absolute configurations were characterized by spectroscopic methods, single-crystal X-ray diffraction, and electronic circular dichroism analyses. Compounds **3** and **5** exhibited activity against Zika virus (ZIKV) with EC_{50} values of 8.07 and 8.50 μM, respectively, and showed no significant cytotoxicity toward Vero cells at 100 μM. Western blot and immunofluorescence experiments showed that compounds **3** and **5** interfered with the replication of the ZIKV by inhibiting the expression of the ZIKV envelope (E) protein.

Reemergence of Cosmopolitan Genotype Dengue Virus Serotype 2, Southern Vietnam.

Tran VT, Inward RPD, Gutierrez B, Nguyen NM, Nguyen PT, Rajendiran I, Cao TT, Duong KTH, Kraemer MUG, Yacoub S.
Oct-2023
Emerg Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37735803/

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

Ball EE, Bennett JL, Keesler RI, Van Rompay KKA, Coffey LL, Bliss-Moreau E.
01-11-2023
Neuroreport.
https://pubmed.ncbi.nlm.nih.gov/37695589/

Zika virus' neural tropism causes significant neural pathology, particularly in developing fetuses. One of the consistent findings from humans and animal models is that prenatal exposure to Zika virus (ZIKV) causes pathology in the eyes and visual pathways of the brain, although the extent to which this pathology persists over development is not clear. In the present report, we build upon our previous work which demonstrated that full-term rhesus monkey (Macaca mulatta) fetuses who were exposed to ZIKV early in gestation had significant pathological abnormalities to the organization of the lateral geniculate nucleus (LGN), a major hub of the visual network. The objective of the present work was to replicate those LGN findings and determine whether such pathology persisted across childhood development. We carried out histological analyses of the LGNs of two juvenile rhesus monkeys who were prenatally exposed to ZIKV and two age-matched controls. Pregnant rhesus monkeys were infected with ZIKV via the intravenous and intra-amniotic routes and tracked across development. Following sacrifice and perfusion, brains were subjected to quantitative neuroanatomical analyses with a focus on the size and structure of the LGN and its composite layers. Early fetal ZIKV exposure resulted in developmental abnormalities within the brains' visual pathway: specifically disorganization, blending of layers, laminar discontinuities, and regions of low cell density within the LGN. These abnormalities were not observed in the control animals. Our findings demonstrate that the ZIKV's damage to the LGN that occurs during fetal development persists into childhood.

Hepatic damage caused by flaviviruses: A systematic review.

Pinheiro BSS, Rodrigues JG, Dias FCR, de Oliveira Gomes A, de Lucca Moreira Gomes M.
15-10-2023
Life Sci.
https://pubmed.ncbi.nlm.nih.gov/37683724/

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

Micro- and nanosystems for the detection of hemorrhagic fever viruses.

Bao M, Waitkus J, Liu L, Chang Y, Xu Z, Qin P, Chen J, Du K.
26-09-2023
Lab Chip.
https://pubmed.ncbi.nlm.nih.gov/37675935/

Hemorrhagic fever viruses (HFVs) are virulent pathogens that can cause severe and often fatal illnesses in humans. Timely and accurate detection of HFVs is critical for effective disease management and prevention. In recent years, micro- and nano-technologies have emerged as promising approaches for the detection of HFVs. This paper provides an overview of the current state-of-the-art systems for micro- and nano-scale approaches to detect HFVs. It covers various aspects of these technologies, including the principles behind their sensing assays, as well as the different types of diagnostic strategies that have been developed. This paper also explores future possibilities of employing micro- and nano-systems for the development of HFV diagnostic tools that meet the practical demands of clinical settings.

Multiplexed Biosensing of Proteins and Virions with Disposable Plasmonic Assays.

Wallace S, Kartau M, Kakkar T, Davis C, Szemiel A, Samardzhieva I, Vijayakrishnan S, Cole S, De Lorenzo G, Maillart E, Gautier K, Lapthorn AJ, Patel AH, Gadegaard N, Kadodwala M, Hutchinson E, Karimullah AS.
22-09-2023
ACS Sens.
https://pubmed.ncbi.nlm.nih.gov/37610841/

Linear epitope identification of monoclonal antibodies against the duck Tembusu virus NS1.

Tan H, Zhang S, Tan W, Hu T, He Y, Wu Z, Wang M, Jia R, Zhu D, Liu M, Zhao X, Yang Q, Wu Y, Zhang S, Huang J, Ou X, Gao Q, Sun D, Cheng A, Chen S.
Oct-2023
Poult Sci.
https://pubmed.ncbi.nlm.nih.gov/37499611/

Downregulation of Microcephaly-Causing Genes as a Mechanism for ZIKV Teratogenesis: A Meta-analysis of RNA-Seq Studies.

Gomes JA, Sgarioni E, Kowalski TW, Giudicelli GC, Recamonde-Mendoza M, Fraga LR, Schüler-Faccini L, Vianna FSL.
Août-2023
J Mol Neurosci.
https://pubmed.ncbi.nlm.nih.gov/37428363/

Zika virus (ZIKV) is a neurotropic teratogen that causes congenital Zika syndrome (CZS), characterized by brain and eye anomalies. Impaired gene expression in neural cells after ZIKV infection has been demonstrated; however, there is a gap in the literature of studies comparing whether the differentially expressed genes in such cells are similar and how it can cause CZS. Therefore, the aim of this study was to compare the differential gene expression (DGE) after ZIKV infection in neural cells through a meta-analysis approach. Through the GEO database, studies that evaluated DGE in cells exposed to the Asian lineage of ZIKV versus cells, of the same type, not exposed were searched. From the 119 studies found, five meet our inclusion criteria. Raw data of them were retrieved, pre-processed, and evaluated. The meta-analysis was carried out by comparing seven datasets, from these five studies. We found 125 upregulated genes in neural cells, mainly interferon-stimulated genes, such as IFI6, ISG15, and OAS2, involved in the antiviral response. Furthermore, 167 downregulated, involved with cellular division. Among these downregulated genes, classic microcephaly-causing genes stood out, such as CENPJ, ASPM, CENPE, and CEP152, demonstrating a possible mechanism by which ZIKV impairs brain development and causes CZS.

An in vitro workflow to create and modify infectious clones using replication cycle reaction.

Marano JM, Cereghino C, Finkielstein CV, Weger-Lucarelli J.
Août-2023
Virology.
https://pubmed.ncbi.nlm.nih.gov/37331111/

Dracunculose

Analysis of the response mechanisms of Pinellia ternata to terahertz wave stresses using transcriptome and metabolic data.

Wang D, Sarsaiya S, Qian X, Jin L, Shu F, Zhang C, Chen J.
12-09-2023
Front Plant Sci.
https://pubmed.ncbi.nlm.nih.gov/37771489/

Pinellia ternata (Thunb.) Breit. (Araceae), a significant medicinal plant, has been used to treat various diseases for centuries. Terahertz radiation (THZ) is located between microwaves and infrared rays on the electromagnetic spectrum. THZ possesses low single-photon energy and a spectral fingerprint, but its effects on plant growth have not yet been investigated. The study's primary objective was to examine the transcriptome and metabolome databases of the SY line to provide a new perspective for identifying genes associated with resistance and growth promotion and comprehending the underlying molecular mechanism. Variations in the biological characteristics of *P. ternata* grown under control and experimental conditions were analyzed to determine the effect of THZ. Compared with the control group, phenotypic variables such as leaf length, petiole length, number of leaves, leaf petiole diameter, and proliferation coefficient exhibited significant differences. *P. ternata* response to THZ was analyzed regarding the effects of various coercions on root exudation. The experimental group contained considerably more sugar alcohol than the control group. The transcriptome analysis revealed 1,695 differentially expressed genes (DEGs), including 509 upregulated and 1,186 downregulated genes. In the KEGG-enriched plant hormone signaling pathway, there were 19 differentially expressed genes, 13 of which were downregulated and six of which were upregulated. In the metabolomic analysis, approximately 416 metabolites were uncovered. There were 112 DEMs that were downregulated, whereas 148 were upregulated. The *P. ternata* leaves displayed significant differences in phytohormone metabolites, specifically in brassinolide (BR) and abscisic acid (ABA). The rise in BR triggers alterations in internal plant hormones, resulting in faster growth and development of *P. ternata*. Our findings demonstrated a link between THZ and several metabolic pathway processes, which will enhance our understanding of *P. ternata* mechanisms.

Evaluation of Anticancer Activity of 76 Plant Species Collected in Andalusia (Spain) against Lung Cancer Cells.

Jiménez-González V, Benítez G, Pastor JE, López-Lázaro M, Calderón-Montaño JM.
15-09-2023
Plants (Basel).
https://pubmed.ncbi.nlm.nih.gov/37765439/

Every year, cancer kills millions of people around the world. Finding more selective anticancer agents is essential to improve the low survival rates of patients with metastatic cancers. Since the research of natural products is a valuable approach to the discovery of new compounds and the Iberian flora offers a rich source of unstudied plants, we have carried out a random screening of 76 plant species from 43 families collected in Andalusia (South of Spain). Using non-malignant cells (HaCaT) and lung cancer cells (A549), we found that the extract from *Arum italicum* Mill. subsp. *italicum* (Araceae), *Mandragora autumnalis* Bertol. (Solanaceae), *Rhamnus alaternus* L. (Rhamnaceae), and *Lomelosia simplex* (Desf.) Raf. subsp. *dentata* (Jord. & Fourr.) Greuter & Burdet (Dipsacaceae) showed selective cytotoxicity against lung cancer cells. Extracts of plant species belonging to the Iridaceae family showed high selective activity against cancer cells, highlighting that the *Xiphion xiphium* (L.) M.B. Crespo, Mart.-Azorín & Mavrodiev flower extract was more selective against lung cancer cells than the standard anticancer drugs, cisplatin and 5-fluorouracil. This extract also showed modest selective cytotoxicity against bladder carcinoma cells (T24). The number of cells in the G1 phase increased after treatment with the extract from *Xiphion xiphium*. Our research indicates that various plants are potential sources for the isolation and development of new anticancer drugs.

Five Different Artemisia L. Species Ethanol Extracts' Phytochemical Composition and Their Antimicrobial and Nematocide Activity.

Nikitin E, Fitsev I, Egorova A, Logvinenko L, Terenzhev D, Bekmuratova F, Rakhmaeva A, Shumatbaev G, Gatiyatullina A, Shevchuk O, Kalinnikova T.
21-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762675/

mRNA-Seq and miRNA-Seq Analyses Provide Insights into the Mechanism of Pinellia ternata Bulbil Initiation Induced by Phytohormones.

Xu W, Fan H, Pei X, Hua X, Xu T, He Q.
29-08-2023
Genes (Basel).
https://pubmed.ncbi.nlm.nih.gov/37761867/

Pinellia ternata (Thunb.) Breit (abbreviated as *P. ternata*) is a plant with an important medicinal value whose yield is restricted by many factors, such as low reproductive efficiency and continuous cropping obstacles. As an essential breeding material for *P. ternata* growth and production, the bulbils have significant advantages such as a high survival rate and short breeding cycles. However, the location effect, influencing factors, and molecular mechanism of bulbil occurrence and formation have not been fully explored. In this study, exogenously applied phytohormones were used to induce in vitro petiole of *P. ternata* to produce bulbil structure. Transcriptome sequencing of mRNA and miRNA were performed in the induced petiole (TCp) and the induced bulbil (TCb). Gene Ontology (GO) term enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis were performed for the identification of key genes and pathways involved in bulbil development. A total of 58,019

differentially expressed genes (DEGs) were identified. The GO and KEGG analysis indicated that DEGs were mainly enriched in plant hormone signal transduction and the starch and sucrose metabolism pathway. The expression profiles of miR167a, miR171a, and miR156a during bulbil induction were verified by qRT-PCR, indicating that these three miRNAs and their target genes may be involved in the process of bulbil induction and play an important role. However, further molecular biological experiments are required to confirm the functions of the identified bulbil development-related miRNAs and targets.

Susceptibility of centipede tongavine (Epipremnum pinnatum) commercially grown in nurseries in Florida to aroid leaf rust (Pseudocerradoa paullula).

Urbina H, Jones C, Moore M, Gazis R.
27-09-2023
Plant Dis.
https://pubmed.ncbi.nlm.nih.gov/37755418/

Complete assembly of the chloroplast genome of Amorphophallus coaetaneus S. Y. Liu & S. J. Wei 1986 (Araceae) from southwestern China.

Gao Y, Dong K, Xiao P, Wu W, Yin S.
25-07-2023
Mitochondrial DNA B Resour.
https://pubmed.ncbi.nlm.nih.gov/37753189/

Plant neopolyploidy and genetic background differentiate the microbiome of duckweed across a variety of natural freshwater sources.

Anneberg TJ, Turcotte MM, Ashman TL.
26-09-2023
Mol Ecol.
https://pubmed.ncbi.nlm.nih.gov/37750335/

Whole-genome duplication has long been appreciated for its role in driving phenotypic novelty in plants, often altering the way organisms interface with the abiotic environment. Only recently, however, have we begun to investigate how polyploidy influences interactions of plants with other species, despite the biotic niche being predicted as one of the main determinants of polyploid establishment. Nevertheless, we lack information about how polyploidy affects the diversity and composition of the microbial taxa that colonize plants, and whether this is genotype-dependent and repeatable across natural environments. This information is a first step towards understanding whether the microbiome contributes to polyploid establishment. We, thus, tested the immediate effect of polyploidy on the diversity and composition of the bacterial microbiome of the aquatic plant Spirodela polyrhiza using four pairs of diploids and synthetic autotetraploids. Under controlled conditions, axenic plants were inoculated with pond waters collected from 10 field sites across a broad environmental gradient. Autotetraploids hosted 4%-11% greater bacterial taxonomic and phylogenetic diversity than their diploid progenitors. Polyploidy, along with its interactions with the inoculum source and genetic lineage, collectively explained 7% of the total variation in microbiome composition. Furthermore, polyploidy broadened the core microbiome, with autotetraploids having 15 unique bacterial taxa in addition to the 55 they shared with diploids. Our results show that whole-genome duplication directly leads to novelty in the plant microbiome and importantly that the effect is dependent on the genetic ancestry of the polyploid and generalizable over many environmental contexts.

Proposal of Allomuricauda gen. nov. and Allofranklinella gen. nov. as replacement names for the illegitimate prokaryotic generic names Muricauda and Franklinella, respectively.

Deshmukh UB, Oren A.
Sept-2023
Int J Syst Evol Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37747448/

The prokaryotic generic names *Muricauda* Bruns *et al*. 2001 and *Franklinella* Bernard *et al*. 2022 are illegitimate because they are later homonyms of the genus names *Muricauda* Small 1903 (synonym of *Arisaema*; *Tracheophyta - Liliopsida - Araceae*) and *Franklinella* Stewart and Hendrix 1945 (a Devonian ostracod genus) and *Franklinella* Lenz 1973 (a Devonian brachiopod genus), respectively (Principle 2 and Rule 51b(4) of the International Code of Nomenclature of Prokaryotes). We therefore propose the replacement generic names *Allomuricauda* and *Allofranklinella*, with type species *Allomuricauda ruestringensis* and *Allofrankinella schreckenbergeri*, respectively.

Taguchi-TOPSIS based optimization of comfort in compression stockings for vascular disorders.

Nadeem M, Jamshaid H, Mishra R, Ahmed N, Chandan V, Jirku P, Kolar V, Muller M.
23-09-2023
Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37741942/

Compression stockings/socks are one of the most essential materials to treat vascular disorders in veins. However, the comfort of wearing such stockings over prolonged period of time is a major problem. There is limited research in the area of comfort optimization while retaining the compressional performance. The current work is carried out with an aim to determine the optimum level of the input factors e.g., knitting structure, plaiting yarn linear density and main yarn linear density for achieving desired stretch recovery percentage and thermo-physiological comfort properties of compression socks used in treatment of vascular disorders. Their optimum combination was determined by using Taguchi based techniques for order of preference by similarity to ideal solution i.e., TOPIS. In this study, thickness, areal density, air permeability, thermal resistance, over all moisture management capacity (OMMC), stretch and recovery % were optimized simultaneously by using Taguchi-TOPSIS method. The results showed that linear density of plaiting

and main yarn has significant influence on all the comfort related properties for compression stockings/socks. The optimum sample had linear density 20 denier for Lycra covered by 70 denier of nylon 66 in the plaiting yarn. It also suggested 120 denier nylon 66 in the main yarn knitted into a plain single jersey structure. The percentage contribution of the factors i.e., structure, plaiting yarn linear density and main yarn linear density was obtained by using ANOVA which are 7%, 31% and 42% respectively. It is worth mentioning that in case of compression stockings, the main yarn linear density has more significant effect on comfort properties as compared to other independent parameters. The results were verified by experiment, and the accuracy was relatively high (maximum error 8.533%). This study helped to select suitable knit structure with the change of linear densities of plaiting yarn and main yarn for comfortable compression stocking/sock and will fulfill the potential requirement for treatment of venous/vascular disorders. The novel methodology involving TOPSIS method helped in analyzing the cumulative contribution of the input parameters to achieve optimum compression as well as comfort performance. This modern approach is based on contemporary scientific principles and statistical approximations. This study may provide benchmark solutions to complex problems involving multiple interdependent criteria.

Translocation of TiO_2 nanoparticles enhances phosphorus uptake by wetland plants: Evidence from Pistia stratiotes and Alisma plantago-aquatica.

Hou L, Liang Q, Yang G, Gao L, Liu X.
01-11-2023
J Environ Manage.
https://pubmed.ncbi.nlm.nih.gov/37591090/

Echinococcose

Biliary fistula and late recurrence of liver hydatid cyst: Role of cysto-biliary communication: A prospective multicenter study.

Habeeb TAAM, Podda M, Tadic B, Shelat VG, Tokat Y, Abo Alsaad MI, Kalmoush AE, Nassar MS, Mustafa FM, Morsi Badawy MH, Sobhy Shaaban M, Mohamed TZ, El Sayed Henish MI, Elbelkasi H, Abdou Yassin M, Mostafa A, Ibrahim A, A-Abdelhady W, Elshahidy TM, Mansour MI, Moursi AM, Abdallah Zaitoun M, Abd-Allah ES, Abdelmonem Elsayed A, S Elsayed R, M Yehia A, Abdelghani A, Negm M, Abo-Alella HA, Elaidy MM.
20-09-2023
World J Methodol.
https://pubmed.ncbi.nlm.nih.gov/37771864/

Background: Hydatid cyst disease (HCD) is common in certain locations. Surgery is associated with postoperative biliary fistula (POBF) and recurrence. The primary aim of this study was to identify whether occult cysto-biliary communication (CBC) can predict recurrent HCD. The secondary aim was to assess the role of cystic fluid bilirubin and alkaline phosphatase (ALP) levels in predicting POBF and recurrent HCD. Aim: To identify whether occult CBC can predict recurrent HCD. The secondary aim was to assess the role of cystic fluid bilirubin and ALP levels in predicting POBF and recurrent HCD. Methods: From September 2010 to September 2016, a prospective multicenter study was undertaken involving 244 patients with solitary primary superficial stage cystic echinococcosis 2 and cystic echinococcosis 3b HCD who underwent laparoscopic partial cystectomy with omentoplasty. Univariable logistic regression analysis assessed independent factors determining biliary complications and recurrence. Results: There was a highly statistically significant association ($P \leq 0.001$) between cystic fluid biochemical indices and the development of biliary complications (of 16 patients with POBF, 15 patients had high cyst fluid bilirubin and ALP levels), where patients with high bilirubin-ALP levels were 3405 times more likely to have biliary complications. There was a highly statistically significant association ($P \leq 0.001$) between biliary complications, biochemical indices, and the occurrence of recurrent HCD (of 30 patients with recurrent HCD, 15 patients had high cyst fluid bilirubin and ALP; all 16 patients who had POBF later developed recurrent HCD), where patients who developed biliary complications and high bilirubin-ALP were 244.6 and 214 times more likely to have recurrent hydatid cysts, respectively. Conclusion: Occult CBC can predict recurrent HCD. Elevated cyst fluid bilirubin and ALP levels predicted POBF and recurrent HCD.

Development of an oral nanovaccine for dogs against Echinococcus granulosus.

Leroux M, Benavides U, Hellel-Bourtal I, Silvarrey C, Milhau N, Marchal T, Bourgeois S, Lawton P, Briançon S, Petavy AF, Lahmar S, Esteves A, Almouazen E, Azzouz-Maache S.
26-09-2023
Eur J Pharm Biopharm.
https://pubmed.ncbi.nlm.nih.gov/37769880/

MUSKRATS (ONDATRA ZIBETHICUS) ARE COMPETENT INTERMEDIATE HOSTS OF ECHINOCOCCUS MULTILOCULARIS IN NORTH AMERICA.

Trudeau MJ, Goldsmith D, Letain C, Stamler S, Rothenburger JL.
28-09-2023
J Wildl Dis.
https://pubmed.ncbi.nlm.nih.gov/37768814/

The tapeworm Echinococcus multilocularis is an emerging pathogen of significance to human and animal health in Canada, yet little is known about key rodent intermediate hosts in local urban ecosystems. In Europe, invasive muskrats (Ondatra zibethicus) are an important indicator intermediate host species; however, the role of this semiaquatic rodent in the ecology of E. multilocularis is undetermined in the North American context. We examined 93 muskrats that were livetrapped in the spring of 2017 within Calgary, Alberta, Canada, for the presence of E. multilocularis infection. The objectives of this study

were to 1) diagnose alveolar echinococcosis using macroscopic assessment, histopathology, and molecular analyses; 2) quantify infection severity; and 3) assess host demographic risk factors for infection. Macroscopic cysts consistent with alveolar echinococcosis were present in 24% of muskrats (22/93). Most individuals had hepatic cysts; however, cysts were also occasionally detected in the mesentery, reproductive organs, omentum, peritoneum, spleen, diaphragm, lung, or kidney. The mean number of cysts per liver was 2.1 (range, 1-4). We examined hepatic cysts from 18 individuals using histology; all had lesions compatible with alveolar echinococcosis. Protoscoleces, indicative of patent infections, were present in 14/18 (78%). No demographic risk factors (sex, body condition, body mass) were significantly associated with infection. Muskrats in the North American context are competent intermediate hosts with high infection prevalence and may play an important role in the ecology of this emerging parasite.

The First Identification of Trichinella britovi in the Raccoon Dog (Nyctereutes procyonoides) in Romania.

Marin AM, Popovici DC, Dărăbuș G, Marian C, Nițușcă D, Mederle N.
05-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764940/

The Evolution of Cystic Echinococcosis in Humans and Ruminants in Portugal-A One Health Approach.

Alho AM, Dias MC, Cardo M, Aguiar P, de Carvalho LM.
21-09-2023
Vet Sci.
https://pubmed.ncbi.nlm.nih.gov/37756107/

Very Prolonged Treatment with Albendazole of a Case of Disseminated Abdominal Cystic Echinococcosis.

Buscemi C, Randazzo C, Buscemi P, Caldarella R, Lombardo M, Buscemi S.
15-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755910/

Cystic echinococcosis is a zoonosis caused by the ingestion of food or water contaminated by *Echinococcus* eggs. E. granulosus is the most common causative agent of cystic echinococcosis that still has a relevant incidence in Italy, especially on the islands of Sicily and Sardinia. We report the case of a 64-year-old man with disseminated abdominal cystic echinococcosis (liver, spleen, peritoneum). The patient was asymptomatic and non-eligible for surgical treatment. Treatment with albendazole 400 mg/twice daily was started in 2012 for 15 cycles (each cycle consisted of three 28-day treatments at 14-day intervals) over 10 years for a total of 1260 days of treatment. Serum anti-*Echinococcus* antibody titers and imaging (echography, TC) were evaluated to monitor the evolution of the disease. Imaging techniques documented the regression of all cyst lesions, but it was less evident for the peritoneal localizations that still are in follow-up. In this case, the prolonged treatment with albendazole was effective, safe and free of side effects. Until today, the patient displays a good clinical condition.

Hydatid cyst of the hepatopancreatic groove - A case report.

Jan ZU, Ahmed N, Khan MY, Samin Y, Sohail R.
09-09-2023
Int J Surg Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37748385/

Introduction and importance: Hydatid cysts are zoonoses caused by Echinococcus granulosus. It can affect any part of the body. The most common sites are the liver and lungs. Hydatid cyst of the hepatopancreatic groove is rare and to the best of our knowledge, this has not been reported in the literature before. Case presentation: We present a case of a young male patient who presented with abdomimal pain and jaundice. His workup revealed a hydatid cyst in the hepatopancreatic groove. Surgery for the hydatid cyst was done and the postoperative course was uneventful. Clinical discussion: Hepatopancreatic groove is an atypical site for a hydatid cyst. The main symptoms of a patient include vomiting, discomfort as well as pain in the epigastrium. The diagnostic imaging techniques include an ultrasound, CT scan as well as an MRI. Definitive treatment includes the cyst to be surgically removed. Conclusion: Hydatid cyst of the hepatopancreatic groove is rare. The diagnosis is usually not very easy and imaging can help in this regard. Surgery is the treatment modality of choice.

Comparison of Native Hydatid Cyst Fluid (HCF), Lyophilized HCF, Antigen B (AgB) and Lyophilized AgB (LAgB) Originated from Echinococcus granulosus Sensu Stricto for Sero-Diagnosis of Active, Transitional and Inactive Human Liver Cystic Echinococcosis.

Sadjjadi FS, Mohammadzadeh T, Jafari SH, Sharifi Y, Deilami HN, Hafezi F, Sadjjadi SM.
Août-2023
Iran J Public Health.
https://pubmed.ncbi.nlm.nih.gov/37744545/

Background: Cystic echinococcosis (CE) is an important zoonotic parasitic disease caused by the larval stage or metacestode of the tapeworm *Echinococcus granulosus* sensu lato. Due to treatment protocols for different liver cysts, diagnosis of cyst stages is very important. Different antigens have been used for CE diagnosis. However, each one is more sensitive and effective for the diagnosis of specific CE stages is not known well. We aimed to compare Native Hydatid Cyst Fluid (HCF), Lyophilized Hydatid Cyst Fluid (LHCF), antigen B (AgB) and Lyophilized antigen B (LAgB) originated from *E. granulosus* sensu stricto (G1-G3) genotype, for sero- diagnosis of active, transitional and inactive human liver CE using ELISA technique. Methods: The HCF was collected aseptically from liver CE cysts of sheep slaughtered from 2018 to 2019 in Shiraz slaughterhouse, Southern, Iran. The cysts were

characterized by PCR and sequencing for genotype specification. Four types of antigens were used: HCF, LHCF, AgB and LAgB originated from *E. granulosus* sensu stricto (G1-G3) genotype. Thirty-three serum samples from active, transitional, and inactive human cysts were collected. Overall, 48 samples from other parasitic diseases and 60 samples from healthy subjects as negative controls were checked using four antigens by ELISA method. **Results:** The best diagnostic sensitivity with 96.97% was observed by anti-LHCF IgG ELISA test. The best specificity with 95.37% was observed in ELISA test using LAgB. **Conclusion:** Simultaneous test of sera with anti-LHCF IgG ELISA and anti-LAgB IgG ELISA would be the best in the diagnosis of human liver cystic echinococcosis.

Pulmonary cystic echinococcosis in a child.

Peulier-Maitre E, Hervieux E, Bigot J, Sileo C, Denamur S, Corvol H.
Oct-2023
Pediatr Pulmonol.
https://pubmed.ncbi.nlm.nih.gov/37401873/

Editorial: Host-pathogen interaction in cestodes infection.

Tharmalingam J, Brehm K, Kundu S, Młocicki D, Paredes R.
11-09-2023
Front Cell Infect Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37767200/

When wildlife comes to town: interaction of sylvatic and domestic host animals in transmission of *Echinococcus* spp. in Namibia.

Aschenborn O, Aschenborn J, Kern P, Mackenstedt U, Romig T, Wassermann M.
22-09-2023
Helminthologia.
https://pubmed.ncbi.nlm.nih.gov/37745225/

The present study was conducted in the isolated desert town of Oranjemund in the far south of Namibia. It is an extremely arid region where no livestock husbandry is practiced and only animals adapted to the desert can be found. However, in and around the city, artificial irrigation maintains lush green patches of grass that attract wild animals, in particular oryx antelopes (*Oryx gazella*). In 2015 four oryx antelopes were euthanised due to poor conditions and a post-mortem examination was conducted. Two were found positive for cystic echinococcosis and 16 cysts were collected for molecular analyses. In addition, faecal samples from black-backed jackals (n=5) and domestic dogs (n=9), which were regularly observed to feed on oryx carcasses, were collected and taeniid eggs isolated. Parasite species identification of the cysts and eggs was done by amplifying and sequencing the mitochondrial *nad1* gene. Both oryx antelopes were found infected with *E. ortleppi* and one co-infected with *E. canadensis* G6/7. Both *Echinococcus* species were able to develop fertile cysts in oryx, making oryx antelopes competent hosts for these parasites. Therefore, the analysis of faecal samples was of high interest and although the numbers were quite small, taeniid eggs were found in three out of five faecal samples of jackals and in all nine dog samples. However, species determination was only successful with two jackal and one dog sample. All three were positive for *E. canadensis* G6/7. The absence of *E. ortleppi* may be due to the low number of faecal samples examined. In our small study, we discovered a rather unique lifecycle of *Echinococcus* spp. between jackals and domestic dogs as definitive hosts and oryx antelopes as intermediate hosts. Here, the presence of *E. canadensis* G6/7 is of particular concern, as it is the second most important causative agent of CE in humans.

Filariose lymphatique

Xenorhabdus and Photorhabdus Bacteria as Potential Candidates for the Control of Culex pipiens L. (Diptera: Culicidae), the Principal Vector of West Nile Virus and Lymphatic Filariasis.

Yüksel E, Yıldırım A, İmren M, Canhilal R, Dababat AA.
28-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764903/

Vector-borne diseases pose a severe threat to human and animal health. *Culex pipiens* L. (Diptera: Culicidae) is a widespread mosquito species and serves as a vector for the transmission of infectious diseases such as West Nile disease and Lymphatic Filariasis. Synthetic insecticides have been the prime control method for many years to suppress *Cx. pipiens* populations. However, recently, the use of insecticides has begun to be questioned due to the detrimental impact on human health and the natural environment. Therefore, many authorities urge the development of eco-friendly control methods that are nontoxic to humans. The bacterial associates [*Xenorhabdus* and *Photorhabdus* spp. (Enterobacterales: Morganellaceae)] of entomopathogenic nematodes (EPNs) (*Sterinernema* spp. and *Heterorhabditis* spp.) (Rhabditida: Heterorhabditidae and Steinernematidae) are one of the green approaches to combat a variety of insect pests. In the present study, the mosquitocidal activity of the cell-free supernatants and cell suspension (4×10^7 cells mL^{-1}) of four different symbiotic bacteria (*Xenorhabdus nematophila*, *X. bovienii*, *X. budapestensis*, and *P. luminescens* subsp. *kayaii*) was assessed against different development stages of *Cx. pipiens* (The 1st/2nd and 3rd/4th instar larvae and pupa) under laboratory conditions. The bacterial symbionts were able to kill all the development stages with varying levels of mortality. The 1st/2nd instar larvae exhibited the highest susceptibility to the cell-free supernatants and cell suspensions of symbiotic bacteria and the efficacy of the cell-free supernatants and cell suspensions gradually declined with increasing phases of growth. The highest effectiveness was achieved by the *X. bovienii* KCS-4S strain inducing 95% mortality to the 1st/2nd instar larvae. The results indicate that tested bacterial symbionts have great potential as an eco-friendly alternative to insecticides.

A Health Survey Revealing Prevalence of Vector-Borne Diseases and Tuberculosis in Papua New Guinea Defence Force Personnel and Families.

McCallum F, Mond K, Cheng Q, Furuya-Kanamori L, Auliff A, Kaminiel P; ADFMIDI/PNGDF Health Services Survey Team.
25-09-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37748766/

Gale

Implementation of a Community-Based Public Model for the Prevention and Control of Communicable Diseases in Migrant Communities in Catalonia.

Gómez I Prat J, Alguacil HM, Pequeño Saco S, Ouaarab Essadek H, Montero I Garcia J, Catasús I Llena O, Mendioroz Peña J.
14-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755907/

In high-income countries, migrant populations have a greater epidemiological vulnerability: increased exposure to infectious diseases, difficulties in diagnosis, case follow-up and contact tracing, and obstacles following preventive measures related to cultural and administrative barriers. This study aims to describe the implementation of a community-based program to address these challenges. The target population is the migrant native population from North Africa, South Asia, Sub-Saharan Africa, Eastern Europe, and Latin America resident in Catalonia during 2023. Implementation phases include the identification of the perceived needs, search, recruitment and capacity building of 16 community health workers, and the development of a computer software. From January to June 2023, 117 community-based interventions have been implemented, reaching 677 people: 73 community case and contacts management interventions, 17 community in-situ screenings (reaching 247 people) and 27 culturally adapted health awareness and education actions (reaching 358 people). The program addresses the following infectious diseases: tuberculosis, Chagas disease, hepatitis C, typhoid, scabies, hepatitis B, mumps and tinea capitis. The implementation of a community-based model may be key to improving surveillance communicable diseases, promoting an equitable and comprehensive epidemiological surveillance system.

Dermoscopic and reflectance confocal microscopic features of children scabies.

Guan Z, Bi T, Li Q.
Sept-2023
Skin Res Technol.
https://pubmed.ncbi.nlm.nih.gov/37753693/

Crusted Scabies in an Elderly Patient.

Yang Y, Shen H, Liu ZH.
25-09-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37748763/

Comparing the Trends of Vector-Borne Diseases (VBDs) before and after the COVID-19 Pandemic and Their Spatial Distribution in Southern Iran.

Gheibi Z, Boroomand M, Soltani A.
15-09-2023
J Trop Med.
https://pubmed.ncbi.nlm.nih.gov/37745307/

Objectives: We aimed to model and predict the changes in the trend of vector-borne diseases (VBDs) before and after the COVID-19 pandemic in a high-risk area of Iran. Methods: This case-series study was conducted in Fars province, south of Iran, between April 2016 and July 2021. All referred cases of VBDs were considered during the five years to investigate the effect of the lockdown on the epidemiological profile of these diseases. We used time-series autoregressive integrated moving average (ARIMA) and seasonal ARIMA (SARIMA) models. Results: Pediculosis incidence trend was rising with a peak of 1,146 per 100,000 in 2018, followed by a dramatic decrease reached to the minimum amount of 157.8 per 100,000 in 2021. In contrast, malaria and scabies had a smooth decreasing trend ranging from 2.2 per 100,000 and 7.3 per 100,000 in 2016 to a minimum of 0.2 per 100,000 in 2021, respectively. Likewise, leishmaniasis had a falling trend, with a maximum rate of 82.9 per 100,000 in 2016 to the lowest rate of 9.4 per 100,000 in 2021. However, the difference between observed and expected values revealed that the consequences of the COVID-19 pandemic had increased the number of leishmaniasis cases. Conclusion: Tropical regions of Iran, including Fars province, are the favorite destinations for travelers. During COVID-19 outbreaks, some reasons, such as quarantine, movement restrictions, and social distancing, reduced human-vector contact and finally led to the reduction of VBDs in this area.

Scabies: UK treatment shortage poses public health threat, warn dermatologists.

Mahase E.
21-09-2023
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37734758/

Modelling mass drug administration strategies for reducing scabies burden in Monrovia, Liberia.

Tellioglu N, Chisholm RH, Campbell PT, Collinson S, Timothy J, Kollie K, Zayzay S, Devine A, McVernon J, Marks M, Geard N.
18-09-2023
Epidemiol Infect.
https://pubmed.ncbi.nlm.nih.gov/37593956/

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

Quantitative microbial risk assessment associated with the use of container-based toilets in Haiti.

Jean-Baptiste D, De Giudici P, Monette F.
Sept-2023
Water Sci Technol.
https://pubmed.ncbi.nlm.nih.gov/37771230/

The Impact of Intestinal Inflammation on Nematode's Excretory-Secretory Proteome.

Maruszewska-Cheruiyot M, Szewczak L, Krawczak-Wójcik K, Kierasińska M, Stear M, Donskow-Łysoniewska K.
15-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762428/

Parasitic nematodes and their products are promising candidates for therapeutics against inflammatory bowel diseases (IBD). Two species of nematodes, the hookworm *Necator americanus* and the whipworm *Trichuis suis*, are being used in clinical treatment trials of IBD referred to as "helminth therapy". *Heligmosomoides polygyrus* is a well-known model for human hookworm infections. Excretory-secretory (ES) products of *H. polygyrus* L4 stage that developed during colitis show a different immunomodulatory effect compared to the ES of *H. polgyrus* from healthy mice. The aim of the study was to evaluate excretory-secretory proteins produced by *H. polygyrus* L4 stage males and females that developed in the colitic milieu. Mass spectrometry was used to identify proteins. Blast2GO was used to investigate the functions of the discovered proteins. A total of 387 proteins were identified in the ES of *H. polygyrus* L4 males (HpC males), and 330 proteins were identified in the ES of L4 females that developed in the colitic milieu (HpC females). In contrast, only 200 proteins were identified in the ES of L4 males (Hp males) and 218 in the ES of L4 females (Hp females) that developed in control conditions. Most of the proteins (123) were detected in all groups. Unique proteins identified in the ES of HpC females included annexin, lysozyme-2, apyrase, and galectin. Venom allergen/Ancylostoma-secreted protein-like, transthyretin-like family proteins, and galectins were found in the secretome of HpC males but not in the secretome of control males. These molecules may be responsible for the therapeutic effects of nematodes in DSS-induced colitis.

Prevalence and intensity of soil-transmitted helminth infections in Uganda: Results from population-based prevalence surveys in five districts.

Tinkitina B, Beinamaryo P, Adriko M, Nabatte B, Arinaitwe M, Mubangizi A, Emerson P, Dhakal S, Sullivan KM.
26-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37751418/

Background: Soil-transmitted helminth (STH) infections are caused by roundworms (Ascaris lumbricoides), whipworms (Trichuris trichiura), and hookworms (Necator americanus and Ancylostoma duodenale). In Uganda, baseline surveys conducted during the late 1990s and early 2000s suggested STH infections were common, with prevalence >50% among surveyed schoolchildren. In 2003, a national program was launched with mass preventative chemotherapy (PC) and health education for children 1-14 years old. Little evidence is available to show the impact of national deworming. Methods: We conducted population-based, cross-sectional household surveys in five districts (Buikwe, Kassanda, Kiryandongo, Kisoro, and Rubanda) in March and May 2022. Our primary objective was to estimate STH prevalence by species due to infections of any intensity and infections of moderate-to-heavy intensity among preschool-aged children (PSAC, 1-4 years old), school-aged children (SAC, 5-14 years old), and women of reproductive age (WRA, 15-49 years old). Laboratory technicians used duplicate Kato-Katz microscopy to determine fecal egg count. Results: Overall, 3,352 PSAC; 3,884 SAC; and 1,226 WRA provided stool samples. The prevalence of any infection remained high in Kisoro at or above ~50% within all risk groups. In other districts, the prevalence of any infection ranged from approximately 5 to 16% among PSAC, 6 to 23% among SAC, and 12 to 19% among WRA. Moderate-to-heavy intensity infection prevalence was highest in Kisoro (~15-26%), followed by Rubanda (<5%), and was ≤1% in other districts. A. lumbricoides and T. trichiura infections were largely confined to Kisoro and Rubanda, whereas hookworm was most common in other districts. Conclusions: The STH prevalence has decreased markedly in three districts in Uganda. Based on our findings, the national deworming program should consider decreasing PC distribution frequency in these districts per the World Health Organization guidelines. Efforts are needed to understand why the Kisoro and Rubanda districts did not demonstrate similar gains.

Noninvasive diagnosis of Ascaris lumbricoides in the common bile duct: A pediatric case report of acute pancreatitis.

Samir K, Subash T, Subash A, Bilal H, Shah HH, Dave T.
22-09-2023
Clin Case Rep.
https://pubmed.ncbi.nlm.nih.gov/37744625/

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

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

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

Leishmaniose

Leishmania species infection of bats: A systematic review.

de Souza NN, Ursine RL, Cruz DS, Xavier EMS, Queiroz LDRP, Falcão LAD, de Araújo WS, Gontijo CMF, Melo MN, Vieira TM.
26-09-2023
Acta Trop.
https://pubmed.ncbi.nlm.nih.gov/37769863/

Immunization with recombinant LiHyp1 protein plus adjuvant is protective against tegumentary leishmaniasis.

Jesus MM, Lage DP, Vale DL, Freitas CS, Pimenta BL, Moreira GJL, Ramos FF, Pereira IAG, Bandeira RS, Ludolf F, Tavares GSV, Galdino AS, Duarte MC, Menezes-Souza D, Chávez-Fumagalli MA, Teixeira AL, Gonçalves DU, Roatt BM, Christodoulides M, Martins VT, Coelho EAF.
28-09-2023
Parasitol Res.
https://pubmed.ncbi.nlm.nih.gov/37768367/

Tegumentary leishmaniasis (TL) is the main clinical manifestation of leishmaniasis, and it can cause the infected hosts to self-healing cutaneous lesions until mutilating scars in mucosal membranes, particularly in the nose and throat. The treatment against disease presents problems, and the diagnosis is hampered by variable sensitivity and/or specificity of the tests. In this context, the development of prophylactic vaccines could be considered as a strategy to control the disease. Previously, we showed that the recombinant LiHyp1 protein plus adjuvant protected mice from infection with Leishmania infantum, which causes visceral leishmaniasis. In the present study, we tested whether rLiHyp1 could induce protection against infection with L. amazonensis, a parasite species able to cause TL. We immunized BALB/c mice with rLiHyp1 plus saponin (rLiHyp1/S) or incorporated in micelles (rLiHyp1/M) as adjuvants and performed parasitological and immunological evaluations before and after infection. Results showed that after in vitro stimulation from spleen cell cultures using rLiHyp1 or a Leishmania antigenic extract (SLA), rLiHyp1/S and rLiHyp1/M groups developed a Th1-type immune response, which was characterized by high levels of IFN-γ, IL-2, TNF-α and IL-12 cytokines, nitrite, and IgG2a isotype antibodies when compared to values found in the control (saline, saponin, micelles alone) groups, which showed higher levels of anti-SLA IL-4, IL-10, and IgG1 antibodies before and after challenge. In addition, mice receiving rLiHyp1/S or rLiHyp1/M presented significant reductions in the lesion average diameter and parasite load in the infected tissue and internal organs. Blood samples were collected from healthy subjects and TL patients to obtain PBMC cultures, which were in vitro stimulated with rLiHyp1 or SLA, and results showed higher lymphoproliferation and IFN-γ production after stimulus using rLiHyp1, as compared to values found using SLA. These results suggest that rLiHyp1 plus adjuvant was protective against experimental TL and could also be considered for future studies as a vaccine candidate against human disease.

(-)-5-Demethoxygrandisin B a New Lignan from Virola surinamensis (Rol.) Warb. Leaves: Evaluation of the Leishmanicidal Activity by In Vitro and In Silico Approaches.

Paes SS, Silva-Silva JV, Portal Gomes PW, Silva LOD, Costa APLD, Lopes Júnior ML, Hardoim DJ, Moragas-Tellis CJ, Taniwaki NN, Bertho AL, Molfetta FA, Almeida-Souza F, Santos LS, Calabrese KDS.
07-09-2023
Pharmaceutics.
https://pubmed.ncbi.nlm.nih.gov/37765261/

Modulation of Macrophage Redox and Apoptotic Processes to Leishmania infantum during Coinfection with the Tick-Borne Bacteria Borrelia burgdorferi.

Pessôa-Pereira D, Scorza BM, Cyndari KI, Beasley EA, Petersen CA.
04-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764937/

Canine leishmaniosis (CanL) is a zoonotic disease caused by protozoan *Leishmania infantum*. Dogs with CanL are often coinfected with tick-borne bacterial pathogens, including *Borrelia burgdorferi* in the United States. These coinfections have been causally associated with hastened disease progression and mortality. However, the specific cellular mechanisms of how coinfections affect microbicidal responses against *L. infantum* are unknown. We hypothesized that *B. burgdorferi* coinfection impacts host macrophage effector functions, prompting *L. infantum* intracellular survival. In vitro experiments demonstrated that exposure to *B. burgdorferi* spirochetes significantly increased *L. infantum* parasite burden and pro-inflammatory responses in DH82 canine macrophage cells. Induction of cell death and generation of mitochondrial ROS were significantly decreased in coinfected DH82 cells compared to uninfected and *L. infantum*-infected cells. Ex vivo stimulation of PBMCs from *L. infantum*-seronegative and -seropositive subclinical dogs with spirochetes and/or total *Leishmania* antigens promoted limited induction of IFNγ. Coexposure significantly induced expression of pro-inflammatory cytokines and chemokines associated with Th17 differentiation and neutrophilic and monocytic recruitment in PBMCs from *L. infantum*-seropositive dogs. Excessive pro-inflammatory responses have previously been shown to cause CanL pathology. This work supports effective tick prevention and risk management of coinfections as critical strategies to prevent and control *L. infantum* progression in dogs.

Mucosal Relapse of Visceral Leishmaniasis in a Child with SARS-CoV-2 Infection.

Colomba C, Boncori G, Albano C, Garbo V, Bagarello S, Condemi A, Giordano S, Cascio A.
03-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764934/

A Fatal Case of Disseminated Histoplasmosis by Histoplasma capsulatum var. capsulatum Misdiagnosed as Visceral Leishmaniasis-Molecular Diagnosis and Identification.

Calvopiña M, Toro M, Bastidas-Caldes C, Vasco-Julio D, Muñoz G.
30-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764920/

Exploring Host-Specificity: Untangling the Relationship between Leishmania (Viannia) Species and Its Endosymbiont Leishmania RNA Virus 1.

Santana MCO, Chourabi K, Cantanhêde LM, Cupolillo E.
12-09-2023
Microorganisms.
https://pubmed.ncbi.nlm.nih.gov/37764139/

Molecular Mechanisms of Persistence in Protozoan Parasites.

Tarannum A, Rodríguez-Almonacid CC, Salazar-Bravo J, Karamysheva ZN.
07-09-2023
Microorganisms.
https://pubmed.ncbi.nlm.nih.gov/37764092/

Protozoan parasites are known for their remarkable capacity to persist within the bodies of vertebrate hosts, which frequently results in prolonged infections and the recurrence of diseases. Understanding the molecular mechanisms that underlie the event of persistence is of paramount significance to develop innovative therapeutic approaches, given that these pathways still need to be thoroughly elucidated. The present article provides a comprehensive overview of the latest developments in the investigation of protozoan persistence in vertebrate hosts. The focus is primarily on the function of persisters, their formation within the host, and the specific molecular interactions between host and parasite while they persist. Additionally, we examine the metabolomic, transcriptional, and translational changes that protozoan parasites undergo during persistence within vertebrate hosts, focusing on major parasites such as *Plasmodium* spp., *Trypanosoma* spp., *Leishmania* spp., and *Toxoplasma* spp. Key findings of our study suggest that protozoan parasites deploy several molecular and physiological strategies to evade the host immune surveillance and sustain their persistence. Furthermore, some parasites undergo stage differentiation, enabling them to acclimate to varying host environments and immune challenges. More often, stressors such as drug exposure were demonstrated to impact the formation of protozoan persisters significantly. Understanding the molecular mechanisms regulating the persistence of protozoan parasites in vertebrate hosts can reinvigorate our current insights into host-parasite interactions and facilitate the development of more efficacious disease therapeutics.

Diagnostic Tools for Cutaneous Leishmaniasis Caused by Leishmania donovani: A Narrative Review.

Piyasiri SB, Dewasurendra R, Samaranayake N, Karunaweera N.
18-09-2023
Diagnostics (Basel).
https://pubmed.ncbi.nlm.nih.gov/37761356/

Leishmaniasis, a neglected tropical disease, encompasses a spectrum of clinical conditions and poses a significant risk of infection to over one billion people worldwide. Visceral leishmaniasis (VL) in the Indian sub-continent (ISC), where the causative parasite is *Leishmania donovani*, is targeted for elimination by 2025, with some countries already reaching such targets. Other clinical phenotypes due to the same species could act as a reservoir of parasites and thus pose a challenge to successful control and elimination. Sri Lanka has consistently reported

cutaneous leishmaniasis (CL) due to *L. donovani* as the primary disease presentation over several decades. Similar findings of atypical phenotypes of *L. donovani* have also been reported from several other countries/regions in the Old World. In this review, we discuss the applicability of different methods in diagnosing CL due to *L. donovani* and a comprehensive assessment of diagnostic methods spanning clinical, microscopic, molecular, and immunological approaches. By incorporating evidence from Sri Lanka and other regions on *L. donovani*-related CL, we thoroughly evaluate the accuracy, feasibility, and relevance of these diagnostic tools. We also discuss the challenges and complexities linked to diagnosing CL and review novel approaches and their applicability for detecting CL.

Systematic Exploration of Functional Group Relevance for Anti-Leishmanial Activity of Anisomycin.

Nguyen AMT, Shalev-Benami M, Rosa-Teijeiro C, Ibarra-Meneses AV, Yonath A, Bashan A, Jaffe CL, Olivier M, Fernandez-Prada C, Lubell WD.
15-09-2023
Biomedicines.
https://pubmed.ncbi.nlm.nih.gov/37760981/

Assessment of structure-activity relationships for anti-protozoan activity revealed a strategy for preparing potent anisomycin derivatives with reduced host toxicity. Thirteen anisomycin analogs were synthesized by modifying the alcohol, amine, and aromatic functional groups. Examination of anti-protozoal activity against various strains of *Leishmania* and cytotoxicity against leucocytes with comparison against the parent natural product demonstrated typical losses of activity with modifications of the alcohol, amine, and aromatic meta-positions. On the other hand, the para-phenol moiety of anisomycin proved an effective location for introducing substituents without significant loss of anti-protozoan potency. An entry point for differentiating activity against *Leishmania* versus host has been uncovered by this systematic study.

Antimicrobial Peptides (AMP) in the Cell-Free Culture Media of Xenorhabdus budapestensis and X. szentirmaii Exert Anti-Protist Activity against Eukaryotic Vertebrate Pathogens including Histomonas meleagridis and Leishmania donovani Species.

Fodor A, Hess C, Ganas P, Boros Z, Kiss J, Makrai L, Dublecz K, Pál L, Fodor L, Sebestyén A, Klein MG, Tarasco E, Kulkarni MM, McGwire BS, Vellai T, Hess M.
19-09-2023
Antibiotics (Basel).
https://pubmed.ncbi.nlm.nih.gov/37760758/

Prevalence and Factors Related to Leishmania infantum Infection in Healthy Horses (Equus caballus) from Eastern Spain.

Martínez-Sáez L, Dulac Q, Montaner-Angoiti E, Marín-García PJ, Llobat L.
11-09-2023
Animals (Basel).
https://pubmed.ncbi.nlm.nih.gov/37760289/

Evidence of Horse Exposure to Anaplasma phagocytophilum, Borrelia burgdorferi, and Leishmania infantum in Greece through the Detection of IgG Antibodies in Serum and in an Alternative Diagnostic Sample-The Saliva.

Athanasiou LV, Katsogiannou EG, Tyrnenopoulou P, Gougoulis D, Apostolidis KN, Papadakis SM, Kokkinaki KCG, Papatsiros VG, Tsokana CN.
11-09-2023
Biomolecules.
https://pubmed.ncbi.nlm.nih.gov/37759774/

Among the various zoonotic pathogens that infect horses, *Anaplasma phagocytophilum, Borrelia* spp. and *Leishmania* spp. have gained scientific interest, and relevant molecular and serological studies in horses have been conducted worldwide. Moreover, human and veterinary medicine have extensively applied alternatives to serum diagnostic samples-such as saliva-for detecting pathogens or antibodies. In this study, we investigated the exposure of horses in Greece to *A. phagocytophilum*, *B. burgdorferi*, and *L. infantum*, and we assessed the diagnostic accuracy of saliva compared to serum in detecting IgG antibodies against the abovementioned pathogens. Paired saliva and serum samples were collected from 317 horses from different regions in Greece. The paired samples were examined using the indirect fluorescent antibody test (IFAT) for detecting IgG antibodies against *A. phagocytophilum, B. burgdorferi*, and *L. infantum.* Sensitivity, specificity, positive likelihood ratio (PLR), and negative likelihood ratio (NLR) were determined to assess the validity of saliva as an alternative to serum. The receiver operating characteristic (ROC) curve revealed that the optimal cut-off value for detecting antibodies against all the examined pathogens in saliva was 1/10. Higher seropositivity rates were found for *B. burgdorferi* (15.14%) and *A. phagocytophilum* (14.19%) compared to *L. infantum* (1.26%). The detection of IgG antibodies using IFAT in saliva samples had a good test performance compared to serum. The two sample types had a substantial to almost perfect agreement. Although the sensitivity was moderate (70.83-75.56%) in all cases, the specificity was almost perfect to perfect (99.63-100%). This study provides the first evidence that horses in Greece are exposed to *A. phagocytophilum* and *B. burgdorferi* and confirms that the seroprevalence of *L. infantum* in horses in Greece remains low. Our findings suggest that saliva sampling coupled with IFAT could be successfully applied for detecting IgG antibodies against these important zoonotic pathogens in large-scale epidemiological studies in horses, at the population level, as an alternative to serum.

Endemic infectious cutaneous ulcers syndrome in the Oti Region of Ghana:

Study of cutaneous leishmaniasis, yaws and Haemophilus ducreyi cutaneous ulcers.

Akuffo RA, Sanchez C, Amanor I, Amedior JS, Kotey NK, Anto F, Azurago T, Ablordey A, Owusu-Antwi F, Beshah A, Amoako YA, Phillips RO, Wilson M, Asiedu K, Ruiz-Postigo JA, Moreno J, Mokni M.
27-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37756291/

Background: A recent study detected cutaneous leishmaniasis (CL) in 31.9% of persons with skin ulcers in the Oti Region of Ghana, resulting in a need to investigate other potential causes of the unexplained skin ulcers. Methodology/principal findings: A community based cross-sectional study was conducted in the Oti region to investigate skin ulcers of undetermined aetiologies. To confirm a diagnosis of cutaneous leishmaniasis, Buruli ulcer, Haemophilus ducreyi ulcers, or yaws, DNA obtained from each patient skin ulcer sample was systematically subjected to polymerase chain reaction (PCR) for Leishmania spp., Mycobacterium ulcerans, Haemophilus ducreyi, and Treponema pallidum sub species pertenue. A total of 101 skin ulcer samples were obtained from 101 persons. Co-infection of more than one organism was observed in 68.3% of the samples. Forty (39.6%) participants had a positive result for Leishmania spp., 68 (67.3%) for Treponema pallidum sub. Sp. pertenue, and 74 (73.3%) for H. ducreyi. Twenty (19.8%) of the patient ulcers were simultaneously infected with Leishmania spp., Treponema pallidum sub. Sp. pertenue, and H. ducreyi. None of the patients' lesions yielded a positive result for Mycobacterium ulcerans. Conclusions/significance: This study detected single and mixed occurrence of the causative organisms of CL, yaws, and H. ducreyi cutaneous ulcers in CL endemic communities of the Oti Region in Ghana. These findings emphasize the importance of integrating multiple skin diseases on a common research platform and calls for the development of a comprehensive guideline for diagnosing and treating tropical ulcers in the study areas.

Subcutaneous, Oral, and Intranasal Immunization of BALB/c Mice with Leishmania infantum K39 Antigen Induces Non-Protective Humoral Immune Response.

Silva BBD, Silva Junior ABD, Araújo LDS, Santos ENFN, Silva ACMD, Florean EOPT, van Tilburg MF, Guedes MIF.
12-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755905/

Systematic Review of Treatment Failure and Clinical Relapses in Leishmaniasis from a Multifactorial Perspective: Clinical Aspects, Factors Associated with the Parasite and Host.

Santos GA, Sousa JM, Aguiar AHBM, Torres KCS, Coelho AJS, Ferreira AL, Lima MIS.
29-08-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755891/

Double Staining with Fluorescent Tracers to Determine Myeloid Cell Migration of Leishmania-infected Cells from Mouse Skin to Lymphatic Tissues by Flow Cytometry.

Uscanga-Palomeque AC, Osorio YE, Melby PC.
20-09-2023
Bio Protoc.
https://pubmed.ncbi.nlm.nih.gov/37753467/

Biochemical and structural characterization of the RT domain of Leishmania sp. telomerase reverse transcriptase.

da Silva VL, de Paiva SC, de Oliveira HC, Fernandes CAH, Salvador GHM, Fontes MRM, Cano MIN.
24-09-2023
Biochim Biophys Acta Gen Subj.
https://pubmed.ncbi.nlm.nih.gov/37751810/

Background: The Leishmania genus comprises parasites that cause leishmaniasis, a neglected disease spread worldwide. Leishmania sp. telomeres are composed of TTAGGG repeats maintained by telomerase. In most eukaryotes, the enzyme minimal complex contains the TER (telomerase RNA) and the TERT (telomerase reverse transcriptase) components. The TERT holds the enzyme catalytic core and is formed by four structural and functional domains (TEN, Telomerase Essential N-terminal; TRBD, Telomerase RNA Binding Domain; RT, the reverse transcriptase domain and CTE, C-Terminal Extension domain). Methods and results: Amino acid sequence alignments, protein structure prediction analysis, and protein: nucleic acid interaction assays were used to show that the Leishmania major RT domain preserves the canonical structural elements found in higher eukaryotes, including the canonical motifs and the aspartic acid residues that stabilize the Mg^{2+} ion cofactor. Furthermore, amino acid substitutions specific to the Leishmania genus and partial conservation of the residues involved with nucleic acid interactions are shown. The purified recombinant Leishmania RT protein is biochemically active and interacts with the G-rich telomeric strand and the TER template sequence. Conclusion: Our results highlight that the telomerase catalysis mechanism is conserved in a pathogen of medical importance despite the structural peculiarities present in the parasite's RT domain.

RNA Polymerase II evolution and adaptations: Insights from Plasmodium and other parasitic protists.

Purkayastha D, Karmodiya K.
23-09-2023
Infect Genet Evol.
https://pubmed.ncbi.nlm.nih.gov/37748526/

Visceral Leishmaniasis With Blastocystis Co-infection: A Case Report.

Wang T, Rampisela D.
24-08-2023
Cureus.
https://pubmed.ncbi.nlm.nih.gov/37746419/

Visceral leishmaniasis (VL) is a form of leishmaniasis, which causes significant mortality if untreated. The coexistence of VL with *Blastocystis* infection has not been well-documented in the literature. In this paper, we present the case of a 72-year-old male who experienced four months of recurrent diarrhea and later developed weight loss, fever, night sweats, and pancytopenia. The stool ova and parasite (O&P) examination revealed *Blastocystis* spp. vacuolar bodies and he was treated with metronidazole which resolved the diarrhea but not other symptoms. Further evaluation, including an abdominal Computed Tomogram (CT) scan and ultrasonography (USG), revealed splenomegaly. A splenic biopsy confirmed VL with numerous *Leishmania* amastigotes. Treatment with Amphotericin B led to clinical improvement. This paper discusses the clinical and diagnostic features of VL and *Blastocystis*, highlighting their differential diagnosis, and available treatments.

Within-Host Bayesian Joint Modeling of Longitudinal and Time-to-Event Data of Leishmania Infection.

Pabon-Rodriguez FM, Brown GD, Scorza BM, Petersen CA.
19-09-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37745423/

The host immune system plays a significant role in managing and clearing pathogen material during an infection, but this complex process presents numerous challenges from a modeling perspective. There are many mathematical and statistical models for these kinds of processes that take into account a wide range of events that happen within the host. In this work, we present a Bayesian joint model of longitudinal and time-to-event data of Leishmania infection that considers the interplay between key drivers of the disease process: pathogen load, antibody level, and disease. The longitudinal model also considers approximate inflammatory and regulatory immune factors. In addition to measuring antibody levels produced by the immune system, we adapt data from CD4+ and CD8+ T cell proliferation, and expression of interleukin 10, interferon-gamma, and programmed cell death 1 as inflammatory or regulatory factors mediating the disease process. The model is developed using data collected from a cohort of dogs naturally exposed to Leishmania infantum. The cohort was chosen to start with healthy infected animals, and this is the majority of the data. The model also characterizes the relationship features of the longitudinal outcomes and time of death due to progressive Leishmania infection. In addition to describing the mechanisms causing disease progression and impacting the risk of death, we also present the model's ability to predict individual trajectories of Canine Leishmaniosis (CanL) progression. The within-host model structure we present here provides a way forward to address vital research questions regarding the understanding progression of complex chronic diseases such as Visceral Leishmaniasis, a parasitic disease causing significant morbidity worldwide.

Anti-SpCas9 IgY Polyclonal Antibodies Production for CRISPR Research Use.

León E, Ortiz V, Pérez A, Téllez J, Díaz GJ, Ramírez H MH, Contreras R LE.
06-09-2023
ACS Omega.
https://pubmed.ncbi.nlm.nih.gov/37744827/

Development of New Leishmanicidal Compounds via Bioconjugation of Antimicrobial Peptides and Antileishmanial Guanidines.

Costa NCS, Dos Anjos LR, de Souza JVM, Brasil MCOA, Moreira VP, Graminha MAS, Lubec G, Gonzalez ERP, Cilli EM.
06-09-2023
ACS Omega.
https://pubmed.ncbi.nlm.nih.gov/37744786/

Leishmaniasis refers to a collection of diseases caused by protozoa from the *Leishmania* genus. These diseases, along with other parasitic afflictions, pose a significant public health issue, particularly given the escalating number of at-risk patients. This group includes immunocompromised individuals and those residing in impoverished conditions. The treatment of leishmaniasis is crucial, particularly in light of the mortality rate associated with nontreatment, which stands at 20-30,000 deaths per year globally. However, the therapeutic options currently available are limited, often ineffective, and potentially toxic. Consequently, the pursuit of new therapeutic alternatives is warranted. This study aims to design, synthesize, and evaluate the leishmanicidal activity of antimicrobial peptides functionalized with guanidine compounds and identify those with enhanced potency and selectivity against the parasite. Accordingly, three bioconjugates were obtained by using the solid-phase peptide synthesis protocol. Each proved to be more potent against intracellular amastigotes than their respective peptide or guanidine compounds alone and demonstrated higher selectivity to the parasites than to the host cells. Thus, the conjugation strategy employed with these compounds effectively contributes to the development of new molecules with leishmanicidal activity.

Leishmania mexicana centrin knockout parasites promote M1-polarizing metabolic changes.

Volpedo G, Pacheco-Fernandez T, Oljuskin T, Markle HL, Azodi N, Hamano S, Matlashewski G, Gannavaram S, Nakhasi HL, Satoskar AR.
29-08-2023
iScience.
https://pubmed.ncbi.nlm.nih.gov/37744404/

Leishmania major centrin knock-out parasites reprogram tryptophan metabolism to induce a pro-inflammatory response.

Oljuskin T, Azodi N, Volpedo G, Bhattacharya P, Markle HL, Hamano S, Matlashewski G, Satoskar AR, Gannavaram S, Nakhasi HL.
29-08-2023
iScience.
https://pubmed.ncbi.nlm.nih.gov/37744403/

Leishmaniasis is a parasitic disease that is prevalent in 90 countries, and yet no licensed human vaccine exists against it. Toward control of leishmaniasis, we have developed *Leishmania major centrin* gene deletion mutant strains (*LmCen*$^{-/-}$) as a live attenuated vaccine, which induces a strong IFN-γ-mediated protection to the host. However, the immune mechanisms of such protection remain to be understood. Metabolomic reprogramming of the host cells following *Leishmania* infection has been shown to play a critical role in pathogenicity and shaping the immune response following infection. Here, we applied untargeted mass spectrometric analysis to study the metabolic changes induced by infection with *LmCen*$^{-/-}$ and compared those with virulent *L. major* parasite infection to identify the immune mechanism of protection. Our data show that immunization with *LmCen*$^{-/-}$ parasites, in contrast to virulent *L. major* infection promotes a pro-inflammatory response by utilizing tryptophan to produce melatonin and downregulate anti-inflammatory kynurenine-AhR and FICZ-AhR signaling.

No place to hide! A method for revealing hidden loci of infection.

Kima PE.
22-09-2023
Trends Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37743113/

Epidemiological features of Leishmania infantum in dogs (Canis lupus familiaris) suggest a latent risk of visceral leishmaniasis in the metropolitan area of Bucaramanga, Santander, Eastern Colombia.

Jaimes-Dueñez J, Castillo-Castañeda A, Jiménez-Leaño Á, Duque JE, Cantillo-Barraza O, Cáceres-Rivera DI, Granada Y, Triana-Chávez O, Ramírez JD.
09-09-2023
Prev Vet Med.
https://pubmed.ncbi.nlm.nih.gov/37738753/

Visceral leishmaniasis (VL) is a disease caused by species of the Leishmania donovani complex that is mainly transmitted through the urban cycle involving dogs as the primary reservoir. In Colombia, the incidence of VL is increasing, along with the spread of potential vectors. This study aims to investigate the eco-epidemiological factors associated with Leishmania spp. infection in dogs from the Metropolitan Area of Bucaramanga (MAB), Santander, eastern Colombia, which is a region at risk for VL. We conducted molecular and serological surveillance of Leishmania spp. in 207 dogs from MAB to determine the epidemiological factors associated with infection. Subsequently, we carried out a molecular and serological analysis of phlebotomine and humans, respectively, in areas with a higher prevalence of infection, aiming to describe the main features associated with the transmission cycle. Out of the 207 dogs tested, 37 (17.8%, 95% CI = 12.6-23.1%) were positive for the presence of Leishmania antibodies by the IFAT test, and only 9 (4.3%, 95% CI = 1.55-7.15%) were positive for L. infantum by PCR. Multivariate analyses indicated that canine shelters and dogs with clinical signs commonly associated with canine VL had a higher prevalence of infection ($P < 0.05$). In the entomological survey, 69 blood-fed female phlebotomine of the genus Lutzomyia were captured in canine shelters, among them, 55% were identified as Lutzomyia camposi, 29% as Lu. ovallesi, 7% as Lu. dubitans, 6% as Lu. torvida, and 3% as Lu. cayennensis. The identified meal sources of the phlebotomine included human, pig, avian, cattle, and porcupine (Coendou quichua) blood. However, no phlebotomine positive for Leishmania spp. were detected by molecular analyses. Finally, 14 humans who had frequent contact with L. infantum-positive dogs were analyzed through rK39 test, but none tested was positive for IgG/IgM antibodies. The molecular and serological analyses indicate the circulation of L. infantum in dogs from MAB, with canine shelters having the highest prevalence of infection. The entomological survey of canine shelters showed a significant diversity of phlebotomine without potential vectors of L. infantum, suggesting the presence of infection in dogs from these areas could take place in other locations or through other transmission routes. The circulation of L. infantum in multiple dogs from MAB suggests a latent risk of zoonotic transmission of VL in these cities.

Enhanced antibacterial activity of dimethyl gallium quinolinolates toward drug-resistant Klebsiella pneumoniae in low iron environments.

Duffin RN, Andrews PC.
17-09-2023
J Inorg Biochem.
https://pubmed.ncbi.nlm.nih.gov/37738699/

A series of dimethylgallium quinolinolate [$GaMe_2L$] (L = 5-chloroquinolinolate, 5, 7-dichloroquinolinolate, 5, 7-dibromoquinolinolate or 5, 7-doiodoquinolinolate) complexes, shown previously to be active toward the Leishmania parasite, have been studied for their antibacterial activity toward a reference and drug resistant strain of Klebsiella pneumoniae (KP). The assays were conducted in standard iron-rich LB media and in the iron depleted RPMI and RPMI-HS media to better understand the effect of Fe concentration on the activity of the Ga complexes. In LB broth the parent quinolinols and the gallium complexes were inactive up to the highest concentration tested, 100 μM. In the more physiologically relevant 'iron-poor' RPMI-HS media the quinolonols remained inactive, however, the gallium complexes showed exceptional activity in the range 48-195 nM. Only in RPMI without any added HS did both the quinolinols and the gallium complexes show good activity. The significant

differences in activity across the various media types suggest that the unnaturally high iron content of conventional LB media may provide false negative results for potentially potent Ga therapeutics. A protein binding assay on the organometallic gallium complexes showed a much slower uptake of Ga by Fe-binding proteins than is typically observed for gallium salts. This indicates that their greater lipophilicity and greater hydrolytic stability could account for their increased biological activity in RPMI-HS media.

Reactive oxygen species trigger inflammasome activation after intracellular microbial interaction.

Rosa CP, Belo TCA, Santos NCM, Silva EN, Gasparotto J, Corsetti PP, de Almeida LA.
15-10-2023
Life Sci.
https://pubmed.ncbi.nlm.nih.gov/37683723/

The intracellular production of reactive oxygen species (ROS), composed of oxygen-reduced molecules, is important not only because of their lethal effects on microorganisms but also due to their potential inflammatory and metabolic regulation properties. The ROS pro-inflammatory properties are associated with the second signal to inflammasome activation, leading to cleaving pro-IL-1β and pro-IL18 before their secretion, as well as gasdermin-D, leading to pyroptosis. Some microorganisms can modulate NLRP3 and AIM-2 inflammasomes through ROS production: whilst Mycobacterium bovis, Mycobacterium kansasii, Francisella novicida, Brucella abortus, Listeria monocytogenes, Influenza virus, Syncytial respiratory virus, Porcine reproductive and respiratory syndrome virus, SARS-CoV, Mayaro virus, Leishmania amazonensis and Plasmodium sp. enhance inflammasome assembly, Hepatitis B virus, Mycobacterium marinum, Mycobacterium tuberculosis, Francisella tularensis and Leishmania sp. disrupt it. This process represents a recent cornerstone in our knowledge of the immunology of intracellular pathogens, which is reviewed in this mini-review.

Synthesis of new 3-acetyl-1,3,4-oxadiazolines combined with pyrimidines as antileishmanial and antiviral agents.

Lachhab S, El Mansouri AE, Mehdi A, Dennemont I, Neyts J, Jochmans D, Andrei G, Snoeck R, Sanghvi YS, Ait Ali M, Loiseau PM, Lazrek HB.
Oct-2023
Mol Divers.
https://pubmed.ncbi.nlm.nih.gov/36251201/

Lèpre

Bilateral Thickened Transverse Cervical Nerve in a Leprosy Patient.

Prabha N, Khare S, Yadav H.
29-09-2023
Skinmed.
https://pubmed.ncbi.nlm.nih.gov/37771020/

Highly sensitive and rapid determination of Mycobacterium leprae based on real-time multiple cross displacement amplification.

Huang J, Tong Y, Chen Y, Yang X, Wei X, Chen X, Li J, Li S.
28-09-2023
BMC Microbiol.
https://pubmed.ncbi.nlm.nih.gov/37770823/

A cluster onset of acute and accelerated silicosis cases in workers of ramming mass industries in Jharkhand, Eastern India.

Singh D, Carr SK, Sarkar B, Ali SI, Sarkar K.
Août-2023
J Family Med Prim Care.
https://pubmed.ncbi.nlm.nih.gov/37767429/

Introduction and methodology: A cross-sectional study was conducted among workers of ramming mass industries in the East Singhbhum district of Jharkhand, eastern India. Workers had occupational exposure to respirable crystalline silica dust of varied duration between 1 and 6 years. A total of 122 subjects participated in it. Relevant epidemiological information was collected from them. All were x-rayed using 300 mA radiation for the detection of the presence of silicotic opacities if any as described by the International Labour Organisation (ILO) for the detection of silicosis. Results: The study revealed that 61.4% (n = 75) of subjects had silicosis. Of them, 19 had acute silicosis (having a duration of silica dust exposure of 2 years or lesser) and 56 had accelerated silicosis (a duration of occupational exposure of > 2 to 6 years). The offending agent was clouds of respirable crystalline silica dust from the ramming mass industries. Epidemiological interpretation: To the best of our knowledge, this is the first report of an outbreak of acute and accelerated silicosis cases because of occupational inhalational exposure to ramming mass in India with a sizable portion of female workers with silicosis. Regional as well as national authorities need to take appropriate interventional measures in a programmatic mode as soon as possible. Conclusion: An in-depth investigation on the existence and magnitude of the problem of silico-tuberculosis is needed to be performed in them as silicosis increases the vulnerability of pulmonary tuberculosis among the affected workers.

Integrated control of neglected tropical diseases in Brazil: document review of a national campaign in light of WHO recommendations.

Soares RCR, de Carvalho AG, Luz JGG, Lucas ALZ, Ignotti E.
26-09-2023
Rev Panam Salud Publica.
https://pubmed.ncbi.nlm.nih.gov/37767238/

Objective: To describe the results of a national campaign aimed at the integrated control of neglected tropical diseases in Brazil in light of the World Health Organization (WHO) official documentation related to the integration of strategies for the prevention, control, and elimination or eradication of neglected tropical diseases. **Methods:** A document review that included official WHO documents published between 2007 and 2020 and campaign results extracted from the official technical report produced by the Brazilian Ministry of Health. **Results:** The integrated control of neglected tropical diseases was gradually incorporated in the WHO documentation over time. Preventive chemotherapy through mass drug administration, intensified case management, and integrated vector management were extensively recommended as strategies for integrated control. The Brazilian campaign was carried out in four iterations between 2013 and 2017. Children aged 5 to 14 years enrolled in municipal public schools nationwide were targeted. In summary, a total of 1 074 and 73 522 new cases of leprosy and trachoma, respectively, were detected. Nearly 18 million doses of preventive chemotherapy for soil-transmitted helminthiasis were administered. More than 700 cases of schistosomiasis were diagnosed and treated. **Conclusions:** The integrated strategies implemented in Brazil throughout the campaign generated results aligned with the WHO recommendations for the control of neglected tropical diseases, especially those regarding mass drug administration, active case detection, and intensified case management. Therefore, the continuity of the campaign with adequate evaluation tools must be encouraged as a constant public health policy in the Brazilian government agenda.

Distinguishing the Concentration- vs. Bioaccumulation-Dependent Immunological and Metabolic Effects of Clofazimine.

Willmer AR, Diaz-Espinosa J, Zhou A, Stringer KA, Rosania GR.
20-09-2023
Pharmaceutics.
https://pubmed.ncbi.nlm.nih.gov/37765318/

Leprosy Neuropathy in a Non-Endemic Area: A Clinical and Pathological Study.

Cotti Piccinelli S, Tagliapietra M, Cavallaro T, Labella B, Risi B, Caria F, Damioli S, Poli L, Padovani A, Ferrari S, Filosto M.
06-09-2023
Biomedicines.
https://pubmed.ncbi.nlm.nih.gov/37760909/

The extent of nerve involvement in leprosy is highly variable in distribution and clinical presentation. Mononeuropathies, multiple mononeuropathies, and polyneuropathies can present both in the context of a cutaneous and/or systemic picture and in the form of pure neuritic leprosy (PNL). The differential diagnosis of leprosy neuropathy remains challenging because it is a very rare condition and, especially in Western countries, is often overlooked. We report one case of the polyneuropathic form of PNL (P-PNL) and one case of multiple mononeuropathy in paucibacillary leprosy. In both cases, the diagnosis was achieved by performing a sural nerve biopsy, which showed subverted structure, severe infiltration of inflammatory cells in nerve fascicles, granulomatous abnormalities, and the presence of alcohol-acid-resistant, Ziehl-Neelsen-positive bacilli inside the nerve bundles. Leprosy remains an endemic disease in many areas of the world, and globalization has led to the spread of cases in previously disease-free countries. In this perspective, our report emphasizes that the diagnostic possibility of leprosy neuropathy should always be taken into account, even in Western countries, in the differential diagnostic process of an acquired sensory polyneuropathy or multineuropathy and confirms that nerve biopsy remains a useful procedure in working up neuropathies with unknown etiology.

Leprosy-specific subsets of macrophages and Schwann cells identified by single-cell RNA-sequencing.

Shin S, Choi EJ, Moon SW, Lee SB, Chung YJ, Lee SH.
22-09-2023
Pathol Res Pract.
https://pubmed.ncbi.nlm.nih.gov/37757621/

A case-control study addressing the population of epidermal and dermal inflammatory infiltrate including neural milieu in primary prurigo nodularis using S-100 and toluidine blue stain and its therapeutic implications.

Agrawal D, Sardana K, Mathachan SR, Bhardwaj M, Ahuja A, Jain S, Panesar S.
27-09-2023
Int J Dermatol.
https://pubmed.ncbi.nlm.nih.gov/37753716/

One Case of Tuberculosis-Like Leprosy with a Type I Leprosy Reaction.

Li J, Wang CH, Yu DH, He Q, He W.
18-09-2023
Clin Cosmet Investig Dermatol.
https://pubmed.ncbi.nlm.nih.gov/37745274/

Clofazimine: A journey of a drug.

Xu J, Koval A, Katanaev VL.
22-09-2023
Biomed Pharmacother.
https://pubmed.ncbi.nlm.nih.gov/37742606/

Among different strategies to develop novel therapies, drug repositioning (aka repurposing) aims at identifying new uses of an already approved or investigational drug. This approach has the advantages of availability of the extensive pre-existing knowledge of the drug's safety, pharmacology and toxicology, manufacturing and formulation. It provides advantages to the risk-versus-rewards trade-off as compared to the costly and time-consuming de novo drug discovery process. Clofazimine, a

red-colored synthetic derivative of riminophenazines initially isolated from lichens, was first synthesized in the 1950 s, and passed through several phases of repositioning in its history as a drug. Being initially developed as an anti-tuberculosis treatment, it was repurposed for the treatment of leprosy, prior to re-repositioning for the treatment of multidrug-resistant tuberculosis and other infections. Since 1990 s, reports on the anticancer properties of clofazimine, both in vitro and in vivo, started to appear. Among the diverse mechanisms of action proposed, the activity of clofazimine as a specific inhibitor of the oncogenic Wnt signaling pathway has recently emerged as the promising targeting mechanism of the drug against breast, colon, liver, and other forms of cancer. Seventy years after the initial discovery, clofazimine's journey as a drug finding new applications continues, serving as a colorful illustration of drug repurposing in modern pharmacology.

High-Resolution Plasma Metabolomics Identifies Alterations in Fatty Acid, Energy, and Micronutrient Metabolism in Adults across the Leprosy Spectrum.

Fairley JK, Ferreira JA, Fraga LAO, Lyon S, Valadão Cardoso TM, Campos Boson V, Nunes ACM, Medeiros Cinha EH, de Oliveira LBP, Magueta EB, Marçal PHF, Branco AC, Grossi MAF, Jones DP, Ziegler TR, Collins JM.
22-09-2023
J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37740551/

Background: High resolution metabolomics (HRM) is an innovative tool to study challenging infectious diseases like leprosy, where the pathogen cannot be grown with standard methods. Here, we use HRM to better understand associations between disease manifestations, nutrition, and host metabolism. Methods: From 2018-2019, adults with leprosy and controls were recruited in Minas Gerais, Brazil. Plasma metabolites were detected using an established HRM workflow and characterized by accurate mass m/z and retention time. The mummichog informatics package compared metabolic pathways between cases and controls and between multibacillary (MB) and paucibacillary (PB) leprosy. Additionally, select individual metabolites were quantified and compared. Results: Thirty-nine cases (62% MB and 38% PB) and 25 controls were enrolled. We found differences ($p<0.05$) in several metabolic pathways, including fatty acid metabolism, carnitine shuttle, retinol, vitamin D3, and C-21 steroid metabolism between cases and controls with lower retinol and associated metabolites in cases. Between MB and PB, leukotrienes, prostaglandins, tryptophan, and cortisol were all found to be lower in MB ($p<0.05$). Discussion: Metabolites associated with several nutrient-related metabolic pathways appeared differentially regulated in leprosy, especially MB vs PB. This pilot study demonstrates the metabolic interdependency of these pathways, which may play a role in the pathophysiology of disease.

Biosensor-Based Multiple Cross Displacement Amplification for the Rapid Detection of Mycobacterium leprae.

Huang J, Tong Y, Yang X, Chen Y, Wei X, Chen X, Li J, Li S.
22-09-2023
ACS Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37738642/

Leprosy is an ancient disease caused by *Mycobacterium leprae* (ML) that remains a public health problem in poverty-stricken areas worldwide. Although many ML detection techniques have been used, a rapid and sensitive tool is essential for the early detection and treatment of leprosy. Herein, we developed a rapid ML detection technique by combining multiple cross displacement amplification (MCDA) with a nanoparticle-based lateral flow biosensor (LFB), termed ML-MCDA-LFB. MCDA induced a rapid isothermal reaction using specific primers targeting the RLEP gene, and the LFB enabled instant visual amplicon detection. The pure genomic DNA of ML and nucleic acids from various pathogens were employed to evaluate and optimize the ML-MCDA-LFB assay. The optimal conditions for ML-MCDA-LFB were 68 °C and 35 min, respectively. The limit of detection for pure ML genomic DNA was 150 fg per vessel, and the specificity of detection was 100% for the experimental strains. Additionally, the entire detection process could be performed within 40 min, including the isothermal amplification (35 min) and result confirmation (1-2 min). Hence, the ML-MCDA-LFB assay was shown to be a rapid, sensitive, and visual method for detecting ML and could be used as a potential tool for early clinical diagnosis and field screening of leprosy.

Efficacy and safety of an inactivated virus-particle vaccine for SARS-CoV-2, BIV1-CovIran: randomised, placebo controlled, double blind, multicentre, phase 3 clinical trial.

Mohraz M, Vahdat K, Ghamari SH, Abbasi-Kangevari M, Ghasemi E, Ghabdian Y, Rezaei N, Pouya MA, Abdoli A, Malekpour MR, Koohgir K, Saeedi Moghaddam S, Tabarsi P, Moghadami M, Khorvash F, Khodashahi R, Salehi M, Hosseini H.
21-09-2023
BMJ.
https://pubmed.ncbi.nlm.nih.gov/37734752/

Automated chronic wounds medical assessment and tracking framework based on deep learning.

Monroy B, Sanchez K, Arguello P, Estupiñán J, Bacca J, Correa CV, Valencia L, Castillo JC, Mieles O, Arguello H, Castillo S, Rojas-Morales F.
Oct-2023
Comput Biol Med.
https://pubmed.ncbi.nlm.nih.gov/37633087/

Chronic wounds are a latent health problem worldwide, due to high incidence of diseases such as diabetes and Hansen. Typically, wound evolution is tracked by medical staff through visual inspection, which becomes problematic for patients in rural areas with poor

transportation and medical infrastructure. Alternatively, the design of software platforms for medical imaging applications has been increasingly prioritized. This work presents a framework for chronic wound tracking based on deep learning, which works on RGB images captured with smartphones, avoiding bulky and complicated acquisition setups. The framework integrates mainstream algorithms for medical image processing, including wound detection, segmentation, as well as quantitative analysis of area and perimeter. Additionally, a new chronic wounds dataset from leprosy patients is provided to the scientific community. Conducted experiments demonstrate the validity and accuracy of the proposed framework, with up to 84.5% in precision.

Lapatinib-induced PRIDE complex: a new kid on the block.

Sil A, Sikder B, Biswas SK, Chandra A.
21-09-2023
Postgrad Med J.
https://pubmed.ncbi.nlm.nih.gov/37535871/

Morsures de serpent

Clinical, laboratory profile and outcomes in children with snakebite from Eastern India.

Pattanaik B, Mahapatra C, Karthika IK, Satapathy AK, John J, Das RR, Dwibedi B, Mahapatro S, Gulla KM.
Août-2023
J Family Med Prim Care.
https://pubmed.ncbi.nlm.nih.gov/37767426/

Novel Toxicodynamic Model of Subcutaneous Envenomation to Characterize Snake Venom Coagulopathies and Assess the Efficacy of Site-Directed Inorganic Antivenoms.

Nielsen VG.
11-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762243/

Venomous snake bite adversely affects millions of people yearly, but few animal models allow for the determination of toxicodynamic timelines with hemotoxic venoms to characterize the onset and severity of coagulopathy or assess novel, site-directed antivenom strategies. Thus, the goals of this investigation were to create a rabbit model of subcutaneous envenomation to assess venom toxicodynamics and efficacy of ruthenium-based antivenom administration. New Zealand White rabbits were sedated with midazolam via the ear vein and had viscoelastic measurements of whole blood and/or plasmatic coagulation kinetics obtained from ear artery samples. Venoms derived from *Crotalus scutulatus scutulatus*, *Bothrops moojeni*, or *Calloselasma rhodostoma* were injected subcutaneously, and changes in coagulation were determined over three hours and compared to samples obtained prior to envenomation. Other rabbits had ruthenium-based antivenoms injected five minutes after venom injection. Viscoelastic analyses demonstrated diverse toxicodynamic patterns of coagulopathy consistent with the molecular composition of the proteomes of the venoms tested. The antivenoms tested attenuated venom-mediated coagulopathy. A novel rabbit model can be used to characterize the onset and severity of envenomation by diverse proteomes and to assess site-directed antivenoms. Future investigation is planned involving other medically important venoms and antivenom development.

Oral and IV Varespladib Rescue Experiments in Juvenile Pigs with Weakness Induced by Australian and Papuan Oxyuranus scutellatus Venoms.

Gilliam LL, Gilliam J, Samuel SP, Carter RW, Ritchey J, Bulfone T, Gutiérrez JM, Williams DJ, Durkin DM, Stephens SI, Lewin MR.
07-09-2023
Toxins (Basel).
https://pubmed.ncbi.nlm.nih.gov/37755983/

Inflammatory Profile Associated with Secondary Infection from Bothrops atrox Snakebites in the Brazilian Amazon.

Cavalcante TTA, de Souza MBS, Neves JCF, Ibiapina HNS, Barbosa FBA, Bentes KO, Alves EC, Marques HO, Colombini M, Sampaio SV, Pucca MB, Silva IMD, Ferreira LCL, Sampaio VS, Moura-da-Silva AM, Costa AG, Monteiro WM, Sachett JAG, Sartim MA.
26-08-2023
Toxins (Basel).
https://pubmed.ncbi.nlm.nih.gov/37755950/

Bothrops snakebite envenomation (SBE) is consider an important health problem in Brazil, where *Bothrops atrox* is mainly responsible in the Brazilian Amazon. Local effects represent a relevant clinical issue, in which inflammatory signs and symptoms in the bite site represent a potential risk for short and long-term disabilities. Among local complications, secondary infections (SIs) are a common clinical finding during *Bothrops atrox* SBE and are described by the appearance of signs such as abscess, cellulitis or necrotizing fasciitis in the affected site. However, the influence of SI in the local events is still poorly understood. Therefore, the present study describes for the first time the impact of SBE wound infection on local manifestations and inflammatory response from patients of *Bothrops atrox* SBE in the Brazilian Amazon. This was an observational study carried out at the Fundação de Medicina Tropical Dr. Heitor Vieira Dourado, Manaus (Brazil), involving victims of *Bothrops* SBE. Clinical and laboratorial data were collected along with blood samples for the quantification of circulating cytokines and chemokines before antivenom administrations (T0) and 24 h (T1), 48 h (T2), 72 h (T3) and 7 days after (T4). From the 94 patients included in this study, 42 presented SI (44.7%) and 52 were without SI (NSI, 55.3%). Patients classified as moderate envenoming presented an increased risk of developing SI (OR = 2.69; CI 95% = 1.08-6.66, p = 0.033), while patients with bites in hands showed a lower risk (OR

= 0.20; CI 95% = 0.04-0.96, *p* = 0.045). During follow-up, SI patients presented a worsening of local temperature along with a sustained profile of edema and pain, while NSI patients showed a tendency to restore and were highlighted in patients where SI was diagnosed at T2. As for laboratorial parameters, leukocytes, erythrocyte sedimentation ratio, fibrinogen and C-reactive protein were found increased in patients with SI and more frequently in patients diagnosed with SI at T3. Higher levels of circulating IL-2, IL-10, IL-6, TNF, INF-γ and CXCL-10 were observed in SI patients along with marked correlations between these mediators and IL-4 and IL-17, showing a plurality in the profile with a mix of Th1/Th2/Th17 response. The present study reports for the first time the synergistic effects of local infection and envenoming on the inflammatory response represented by local manifestations, which reflected on laboratorial parameters and inflammatory mediators and thus help improve the clinical management of SI associated to *Bothrops* SBE.

Barriers and opportunities for improving management of snakebites: Perspectives of healthcare workers in Northern Uganda.

Wafula ST, Namakula LN, Ninsiima LR, Ssekamatte NK, Walekhwa AW, Mugume IB, Musoke D.
25-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37747844/

Background: Snakebites are a neglected public health problem that pose a significant burden on affected individuals and communities in many sub-Saharan African countries, including Uganda. However, the barriers and facilitators to snakebite management within healthcare settings are not as well understood and well-documented. The aim of this study was to explore the experiences and perspectives of healthcare workers involved in handling snakebite incidents at individual and health system levels in Arua and Gulu districts in Northern Uganda. We sought to understand how healthcare workers manage snakebite cases, what challenges they encounter, and what opportunities they perceive for improvement. Methods: We conducted a qualitative study using in-depth interviews with 18 healthcare workers from different cadres, seniority levels, and facility types. We used iterative thematic analysis to explore the management procedures, challenges, and opportunities for snakebite management. Using thematic analysis, we identified the overarching themes and subthemes related to snakebite management and associated barriers and opportunities. Results: The main barriers to snakebite management identified by healthcare workers were inadequate knowledge and skills; limited availability of antivenom; lack of protocols for snakebite management; delayed treatment-seeking for patients; and poor referral systems. The main opportunities for improvement were regular in-service training; increasing public education and awareness about snakebite prevention and management; and increased funding and research. Conclusion: This study highlights the need for interventions to address the identified barriers while leveraging the existing opportunities to enhance snakebite management in Uganda. Specifically, we recommend the provision of regular training and support to healthcare workers, developing clinical guidelines, and improving the availability of antivenoms.

Antivenom supply and demand: An analysis of antivenom availability and utilization in South Africa.

Neumann NR, du Plessis A, van Hoving DJ, Hoyte CO, Lermer A, Wittels S, Marks C.
Dec-2023
Afr J Emerg Med.
https://pubmed.ncbi.nlm.nih.gov/37745277/

Snakebite Envenoming in Avian Species: A Systematic Scoping Review and Practitioner Experience Survey.

Cummings CO, Eisenbarth JM.
Sep-2023
J Avian Med Surg.
https://pubmed.ncbi.nlm.nih.gov/37733451/

Snakebite envenoming in avian species is infrequently reported in the veterinary literature, although perhaps not as rarely as recent publications suggest. A systematic scoping review was performed on the topic using PubMed and Google Scholar, 21 veterinary textbooks, and 139 conference proceedings. A practitioner experience survey was also performed, with recruitment from Facebook groups for exotic animal practitioners and professional organization email listservs. Only 31 texts met our inclusion/exclusion criteria, which meant they described clinicopathologic signs of snakebite envenomation in avian species, the treatment of snakebite envenomation in avian species, or expanded the geographic range or the number of captive avian and snake species involved. Reports included approximately 15-20 different species of both snakes and birds worldwide; however, no reports described clinicopathologic signs of naturally occurring snakebites from Asia, Australasia, or Europe. The few responses from our practitioner experience survey suggest that snakebite envenomation may be more common than previously reported. Clinical signs of snake envenomation in birds appear to depend on the snake species involved but often include local swelling and subcutaneous edema or hemorrhage with paired fang marks; weakness, bleeding, neurologic deficits, and death may follow. A wide variety of treatment protocols have been used to counter snakebite envenomation in birds, including the successful use of antivenom. Based on this body of evidence, much remains to be learned about snakebite envenomation of birds, particularly about the efficacy of different treatment protocols.

Mycétome

Effect of Mycetoma in Lung Transplant Patients - a Single Center Experience.

Singh S, Lum J, Majeed A.
25-09-2023

Transplant Proc.
https://pubmed.ncbi.nlm.nih.gov/37758562/

Background: Mycetomas are uncommon in lung transplant recipients. Prior studies have shown increased mortality associated with mycetoma in lung transplant recipients (LTR). We reviewed our center's experience in outcome of LTRs with pre -or post-transplant mycetoma. **Methods:** We retrospectively reviewed electronic health records of LTRs performed at our institute between January 1, 2013 to December 31, 2020. **Results:** Mycetoma was present in less than 1 percent of LTR patients (7/1086). Mean age at the time of the transplant was 65 years. Idiopathic pulmonary fibrosis (5/7), interstitial lung disease (1/7), and sarcoidosis (1/7) were underlying pulmonary diagnoses. Seventy-one percent (5/7) received single lung transplant and 29% received double lung transplant. Seventy-one percent had negative serum galactomannan vs 29% (2/7) of patients who had positive serum galactomannan (one post and one pre). Fifty-seven percent had positive bronchoalveolar aspergillus galactomannan (23% had negative). A total of 42% (3/7) were found to have mycetoma before transplant and 58% (4/7) had mycetoma post transplant. Chest computed tomography findings in all patients were consistent with mycetoma. **Conclusions:** In our cohort of patients, mycetoma was not found to be the primary cause of death if diagnosed pre transplant. Transplant recipients with mycetoma pre transplant did not develop invasive fungal infection or mycetoma post transplant. Careful evaluation of lung transplant candidates with mycetoma is critical. Further studies are needed to determine optimal duration of antifungal therapy and to determine if surgical resection may be needed to manage post-lung transplant mycetoma.

Subcutaneous mycoses: Endemic but neglected among the Neglected Tropical Diseases in Ethiopia.

Enbiale W, Bekele A, Manaye N, Seife F, Kebede Z, Gebremeskel F, van Griensven J.
27-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37756346/

Background: Subcutaneous (deep) mycoses are a chronic infectious disease of the skin and underlying structures endemic in tropical countries. The disease has serious medical and socioeconomic consequences for patients, communities and health services in endemic areas. The inclusion of mycetoma and other subcutaneous mycoses in the list of Neglected Tropical Diseases by WHO highlights the need to assess the burden of these diseases and establish control programs where necessary. In Ethiopia no strategies can be devised because of a lack of epidemiologic information. To address this evidence gap, we performed a national rapid assessment of the geographic distribution of subcutaneous mycoses. **Methodology:** We conducted a rapid retrospective assessment using hospital records to identify all suspected and confirmed cases of subcutaneous mycoses in 13 referral hospitals across the country between 2015 and 2022. In each hospital the logbooks were reviewed for diagnoses of subcutaneous mycosess, as diagnosed per routine practice. Descriptive analysis was done. **Result:** From 13 hospitals we extracted 143 cases of subcutaneous mycoses, registered from July 2018 to September 2022. 118 (82.5%) patients were diagnosed as mycetoma, 21 (14.7%) as chromoblastomycosis and the remaining 4 (2.8%) as sporotrichosis. The mean age of patients was 35.8 years (SD = 14.5). 101 (70.6%) patients were male and 96 (67.1%) patients were farmers. 64 (44.8%) cases were from the Tigray regional state. 56 (65.9%) patients had information on diagnostic microscopic evaluation: for mycetoma histopathologic evaluation and fine needle aspiration cytology had a higher positivity rate while for chromoblastomycosis potassium hydroxide (KOH) staining had a better yield. The main clinical presentations were nodules, sinuses and infiltrative plaques on the skin. Radiologic findings of bone involvement was present in some. **Conclusions:** Mycetoma and other subcutaneous mycoses are endemic in Ethiopia, with cases reported from almost all regions with the highest cases numbers reported from the northern part of the country. A routine program and systems should be developed to identify and document the burden of subcutaneous fungal infections in the country. Diagnosis and treatment guidelines should be developed.

Onchocercose

Procedure for Handling and Storage of Onchocerca volvulus Microfilariae Obtained from Skin Snips for Downstream Genetic Work.

Hedtke SM, Kode A, Ukety TO, Mande JL, Abhafule GM, Raciu AA, Uvon CB, Jada SR, Hotterbeekx A, Siewe Fodjo JN, Mitreva M, Sebit W, Colebunders R, Grant WN, Kuesel AC.
12-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755906/

Pian

Endemic infectious cutaneous ulcers syndrome in the Oti Region of Ghana: Study of cutaneous leishmaniasis, yaws and Haemophilus ducreyi cutaneous ulcers.

Akuffo RA, Sanchez C, Amanor I, Amedior JS, Kotey NK, Anto F, Azurago T, Ablordey A, Owusu-Antwi F, Beshah A, Amoako YA, Phillips RO, Wilson M, Asiedu K, Ruiz-Postigo JA, Moreno J, Mokni M.
27-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37756291/

Background: A recent study detected cutaneous leishmaniasis (CL) in 31.9% of persons with skin ulcers in the Oti Region of Ghana, resulting in a need to investigate other potential causes of the unexplained skin ulcers. **Methodology/principal findings:** A community based cross-sectional study was conducted in the Oti region to investigate skin ulcers of undetermined aetiologies. To confirm a diagnosis of cutaneous leishmaniasis, Buruli

ulcer, Haemophilus ducreyi ulcers, or yaws, DNA obtained from each patient skin ulcer sample was systematically subjected to polymerase chain reaction (PCR) for Leishmania spp., Mycobacterium ulcerans, Haemophilus ducreyi, and Treponema pallidum sub species pertenue. A total of 101 skin ulcer samples were obtained from 101 persons. Co-infection of more than one organism was observed in 68.3% of the samples. Forty (39.6%) participants had a positive result for Leishmania spp., 68 (67.3%) for Treponema pallidum sub. Sp. pertenue, and 74 (73.3%) for H. ducreyi. Twenty (19.8%) of the patient ulcers were simultaneously infected with Leishmania spp., Treponema pallidum sub. Sp. pertenue, and H. ducreyi. None of the patients' lesions yielded a positive result for Mycobacterium ulcerans. Conclusions/significance: This study detected single and mixed occurrence of the causative organisms of CL, yaws, and H. ducreyi cutaneous ulcers in CL endemic communities of the Oti Region in Ghana. These findings emphasize the importance of integrating multiple skin diseases on a common research platform and calls for the development of a comprehensive guideline for diagnosing and treating tropical ulcers in the study areas.

Rage

mAb therapy controls CNS-resident lyssavirus infection via a CD4 T cell-dependent mechanism.

Mastraccio KE, Huaman C, Coggins SA, Clouse C, Rader M, Yan L, Mandal P, Hussain I, Ahmed AE, Ho T, Feasley A, Vu BK, Smith IL, Markotter W, Weir DL, Laing ED, Broder CC, Schaefer BC.
28-09-2023
EMBO Mol Med.
https://pubmed.ncbi.nlm.nih.gov/37767784/

Infections with rabies virus (RABV) and related lyssaviruses are uniformly fatal once virus accesses the central nervous system (CNS) and causes disease signs. Current immunotherapies are thus focused on the early, pre-symptomatic stage of disease, with the goal of peripheral neutralization of virus to prevent CNS infection. Here, we evaluated the therapeutic efficacy of F11, an anti-lyssavirus human monoclonal antibody (mAb), on established lyssavirus infections. We show that a single dose of F11 limits viral load in the brain and reverses disease signs following infection with a lethal dose of lyssavirus, even when administered after initiation of robust virus replication in the CNS. Importantly, we found that F11-dependent neutralization is not sufficient to protect animals from mortality, and a CD4 T cell-dependent adaptive immune response is required for successful control of infection. F11 significantly changes the spectrum of leukocyte populations in the brain, and the FcRγ-binding function of F11 contributes to therapeutic efficacy. Thus, mAb therapy can drive potent neutralization-independent T cell-mediated effects, even against an established CNS infection by a lethal neurotropic virus.

Sequencing and Partial Molecular Characterization of BAB-TMP, the Babeş Strain of the Fixed Rabies Virus Adapted for Multiplication in Cell Lines.

Podgoreanu P, Petre A, Tănasă RI, Dinu S, Oprea M, Marandiuc IM, Vlase E.
31-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766258/

Genomic Surveillance of Rabies Virus in Georgian Canines.

Huaman C, Paskey AC, Clouse C, Feasley A, Rader M, Rice GK, Luquette AE, Fitzpatrick MC, Drumm HM, Yan L, Cer RZ, Donduashvili M, Buchukuri T, Nanava A, Hulseberg CE, Washington MA, Laing ED, Malagon F, Broder CC, Bishop-Lilly KA, Schaefer BC.
24-08-2023
Viruses.
https://pubmed.ncbi.nlm.nih.gov/37766204/

Rabies is a fatal zoonosis that is considered a re-emerging infectious disease. Although rabies remains endemic in canines throughout much of the world, vaccination programs have essentially eliminated dog rabies in the Americas and much of Europe. However, despite the goal of eliminating dog rabies in the European Union by 2020, sporadic cases of dog rabies still occur in Eastern Europe, including Georgia. To assess the genetic diversity of the strains recently circulating in Georgia, we sequenced seventy-eight RABV-positive samples from the brain tissues of rabid dogs and jackals using Illumina short-read sequencing of total RNA shotgun libraries. Seventy-seven RABV genomes were successfully assembled and annotated, with seventy-four of them reaching the coding-complete status. Phylogenetic analyses of the nucleoprotein (N) and attachment glycoprotein (G) genes placed all the assembled genomes into the Cosmopolitan clade, consistent with the Georgian origin of the samples. An amino acid alignment of the G glycoprotein ectodomain identified twelve different sequences for this domain among the samples. Only one of the ectodomain groups contained a residue change in an antigenic site, an R264H change in the G5 antigenic site. Three isolates were cultured, and these were found to be efficiently neutralized by the human monoclonal antibody A6. Overall, our data show that recently circulating RABV isolates from Georgian canines are predominantly closely related phylogroup I viruses of the Cosmopolitan clade. Current human rabies vaccines should offer protection against infection by Georgian canine RABVs. The genomes have been deposited in GenBank (accessions: OQ603609-OQ603685).

Does Perioperative Administration of Rabies Vaccine in Dogs Undergoing Surgical Sterilization Induce an Adequate Antibody Response?

Peda A, Samaniego P, Daugherty C, Wood T, Wang C, Knobel D.
25-08-2023
Vaccines (Basel).

https://pubmed.ncbi.nlm.nih.gov/37766095/

High-volume spay/neuter events may facilitate access to free-roaming dogs to administer rabies vaccination, but important questions remain regarding the effect of surgery and anesthesia on the immune response to a vaccine administered in the perioperative period. This study evaluated the immunogenicity of primary rabies vaccination in dogs when administered during the immediate perioperative period at the time of surgical sterilization (ovariohysterectomy/orchidectomy). Healthy dogs of both sexes presenting for surgical sterilization who had never been vaccinated against rabies virus were eligible for enrollment in the study. Fifty dogs ranging in age from 5 to 96 months were enrolled and were vaccinated against rabies virus during the recovery period following anesthesia and surgery. Rabies virus neutralizing antibody (RVNA) titers were measured preoperatively and 28 days postoperatively. This cohort was compared to a historical control cohort of 57 dogs who received primary rabies vaccination for travel purposes and had RVNA titers measured at the same laboratory as the study group 28-35 days post-vaccination. After controlling for age and sex, there was no statistically significant difference in immunogenicity of a rabies vaccine administered to dogs during the perioperative period in comparison to dogs that received the rabies vaccine for travel alone in the absence of surgery. Perioperative administration of a rabies vaccine in dogs undergoing surgical sterilization induces an adequate antibody response. We recommend that rabies vaccine be administered perioperatively during spay/neuter campaigns in canine rabies endemic areas if other opportunities to access veterinary care and rabies vaccination are limited.

Phylogeographic Aspects of Bat Lyssaviruses in Europe: A Review.

Dundarova H, Ivanova-Aleksandrova N, Bednarikova S, Georgieva I, Kirov K, Miteva K, Neov B, Ostoich P, Pikula J, Zukal J, Hristov P.
27-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764897/

Epidemiology and Control of Rabies in Cattle and Equines in Rondônia State, a Brazilian's Legal Amazon Area.

Sodré DNA, Rossi GAM, Mathias LA, de Andrade Belo MA.
20-09-2023
Animals (Basel).
https://pubmed.ncbi.nlm.nih.gov/37760375/

Rabies is a fatal neglected tropical zoonosis, and its significance for domestic herbivores in the rural cycle is probably associated with rainforest deforestation, livestock, and agricultural expansion. This epidemiological survey aimed to study the occurrence of rabies in bovines and equines in the state of Rondônia, located in the Brazilian's Legal Amazon, between the years 2002 and 2021, correlating these findings with the prophylactic strategies adopted by the local sanitary agency for rabies control. During this period, 201 cases were observed in bovines and 23 in equines. A downward trend in rabies incidence was observed for both domestic herbivores. Rabies did not show a higher occurrence in any specific time of the year, and epidemic periods varied during some years for bovines and equines. Using the Generalized estimating equations (GEE) method, a multiple model approach was obtained with the explanatory variables significantly associated with the decrease in rabies incidence in cattle and horses during the study period: the ratio of treated bats and ratio of vaccine doses sold. Furthermore, the ratio of printed educative material was positively associated with rabies incidence. Despite a decreasing trend in rabies occurrences in this Amazon rainforest area, likely due to the actions taken by the animal sanitary agency, rabies remains endemic and requires monitoring, as well as prophylactic strategies to control this disease.

ATLAS: A rationally designed anterograde transsynaptic tracer.

Rivera JF, Weng W, Huang H, Rao S, Herring BE, Arnold DB.
13-09-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37745471/

Neural circuits, which constitute the substrate for brain processing, can be traced in the retrograde direction, from postsynaptic to presynaptic cells, using methods based on introducing modified rabies virus into genetically marked cell types. These methods have revolutionized the field of neuroscience. However, similarly reliable, transsynaptic, and non-toxic methods to trace circuits in the anterograde direction are not available. Here, we describe such a method based on an antibody-like protein selected against the extracellular N-terminus of the AMPA receptor subunit GluA1 (AMPA.FingR). ATLAS (A nterograde T ranssynaptic L abel based on A ntibody-like S ensors) is engineered to release the AMPA.FingR and its payload, which can include Cre recombinase, from presynaptic sites into the synaptic cleft, after which it binds to GluA1, enters postsynaptic cells through endocytosis and subsequently carries its payload to the nucleus. Testing in vivo and in dissociated cultures shows that ATLAS mediates monosynaptic tracing from genetically determined cells that is strictly anterograde, synaptic, and non-toxic. Moreover, ATLAS shows activity dependence, which may make tracing active circuits that underlie specific behaviors possible.

A brain circuit and neuronal mechanism for decoding and adapting to change in daylength.

Maddaloni G, Chang YJ, Senft RA, Dymecki SM.
13-09-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37745319/

Changes in daylight amount (photoperiod) drive pronounced alterations in physiology and behaviour [1,2] . Adaptive responses to seasonal photoperiods are vital to all organisms - dysregulation is associated with disease, from affective disorders [3] to metabolic syndromes [4] . Circadian rhythm circuitry has been implicated [5,6] yet little

is known about the precise neural and cellular substrates that underlie phase synchronization to photoperiod change. Here we present a previously unknown brain circuit and novel system of axon branch-specific and reversible neurotransmitter deployment that together prove critical for behavioural and sleep adaptation to photoperiod change. We found that the recently defined neuron type called mr *En1-Pet1* [7] located in the mouse brainstem Median Raphe Nucleus (MRN) segregates serotonin versus VGLUT3 (here proxy for the neurotransmitter glutamate) to different axonal branches innervating specific brain regions involved in circadian rhythm and sleep/wake timing [8,9] . We found that whether measured during the light or dark phase of the day this branch-specific neurotransmitter deployment in mr *En1-Pet1* neurons was indistinguishable; however, it strikingly reorganizes on photoperiod change. Specifically, axonal boutons but not cell soma show a shift in neurochemical phenotype upon change away from equinox light/dark conditions that reverses upon return to equinox. When we genetically disabled the deployment of VGLUT3 in mr *En1-Pet1* neurons, we found that sleep/wake periods and voluntary activity failed to synchronize to the new photoperiod or was significantly delayed. Combining intersectional rabies virus tracing and projection-specific neuronal silencing *in vivo* , we delineated a Preoptic Area-to-mr *En1Pet1* connection responsible for decoding the photoperiodic inputs, driving the neurochemical shift and promoting behavioural synchronization. Our results reveal a previously unrecognized brain circuit along with a novel form of periodic, branch-specific neurotransmitter deployment that together regulate organismal adaptation to photoperiod changes.

Biodegradable Polyester Nanoparticle Vaccines Deliver Self-Amplifying mRNA in Mice at Low Doses.

Wilson DR, Tzeng SY, Rui Y, Neshat SY, Conge MJ, Luly KM, Wang E, Firestone JL, McAuliffe J, Maruggi G, Jalah R, Johnson R, Doloff JC, Green JJ.
Mai-2023
Adv Ther (Weinh).
https://pubmed.ncbi.nlm.nih.gov/37743930/

Spatio-temporal investigation of reported cases of animal rabies in Ghana from 2010 to 2017.

Turkson PK.
23-09-2032
Vet Med Sci.
https://pubmed.ncbi.nlm.nih.gov/37742084/

Background: Rabies is a zoonotic disease transmitted mainly by animals, especially dogs. Objective: The aim of the article was to examine reported cases of animal rabies in Ghana for trends to provide information that could be helpful to control the disease. Method: Retrospective analyses of reported cases of rabies in Ghana from 2010 to 2017. Results: In all, 328 rabies cases were recorded in animals in the period under review. The predominant species involved were dogs (299; 91.2%) and cats (12; 3.7%). Other species included pigs (4; 1.2%), goats (4; 1.2%), monkeys (4; 1.2%), sheep (2; 0.6%), bats (2; 0.6%) and cattle (1; 0.3%). The numbers of reported cases in animals were markedly higher than those in humans except in 2013 and 2017. There was a positive but weak correlation between cases in animals and humans which could be due to lack of reporting collaboration between institutions responsible for these. Greater Accra and Ashanti Regions were identified as hotspots in the period under review, while January and August were the months with the highest peaks for cases reported. Cases reported in rainy season were significantly higher than those in dry season. Poisson regression for spatio-temporal analyses showed no statistical significance in predicting number of rabies cases (response variable) from year, month, season, region and affected species (predictor variables). Conclusion: Rabies remained endemic in Ghana during 2010-2017 with cases reported in nearly every month of the year during this period. There was a significant seasonal pattern with higher proportion of cases reported in the rainy/wet season compared to the dry season.

Monkeypox virus-infected individuals mount comparable humoral immune responses as Smallpox-vaccinated individuals.

Otter AD, Jones S, Hicks B, Bailey D, Callaby H, Houlihan C, Rampling T, Gordon NC, Selman H, Satheshkumar PS, Townsend M, Mehta R, Pond M, Jones R, Wright D, Oeser C, Tonge S, Linley E, Hemingway G, Coleman T, Millward S, Lloyd A, Damon I, Brooks T, Vipond R, Rowe C, Hallis B.
23-09-2023
Nat Commun.
https://pubmed.ncbi.nlm.nih.gov/37741831/

In early 2022, a cluster of monkeypox virus (MPXV) infection (mpox) cases were identified within the UK with no prior travel history to MPXV-endemic regions. Subsequently, case numbers exceeding 80,000 were reported worldwide, primarily affecting gay, bisexual, and other men who have sex with men (GBMSM). Public health agencies worldwide have offered the IMVANEX Smallpox vaccination to these individuals at high-risk to provide protection and limit the spread of MPXV. We have developed a comprehensive array of ELISAs to study poxvirus-induced antibodies, utilising 24 MPXV and 3 Vaccinia virus (VACV) recombinant antigens. Panels of serum samples from individuals with differing Smallpox-vaccine doses and those with prior MPXV infection were tested on these assays, where we observed that one dose of Smallpox vaccination induces a low number of antibodies to a limited number of MPXV antigens but increasing with further vaccination doses. MPXV infection induced similar antibody responses to diverse poxvirus antigens observed in Smallpox-vaccinated individuals. We identify MPXV A27 as a serological marker of MPXV-infection, whilst MPXV M1 (VACV L1) is likely IMVANEX-specific. Here, we demonstrate analogous humoral antigen recognition between both MPXV-infected or Smallpox-vaccinated individuals, with binding to diverse yet core set of poxvirus antigens, providing opportunities for future vaccine (e.g., mRNA) and therapeutic (e.g., mAbs) design.

Schistosomiase

Discovery of long non-coding RNAs in the liver fluke, Fasciola hepatica.

McVeigh P, McCammick E, Robb E, Brophy P, Morphew RM, Marks NJ, Maule AG.
28-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37769025/

Long non-coding (lnc)RNAs are a class of eukaryotic RNA that do not code for protein and are linked with transcriptional regulation, amongst a myriad of other functions. Using a custom in silico pipeline we have identified 6,436 putative lncRNA transcripts in the liver fluke parasite, Fasciola hepatica, none of which are conserved with those previously described from Schistosoma mansoni. F. hepatica lncRNAs were distinct from F. hepatica mRNAs in transcript length, coding probability, exon/intron composition, expression patterns, and genome distribution. RNA-Seq and digital droplet PCR measurements demonstrated developmentally regulated expression of lncRNAs between intra-mammalian life stages; a similar proportion of lncRNAs (14.2%) and mRNAs (12.8%) were differentially expressed ($p<0.001$), supporting a functional role for lncRNAs in F. hepatica life stages. While most lncRNAs (81%) were intergenic, we identified some that overlapped protein coding loci in antisense (13%) or intronic (6%) configurations. We found no unequivocal evidence for correlated developmental expression within positionally correlated lncRNA:mRNA pairs, but global co-expression analysis identified five lncRNA that were inversely co-regulated with 89 mRNAs, including a large number of functionally essential proteases. The presence of micro (mi)RNA binding sites in 3135 lncRNAs indicates the potential for miRNA-based post-transcriptional regulation of lncRNA, and/or their function as competing endogenous (ce)RNAs. The same annotation pipeline identified 24,141 putative lncRNAs in F. gigantica. This first description of lncRNAs in F. hepatica provides an avenue to future functional and comparative genomics studies that will provide a new perspective on a poorly understood aspect of parasite biology.

Efficacy of Single-Dose Praziquantel for the Treatment of Schistosoma mansoni Infections among School Children in Rwanda.

Kabatende J, Ntirenganya L, Mugisha M, Barry A, Ruberanziza E, Bienvenu E, Bergman U, Aklillu E.
17-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764978/

Plumbagin: A Promising In Vivo Antiparasitic Candidate against Schistosoma mansoni and In Silico Pharmacokinetic Properties (ADMET).

Silva LMN, França WWM, Santos VHB, Souza RAF, Silva AM, Diniz EGM, Aguiar TWA, Rocha JVR, Souza MAA, Nascimento WRC, Lima Neto RG, Cruz Filho IJ, Ximenes ECPA, Araújo HDA, Aires AL, Albuquerque MCPA.
22-08-2023
Biomedicines.
https://pubmed.ncbi.nlm.nih.gov/37760782/

Schistosomiasis, a potentially fatal chronic disease whose etiological agents are blood trematode worms of the genus *Schistosoma* spp., is one of the most prevalent and debilitating neglected diseases. The treatment of schistosomiasis depends exclusively on praziquantel (PZQ), a drug that has been used since the 1970s and that already has reports of reduced therapeutic efficacy, related with the development of *Schistosoma*-resistant or -tolerant strains. Therefore, the search for new therapeutic alternatives is an urgent need. Plumbagin (PLUM), a naphthoquinone isolated from the roots of plants of the genus *Plumbago*, has aroused interest in research due to its antiparasitic properties against protozoa and helminths. Here, we evaluated the in vivo schistosomicidal potential of PLUM against *Schistosoma mansoni* and the in silico pharmacokinetic parameters. ADMET parameters and oral bioavailability were evaluated using the PkCSM and SwissADME platforms, respectively. The study was carried out with five groups of infected mice and divided as follows: an untreated control group, a control group treated with PZQ, and three groups treated orally with 8, 16, or 32 mg/kg of PLUM. After treatment, the Kato-Katz technique was performed to evaluate a quantity of eggs in the feces (EPG). The animals were euthanized for worm recovery, intestine samples were collected to evaluate the oviposition pattern, the load of eggs was determined on the hepatic and intestinal tissues and for the histopathological and histomorphometric evaluation of tissue and hepatic granulomas. PLUM reduced EPG by 65.27, 70.52, and 82.49%, reduced the total worm load by 46.7, 55.25, and 72.4%, and the female worm load by 44.01, 52.76, and 71.16%, for doses of 8, 16, and 32 mg/kg, respectively. PLUM also significantly reduced the number of immature eggs and increased the number of dead eggs in the oogram. A reduction of 36.11, 46.46, and 64.14% in eggs in the hepatic tissue, and 57.22, 65.18, and 80.5% in the intestinal tissue were also observed at doses of 8, 16, and 32 mg/kg, respectively. At all doses, PLUM demonstrated an effect on the histopathological and histomorphometric parameters of the hepatic granuloma, with a reduction of 41.11, 48.47, and 70.55% in the numerical density of the granulomas and 49.56, 57.63, and 71.21% in the volume, respectively. PLUM presented itself as a promising in vivo antiparasitic candidate against *S. mansoni*, acting not only on parasitological parameters but also on hepatic granuloma. Furthermore, in silico, PLUM showed good predictive pharmacokinetic profiles by ADMET.

Revisiting Schistosoma mansoni Micro-Exon Gene (MEG) Protein Family: A Tour into Conserved Motifs and Annotation.

Nedvědová Š, De Stefano D, Walker O, Hologne M, Miele AE.
22-08-2023
Biomolecules.

https://pubmed.ncbi.nlm.nih.gov/37759676/

Genome sequencing of the human parasite *Schistosoma mansoni* revealed an interesting gene superfamily, called micro-exon gene (*meg*), that encodes secreted MEG proteins. The genes are composed of short exons (3-81 base pairs) regularly interspersed with long introns (up to 5 kbp). This article recollects 35 *S. mansoni* specific *meg* genes that are distributed over 7 autosomes and one pair of sex chromosomes and that code for at least 87 verified MEG proteins. We used various bioinformatics tools to produce an optimal alignment and propose a phylogenetic analysis. This work highlighted intriguing conserved patterns/motifs in the sequences of the highly variable MEG proteins. Based on the analyses, we were able to classify the verified MEG proteins into two subfamilies and to hypothesize their duplication and colonization of all the chromosomes. Together with motif identification, we also proposed to revisit MEGs' common names and annotation in order to avoid duplication, to help the reproducibility of research results and to avoid possible misunderstandings.

Dried urine spot method for detection of Schistosoma mansoni circulating cathodic antigen in resource-limited settings: a proof of concept study.

Zacharia A, Makene T, Kinabo C, Ogweno G, Lyamuya F, Ngasala B.
11-09-2023
Front Immunol.
https://pubmed.ncbi.nlm.nih.gov/37753086/

Schistosoma mansoni excretory-secretory products induce protein kinase signalling, hyperkinesia, and stem cell proliferation in the opposite sex.

Shakir EMN, Rinaldi G, Kirk RS, Walker AJ.
26-09-2023
Commun Biol.
https://pubmed.ncbi.nlm.nih.gov/37752334/

The Efficiency of Schistosoma mansoni Crude Antigens in Inhibition of Heat Shock Protein, Apoptosis, and Lysosomal Activity: An Immunohistochemical Study.

Alnasser SM, Alotaibi M, Ramadan NK, Abd ElHafeez HH, Abdel-Hakeem SS.
05-04-2023
Microsc Microanal.
https://pubmed.ncbi.nlm.nih.gov/37749745/

The adverse impact of schistosomiasis on tissues is considered in generating a schistosomal vaccine. The purpose of this study was to evaluate the effectiveness of Schistosoma mansoni crude antigens as a therapeutic and prophylactic formulation in the inhibition of heat shock protein, apoptosis, and CD3/CD20 expression in a liver and spleen mouse models using the immunohistochemistry method. A total of 65 mice were divided into five groups: (i) infected untreated group (G1), (ii) therapeutic treated group (G2) with egg soluble egg antigen (SEA), and soluble worm antigen preparation (SWAP), (iii) prophylactically treated group (G3) with cercarial antigen preparation (CAP), (iv) combined treated group with three antigens (G4), and (v) control group (G5). The results we obtained showed that CAP, SEA, and SWAP antigens mitigated the deterioration and inflammation induced by infection. Apoptosis and sinusoidal injuries were significantly reduced when treated with CAP antigen before infection. After infection, using SEA and SWAP antigens may help lighten the liver's load. A high degree of activation in T and B cells in the liver and spleen is linked to this. Our findings shed light on the immunological mechanisms that contribute to the recovery from therapy and vaccination against schistosome damage.

In Vitro Cercaricidal Activity, Acute Toxicity, and GC/MS Analysis of Some Selected Ghanaian Medicinal Plants.

Osei-Mensah B, Boakye YD, Anyan WK, Agana TA, Aboagye EA, Bentil I, Lomotey ES, Adu F, Agyare C.
15-09-2023
J Parasitol Res.
https://pubmed.ncbi.nlm.nih.gov/37745984/

Schistosomiasis is a human parasitic disease caused by the *Schistosoma* species and is recognised in public health as second to malaria in terms of its socioeconomic impact on humans. Four local plants native to many tribes in Ghana and known for their medicinal properties against some diseases were assessed for their cercaricidal activity against *Schistosoma mansoni* cercariae. The plants, namely, *Newbouldia laevis* stem bark (NLSB), *Spathodea campanulata* stem bark (SCSB), *Momordica charantia* leaves (MCL), and *Ocimum viride* leaves (OVL), were extracted for their active metabolites using methanol. Preliminary phytochemical screening was carried out on all plant extracts and powdered samples. The crude extracts were tested against *S. mansoni* cercariae *in vitro* using *Balanites aegyptiaca* as the positive control. The percentage of mortalities for each extract was recorded. Gas chromatography/mass spectrometry (GC/MS) analysis was conducted on all the plant extracts. Phytochemical analysis revealed the presence of saponins, glycosides, triterpenoids, sterols, alkaloids, flavonoids, and tannins in almost all the extracts. GC/MS analysis showed the presence of medicinally important active volatile compounds in each extract such as thymol, n-hexadecanoic acid, phytol, and maltol. All four plants showed relatively different levels of activity against *S. mansoni* cercariae at different times and concentrations. The LC_{50} values of the plant extracts were determined at the end of the assay. At 240 min, NLSB, SCSB, MCL, and OVL extracts had LC_{50} values of 487.564, 429.898, 197.696, and 0.129 μg/mL, respectively. Hence, this study revealed the potency of *Ocimum viride* leaves, *Momordica charantia* leaves, *Spathodea campanulata* stem bark, and *Newbouldia laevis* stem bark against *S. mansoni*. These plants could therefore be exploited as possible candidates for curbing schistosomiasis.

Nanoparticles as Potent Agents for Treatment of Schistosoma Infections: A Systematic Review.

Shakib P, Zivdari M, Khalaf AK, Marzban A, Ganjalikhani-Hakemi M, Parvaneh J, Mahmoudvand H, Cheraghipour K.
22-08-2023
Curr Ther Res Clin Exp.
https://pubmed.ncbi.nlm.nih.gov/37743882/

Background: Schistosomiasis is an acute and chronic parasitic disease caused by blood flukes of the genus *Schistosoma*. The current drugs for treating schistosomiasis are associated with some side effects. **Objective:** The aim of this systematic study was an overview of the treatment of diseases caused by *Schistosoma* based on nanoparticles. **Methods:** In the present systematic research with keywords "*Schistosoma*", "parasitism", "anti-*Schistosoma* activity", "nanoparticles", "metal nanoparticles", "silver nanoparticles", "gold nanoparticles", "polymer nanoparticles", "PLGA nanoparticles", "nanoemulsions", "*in vitro*", and "*in vivo*" from five English-language databases, including ScienceDirect, europePMC, PubMed, Scopus, Ovid, and Cochrane were searched from 2000 to 2022 by 2 researchers. **Results:** In the initial search, 250 studies were selected. Based on the inclusion and exclusion criteria, 27 articles were finally selected after removing duplicate, unrelated, and articles containing full text. In present article, the most nanoparticles used against *Schistosoma* were gold nanoparticles (22%). **Conclusions:** The results indicate the high potential of various nanoparticles, including metal nanoparticles, against *Schistosoma*. Also, the remarkable anti-schistosomal activity of nanoparticles suggests their use in different fields to eliminate this pathogenic microorganism so that it can be used as an effective candidate in the preparation of anti-schistosomal compounds because these compounds have fewer side effects than chemical drugs. *Ther Res Clin Exp*. 2023; XX:XXX-XXX).

A case of chronic hepatitis C combined with autoimmune hepatitis with schistosomal liver disease.

Sun W, Xiao P, Wei C, Wang J.
22-09-2023
Asian J Surg.
https://pubmed.ncbi.nlm.nih.gov/37743177/

Schistosoma japonicum EKLF/KLF1 is a potential immune target to tackle schistosomiasis.

Piao X, Jiang N, Liu S, Duan J, Dai H, Hou N, Chen Q.
23-09-2023
Parasit Vectors.
https://pubmed.ncbi.nlm.nih.gov/37742024/

Background: Interruption of parasite reproduction by targeting migrating schistosomula is a promising strategy for managing schistosomiasis. Hepatic schistosomula proteins previously identified based on second-generation schistosome DNA sequencing were found to hold excellent potential for schistosomiasis japonica diagnosis and as vaccine candidates. However, there are still many unknown schistosomula proteins that warrant further investigations. Herein, a novel schistosomula protein, the Schistosoma japonicum erythroid Krüppel-like factor (SjEKLF/KLF1), was explored. **Methods:** Sequence alignment was carried out to detect the amino acid sequence characteristics of SjEKLF. The expression profile of SjEKLF was determined by western blot and immunofluorescence analysis. Enzyme-linked immunosorbent assay was used to determine the antigenicity of SjEKLF in hosts. Mice immunised with recombinant SjEKLF were challenged to test the potential value of the protein as an immunoprotective target. **Results:** SjEKLF is defined as EKLF/KLF1 for its C-terminal DNA-binding domain. SjEKLF is mainly expressed in hepatic schistosomula and male adults and located within the intestinal intima of the parasites. Notably, high levels of SjEKLF-specific antibodies were detected in host sera and SjEKLF exhibited outstanding sensitivity and specificity for schistosomiasis japonica immunodiagnosis but failed to distinguish between ongoing infection and previous exposure. In addition, SjEKLF immunisation reduced the infection in vivo, resulting in decreased worm and egg counts, and alleviated body weight loss and hepatomegaly in infected mice. **Conclusions:** Overall, these findings demonstrate that SjEKLF is critical for the infection of S. japonicum and may be a potential target to help control S. japonicum infection and transmission.

Comparative assessment of the SjSAP4-incorporated gold immunochromatographic assay for the diagnosis of human schistosomiasis japonica.

Mu Y, Rivera J, McManus DP, Weerakoon KG, Ross AG, Olveda RM, Gordon CA, You H, Jones MK, Cai P.
01-09-2023
Front Public Health.
https://pubmed.ncbi.nlm.nih.gov/37736084/

Background: Schistosomiasis, a disease caused by parasites of the genus *Schistosoma*, remains a global public health threat. This study aimed to validate the diagnostic performance of a recently developed gold immunochromatographic assay (GICA) for the detection of *S. japonicum* infection in a rural endemic area of the Philippines. **Methods:** Human clinical samples were collected from 412 subjects living in Laoang and Palapag municipalities, Northern Samar, the Philippines. The presence of *Schistosoma*-specific antibodies in serum samples was tested with the SjSAP4-incorporated GICA strips and the results were converted to fully quantitative data by introducing an *R* value. The performance of the established GICA was further compared with other diagnostic tools, including the Kato-Katz (KK) technique, point-of-care circulating cathodic antigen (POC-CCA), droplet digital (dd) PCR, and enzyme-linked immunosorbent assays (ELISAs). **Results:** The developed GICA strip was able to detect KK positive individuals with a sensitivity of 83.3% and absolute specificity. When calibrated with the highly sensitive faecal ddPCR assay, the immunochromatographic assay displayed an accuracy of 60.7%. Globally, the GICA assay showed a high concordance with the SjSAP4-ELISA assay. The schistosomiasis positivity rate determined by the GICA test

was similar to those obtained with the SjSAP4-ELISA assay and the ddPCR assay performed on serum samples (SR_ddPCR), and was 2.3 times higher than obtained with the KK method. **Conclusion:** The study further confirms that the developed GICA is a valuable diagnostic tool for detecting light *S. japonicum* infections and implies that this point-of-care assay is a viable solution for surveying endemic areas of low-intensity schistosomiasis and identifying high-priority endemic areas for targeted interventions.

Metabolism of (R)-Praziquantel versus the Activation of a Parasite Transient Receptor Potential Melastatin Ion Channel.

Friedrich L, Park SK, Ballard P, Ho Baeurle TH, Maillard D, Bödding M, Keiser J, Marchant JS, Spangenberg T.
15-09-2023
ChemMedChem.
https://pubmed.ncbi.nlm.nih.gov/37272317/

Schistosoma Infection Burden and Risk Factors among School-Aged Children in a Rural Area of the Democratic Republic of the Congo.

Linsuke S, Ilombe G, Disonama M, Nzita JD, Mbala P, Lutumba P, Van Geertruyden JP.
21-09-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755916/

Trachome

Integrated control of neglected tropical diseases in Brazil: document review of a national campaign in light of WHO recommendations.

Soares RCR, de Carvalho AG, Luz JGG, Lucas ALZ, Ignotti E.
26-09-2032
Rev Panam Salud Publica.
https://pubmed.ncbi.nlm.nih.gov/37767238/

Effectiveness of Trachomatous Trichiasis Case-identification Approaches in Ethiopia.

Diallo AO, Bayissasse B, Sisay A, Seyum D, Weaver J, Munoz B, Merbs SL, Gower EW.
Nov-2023
Epidemiology.
https://pubmed.ncbi.nlm.nih.gov/37757880/

Background: Trachoma control programs use multiple approaches to identify individuals with trachomatous trichiasis (TT). Evidence is limited regarding which approaches are most effective and cost-efficient. **Methods:** We evaluated the effectiveness of two TT case-identification approaches in Ethiopia: community mobilization to encourage self-referral for centralized screening and house-to-house screenings conducted by case finders. We compared the number of true cases found per 1000 population and costs associated with case identification under each approach, stratified by villages that received one or multiple screening visits. **Results:** We conducted screenings in 396 villages. In villages receiving one house-to-house visit, case finders identified 14,229 suspected cases, of whom 10,513 (73.9%) presented for TT confirmation. A median of 17.2% (interquartile range [IQR]: 9.1%-27.8%) of those presenting truly had TT (positive predictive value). In single-visit villages, the community mobilization approach yielded higher rates of confirmed cases than the house-to-house approach (1.5 [IQR: 1.1, 2.6] vs. 1.1 [IQR: 0.5, 1.9] cases per 1000 population), and the median cost of identifying a TT case was less ($5.59 vs. $31.18) using community mobilization than house-to-house. In multiple-visit villages, additional screening visits increased the median rate of confirmed cases to 2.5 per 1000 population in community mobilization villages, but the rate remained unchanged in house-to-house villages. **Conclusions:** Community mobilization-based TT case finding had a higher yield than house-to-house, at a substantially lower cost. Future research should examine whether additional tools to aid case finders in their diagnosis increases case-finding efficiency and accuracy and whether TT prevalence and surgical program duration impact case-finding success.

The 100 most cited articles on trachoma: a bibliometric analysis.

Aquino-Canchari CR, Chavez-Bustamante SG.
Nov-2023
Int Ophthalmol.
https://pubmed.ncbi.nlm.nih.gov/37592115/

Objective: Trachoma is the cause of blindness or visual impairment in 1.9 million people. Few bibliometric studies have been carried out, but none explore the characteristics of the 100 most cited articles on trachoma. **Methods:** A keyword-based search without time restriction was performed in September 2022 using the Scopus database. Search keywords include the following: "trachoma; trachome; tracoma; trachomatis." Two authors independently screened the literature and extracted data. The search result was obtained to classify the 100 articles according to their number of citations. **Results:** The Top 100 articles were published between 1957 and 2015 with a total of 11,102 citations (range 56-689). The country with the most significant contribution was the USA (n = 56). The Lancet was the most active journal (n = 15). Bailey RL was the author with the highest number of publications (n = 30). The Edna McConnell Clark Foundation (n = 26) was the most prominent funding entity. The type of original article was the most published (n = 83), in addition, the most frequent thematic area was prevention (n = 33). The most popular keywords were trachoma (n = 93), chlamydia trachomatis (n = 55), and azithromycin (n = 34). **Conclusions:** The study provides new insight into trachoma research, information that may help healthcare providers, researchers, and stakeholders better understand trends and influential contributions. It highlights under-researched areas that could be the basis for future research.

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

Discovery of long non-coding RNAs in the liver fluke, Fasciola hepatica.

McVeigh P, McCammick E, Robb E, Brophy P, Morphew RM, Marks NJ, Maule AG.
28-09-2023
PLoS Negl Trop Dis.
https://pubmed.ncbi.nlm.nih.gov/37769025/

Reduction of carcinogens in fermented fish (pla-ra and pla-som) by heating.

Artchayasawat A, Sriraj P, Boonmars T, Aukkanimart R, Wisetmora A, Borlace GN, Boueroy P, Pumhirunroj B, Laummaunwai P, Rattanasuwan P, Boonjaraspinyo S, Ekobol N, Pitaksakulrat O, Zhiliang W.
Août-2023
Vet World.
https://pubmed.ncbi.nlm.nih.gov/37766713/

Clinical characteristics of human fascioliasis in Egypt.

Ibrahim N, Abdel Khalek EM, Makhlouf NA, Abdel-Gawad M, Mekky M, Ramadan HK, Abu-Elfatth A, El-Latif NA, Hassan MK, Eldeeb R, Abdelmalek M, Abd-Elsalam S, Attia H, Mohammed AQ, Aboalam H, Farouk M, Alboraie M.
27-09-2023
Sci Rep.
https://pubmed.ncbi.nlm.nih.gov/37758788/

There is a lack of epidemiological data on fascioliasis in Egypt regarding disease characteristics and treatment outcomes across different governorates. We aimed to identify the demographic, epidemiologic, clinical, laboratory, and radiological characteristics and treatment outcomes of patients diagnosed with fascioliasis in Egypt. Data on human fascioliasis were collected retrospectively from patients' medical records in the period between January 2018 and January 2020. The study included 261 patients. More than 40% of enrolled patients were in the age group of 21-40 years old. Geographically, 247 (94.6%) were from Assiut Governorate with 69.3% were from rural areas. The most frequent symptoms were right upper quadrant pain (96.9%), and fever (80.1%). Eosinophilia was found in 250 cases (95.8%). Hepatic focal lesions were detected in 131 (50.2%); out of them 64/131 (48.9%) had a single lesion. All patients received a single dose of 10 mg/kg of triclabendazole, 79.7% responded well to a single dose, while in 20.3% a second ± a third dose of treatment was requested. After therapy, there was a reduction in leucocytes, Fasciola antibodies titer, eosinophilic count, bilirubin, and liver enzymes with an increase in hemoglobin level. According to our findings, a high index of suspicion should be raised in cases with fever, right upper abdominal pain, and peripheral eosinophilia, and further imaging workup is mandated to detect hepatic focal lesions. Prompt treatment by triclabendazole can serve as a standard-of-care regimen even for suspected cases.

Tetraspanins from the liver fluke Opisthorchis viverrini stimulate cholangiocyte migration and inflammatory cytokine production.

Ruangsuwast A, Smout MJ, Brindley PJ, Loukas A, Laha T, Chaiyadet S.
16-09-2023
Folia Parasitol (Praha).
https://pubmed.ncbi.nlm.nih.gov/37752807/

The liver fluke Opisthorchis viverrini (Poirier, 1886) (Digenea) secretes extracellular vesicles (EVs) bearing CD63-like tetraspanins on their surface. Fluke EVs are actively internalised by host cholangiocytes in the bile ducts, where they drive pathology and promote neoplasia through induction of cellular proliferation and secretion of inflammatory cytokines. We investigated the effects of tetraspanins of the CD63 superfamily by co-culturing recombinant forms of the large extracellular loop (LEL) of O. viverrini tetraspanin-2 (rLEL-Ov-TSP-2) and tetraspanin-3 (rLEL-Ov-TSP-3) with non-cancerous human bile duct (H69) and cholangiocarcinoma (CCA, M213) cell lines. The results showed that cell lines co-cultured with excretory/secretory products from adult O. viverrini (Ov-ES) underwent significantly increased cell proliferation at 48 hours but not 24 hours compared to untreated control cells ($P < 0.05$), whereas rLEL-Ov-TSP-3 co-culture resulted in significantly increased cell proliferation at both 24 hours ($P < 0.05$) and 48 hours ($P < 0.01$) time points. In like fashion, H69 cholangiocytes co-cultured with both Ov-ES and rLEL-Ov-TSP-3 underwent significantly elevated Il-6 and Il-8 gene expression for at least one of the time points assessed. Finally, both rLEL-Ov-TSP-2 and rLEL-Ov-TSP-3 significantly enhanced migration of both M213 and H69 cell lines. These findings indicated that O. viverrini CD63 family tetraspanins can promote a cancerous microenvironment by enhancing innate immune responses and migration of biliary epithelial cells.

Prevalence of flukes (Fasciola hepatica and paramphistomids) in cattle in south-eastern Mexico.

Hernández-Hernández JC, González-Garduño R, Ortiz-Pérez DO, Villa-Mancera A, Arias-Vázquez MS, Paz-Silva A.
22-09-2023
Helminthologia.
https://pubmed.ncbi.nlm.nih.gov/37745221/

Exudative pleural effusion caused by lung fluke infection: A practical diagnostic approach.

Wang H, Wang L, Yu D, Luo G, Yang S, Liu Y, Ren T, Wang M.

Oct-2023
Int J Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37507085/

Objectives: Pleural effusion caused by lung fluke is a rare etiology of exudative pleural effusion (EPE), which is often misdiagnosed or delayed. We aim to summarize the diagnosis and treatment course of EPE caused by lung fluke infection and put forward a practical diagnosis approach. **Methods:** We retrospectively analyzed the diagnosis and treatment of 14 cases of EPE caused by lung fluke infection diagnosed by enzyme-linked immunosorbent assay of serum antibodies or egg detection. **Results:** All patients (100%) with an absolute count of eosinophils in peripheral blood exceeded 0.5 × 10^9/l, and 10 patients (71.4%) had a history of special ingestion. Eosinophilic PE occurred in 11 patients (78.6%), pleural biopsy of medical thoracoscopic demonstrated eosinophils infiltration in nine patients (64.3%), and parasite eggs in one patient. All patients showed positive intradermal tests for Paragonimus-specific antigens and enzyme-linked immunosorbent assay of serum antibodies to Paragonimus. **Conclusion:** For patients with unexplained PE, lung fluke infection should be highly suspected when pleural fluid or pleural biopsy shows eosinophilic PE or eosinophils infiltration, especially for patients with certain diet history.

Rapid, sensitive, and visual detection of Clonorchis sinensis with an RPA-CRISPR/Cas12a-based dual readout portable platform.

Huang T, Li L, Li J, Li X, Li S, Wang X, Zhang N, Yu Y, Zhang X, Zhao Z, Guo Y, Cao L, Gong P.
30-09-2023
Int J Biol Macromol.
https://pubmed.ncbi.nlm.nih.gov/37494991/

Fasciola hepatica: an unusual cause of biliary obstruction.

Okasha HH, Delsa H, Gobran BA, Nakhla R.
Oct-2023
Gastrointest Endosc.
https://pubmed.ncbi.nlm.nih.gov/37364704/

Trypanosomes (trypanosomiase et maladie de Chagas)

In vitro trypanocidal activity of extracts and compounds isolated from Vitellaria paradoxa.

Bairy G, Ozzin-Kholy Zolipou CO, Nzoumbou-Boko R.
28-09-2023
BMC Complement Med Ther.
https://pubmed.ncbi.nlm.nih.gov/37770899/

Background: Vitellaria paradoxa is used in traditional medicine for the treatment of various diseases in tropical countries; however, nothing is known about its anti-trypanosomal activity. Human African trypanosomiasis is a neglected tropical disease of Sub-Saharan Africa's poorest rural regions, and the efficacy of its treatment remains a challenge. This study investigates the as-yet-unknown trypanocidal activity of this plant. **Methods:** V. paradoxa, commonly known as shea tree, was selected for study based on an ethnobotanical investigation. Ultrasonicated extracts from bark and seeds were successively treated with ethyl acetate and water. Column chromatography, NMR spectroscopy and mass spectrometry were used to identify isolated compounds. Purified trypanosomes (Trypanosoma brucei brucei) were incubated with serial dilutions of the extracts and isolated compounds at 37 °C in 5% CO_2 for 24 h. Parasite viability was evaluated under a microscope. **Results:** The ethyl acetate extracts of the bark showed the higher in vitro trypanocidal activity against T. brucei brucei with median inhibitory concentration (IC_{50}) of 3.25 µg/mL. However, the triterpene 1α,2β,3β,19α-tretrahydroxyurs-12-en-28-oic acid and the pentadecanoic acid isolated from the ethyl acetate extract of the seeds showed in vitro trypanocidal activity with IC_{50} of 11.30 and 70.1 µM, respectively. **Conclusion:** The results obtained contribute to the validation of the traditional medicinal use of V. paradoxa. Our results encourage further investigations of this plant, mainly with respect to its in vivo efficacy and toxicity.

A novel palladium complex with a coumarin-thiosemicarbazone hybrid ligand inhibits Trypanosoma cruzi release from host cells and lowers the parasitemia in vivo.

Rostán S, Porto S, Barbosa CLN, Assis D, Alvarez N, Machado FS, Mahler G, Otero L.
28-09-2023
J Biol Inorg Chem.
https://pubmed.ncbi.nlm.nih.gov/37768364/

Triosephosphate Isomerase: The Crippling Effect of the P168A/I172A Substitution at the Heart of an Enzyme Active Site.

Hegazy R, Richard JP.
28-09-2023
Biochemistry.
https://pubmed.ncbi.nlm.nih.gov/37768194/

The P168 and I172 side chains sit at the heart of the active site of triosephosphate isomerase (TIM) and play important roles in the catalysis of the isomerization reaction. The phosphodianion of substrate glyceraldehyde 3-phosphate (GAP) drives a conformational change at the TIM that creates a steric interaction with the P168 side chain that is relieved by the movement of P168 that carries the basic E167 side chain into a clamp that consists of the hydrophobic I172 and L232 side chains. The P168A/I172A substitution at TIM from *Trypanosoma brucei brucei* (*Tbb*TIM) causes a large 120,000-fold decrease in k_{cat} for isomerization of GAP that eliminates most of the difference in the reactivity of TIM compared to the small amine base quinuclidinone for deprotonation of catalyst-bound GAP. The I172A substitution causes *a* > 2-unit

decrease in the pK_a of the E167 carboxylic acid in a complex to the intermediate analog PGA, but the P168A substitution at the I172A variant has no further effect on this pK_a. The P168A/I172A substitutions cause a 5-fold decrease in K_m for the isomerization of GAP from a 0.9 kcal/mol stabilization of the substrate Michaelis complexes. The results show that the P168 and I172 side chains play a dual role in destabilizing the ground-state Michaelis complex to GAP and in promoting stabilization of the transition state for substrate isomerization. This is consistent with an important role for these side chains in an induced fit reaction mechanism [Richard, J. P. (2022) Enabling Role of Ligand-Driven Conformational Changes in Enzyme Evolution. Biochemistry 61, 1533-1542].

A phenotypic screen with Trypanosoma brucei for discovering small molecules that target the SLiM-binding pocket of proliferating cell nuclear antigen orthologs.

Actis M, Fujii N, Mackey ZB.
28-09-2023
Chem Biol Drug Des.
https://pubmed.ncbi.nlm.nih.gov/37767622/

Proliferating cell nuclear antigen (PCNA) is a homo-trimeric protein complex that clamps around DNA to tether DNA polymerases to the template during replication and serves as a hub for many other interacting proteins. It regulates DNA metabolic processes and other vital cellar functions through the binding of proteins having short linear motifs (SLiMs) like the PIP-box (PCNA-interacting protein-box) or the APIM (AlkB homolog 2 PCNA-interacting motif) in the hydrophobic pocket where SLiMs bind. However, overproducing TbPCNA or human PCNA (hPCNA) in the pathogenic protist Trypanosoma brucei triggers a dominant-negative phenotype of arrested proliferation. The mechanism for arresting T. brucei proliferation requires the overproduced PCNA orthologs to have functional intact SLiM-binding pocket. Sight-directed mutagenesis studies showed that T. brucei overproducing PCNA variants with disrupted SLiM-binding pockets grew normally. We hypothesized that chemically disrupting the SLiM-binding pocket would restore proliferation in T. brucei, overproducing PCNA orthologs. Testing this hypothesis is the proof-of-concept for a T. brucei-based PCNA screening assay. The assay design is to discover bioactive small molecules that restore proliferation in T. brucei strains that overproduce PCNA orthologs, likely by disrupting interactions in the SLiM-binding pocket. The pilot screen for this assay discovered two hit compounds that linked to predetermined PCNA targets. Compound #1, a known hPCNA inhibitor, had selective bioactivity to hPCNA overproduced in T. brucei, validating the assay. Compound #6 had promiscuous bioactivity for hPCNA and TbPCNA but is the first compound discovered with bioactivity for inhibiting TbPCNA.

Cell-free N-glycosylation of peptides using synthetic lipid-linked hybrid and complex N-glycans.

Wenzel L, Hoffmann M, Rapp E, Rexer TFT, Reichl U.
12-09-2023
Front Mol Biosci.
https://pubmed.ncbi.nlm.nih.gov/37767159/

Cell-free, chemoenzymatic platforms are emerging technologies towards generating glycoconjugates with defined and homogeneous glycoforms. Recombinant oligosaccharyltransferases can be applied to glycosylate "empty," i.e., aglycosyalted, peptides and proteins. While bacterial oligosaccharlytransferases have been extensively investigated, only recently a recombinant eukaryotic single-subunit oligosaccharyltransferase has been successfully used to *in vitro* *N*-glycosylate peptides. However, its applicability towards synthesizing full-length glycoproteins and utilizing glycans beyond mannose-type glycans for the transfer have not be determined. Here, we show for the first time the synthesis of hybrid- and complex-type glycans using synthetic lipid carriers as substrates for *in vitro* *N*-glycosylation reactions. For this purpose, transmembrane-deleted human β-1,2 *N*-acetylglucosamintransferase I and II (MGAT1ΔTM and MGAT2ΔTM) and β-1,4-galactosyltransferase (GalTΔTM) have been expressed in *Escherichia coli* and used to extend an existing multi-enzyme cascade. Both hybrid and agalactosylated complex structures were transferred to the *N*-glycosylation consensus sequence of peptides (10 amino acids: G-S-D-A-N-Y-T-Y-T-Q) by the recombinant oligosaccharyltransferase STT3A from *Trypanosoma brucei*.

Pro-inflammatory cytokines are modified during the multiplication of Trypanosoma cruzi within the placental chorionic villi and are associated with the level of infection via the signaling pathway NF-κB.

Benizio E, Moreira-Espinoza MJ, Triquell MF, Mezzano L, Díaz-Luján CM, Fretes RE.
Oct-2023
Am J Reprod Immunol.
https://pubmed.ncbi.nlm.nih.gov/37766400/

Expression of Proteins, Glycoproteins, and Transcripts in the Guts of Fasting, Fed, and Trypanosoma cruzi-Infected Triatomines: A Systematic Review.

Reynoso-Ducoing OA, González-Rete B, Díaz E, Candelas-Otero FN, López-Aviña JA, Cabrera-Bravo M, Bucio-Torres MI, Torres-Gutiérrez E, Salazar-Schettino PM.
02-09-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764932/

Monocytes from Uninfected Neonates Born to Trypanosoma cruzi-Infected Mothers Display Upregulated Capacity to Produce TNF-α and to Control Infection in Association with Maternally Transferred Antibodies.

Flores A, Alonso-Vega C, Hermann E, Torrico MC, Montaño Villarroel NA, Torrico F, Carlier Y, Truyens C.
29-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764911/

Activated monocytes/macrophages that produce inflammatory cytokines and nitric oxide are crucial for controlling *Trypanosoma cruzi* infection. We previously showed that uninfected newborns from *T. cruzi* infected mothers (M+B- newborns) were sensitized to produce higher levels of inflammatory cytokines than newborns from uninfected mothers (M-B- newborns), suggesting that their monocytes were more activated. Thus, we wondered whether these cells might help limit congenital infection. We investigated this possibility by studying the activation status of M+B- cord blood monocytes and their ability to control *T. cruzi* in vitro infection. We showed that M+B- monocytes have an upregulated capacity to produce the inflammatory cytokine TNF-α and a better ability to control *T. cruzi* infection than M-B- monocytes. Our study also showed that *T. cruzi*-specific Abs transferred from the mother play a dual role by favoring trypomastigote entry into M+B- monocytes and inhibiting intracellular amastigote multiplication. These results support the possibility that some M+B- fetuses may eliminate the parasite transmitted in utero from their mothers, thus being uninfected at birth.

Main Cardiac Histopathologic Alterations in the Acute Phase of Trypanosoma cruzi Infection in a Murine Model.

de Alba Alvarado MC, Torres Gutiérrez E, Cabrera Bravo M, Zenteno Galindo E, Villarreal Muñoz JA, Salazar Schettino PM, Bucio Torres MI.
26-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764892/

Symptoms in the acute phase of Chagas disease are usually mild and nonspecific. However, after several years, severe complications like dilated heart failure and even death may arise in the chronic phase. Due to the lack of specific symptoms in the acute phase, the aim of this work was to describe and analyze the cardiac histopathology during this phase in a CD1 mouse model by assessing parasitism, fibrotic damage, and the presence and composition of a cellular infiltrate, to determine its involvement in the pathogenesis of lesions in the cardiac tissue. Our results indicate that the acute phase lasts about 62 days post-infection (dpi). A significant increase in parasitemia was observed since 15 dpi, reaching a maximum at 33 dpi (4.1×10^6). The presence of amastigote nests was observed at 15-62 dpi, with a maximum count of 27 nests at 35 dpi. An infiltrate consisting primarily of macrophages and neutrophils was found in the cardiac tissue within the first 30 days, but the abundance of lymphocytes showed an 8 ≥ fold increase at 40-62 dpi. Unifocal interstitial fibrosis was identified after 9 dpi, which subsequently showed a 16 ≥ fold increase at 40-60 dpi, along with a 50% mortality rate in the model under study. The increased area of fibrotic lesions revealed progression in the extent of fibrosis, mainly at 50-62 dpi. The presence of perivasculitis and thrombus circulation disorders was seen in the last days (62 dpi); finally, cases of myocytolysis were observed at 50 and 62 dpi. These histopathological alterations, combined with collagen deposition, seem to lead to the development of interstitial fibrosis and damage to the cardiac tissue during the acute phase of infection. This study provides a more complete understanding of the patterns of histopathological abnormalities involved in the acute phase, which could help the development of new therapies to aid the preclinical tests of drugs for their application in Chagas disease.

Molecular Mechanisms of Persistence in Protozoan Parasites.

Tarannum A, Rodríguez-Almonacid CC, Salazar-Bravo J, Karamysheva ZN.
07-09-2032
Microorganisms.
https://pubmed.ncbi.nlm.nih.gov/37764092/

Protozoan parasites are known for their remarkable capacity to persist within the bodies of vertebrate hosts, which frequently results in prolonged infections and the recurrence of diseases. Understanding the molecular mechanisms that underlie the event of persistence is of paramount significance to develop innovative therapeutic approaches, given that these pathways still need to be thoroughly elucidated. The present article provides a comprehensive overview of the latest developments in the investigation of protozoan persistence in vertebrate hosts. The focus is primarily on the function of persisters, their formation within the host, and the specific molecular interactions between host and parasite while they persist. Additionally, we examine the metabolomic, transcriptional, and translational changes that protozoan parasites undergo during persistence within vertebrate hosts, focusing on major parasites such as *Plasmodium* spp., *Trypanosoma* spp., *Leishmania* spp., and *Toxoplasma* spp. Key findings of our study suggest that protozoan parasites deploy several molecular and physiological strategies to evade the host immune surveillance and sustain their persistence. Furthermore, some parasites undergo stage differentiation, enabling them to acclimate to varying host environments and immune challenges. More often, stressors such as drug exposure were demonstrated to impact the formation of protozoan persisters significantly. Understanding the molecular mechanisms regulating the persistence of protozoan parasites in vertebrate hosts can reinvigorate our current insights into host-parasite interactions and facilitate the development of more efficacious disease therapeutics.

From Benznidazole to New Drugs: Nanotechnology Contribution in Chagas Disease.

Gomes DC, Medeiros TS, Alves Pereira EL, da Silva JFO, de Freitas Oliveira JW, Fernandes-Pedrosa MF, de Sousa da Silva M, da Silva-Júnior AA.
07-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762080/

Parameter Estimation for Kinetic Models of Chemical Reaction Networks from Partial Experimental Data of Species' Concentrations.

Gasparyan M, Rao S.
07-09-2023
Bioengineering (Basel).
https://pubmed.ncbi.nlm.nih.gov/37760158/

Effectiveness of Systemic Insecticide Dog Treatment for the Control of Chagas Disease in the Tropics.

Fiatsonu E, Deka A, Ndeffo-Mbah ML.
13-09-2023
Biology (Basel).
https://pubmed.ncbi.nlm.nih.gov/37759635/

Antitrypanosomal Activity of 1,2,3-Triazole-Based Hybrids Evaluated Using In Vitro Preclinical Translational Models.

Orlando LMR, Lara LDS, Lechuga GC, Rodrigues GC, Pandoli OG, de Sá DS, Pereira MCS.
Sept-2023
Biology (Basel).
https://pubmed.ncbi.nlm.nih.gov/37759621/

Chagas disease therapy still relies on two nitroderivatives, nifurtimox and benznidazole (Bz), which have important limitations and serious adverse effects. New therapeutic alternatives for this silent disease, which has become a worldwide public health problem, are essential for its control and elimination. In this study, 1,2,3-triazole analogues were evaluated for efficacy against *T. cruzi*. Three triazole derivatives, **1d** (0.21 µM), **1f** (1.23 µM), and **1g** (2.28 µM), showed potent activity against trypomastigotes, reaching IC_{50} values 10 to 100 times greater than Bz (22.79 µM). Promising candidates are active against intracellular amastigotes ($IC_{50} \leq 6.20$ µM). Treatment of 3D cardiac spheroids, a translational in vitro model, significantly reduced parasite load, indicating good drug diffusion and efficacy. Oral bioavailability was predicted for triazole derivatives. Although infection was significantly reduced without drug pressure in a washout assay, the triazole derivatives did not inhibit parasite resurgence. An isobologram analysis revealed an additive interaction when 1,2,3-triazole analogs and Bz were combined in vitro. These data indicate a strengthened potential of the triazole scaffold and encourage optimization based on an analysis of the structure-activity relationship aimed at identifying new compounds potentially active against *T. cruzi*.

Suramin action in African trypanosomes involves a RuvB-like DNA helicase.

Albisetti A, Hälg S, Zoltner M, Mäser P, Wiedemar N.
19-09-2023
Int J Parasitol Drugs Drug Resist.
https://pubmed.ncbi.nlm.nih.gov/37757728/

Knowledge Production on Congenital Chagas Disease across Time, Borders and Disciplines: A Comprehensive Scoping Review.

Rapp E, Gold M.
22-08-2023
Trop Med Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37755884/

Congenital transmission is a key route of *Trypanosoma cruzi* infection in Latin America and globally, contributing significantly to the burden of Chagas disease. The interruption of transmission from mother to child has recently become a focus issue. However, the research landscape on congenital Chagas disease remains largely unexplored. The purpose of this scoping review is to assess the production of knowledge on congenital Chagas disease (CCD), aiming to identify research trends and potential gaps. Our initial hypothesis was that the CCD literature overly represents the medical sciences and that there is a need for socio-cultural research on the subject. We conducted a systematic search of publications focusing on congenital Chagas disease in six languages (English, Spanish, Portuguese, French, German and Italian). This comprehensive literature search identified 876 studies that met the inclusion criteria, out of a total of 8893 sources. The relevant literature was analyzed by language, year of publication, discipline, source type and research location. The main outcome of this study has been to prove our hypothesis that there is a scarcity of knowledge produced within the non-biomedical sciences on CCD. This underscores the need for further exploration into the social and structural issues surrounding this disease. Visually clear data concerning congenital Chagas disease produced by this study can contribute to hone in future research efforts and support funding applications. Additionally, this article provides a reference list that other researchers can consult for their own studies.

Canine Systemic Insecticides Fluralaner and Lotilaner Induce Acute Mortality of Triatoma gerstaeckeri, North American Vector of the Chagas Disease Parasite.

Busselman RE, Zecca IB, Hamer GL, Hamer SA.
25-09-2023
Am J Trop Med Hyg.
https://pubmed.ncbi.nlm.nih.gov/37748769/

Chagas disease is a health concern for humans and animals across the Americas, and control options targeting the triatomine vectors of Trypanosoma cruzi, the causative agent of Chagas disease, are limited. Host-targeted interventions may be a useful and underused tool in controlling the spread of T. cruzi from vectors to hosts. Domestic dogs are known to be key bloodmeal hosts for triatomines as well as T. cruzi reservoirs and may be an effective and practical target for host-targeted insecticide deployment. We hypothesized that treating dogs with commercially available systemic insecticides (labeled for flea and tick control) would result in mortality of triatomines after consuming treated blood. We enrolled 16 privately owned dogs into five treatment groups to receive either fluralaner (Bravecto) or lotilaner (Credelio),

alone or in combination with ivermectin. Blood from dogs before the initiation of treatment served as controls. Blood was collected 0, 7, 30, 45, and 90 days after the initial canine insecticide treatment and fed to 10 Triatoma gerstaeckeri nymphs through a membrane feeder, and survival was tracked daily for 7 days and weekly thereafter. All triatomines in the control and ivermectin groups survived the initial period, with no significant difference in long-term survival. In contrast, 99.7% of triatomines that fed on blood from dogs treated with either fluralaner or lotilaner died within 3 days. Although the impact of canine treatment on suppressing vector populations is unknown, fluralaner and lotilaner appear to be a compelling option for an integrated vector management approach to triatomine control.

CD39 expression by regulatory T cells drives CD8+ T cell suppression during experimental Trypanosoma cruzi infection.

Araujo Furlan CL, Boccardo S, Rodriguez C, Robson SC, Gruppi A, Montes CL, Acosta Rodríguez EV.
16-09-2023
bioRxiv.
https://pubmed.ncbi.nlm.nih.gov/37745571/

RNA editing catalytic complexes edit multiple mRNA sites non-processively in Trypanosoma brucei.

Carnes J, McDermott SM, Stuart K.
22-09-223
Mol Biochem Parasitol.
https://pubmed.ncbi.nlm.nih.gov/37742784/

At the outer part of the active site in Trypanosoma cruzi glucokinase: The role of phenylalanine 337.

Carey SM, Kearns SP, Millington ME, Buechner GS, Alvarez BE Jr, Daneshian L, Abiskaroon B, Chruszcz M, D'Antonio EL.
21-09-2023
Biochimie.
https://pubmed.ncbi.nlm.nih.gov/37741546/

The hole mutagenesis approach was used to interrogate the importance of F337 in Trypanosoma cruzi glucokinase (TcGlcK) in order to understand the complete set of binding interactions that are made by d-glucosamine analogue inhibitors containing aromatic tail groups that can extend to the outer part of the active site. An interesting inhibitor of this analogue class includes 2-N-carboxybenzyl-2-deoxy-d-glucosamine (CBZ-GlcN), which exhibits strong TcGlcK binding with a K_i of 710 nM. The residue F337 is found at the outer part of the active site that stems from the second protein subunit of the homodimeric assembly. In this study, F337 was changed to leucine and alanine so as to diminish phenylalanine's side chain size and attenuate intermolecular interactions in this region of the binding cavity. Results from enzyme - inhibitor assays revealed that the phenyl group of F337 made dominant hydrophobic interactions with the phenyl group of CBZ-GlcN as opposed to π - π stacking interactions. Moreover, enzymatic activity assays and X-ray crystallographic experiments indicated that each of these site-directed mutants primarily retained their activity and had high structural similarity of their protein fold. A computed structure model of T. cruzi hexokinase (TcHxK), which was produced by the artificial intelligence system AlphaFold, was compared to an X-ray crystal structure of TcGlcK. Our structural analysis revealed that TcHxK lacked an F337 counterpart residue and probably exists in the monomeric form. We proposed that the d-glucosamine analogue inhibitors that are structurally similar to CBZ-GlcN may not bind as strongly in TcHxK as they do in TcGlcK because of absent van der Waals contact from residue side chains.

Revisiting gene typing and phylogeny of Trypanosoma cruzi reference strains: Comparison of the relevance of mitochondrial DNA, single-copy nuclear DNA, and the intergenic region of mini-exon gene.

Barnabé C, Brenière SF, Santillán-Guayasamín S, Douzery EJP, Waleckx E.
20-09-2023
Infect Genet Evol.
https://pubmed.ncbi.nlm.nih.gov/37739149/

Characterisation of TbSmee1 suggests endocytosis allows surface-bound cargo to enter the trypanosome flagellar pocket.

Schichler D, Konle A, Spath EM, Riegler S, Klein A, Seleznev A, Jung S, Wuppermann T, Wetterich N, Borges A, Meyer-Natus E, Havlicek K, Cabrera SP, Niedermüller K, Sajko S, Dohn M, Malzer X, Riemer E, Tumurbaatar T, Djinovic-Carugo K, Dong G, Janzen CJ, Morriswood B.
22-09-2023
J Cell Sci.
https://pubmed.ncbi.nlm.nih.gov/37737012/

All endo- and exocytosis in the African trypanosome Trypanosoma brucei occurs at a single subdomain of the plasma membrane. This subdomain, the flagellar pocket, is a small vase-shaped invagination containing the root of the cell's single flagellum. Several cytoskeleton-associated multiprotein complexes are coiled around the neck of the flagellar pocket on its cytoplasmic face. One of these, the hook complex, was proposed to affect macromolecule entry into the flagellar pocket lumen. In previous work, knockdown of the hook complex component TbMORN1 resulted in larger cargo being unable to enter the flagellar pocket. In this study, the hook complex component TbSmee1 was characterised in bloodstream form Trypanosoma brucei and was found to be essential for cell viability. TbSmee1 knockdown resulted in flagellar pocket enlargement and impaired access to the flagellar pocket membrane by surface-bound cargo, similar to depletion of TbMORN1. Unexpectedly, inhibition of endocytosis by knockdown of clathrin phenocopied TbSmee1 knockdown, suggesting that endocytic activity itself is a prerequisite for the entry of surface-bound cargo into the flagellar pocket.

Ulcère de Buruli

Recent Advances in the Management Strategies for Buruli Ulcers.

Popa GL, Muntean AA, Popa MI.
27-08-2023
Pathogens.
https://pubmed.ncbi.nlm.nih.gov/37764896/

Buruli ulcer (BU) is a bacterial skin infection that is caused by *Mycobacterium ulcerans* and mainly affects people who reside in the rural areas of Africa and in suburban and beach resort communities in Australia. The infection typically begins as a painless papule or nodule that gradually develops into a large ulcer that can cause substantial impairment, damaging soft tissues and even bones. Early detection and immediate treatment are crucial to preventing further tissue damage and any potential complications, although it is worth noting that access to proper therapeutic resources can be limited in certain areas. The most commonly used antibiotics for treating BU are rifampicin, streptomycin, and clarithromycin; efforts have recently been made to introduce new treatments that increase the effectiveness and adherence to therapy. This article presents the latest research and management strategies regarding BU, providing an updated and intriguing perspective on this topic.

What about Current Diversity of Mycolactone-Producing Mycobacteria? Implication for the Diagnosis and Treatment of Buruli Ulcer.

Combe M, Cherif E, Blaizot R, Breugnot D, Gozlan RE.
06-09-2023
Int J Mol Sci.
https://pubmed.ncbi.nlm.nih.gov/37762030/

Endemic infectious cutaneous ulcers syndrome in the Oti Region of Ghana: Study of cutaneous leishmaniasis, yaws and Haemophilus ducreyi cutaneous ulcers.

Akuffo RA, Sanchez C, Amanor I, Amedior JS, Kotey NK, Anto F, Azurago T, Ablordey A, Owusu-Antwi F, Beshah A, Amoako YA, Phillips RO, Wilson M, Asiedu K, Ruiz-Postigo JA, Moreno J, Mokni M.
27-09-2023
PLoS One.
https://pubmed.ncbi.nlm.nih.gov/37756291/

Background: A recent study detected cutaneous leishmaniasis (CL) in 31.9% of persons with skin ulcers in the Oti Region of Ghana, resulting in a need to investigate other potential causes of the unexplained skin ulcers. Methodology/principal findings: A community based cross-sectional study was conducted in the Oti region to investigate skin ulcers of undetermined aetiologies. To confirm a diagnosis of cutaneous leishmaniasis, Buruli ulcer, Haemophilus ducreyi ulcers, or yaws, DNA obtained from each patient skin ulcer sample was systematically subjected to polymerase chain reaction (PCR) for Leishmania spp., Mycobacterium ulcerans, Haemophilus ducreyi, and Treponema pallidum sub species pertenue. A total of 101 skin ulcer samples were obtained from 101 persons. Co-infection of more than one organism was observed in 68.3% of the samples. Forty (39.6%) participants had a positive result for Leishmania spp., 68 (67.3%) for Treponema pallidum sub. Sp. pertenue, and 74 (73.3%) for H. ducreyi. Twenty (19.8%) of the patient ulcers were simultaneously infected with Leishmania spp., Treponema pallidum sub. Sp. pertenue, and H. ducreyi. None of the patients' lesions yielded a positive result for Mycobacterium ulcerans. Conclusions/significance: This study detected single and mixed occurrence of the causative organisms of CL, yaws, and H. ducreyi cutaneous ulcers in CL endemic communities of the Oti Region in Ghana. These findings emphasize the importance of integrating multiple skin diseases on a common research platform and calls for the development of a comprehensive guideline for diagnosing and treating tropical ulcers in the study areas.

Comprehensive Case-Control Study of Protective and Risk Factors for Buruli Ulcer, Southeastern Australia.

McNamara BJ, Blasdell KR, Yerramilli A, Smith IL, Clayton SL, Dunn M, Tay EL, Gibney KB, Waidyatillake NT, Hussain MA, Muleme M, O'Brien DP, Athan E.
Oct-2023
Emerg Infect Dis.
https://pubmed.ncbi.nlm.nih.gov/37735741/