



Réseau MTN Francophone

Veille scientifique Maladies tropicales négligées

Semaine 46

14 au 20 novembre 2022

| | |
|--|----|
| Dengue, chikungunya et maladie à virus Zika | 2 |
| Rage | 4 |
| Trachome..... | 6 |
| Ulcère de Buruli..... | 7 |
| Pian | 7 |
| Lèpre..... | 7 |
| Trypanosomes (trypanosomiase et maladie de Chagas) | 11 |
| Leishmaniose | 13 |
| Cysticercose..... | 15 |
| Dracunculose | 15 |
| Echinococcose | 15 |
| Trématodoses d'origine alimentaire (clonorchiose, opisthorchiase, fasciolase et paragonimose | 16 |
| Filariose lymphatique | 16 |
| Mycétome | 17 |
| Onchocercose..... | 17 |
| Schistosomiase | 17 |
| Helminthiases transmises par le sol (ascaridiose, trichuriase, ankylostomiase) | 18 |
| Gale..... | 19 |
| Morsures de serpent | 20 |

Dengue, chikungunya et maladie à virus Zika

Understanding and tackling snakebite envenoming with transdisciplinary research.

Gutiérrez JM, Borri J, Giles-Vernick T, Duda R, Habib AG, Malhotra A, Martín G, Pintor AFV, Potet J, Scott T, Bolon I, de Castañeda RR.

17-11-2022

PLoS Negl Trop Dis.

<https://pubmed.ncbi.nlm.nih.gov/36395090/>

No Association Between Interleukin 6 and Inducible Nitric Oxide Synthase Polymorphisms and Dengue Infection: A Case-Control Study.

Dos Santos BRC, Melo Dos Santos AC, Magalhaes Bastos D, Silva Santos LD, de Souza Praxedes FA, Sathio Bessoni Tanabe I, Fireman de Farias K, Martins de Souza Figueiredo EV.

17-11-2022

Immunol Invest.

<https://pubmed.ncbi.nlm.nih.gov/36394557/>

Background: Dengue is a life-threatening disease. The factors that lead to severe cases are not completely understood. The host immune system is involved in the response to infections and plays an important role in dengue infection. IL-6 and iNOS are components of the immune system and genetic polymorphisms in these genes may be involved in dengue virus infection. The study aimed to investigate the association of genetic polymorphisms in the IL6 and iNOS genes and dengue.

Methods: We performed a case-control study using 60 dengue-infected individuals and 119 healthy controls. Polymorphisms in the IL6 (T15A) and iNOS (-1173CT) genes were amplified by Real-Time PCR. Statistical analyses were performed using BioEstat 5.0. **Results:** We identified that the frequency of T/A genotype of IL6 was higher in dengue fever patients and C/T genotype of iNOS was higher in dengue hemorrhagic fever patients, however, no association was found between these polymorphisms and dengue. **Conclusion:** Polymorphisms in iNOS and IL6 were not associated with dengue infection.

New self-sexing *Aedes aegypti* strain eliminates barriers to scalable and sustainable vector control for governments and communities in dengue-prone environments

Spinner SAM, Barnes ZH, Puinean AM, Gray P, Dafa'alla T, Phillips CE, Nascimento de Souza C, Frazon TF, Ercit K, Collado A, Naish N, Sulston E, Li Phillips GC, Greene KK, Poletto M, Sperry BD, Warner SA, Rose NR, Frandsen GK, Verza NC, Gorman KJ, Matzen KJ.

25-10-2022

Front Bioeng Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/36394032/>

For more than 60 years, efforts to develop mating-based mosquito control technologies have largely failed to produce solutions that are both effective and scalable, keeping them out of reach of most governments and communities in disease-impacted regions globally. High pest suppression levels in trials have yet to fully translate into broad and effective *Aedes aegypti* control solutions. Two primary challenges to date—the need for complex sex-sorting to prevent female releases, and cumbersome processes for rearing and releasing male adult mosquitoes—present significant barriers for existing methods. As the host range of *Aedes aegypti* continues to advance into new geographies due to increasing globalisation and climate change, traditional chemical-based approaches are under mounting pressure from both more stringent regulatory processes and the ongoing development of insecticide resistance. It is no exaggeration to state that new tools, which are equal parts effective and scalable, are needed now more than ever. This paper describes the development and field evaluation of a new self-sexing strain of *Aedes aegypti* that has been designed to combine targeted vector suppression, operational simplicity, and cost-effectiveness for use in disease-prone regions. This conditional, self-limiting trait uses the sex-determination gene *doublesex* linked to the tetracycline-off genetic switch to cause complete female lethality in early larval development. With no female progeny survival, sex sorting is no longer required, eliminating the need for large-scale mosquito production facilities or physical sex-separation. In deployment operations, this translates to the ability to generate multiple generations of suppression for each mosquito released, while being entirely self-limiting. To evaluate these potential benefits, a field trial was carried out in densely-populated urban, dengue-prone neighbourhoods in Brazil, wherein the strain was able to suppress wild mosquito populations by up to 96%, demonstrating the utility of this self-sexing approach for biological vector control. In doing so, it has shown that such strains offer the critical components necessary to make these tools highly accessible, and thus they harbour the potential to transition mating-based approaches to effective and sustainable vector control tools that are within reach of governments and at-risk communities who may have only limited resources.

Dual-fluorescent reporter for live-cell imaging of the ER during DENV infection.

Corliss L, Holliday M, Lennemann NJ.

25-10-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36389173/>

Infection by flaviviruses leads to dramatic remodeling of the endoplasmic reticulum (ER). Viral replication occurs within virus-induced vesicular invaginations in the ER membrane. A hallmark of flavivirus infection is expansion of the ER membrane which can be observed at specific time points post infection. However, this process has not been effectively visualized in living cells throughout the course of infection at the single cell resolution. In this study, we developed a plasmid-based reporter system to

monitor flavivirus infection and simultaneous virus-induced manipulation of single cells throughout the course of infection in real-time. This system requires viral protease cleavage to release an ER-anchored fluorescent protein infection reporter that is fused to a nuclear localization signal (NLS). This proteolytic cleavage allows for the translocation of the infection reporter signal to the nucleus while an ER-specific fluorescent marker remains localized in the lumen. Thus, the construct allows for the visualization of virus-dependent changes to the ER throughout the course of infection. In this study, we show that our reporter was efficiently cleaved upon the expression of multiple flavivirus proteases, including dengue virus (DENV), Zika virus (ZIKV), and yellow fever virus (YFV). We also found that the DENV protease-dependent cleavage of our ER-anchored reporter exhibited more stringent cleavage sequence specificity than what has previously been shown with biochemical assays. Using this system for long term time-lapse imaging of living cells infected with DENV, we observed nuclear translocation of the reporter signal beginning approximately 8 hours post-infection, which continued to increase throughout the time course. Interestingly, we found that increased reporter signal translocation correlated with increased ER signal intensity, suggesting a positive association between DENV infection and ER expansion in a time-dependent manner. Overall, this report demonstrates that the FlavER platform provides a useful tool for monitoring flavivirus infection and simultaneously observing virus-dependent changes to the host cell ER, allowing for study of the temporal nature of virus-host interactions.

Vitamin D deficiency in dengue fever patients' coinfecting with *H. pylori* in Pakistan. A case-control study.

Mirza WA, Zhang K, Zhang R, Duan G, Khan MSN, Ni P.
31-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388314/>

Entomo-virological surveillance followed by serological active survey of symptomatic individuals is helpful to identify hotspots of early arbovirus transmission.

Leandro AS, Lopes RD, Amaral Martins C, Delai RM, Villela DAM, Maciel-de-Freitas R.
28-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388305/>

Dengue outbreaks prediction in Bangladesh perspective using distinct multilayer perceptron NN and decision tree.

Khan MAR, Akter J, Ahammad I, Ejaz S, Jaman Khan T.
10-11-2022

Health Inf Sci Syst.

<https://pubmed.ncbi.nlm.nih.gov/36387748/>

Dengue fever is a disease that has been outbreak worldwide in the last few years. Dengue is a fatal disease; sometimes, it may cause life-threatening complications and even death. Dengue is considered to be one of the critical diseases which is spreading in more than 110 countries. Nearly 45,000 case reports have been found around Bangladesh in the last year. Dengue fever has become a major health hazard in Bangladesh. Hence, early detection would mitigate major casualties of Dengue disease. Distinct studies have been performed concerning Dengue disease; however, no effective study, particularly from Bangladesh's perspective, it seemed that reveals Dengue outbreaks prediction method. In this scenario, this research work aims to analyse the Dengue disease and build an apposite model to predict dengue outbreaks. This paper also aims to find the best technique to early predicts Dengue disease. The real-time data of the patients admitted to different hospitals in Bangladesh is accumulated to achieve the goal of the current research. Then different multilayer perceptron neural networks and a Decision tree are used for Dengue outbreaks prediction. Twenty-five parameters are analysed to find these parameters' infection rates in this work. A comparative study of the developed models' performances is also accomplished to obtain a better Dengue outbreaks prediction model. The results evidence that the Levenberg-Marquardt is the best technique with 97.3% accuracy and 2.7% error in Dengue disease prediction. On the other hand, the Decision tree may have the second choice to assess Dengue disease.

An epidemiological study of domiciliary practices and health seeking behaviour among animal bite patients attending a hospital in Delhi.

Panda M, Kapoor R.

Jul-2022

J Family Med Prim Care.

<https://pubmed.ncbi.nlm.nih.gov/36387695/>

Probable sociobehavioural and environmental risk factors for dengue transmission in Puducherry, India - An exploratory study.

Jeyapal DR, Krishnakumari A, Srividya A, Kumar A, Purushothaman J.

Jul-2022

J Family Med Prim Care.

<https://pubmed.ncbi.nlm.nih.gov/36387632/>

Context: Dengue is one of the most extensively spread mosquito borne disease. Puducherry has experienced outbreaks during the post monsoon season almost every year since 2003. Understanding the dynamics of disease transmission and the conducive factors favourable for its spread is necessary to plan early control measures to prevent outbreaks. Objective: To describe the sociodemographic details of the dengue recovered cases, their clinical features, management, probable sociobehavioural and environmental risk factors for acquiring infection that could favour disease spread. Methodology: An exploratory descriptive study was

conducted among 23 individuals recovered from dengue during the outbreak in Puducherry in 2018. An interview guide was used to elicit details regarding the course of illness from its onset until recovery as well as the probable sociobehavioural and environmental risk factors from each participant. Descriptive statistics were reported as frequency, percentage, and mean scores. **Results:** All 23 were primary cases of dengue with fever and myalgia being the commonest presentation. Two of them developed dengue haemorrhagic fever, of which one completely recovered. Five were found to have dengue-chikungunya coinfection. Lack of awareness about dengue, noncompliance regarding proper solid waste management and environmental sanitation among the public was clearly evident. **Conclusion:** Local transmission was evident as most cases did not have any relevant travel history outside the State and from the prevailing mosquito-genic environmental conditions. Dengue being a preventable disease can be controlled only with the active participation of all stakeholders including primary care physicians and the community.

Applicability of the Mexican ovitrap system for Aedes vector surveillance in Colombia.

Wright E, Carrillo MA, Matamoros D, Sanchez RC, Yañez J, Di Lorenzo G, Villa JM, Kroeger A.

16-11-2022

Pathog Glob Health

<https://pubmed.ncbi.nlm.nih.gov/36384430/>

Ovitrap can detect Aedes vectors at an early stage and can serve as an alarm indicator for outbreak prediction. This study aimed to summarize the available literature about the ovitrap system and to determine its feasibility, required resources and costs when installing and maintaining this vector surveillance system in the municipality of Los Patios, Colombia. A scoping review to assess the role of ovitraps as a tool for Aedes vector surveillance was conducted. The subsequent fieldwork consisted of mapping the municipality, manufacturing, and installing 40 ovitraps in 10 blocks, revising them weekly for 4 weeks by two half-time employed vector control technicians, and carrying out a cost analysis. A total of 38 studies were included in this review showing that ovitraps had a better performance than other entomological surveillance methods and a positive correlation with other entomological and disease variables. From the field results over 4 weeks, a high proportion of positive ovitraps (80%, 90%, 75%, 97.5%) and positive blocks (100%) as well as a good acceptance by house owners (76.9%), were identified. Operational indicators such as average installation time of the ovitraps (10h15 m), weekly reading and reinstallation (on average 7h27 m) and the cost of the intervention (COL\$1,142,304.47/US\$297) were calculated. Literature shows that ovitraps are sensitive to detect the presence of Aedes mosquitoes, providing data efficiently and timely for outbreak prediction. The field testing showed it is an affordable and feasible method in the context of a Colombian municipality and similar endemic areas.

Dengue beyond the tropics: a time-series study comprising 2015-2016 versus 2019-2020 at a children's hospital in the City of Buenos Aires.

Berberian G, Pérez G, Mangano A, Borgnia D, Buchovsky A, Costa M, Fabbri C, Luppó V, Mistchenko AS, Deschutter V, Botana C, Martiren S, Brizuela M, Arias AP, Rosanova MT.

Dec-2022

Arch Argent Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36374056/>

Identification of Small Molecules with Improved Potency against Orthopoxviruses from Vaccinia to Smallpox

Brown LE, Seitz S, Kondas AV, Marcyk PT, Filone CM, Hossain MM, Schaus SE, Olson VA, Connor JH.

15-11-2022

Antimicrob Agents Chemother.

<https://pubmed.ncbi.nlm.nih.gov/36222522/>

The genus Orthopoxvirus contains several human pathogens, including vaccinia, monkeypox, cowpox, and variola virus, the causative agent of smallpox. Although there are a few effective vaccines, widespread prophylactic vaccination has ceased and is unlikely to resume, making therapeutics increasingly important to treat poxvirus disease. Here, we described efforts to improve the potency of the anti-poxvirus small molecule CMLDBU6128. This class of small molecules, referred to as pyridopyrimidinones (PDPMs), showed a wide range of biological activities. Through the synthesis and testing of several exploratory chemical libraries based on this molecule, we identified several compounds that had increased potency from the micromolar into the nanomolar range. Two compounds, designated (12) and (16), showed inhibitory concentrations of 326 nM and 101 nM, respectively, which was more than a 10-fold increase in potency to CMLDBU6128 with an inhibitory concentration of around 6 µM. We also expanded our investigation of the breadth of action of these molecules and showed that they can inhibit the replication of variola virus, a related orthopoxvirus. Together, these findings highlighted the promise of this new class of antipoxviral agents as broad-spectrum small molecules with significant potential to be developed as antiviral therapy. This would add a small molecule option for therapy of spreading diseases, including monkeypox and cowpox viruses, that would also be expected to have efficacy against smallpox.

Rage

Case report: Blood purification effectively relieves multiple system failure in patient with rabies.

Kuang D, Luo M, Chen J, Liang C, Cai Z, Yuan Z, Zhou Z, Chen J, Fu C.

26-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388383/>

Rabies is an infectious disease of animal origin with a high mortality rate. In the early stages of rabies, the rabies virus (RABV) is usually undetectable in saliva and cerebrospinal fluid (CSF). In addition, there are still no effective drugs and treatments. Here, we present a case in which blood purification alleviated multisystem failures. The patient was a 45-year-old woman who presented with the fear of water and wind, restlessness, and hyperactivity. RABV was detected in her saliva by high-throughput sequencing Next Generation Sequencing (NGS) and polymerase chain reaction (PCR). Based on typical clinical symptoms and the result of NGS and PCR, the patient was diagnosed as a confirmed case of rabies. Hemodialysis combined with antiviral therapy and intensive care unit (ICU) treatment can effectively relieve circulatory failure, respiratory failure, and renal failure. Finally, she died of brain death on the 34th day of admission. The case report showed that blood purification was positive for rabies-induced organ failure. Blood purification combined with antiviral therapy can prolong the lives of patients with rabies to some extent.

Sf9 Cells Metabolism and Viability When Coinfected with Two Monocistronic Baculoviruses to Produce Rabies Virus-like Particles.

Leme J, Guardalini LGO, Bernardino TC, Astray RM, Tonso A, Núñez EGF, Jorge SAC.

18-11-2022

Mol Biotechnol.

<https://pubmed.ncbi.nlm.nih.gov/36396754/>

This work aimed to describe the dynamics of the Sf9 insect cells death and primary metabolism when this host is infected simultaneously by two recombinant baculoviruses (BV) expressing rabies glycoprotein (BVG) and matrix protein (BVM) genes to produce rabies virus-like particles (VLP) at different multiplicities of infection (MOI). Schott flasks essays covering a wide range of MOI for both BV were performed. Viable cell density, cell viability, glucose, glutamine, glutamate, lactate, ammonium, and rabies proteins concentrations were monitored over the infection phase. The expression of both recombinant proteins was not limited by glucose, glutamine, and glutamate in a broad MOI (pfu/cell) range of BVG (0.15-12.5) and BVM (0.1-5.0) using SF900 III serum free culture medium. Death phase initiation and the specific death rate depend on BV MOI. The wave pattern of nutrient/metabolite profiles throughout the viral infection phase is related to the baculovirus lytic cycle. The optimal MOIs ratio between BVG (2.5-4.5) and BVM (1.0-3.0) for maximum protein expression was defined. The produced rabies VLP sizes are close to 78 nm. In general, these work outputs bring a better understanding of the metabolic performance of Sf9 cells when infected by BV for producing VLP, and specifically, for progressing in a rabies VLP vaccine development.

Knowledge, attitude and practice related to rabies among residents of Amhara region, Ethiopia.

Bahiru A, Molla W, Yizengaw L, Mekonnen SA, Jemberu WT.

03-11-2022

Heliyon

<https://pubmed.ncbi.nlm.nih.gov/36387566/>

CRISPR/Cas-Based Biosensor As a New Age Detection Method for Pathogenic Bacteria.

Chakraborty J, Chaudhary AA, Khan SU, Rudayni HA, Rahaman SM, Sarkar H.

18-10-2022

ACS Omega

<https://pubmed.ncbi.nlm.nih.gov/36385843/>

Methods enabling rapid and on-site detection of pathogenic bacteria are a prerequisite for public health assurance, medical diagnostics, ensuring food safety and security, and research. Many current bacteria detection technologies are inconvenient and time-consuming, making them unsuitable for field detection. New technology based on the CRISPR/Cas system has the potential to fill the existing gaps in detection. The clustered regularly interspaced short palindromic repeats (CRISPR) system is a part of the bacterial adaptive immune system to protect them from intruding bacteriophages. The immunological memory is saved by the CRISPR array of bacteria in the form of short DNA sequences (spacers) from invading viruses and incorporated with the CRISPR DNA repeats. Cas proteins are responsible for triggering and initiating the adaptive immune function of CRISPR/Cas systems. In advanced biological research, the CRISPR/Cas system has emerged as a significant tool from genome editing to pathogen detection. By considering its sensitivity and specificity, this system can become one of the leading detection methods for targeting DNA/RNA. This technique is well applied in virus detection like Dengue, ZIKA, SARS-CoV-2, etc., but for bacterial detection, this CRISPR/Cas system is limited to only a few organisms to date. In this review, we have discussed the different techniques based on the CRISPR/Cas system that have been developed for the detection of various pathogenic bacteria like *L. monocytogenes*, *M. tuberculosis*, Methicillin-resistant *S. aureus*, *Salmonella*, *E. coli*, *P. aeruginosa*, and *A. baumannii*.

Treat the "Untreatable" by a Photothermal Agent: Triggering Heat and Immunological Responses for Rabies Virus Inactivation.

Bai Y, Huang P, Feng N, Li Y, Huang J, Jin H, Zhang M, Sun J, Li N, Zhang H, Xia X, Tang BZ, Wang H.

17-11-2022

Adv Sci (Weinh).

<https://pubmed.ncbi.nlm.nih.gov/36385484/>

Rabies is a fatal neurological zoonotic disease caused by the rabies virus (RABV), and the approved post-exposure prophylaxis (PEP) procedure remains unavailable in areas with inadequate medical systems. Although strategies have been proposed for PEP and postinfection treatment (PIT), because of the complexity of the treatment procedures and the limited curative outcome, developing

an effective treatment strategy remains a holy grail in rabies research. Herein, a facile approach is proposed involving photothermal therapy (PTT) and photothermally triggered immunological effects to realize effective PEP and PIT simultaneously. The designed photothermal agent (N+ TT-mCB nanoparticles) featured positively charged functional groups and high photo-to-heat efficiency, which are favorable for virus targeting and inactivation. The level of the virus at the site of infection in mice is significantly decreased upon treatment with orthotopic PTT, and the transfer of the virus to the brain is significantly inhibited. Furthermore, the survival ratio of the mice three days postinfection is increased by intracranial injection of N+ TT-mCB and laser irradiation. Overall, this work provides a platform for the effective treatment of RABV and opens a new avenue for future antiviral studies.

Ascertaining cells' synaptic connections and RNA expression simultaneously with barcoded rabies virus libraries.

Saunders A, Huang KW, Vondrak C, Hughes C, Smolyar K, Sen H, Philson AC, Nemesh J, Wysoker A, Kashin S, Sabatini BL, McCarroll SA.

16-11-2022

Nat Commun.

<https://pubmed.ncbi.nlm.nih.gov/36384944/>

Brain function depends on synaptic connections between specific neuron types, yet systematic descriptions of synaptic networks and their molecular properties are not readily available. Here, we introduce SBARRO (Synaptic Barcode Analysis by Retrograde Rabies ReadOut), a method that uses single-cell RNA sequencing to reveal directional, monosynaptic relationships based on the paths of a barcoded rabies virus from its "starter" postsynaptic cell to that cell's presynaptic partners. Thousands of these partner relationships can be ascertained in a single experiment, alongside genome-wide RNAs. We use SBARRO to describe synaptic networks formed by diverse mouse brain cell types in vitro, finding that different cell types have presynaptic networks with differences in average size and cell type composition. Patterns of RNA expression suggest that functioning synapses are critical for rabies virus uptake. By tracking individual rabies clones across cells, SBARRO offers new opportunities to map the synaptic organization of neural circuits.

Generalized Modules for Membrane Antigens (GMMA), an outer membrane vesicle-based vaccine platform, for efficient viral antigen delivery.

Hu K, Palmieri E, Samnuan K, Ricchetti B, Oldrini D, McKay PF, Wu G, Thorne L, Fooks AR, McElhinney LM, Goharriz H, Golding M, Shattock RJ, Micoli F.

11-11-2022

J Extracell Vesicles.

<https://pubmed.ncbi.nlm.nih.gov/36377074/>

Vaccine platforms enable fast development, testing, and manufacture of more affordable vaccines. Here, we evaluated Generalized Modules for Membrane Antigens

(GMMA), outer membrane vesicles (OMVs) generated by genetically modified Gram-negative bacteria, as a vaccine platform for viral pathogens. Influenza A virus hemagglutinin (HA), either physically mixed with GMMA (HA+STmGMMA mix), or covalently linked to GMMA surface (HA-STmGMMA conjugate), significantly increased antigen-specific humoral and cellular responses, with HA-STmGMMA conjugate inducing further enhancement than HA+STmGMMA mix. HA-STmGMMA conjugate protected mice from lethal challenge. The versatility for this platform was confirmed by conjugation of rabies glycoprotein (RABVG) onto GMMA through the same method. RABVG+STmGMMA mix and RABVG-STmGMMA conjugate exhibited similar humoral and cellular response patterns and protection efficacy as the HA formulations, indicating relatively consistent responses for different vaccines based on the GMMA platform. Comparing to soluble protein, GMMA was more efficiently taken up in vivo and exhibited a B-cell preferential uptake in the draining lymph nodes (LNs). Together, GMMA enhances immunity against viral antigens, and the platform works well with different antigens while retaining similar immunomodulatory patterns. The findings of our study imply the great potential of GMMA-based vaccine platform also against viral infectious diseases.

Trachome

Assessing seroprevalence and associated risk factors for multiple infectious diseases in Sabah, Malaysia using serological multiplex bead assays.

Chan YL, Patterson CL, Priest JW, Stresman G, William T, Chua TH, Tetteh K, Lammie P, Drakeley C, Fornace KM.

25-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388287/>

Background: Infectious diseases continue to burden populations in Malaysia, especially among rural communities where resources are limited and access to health care is difficult. Current epidemiological trends of several neglected tropical diseases in these populations are at present absent due to the lack of habitual and efficient surveillance. To date, various studies have explored the utility of serological multiplex beads to monitor numerous diseases simultaneously. We therefore applied this platform to assess population level exposure to six infectious diseases in Sabah, Malaysia. Furthermore, we concurrently investigated demographic and spatial risk factors that may be associated with exposure for each disease. **Methods:** This study was conducted in four districts of Northern Sabah in Malaysian Borneo, using an environmentally stratified, population-based cross-sectional serological survey targeted to determine risk factors for malaria. Samples were collected between September to December 2015, from 919 villages totaling 10,100 persons. IgG responses to twelve antigens of six diseases (lymphatic filariasis- Bm33, Bm14, BmR1, Wb123; strongyloides- NIE; toxoplasmosis-SAG2A; yaws- Rp17 and TmpA; trachoma- Pgp3, Ct694; and giardiasis- VSP3, VSP5) were measured using serological multiplex bead assays.

Eight demographic risk factors and twelve environmental covariates were included in this study to better understand transmission in this community. **Results:** Seroprevalence of LF antigens included Bm33 (10.9%), Bm14+ BmR1 (3.5%), and Wb123 (1.7%). Seroprevalence of Strongyloides antigen NIE was 16.8%, for Toxoplasma antigen SAG2A was 29.9%, and Giardia antigens GVSP3 + GVSP5 was 23.2%. Seroprevalence estimates for yaws Rp17 was 4.91%, for TmpA was 4.81%, and for combined seropositivity to both antigens was 1.2%. Seroprevalence estimates for trachoma Pgp3 + Ct694 were 4.5%. Age was a significant risk factors consistent among all antigens assessed, while other risk factors varied among the different antigens. Spatial heterogeneity of seroprevalence was observed more prominently in lymphatic filariasis and toxoplasmosis. **Conclusions:** Multiplex bead assays can be used to assess serological responses to numerous pathogens simultaneously to support infectious disease surveillance in rural communities, especially where prevalences estimates are lacking for neglected tropical diseases. Demographic and spatial data collected alongside serosurveys can prove useful in identifying risk factors associated with exposure and geographic distribution of transmission.

Ulcère de Buruli

Pian

Assessing seroprevalence and associated risk factors for multiple infectious diseases in Sabah, Malaysia using serological multiplex bead assays.

Chan YL, Patterson CL, Priest JW, Stresman G, William T, Chua TH, Tetteh K, Lammie P, Drakeley C, Fornace KM. 25-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388287/>

Background: Infectious diseases continue to burden populations in Malaysia, especially among rural communities where resources are limited and access to health care is difficult. Current epidemiological trends of several neglected tropical diseases in these populations are at present absent due to the lack of habitual and efficient surveillance. To date, various studies have explored the utility of serological multiplex beads to monitor numerous diseases simultaneously. We therefore applied this platform to assess population level exposure to six infectious diseases in Sabah, Malaysia. Furthermore, we concurrently investigated demographic and spatial risk factors that may be associated with exposure for each disease. **Methods:** This study was conducted in four districts of Northern Sabah in Malaysian Borneo, using an environmentally stratified, population-based cross-sectional serological survey targeted to determine risk factors for malaria. Samples were collected between September to December 2015, from 919 villages totaling 10,100 persons. IgG responses to twelve antigens of six diseases (lymphatic filariasis- Bm33, Bm14, BmR1, Wb123;

strongyloides- NIE; toxoplasmosis-SAG2A; yaws- Rp17 and TmpA; trachoma- Pgp3, Ct694; and giardiasis- VSP3, VSP5) were measured using serological multiplex bead assays. Eight demographic risk factors and twelve environmental covariates were included in this study to better understand transmission in this community. **Results:** Seroprevalence of LF antigens included Bm33 (10.9%), Bm14+ BmR1 (3.5%), and Wb123 (1.7%). Seroprevalence of Strongyloides antigen NIE was 16.8%, for Toxoplasma antigen SAG2A was 29.9%, and Giardia antigens GVSP3 + GVSP5 was 23.2%. Seroprevalence estimates for yaws Rp17 was 4.91%, for TmpA was 4.81%, and for combined seropositivity to both antigens was 1.2%. Seroprevalence estimates for trachoma Pgp3 + Ct694 were 4.5%. Age was a significant risk factors consistent among all antigens assessed, while other risk factors varied among the different antigens. Spatial heterogeneity of seroprevalence was observed more prominently in lymphatic filariasis and toxoplasmosis. **Conclusions:** Multiplex bead assays can be used to assess serological responses to numerous pathogens simultaneously to support infectious disease surveillance in rural communities, especially where prevalences estimates are lacking for neglected tropical diseases. Demographic and spatial data collected alongside serosurveys can prove useful in identifying risk factors associated with exposure and geographic distribution of transmission.

Lèpre

Effect of systematic tuberculosis detection on mortality in young children with severe pneumonia in countries with high incidence of tuberculosis: a stepped-wedge cluster-randomised trial.

Marcy O, Wobudeya E, Font H, Vessière A, Chabala C, Khosa C, Taguebue JV, Moh R, Mwanga-Amumpaire J, Lounnas M, Mulenga V, Mavale S, Chilundo J, Rego D, Nduna B, Shankalala P, Chirwa U, De Lauzanne A, Dim B, Tiogouo Ngouana E, Folquet Amorrissani M, Cisse L, Amon Tanoh Dick F, Komena EA, Kwedi Nolna S, Businge G, Natukunda N, Cumbe S, Mbekeka P, Kim A, Kheang C, Pol S, Maleche-Obimbo E, Seddon JA, Mao TE, Graham SM, Delacourt C, Borand L, Bonnet M; TB-Speed Pneumonia Study Group.

14-11-2022

Lancet Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36395782/>

The protective role of tissue-resident interleukin 17A-producing gamma delta T cells in Mycobacterium leprae infection.

Liu Y, Shi C, Ma S, Ma Y, Lu X, Zhu J, Yang D.

26-10-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36389696/>

Mycobacterium leprae is a kind of disease-causing bacteria and results in leprosy in human. Gamma delta ($\gamma\delta$) T cell is a T-cell subset that is presented in both human

dermis and epidermis. These cells bridge innate and adaptive immune responses and play critical roles in regulating anti-microbial defense, wound healing, and skin inflammation. Here, we investigated skin resident $\gamma\delta$ T cells in patients with leprosy. Our data showed that $\gamma\delta$ T cells significantly accumulated in skin lesions of leprosy patients with tuberculoid (TT) form. IL-23 can predominantly stimulate dermal $\gamma\delta$ T cells to produce interleukin 17 (IL-17), a cytokine which may lead to disease protection. These $\gamma\delta$ T cells expressed a specific set of surface molecules, and majority of these cells were V δ 1⁺. Also, IL-23 can stimulate the expansion of dermal $\gamma\delta$ T cells expansion. Moreover, our results revealed that the transcription factor ROR γ t was responsible for IL-17A expression in leprosy lesion. Therefore, these data indicated that IL-23-responsive dermal $\gamma\delta$ T cells were the major resource of IL-17A production in the skin and could be a potential target in the treatment of leprosy.

microRNAs associated with the pathogenesis and their role in regulating various signaling pathways during Mycobacterium tuberculosis infection.

Davuluri KS, Chauhan DS.

27-10-2022

Front Cell Infect Microbiol.

<https://pubmed.ncbi.nlm.nih.gov/36389170/>

Despite more than a decade of active study, tuberculosis (TB) remains a serious health concern across the world, and it is still the biggest cause of mortality in the human population. Pathogenic bacteria recognize host-induced responses and adapt to those hostile circumstances. This high level of adaptability necessitates a strong regulation of bacterial metabolic characteristics. Furthermore, the immune response of the host virulence factors such as host invasion, colonization, and survival must be properly coordinated by the pathogen. This can only be accomplished by close synchronization of gene expression. Understanding the molecular characteristics of mycobacterial pathogenesis in order to discover therapies that prevent or resolve illness relies on the bacterial capacity to adjust its metabolism and replication in response to various environmental cues as necessary. An extensive literature details the transcriptional alterations of host in response to *in vitro* environmental stressors, macrophage infection, and human illness. Various studies have recently revealed the finding of several microRNAs (miRNAs) that are believed to play an important role in the regulatory networks responsible for adaptability and virulence in *Mycobacterium tuberculosis*. We highlighted the growing data on the existence and quantity of several forms of miRNAs in the pathogenesis of *M. tuberculosis*, considered their possible relevance to disease etiology, and discussed how the miRNA-based signaling pathways regulate bacterial virulence factors.

Editorial: Leprosy reactions: New knowledge on pathophysiology, diagnosis, treatment and prevention.

Pinheiro RO, Rosa PS, Spencer JS, Soares CT.

01-11-2022

Front Med (Lausanne)

<https://pubmed.ncbi.nlm.nih.gov/36388943/>

Novel approaches in the treatment of Hansen's disease (Leprosy): a case series of multidrug therapy of monthly rifampin, moxifloxacin, and minocycline (RMM) in the United States.

Franco-Paredes C, Garcia-Creighton E, Henao-Martinez A, Kallgren DL, Banjade R, Dyer JA, Nelson T, Zaesim A, Peluso MJ, Jain V, Lee DH, Mincses LR, Wirshup M, Sierra Hoffman M, Katsolis J, Brust K, Giron J, Smiarowski L, Hoosepian-Mer PA, Stryjewska B.

08-11-2022

Ther Adv Infect Dis

<https://pubmed.ncbi.nlm.nih.gov/36387060/>

The World Health Organization (WHO) recommends multidrug therapy (MDT) for the treatment of paucibacillary and multibacillary forms of leprosy, also known as Hansen's disease (HD). MDT combinations of dapsone, rifampin, and clofazimine have reduced the prevalence of the disease but are not without adverse effects impacting regimen adherence. Hence, an urgent need exists to consider alternative MDT regimens with an improved safety profile that promotes treatment adherence. Herein, we described a case series of 10 patients with HD (nine patients with multibacillary leprosy and one with pure neural leprosy) treated with monthly rifampin, moxifloxacin, and minocycline (RMM). The United States National Hansen's Disease Program (NHDP) diagnosed and treated patients across US institutions. All patients received a regimen of 12-24 months of RMM. We reviewed the clinical outcomes, adherence, rate of completion, and adverse events of patients treated with monthly RMM from January 2019 to August 2022. Nine patients had multibacillary leprosy, with some having type-2 reactions. One patient had pure neural leprosy with a reversal reaction. In this case series, we identified that all patients completed the RMM regimen without treatment interruptions. None of the patients experienced any skin hyperpigmentation or any significant side effects. All patients tolerated the monthly RMM regimen with rapid improvement of skin lesions and without logistic hurdles. Based on previous clinical evidence and the results of this case series, the NHDP and other programs should consider the RMM regimen as first-line therapy.

Collodion Baby to Bathing Suit Ichthyosis: A 6-Year Follow-Up.

Grover C, Saha S.

12-10-2022

Indian Dermatol Online J

<https://pubmed.ncbi.nlm.nih.gov/36386759/>

Hemophagocytic Lymphohistiocytosis in Erythema Nodosum Leprosum: Case Report of an Unusual Conundrum.

Mishra P, Krishnan L, Madakshira MG, Rehman N.

21-09-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386753/>

Hemophagocytic lymphohistiocytosis (HLH) and erythema nodosum leprosum (ENL) result from a complex agent-host interaction and form a continuum of the same spectrum. A 30-year-old multi-gravida presented at 36 weeks gestation with fever and erythematous raised lesions over the face and upper and lower limbs after defaulting treatment for borderline lepromatous leprosy. Skin biopsy confirmed ENL, hence multi-drug therapy (MDT) and oral steroids were restarted. However, her condition worsened and she developed icterus, periorbital puffiness, pleural effusion, ascites and splenomegaly. Laboratory investigations showed pancytopenia, conjugated hyperbilirubinemia, transaminitis, elevated lactate dehydrogenase, hypertriglyceridemia, hyperferritinemia and hypofibrinogenemia. Dapsone was stopped on the suspicion of dapsone hypersensitivity but hyperbilirubinemia progressed. Diagnosis of HLH was clinched after bone marrow aspirate showed florid hemophagocytosis and subsequently, intravenous immunoglobulin (2 g/kg) over 5 days and dexamethasone were administered. The patient improved gradually with normalization of laboratory parameters and restarted MDT. This case depicts a rare and potentially catastrophic complication of ENL and emphasizes a vigil for HLH syndrome in such cases.

Ulcerative Growth Over Penis.

Tandel J, Polra R, Parmar D, Nair PA.

21-09-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386752/>

Chocolate and Skin: The Impact of an Insatiable Indulgence.

Sadhasivamohan A, Karthikeyan K.

21-10-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386751/>

Chocolate is the most sought-after delicacy worldwide. Cocoa has been incorporated in various forms, into both foods and cosmetics. Cocoa has not only been used as gourmet food but has also served as medicine for ages. Chocolates are always in vogue and remain a testament to the cocoa bean, but the benefits attained from commercial chocolates remain a fallacy. On a positive note, chocolate has its health benefits but its effects on the skin need a better understanding. Hence this article focuses on the dermatological effects of cocoa, and its use as a dermatological therapeutic agent.

IADVL SIG Pediatric Dermatology (Academy) Recommendations on Childhood Alopecia Areata.

Katakam BK, Behera B, Ranugha P, Puri N, Narayana Rao T, Gulati R, Seetharam KA.

31-10-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386742/>

Alopecia areata (AA) is a chronic inflammatory disease characterized by nonscarring alopecia. In contrast to adult onset AA, the epidemiology, clinical characteristics, and therapy of childhood AA are less explored. This study aims at providing recommendations for the management of childhood AA. The special interest group (SIG) in pediatric dermatology under the Indian Association of Dermatology, Venereology and Leprosy (IADVL) conducted online meetings from February 2021 to September 2021, intending to identify the critical aspects in the diagnosis and treatment of AA. The classification, diagnosis, and tools for assessment of disease activity of childhood AA have been described in this study, along with recommendations for topical and systemic therapy, including newer therapeutic options.

Hypopigmented Skin Lesions with Doubtful/Minimal Sensory Impairment: A Histopathology-Based Analysis.

Sasidharanpillai S, Govindan A, Dominic S, Binitha T, Nandakumar V, Devi K.

18-07-2022

Indian Dermatol Online J

<https://pubmed.ncbi.nlm.nih.gov/36386740/>

Recording of Leprosy Cases in India: Need for a User-Friendly and Effective App.

Bahunuthula RK, Varala S, Rao PN, Suneetha S.

31-10-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386737/>

An Observational Study of Cutaneous Manifestations in Patients on Chemo and Radiation Therapy for Internal Malignancies at Tertiary Care Center.

Tandel JJ, Polra RV, Parmar D, Srivastava P, Panchal R, Nair PA.

31-10-2022

Indian Dermatol Online J.

<https://pubmed.ncbi.nlm.nih.gov/36386735/>

A Practical Approach to the Treatment of Alopecia Areata

Dhurat R, Sharma R.

31-10-2022

Indian Dermatol Online J

<https://pubmed.ncbi.nlm.nih.gov/36386728/>

Alopecia areata is an autoimmune condition which usually presents as non-scarring patchy alopecia. The disease has varied clinical presentations ranging in severity from patchy circumscribed alopecia, reticular pattern, ophiasis, sisaipho, diffuse, or incognito type to alopecia totalis and alopecia universalis. The various available treatment options include topical/intralesional steroids, topical immunotherapy/contact irritants, systemic steroids, and steroid-sparing agents like cyclosporine, azathioprine, methotrexate, and the JAK-STAT inhibitors. This article

aims at providing practical tips to the clinicians based on published data and author's clinical experience which can help them in deciding what and when to choose in a given clinical scenario of AA.

A Comparative Study of the Efficacy of Intralesional 5 Fluorouracil vs Combination of 5 Fluorouracil with Triamcinolone Acetonide in Keloids.

Monteiro RC, Bhat MR, Martis J, Kamath HG.

May/Jun-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386104/>

Toponyms in Dermatology.

Ramesh H, Somashekar S.

May/Jun-2022

Indian J Dermatol

<https://pubmed.ncbi.nlm.nih.gov/36386102/>

The term toponym means any name that is derived from a place name. Numerous dermatological conditions have their names derived from geographic places. Although most conditions may have some association to the place they have been derived from, some of them are fortuitous.

Acquired Epidermodysplasia Verruciformis During Highly Active Antiretroviral Therapy.

Sil A, Bhanja DB, Panigrahi A, Biswas SK.

May/Jun-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386098/>

A Clinical Study of Premature Canities and Its Association with Hemoglobin, Ferritin and Calcium Levels

Chandran S, Simon SA, George AE.

May/Jun-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386090/>

Chronic Mucocutaneous Candidiasis in An 11-Year-Old Child - A Case Report from South India

Gunasekaran P, Gopalan G.

May/Jun-2022

Indian J Dermatol

<https://pubmed.ncbi.nlm.nih.gov/36386076/>

Acquired Fibrokeratoma: A Retrospective Study in a Tertiary Centre in South India.

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

May/Jun-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386073/>

Background: Acquired fibrokeratoma (AFK) is an uncommon, sporadic, benign, acquired, slow-growing dermo-epidermal tumour. **Aims and objectives:** The purpose of this study was to summarize the demographic, clinical characteristics and treatment outcomes of patients with AFK in a tertiary care centre in South India. **Methods:** We evaluated the records of 26 patients with AFK who were diagnosed and treated in our centre between January 2017 and December 2021. The retrospective data related to age, sex, occupation, consistency, duration of lesions, history of trauma, anatomical site, morphological appearance, histopathological type, treatment provided and recurrence were taken into account and analysed. **Results:** Of the 26 patients, there were 21 males and 5 females. Fingers (n = 23) were the most common site involved, followed by toes (n = 2) and palm (n = 1). A total of 18 patients had finger-like projected lesions and eight patients had dome-shaped lesions. In histopathology, Type I AFK type was observed in 16 cases and Type II in 10 cases. **Conclusion:** We believe that our study would contribute by providing the clinical, histopathology and treatment outcomes of this uncommon dermo-epidermal tumour. The frequency of this condition is often underestimated as it is misdiagnosed for many other dermatological conditions.

Dermoscopy of Dermatopathia Pigmentosa Reticularis.

Maheshwari A, Garg T, Sanke S.

May/Jun-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386069/>

Multiple COVID reinfections in a vaccinated psoriatic patient receiving adalimumab.

Zargari O, Azimi SZ.

17-11-2022

J Dermatolog Treat.

<https://pubmed.ncbi.nlm.nih.gov/36384391/>

Currently, psoriasis patients are advised to follow their standard therapeutic regimen, and are advised to be vaccinated against Covid-19. However, the data about the antibody responses, induced by the various kinds of SARS-CoV-2 vaccines in psoriasis patients who require systemic immunosuppressive treatment is scant. In this case report, we describe antibody responses induced by COVID-19 vaccine, in a 26-year-old male patient with psoriasis being treated with anti-TNF biotherapy, adalimumab biosimilar every two weeks. The patient was vaccinated against COVID-19, according to the national protocol. He experienced three episodes of symptomatic COVID-19. His first and second exposures did not result in antibody production. After the third episode of COVID-19, The SARS-CoV-2 anti-spike antibody (IgG) was more than 100 Ru/mL (ELISA; ≥ 8 Ru/mL is considered positive), and SARS-CoV-2 neutralizing antibody (total) was more than 40 micg/mL (ELISA; ≥ 2.5 micg/mL is considered positive). This is the first case with weak antibody response to vaccination and multiple episodes of COVID infection in a

psoriatic patient with adalimumab biosimilar. However, we cannot assume causality due to the treatment.

Solitary plaque of borderline lepromatous leprosy clinically masquerading as paucibacillary leprosy

Gurjar R, Khullar G, Dewan K, Yadav AK.

16-11-2022

Trop Doct.

<https://pubmed.ncbi.nlm.nih.gov/36384324/>

Borderline lepromatous (BL) leprosy typically manifests as numerous asymmetric ill-defined macules or infiltrated plaques. Localized cutaneous involvement in BL leprosy is infrequently reported. Type 2 reaction (T2R), an immune complex syndrome, occurs in patients with BL and lepromatous leprosy, as crops of tender evanescent papules or nodules with constitutional symptoms. T2R can also present with various atypical morphologies and rarely as type 1 reaction (T1R), thereby creating a diagnostic dilemma.

Alice Augusta Ball: The African-American Woman Chemist Who Pioneered the First Viable Treatment for Hansen's Disease

Mushtaq S, Wermager P.

13-11-2022

Clin Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36384187/>

Alice Augusta Ball was a young and dynamic chemist who achieved extraordinary milestones in her short lifespan of 24 years. As an African American and as a woman in the early 20th century, her work and achievements set a benchmark. Her breakthrough work on the extraction of the water-soluble ethyl esters of Chaulmoogra oil changed the lives of millions of people affected with Hansen's disease who were socially boycotted and segregated to leprosy colonies and asylums. The Chaulmoogra oil esters which continued to be used for almost two decades were the first viable treatment of leprosy. Unfortunately, Alice Ball did not receive the recognition and honor for her work, and she was forgotten soon after her untimely death.

Financing care for Severe Stigmatizing Skin Diseases (SSSDs) in Liberia: challenges and opportunities

Smith JS Jr, Diaconu K, Witter S, Weiland S, Zaizay FZ, Theobald S, McCollum R, Kollie K, Kollie J, Berrian H, Hotopf I, Sempe L, Tate W, Dean L.

14-11-2022

Int J Equity Health.

<https://pubmed.ncbi.nlm.nih.gov/36376897/>

Congenital smooth muscle hamartoma: an atypical presentation.

Sangwan P, Dhiman A, Kansal NK.

14-11-2022

BMJ Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/36375854/>

Multidrug resistant tinea corporis/cruris: Response to voriconazole.

Khurana A, Agarwal A, Agrawal D, Sardana K, Singh A, Chowdhary A.

Nov-2022

J Mycol Med.

<https://pubmed.ncbi.nlm.nih.gov/35785725/>

The increasing worldwide resistance to terbinafine and older antifungal drugs, coupled with often erratic clinical responses to itraconazole, leaves dermatologists with limited options to deal with dermatophytic infections. Recalcitrant dermatophytoses has however, over past few years, become a significant public health issue, especially in India. In this context, we present a patient who failed four systemic antifungals sequentially and was subsequently cured with a 2 week course of voriconazole, an antifungal not routinely used for dermatophytoses as yet.

Trypanosomes (trypanosomiasis et maladie de Chagas)

Diagnosis of Acute Chagas Disease in a Belizean Child with Evidence of a Multiclonal Trypanosoma cruzi Infection.

Murray KO, Saldaña MA, Gunter SM, Manzanero R, Zielinski-Gutierrez E, Herrera C, Thompson JM, Maliga A, Bautista K, Lino A, Hawes E, Ronca SE, Morey F, Fuentes RC, Lopez B, Dumonteil E, Morazan GH.

14-11-2022

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36395748/>

In January 2020, we instituted acute febrile illness surveillance in 11 hospitals and clinics across Belize. Within 3 months, we diagnosed an acute case of Chagas disease by polymerase chain reaction in a 7-year-old child in the northern part of the country. Phylogenetic analyses of the parasite from the acute blood specimen revealed a multiclonal *Trypanosoma cruzi* infection, including parasites from the TcII (25.0% of haplotypes), TcIV (2.5% of haplotypes), and TcV (72.5% of haplotypes) discrete typing units. The family reported no history of travel, and three *Triatoma* species vectors were found within the home. The child's mother was seronegative for antibodies to *T. cruzi*, ruling out congenital transmission. Convalescent blood samples documented seroconversion and confirmed acute infection. The child was successfully treated with nifurtimox. This is the first known diagnosed case of acute Chagas infection in Belize, highlighting the need for further investigation and public health prevention measures.

Chagas Disease and Domestic Medical Screening Guidance for Newly Arrived Individuals Under a Humanitarian-

Based Immigration Status: A Call for Action.

Agudelo Higuaita NI, Franco-Paredes C, Henao-Martínez AF, Beatty NL, Manne-Goehler J, Forsyth CJ.

14-11-2022

Am J Trop Med Hyg.

<https://pubmed.ncbi.nlm.nih.gov/36395747/>

Chagas disease is considered one of the most important neglected tropical diseases in the Western Hemisphere, given its morbidity, mortality, and societal and economic burden. The United States has the fifth highest global burden of Chagas disease. Every year, thousands of migrant people from Latin America and throughout the globe travel to the U.S.- Mexico border searching for asylum. The U.S. CDC's Guidance for the U.S. Domestic Medical Examination for Newly Arriving Refugees provides recommendations to safeguard the health of individuals who enter the United States with a humanitarian-based immigration status as defined by the CDC's guidance under Key Considerations and Best Practices. We encourage the inclusion of *Trypanosoma cruzi* infection screening recommendations in this guidance as an important step toward understanding the risk and burden of Chagas disease in this vulnerable population, strengthening their access to care and contributing to the 2030 objectives of the WHO's neglected tropical diseases road map.

Modulation of STAT-1, STAT-3, and STAT-6 activities in THP-1 derived macrophages infected with two *Trypanosoma cruzi* strains.

Oliveira MM, Bonturi CR, Salu BR, Oliva MLV, Mortara RA, Orikaza CM.

26-10-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36389843/>

Trypanosoma cruzi is the causative protozoan of Chagas' Disease, a neglected tropical disease that affects 6-7 million people worldwide. Interaction of the parasite with the host immune system is a key factor in disease progression and chronic symptoms. Although the human immune system is capable of controlling the disease, the parasite has numerous evasion mechanisms that aim to maintain intracellular persistence and survival. Due to the pronounced genetic variability of *T. cruzi*, co-infections or mixed infections with more than one parasite strain have been reported in the literature. The intermodulation in such cases is unclear. This study aimed to evaluate the co-infection of *T. cruzi* strains G and CL compared to their individual infections in human macrophages derived from THP-1 cells activated by classical or alternative pathways. Flow cytometry analysis demonstrated that trypomastigotes were more infective than extracellular amastigotes (EAs) and that strain G could infect more macrophages than strain CL. Classically activated macrophages showed lower number of infected cells and IL-4-stimulated cells displayed increased CL-infected macrophages. However, co-infection was a rare event. CL EAs decreased the production of reactive oxygen species (ROS), whereas G trypomastigotes displayed increased ROS detection in classically activated cells. Co-infection did

not affect ROS production. Mono-infection by strain G or CL mainly induced an anti-inflammatory cytokine profile by decreasing inflammatory cytokines (IFN- γ , TNF- α , IL-1 β) and/or increasing IL-4, IL-10, and TGF- β . Co-infection led to a predominant inflammatory milieu, with reduced IL-10 and TGF- β , and/or promotion of IFN- γ and IL-1 β release. Infection by strain G reduced activation of intracellular signal transducer and activator of transcription (STAT) factors. In EAs, mono-infections impaired STAT-1 activity and promoted phosphorylation of STAT-3, both changes may prolong cell survival. Co-infected macrophages displayed pronounced activation of all STATs examined. These activations likely promoted parasite persistence and survival of infected cells. The collective results demonstrate that although macrophages respond to both strains, *T. cruzi* can modulate the intracellular environment, inducing different responses depending on the strain, parasite infective form, and co-infection or mono-infection. The modulation influences parasite persistence and survival of infected cells.

Functional antibodies against G-protein coupled receptors in Beagle dogs infected with two different strains of *Trypanosoma cruzi*.

Wallukat G, Botoni FA, Rocha MODC, Louise V, Müller J, Talvani A.

25-10-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36389686/>

The interaction of the anti-beta1-adrenergic receptor autoantibodies (β 1ARAb) and the anti-muscarinic M2 receptor autoantibodies (M2RAB) with cardiac neurotransmitter receptors were identified in human chronic Chagas cardiomyopathy (CCC) related to the ECG and dysautonomia disturbances. Dogs are considered gold model to the study of *Trypanosoma cruzi* infection due the clinical similarities with CCC. This study aims to evaluate whether anti- β 1ARAb, anti- β 2ARAb, and anti-muscarinic M2RAB are generated in Beagle dogs infected by *T. cruzi* using Y and Berenice-78 strains of *T. cruzi*. Animals were infected with 4.0×10^3 bloodstream trypomastigotes/kg of body weight and, after 25 months of infection, blood sample was collected, and serum stored at -80°C. Dog serum was treated by ammonium sulphate precipitation and the IgG antibodies isolated and added to the beating neonatal rats' cardiomyocytes. All *T. cruzi*-infected dogs developed agonistic β 1ARAb, β 2ARAb, and M2RAB. Animals infected by Berenice strain presented less β 2ARAb and M2RAB activities than dogs infected by Y strain of the parasite. In cardiomyocytes culture, the antibodies recognized an epitope on the second extracellular loop of the receptors which were similar to findings in human Chagas disease. There was no detection of antibody against G protein-coupled receptor in serum from uninfected dogs. In conclusion, both Y and Berenice-78 strains of *T. cruzi* induced dog antibodies, whose targets located in the second extracellular loop of the adrenergic and muscarinic receptors were similar to those observed in individuals with CCC. Therefore, our findings highlight dogs as a promisor model to investigate

pathogenic roles of functional Ab against G-protein coupled receptors.

Leishmaniose

Erratum: A case report of two Kala-azar cases in China diagnosed by metagenomic next-generation sequencing.

27-10-2022

Frontiers Production Office.

<https://pubmed.ncbi.nlm.nih.gov/36395465/>

Self-Hybridization in *Leishmania major*.

Ferreira TR, Inbar E, Shaik J, Jeffrey BM, Ghosh K, Dobson DE, Beverley SM, Sacks D

17-11-2022

mBio

<https://pubmed.ncbi.nlm.nih.gov/36394334/>

Genetic exchange between different *Leishmania* strains in the sand fly vector has been experimentally demonstrated and is supported by population genetic studies. In nature, opportunities for *Leishmania* interstrain mating are restricted to flies biting multiply infected hosts or through multiple bites of different hosts. In contrast, self-mating could occur in any infected sand fly. By crossing two recombinant lines derived from the same *Leishmania major* strain, each expressing a different drug-resistance marker, self-hybridization in *L. major* was confirmed in a natural sand fly vector, *Phlebotomus duboscqi*, and in frequencies comparable to interstrain crosses. We provide the first high resolution, whole-genome sequencing analysis of large numbers of selfing progeny, their parents, and parental subclones. Genetic exchange consistent with classical meiosis is supported by the biallelic inheritance of the rare homozygous single nucleotide polymorphisms (SNPs) that arose by mutation during the generation of the parental clones. In contrast, heterozygous SNPs largely failed to be transmitted in Mendelian ratios for reasons not understood. SNPs that were heterozygous in both parents, however, recombined to produce homozygous alleles in some hybrids. For trisomic chromosomes present in both parents, transmittal to the progeny was only altered by self-hybridization, involving a gain or loss of some in frequencies predicted by a meiotic process. Whole-genome polyploidization was also observed in the selfing progeny. Thus, self-hybridization in *Leishmania*, with its potential to occur in any infected sand fly, may be an important source of karyotype variation, loss of heterozygosity, and functional diversity.

Expanded Proteomic Survey of the Human Parasite *Leishmania major* Focusing on Changes in Null Mutants of the Golgi GDP-Mannose/Fucose/Arabinopyranose Transporter *LPG2* and of the Mitochondrial Fucosyltransferase *FUT1*.

Polanco G, Scott NE, Lye LF, Beverley SM.

17-11-2022

Microbiol Spectr.

<https://pubmed.ncbi.nlm.nih.gov/36394313/>

The trypanosomatid protozoan parasite *Leishmania* has a significant impact on human health globally. Understanding the pathways associated with virulence within this significant pathogen is critical for identifying novel vaccination and chemotherapy targets. Within this study we leverage an ultradeep proteomic approach to improve our understanding of two virulence-associated genes in *Leishmania*, encoding the Golgi mannose/arabinopyranose/fucose nucleotide-sugar transporter (*LPG2*) and the mitochondrial fucosyltransferase (*FUT1*). Using deep peptide fractionation followed by complementary fragmentation approaches with higher-energy collisional dissociation (HCD) and electron transfer dissociation (ETD) allowed the identification of over 6,500 proteins, nearly doubling the experimentally known *Leishmania major* proteome. This deep proteomic analysis revealed significant quantitative differences in both $\Delta lpg2$ and $\Delta fut1^s$ mutants with *FUT1*-dependent changes linked to marked alterations within mitochondrion-associated proteins, while *LPG2*-dependent changes impacted many pathways, including the secretory pathway. While the *FUT1* enzyme has been shown to fucosylate peptides *in vitro*, no evidence for protein fucosylation was identified within our ultradeep analysis, nor did we observe fucosylated glycans within *Leishmania* glycopeptides isolated using hydrophilic interaction liquid chromatography (HILIC) enrichment. This work provides a critical resource for the community on the observable *Leishmania* proteome as well as highlighting phenotypic changes associated with *LPG2* or *FUT1*, ablation of which may guide the development of future therapeutics

A Case Report of Two Kala-Azar Cases in China Diagnosed by Metagenomic Next-Generation Sequencing.

Gao H, Wang J, Zhang S, Li T.

30-08-2022

Front Microbiol

<https://pubmed.ncbi.nlm.nih.gov/36386640/>

Background: Leishmaniasis being a local disease, as kala-azar this particular form is a visceral form. It is transmitted by sandflies, and is a parasitic disease involving the reticuloendothelial system of mononuclear macrophages. Due to its poor prognosis and high fatality rate, the fatality rate of patients without effective treatment can exceed 95%. Thereby, early diagnosis and treatment can significantly improve its prognosis. The metagenomic next-generation sequencing (mNGS) has the advantage of being able to find pathogens that cannot be detected by traditional methods. More importantly, it can conduct nucleic acid detection of pathogens covering a wide range in a short time. For infectious diseases like kala-azar, which is clinically complicated and difficult, mNGS detection provides a basis for accurate etiological diagnosis. **Case report:** We report 2 cases of kala-azar in West China Hospital, Chengdu, China. The first case is a 47-year-old male patient who had recurrent fever for 4 months,

accompanied by reduction of red blood cell, white blood cell, and blood platelet. He was detected by mNGS and clinically diagnosed as kala-azar (*Leishmania* detection), finally died of multiple organ failure. The second patient was a 15-year-old male who had fever for more than 10 days. He was detected by mNGS and clinically diagnosed as kala-azar (*Leishmania* detection). He recovered and discharged quickly after treatment with sodium stibogluconate. **Conclusion:** Efforts should be made to improve early etiological diagnosis in order to improve patient prognosis. mNGS detection is beneficial to the diagnosis and treatment of infectious diseases with unknown causes in the early stage of emergency treatment.

The Treatment Based on Ruxolitinib and Amphotericin B is Effective for Relapsed Leishmaniasis-Related Hemophagocytic Lymphohistiocytosis: A Case Report and Literature Review.

Cui T, Wang J, Wang Z.

11-11-2022

Infect Drug Resist.

<https://pubmed.ncbi.nlm.nih.gov/36386416/>

Background: Hemophagocytic lymphohistiocytosis (HLH) is known as a life-threatening syndrome, and *Leishmania* is the most common protozoan that triggers infection-related HLH. It is thus important to find the root cause and treat it effectively. **Case report:** This paper reports a 44-year-old man who developed antisynthetase antibody syndrome previously. The patient progressed rapidly to the extent of meeting the HLH-2004 diagnostic criteria, despite the unknown etiology. Although the patient was promptly treated in line with the HLH-1994 protocol to achieve remission, he still relapsed after glucocorticoid reduction. Afterwards, it was found out that HLH was secondary to *Leishmania* infection. The symptoms of HLH were alleviated quickly by the treatment with Ruxolitinib and Amphotericin B. **Conclusion:** Etiological screening plays a crucial role in leishmaniasis-related HLH. An experienced pathologist and real-time PCR are essential for treating *Leishmania*. The treatment of Ruxolitinib and Amphotericin B proved effective in alleviating the relapse of visceral leishmaniasis-related HLH.

The Clinical Phenotypes of Cutaneous Leishmaniasis in Central and Southwest Regions of Yemen.

Muthanna AM, Malhomme HD, Schwartz RA, Al-Qubati YA.

May-June 2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386068/>

Antileishmanial Activities of (Z)-2-(Nitroimidazolymethylene)-3(2H)-Benzofuranones: Synthesis, In Vitro Assessment, and Bioactivation by NTR 1 and 2.

Navidpour L, Lima ML, Milne R, Wyllie S, Hadj-Esfandiari N, Choudhary MI, Khan S, Yousuf S.

15-11-2022

Antimicrob Agents Chemother

<https://pubmed.ncbi.nlm.nih.gov/36286539/>

The antileishmanial activity of a series of (Z)-2-(heteroarylmethylene)-3(2H)-benzofuranone derivatives, possessing 5-nitroimidazole or 4-nitroimidazole moieties, was investigated against *Leishmania* major promastigotes and some analogues exhibited prominent activities. Compounds with IC₅₀ values lower than 20 μM were further examined against *L. donovani* axenic amastigotes. Evaluated analogues in 5-nitroimidazole subgroup demonstrated significantly superior activity (~17-88-folds) against *L. donovani* in comparison to *L. major*. (Z)-7-Methoxy-2-(1-methyl-5-nitroimidazole-2-ylmethylene)-3(2H)-benzofuranone (5n) showed the highest *L. donovani* anti-axenic amastigote activity with IC₅₀ of 0.016 μM. The cytotoxicity of these analogues was determined using PMM peritoneal mouse macrophage and THP-1 human leukemia monocytic cell lines and high selectivity indices of 26 to 431 were obtained for their anti-axenic amastigote effect over the cytotoxicity on PMM cells. Further studies on their mode of action showed that 5-nitroimidazole compounds were bioactivated predominantly by nitroreductase 1 (NTR1) and 4-nitroimidazole analogues by both NTR1 and 2. It is likely that this bioactivation results in the production of nitroso and hydroxylamine metabolites that are cytotoxic for the *Leishmania* parasite.

Immune Response to LinB13, a Lutzomyia Intermedia Salivary Protein Correlates With Disease Severity in Tegumentary Leishmaniasis

Carvalho AM, Viana SM, Andrade BB, Oliveira F, Valenzuela JG, Carvalho EM, de Oliveira CI.

14-11-2022

Clin Infect Dis

<https://pubmed.ncbi.nlm.nih.gov/35385578/>

Background: We have previously shown that seropositivity to rLinB-13, a salivary protein from *Lutzomyia intermedia*, predicted sand fly exposure and was associated with increased risk of developing cutaneous leishmaniasis (CL).

Methods: Here, we investigated the cellular immune response to saliva from *Lu. intermedia*, using rLinB-13 as a surrogate antigen in naturally exposed individuals presenting positive serology to LinB-13. We also investigated the response to rLinB-13 in leishmaniasis patients, displaying active ulcers and positive PCR for *Leishmania braziliensis*. **Results:** Peripheral blood mononuclear cells (PBMCs) stimulated in vitro with rLinB-13 secreted elevated levels of interleukin-10 (IL-10), IL-4, IL-1β, IL-1α, IL-6, and chemokines (CCL3, CCL4, CCL5, and CXCL5). CL and disseminated leishmaniasis (DL) patients displayed a significantly higher immunoglobulin G (IgG) response to rLinB-13 compared with healthy subjects, and anti-rLinB-13 IgG was positively correlated with the number of lesions in DL patients. Positive serology to rLinB-13 was also associated with chemotherapy failure. PBMCs from DL patients stimulated with rLinB-13 secreted significantly higher levels of IL-10 and IL-1β compared with CL individuals. **Conclusions:** In this study,

we observed an association between humoral and cellular immune response to the sand fly salivary protein rLinB-13 and disease severity in tegumentary leishmaniasis. This study brings evidence that immunity to rLinB-13 influences disease outcome in *L. braziliensis* infection and results indicate that positive serology to rLinB-13 IgG can be used as a marker of DL, an emerging and severe form of disease caused by *L. braziliensis* where no cases of leishmaniasis have been recorded. Six sand fly species were identified. The genus *Phlebotomus* was represented by five species: *Phlebotomus ariasi*, *Phlebotomus longicuspis*, *Phlebotomus perniciosus*, *Phlebotomus kazeruni*, and *Phlebotomus sergenti*, while the genus *Sergentomyia* was represented by only one species *Sergentomyia minuta*. *Phlebotomus perniciosus* was dominant in the nonendemic area (47%) while *Phlebotomus sergenti* was dominant in the endemic area (51%). The spatio-temporal distribution of sand fly populations is discussed according to biotic and abiotic variables. Seasonal fluctuation in sand fly density showed a bimodal pattern for the subgenus *Larrousius* and a unimodal pattern for the subgenus *Paraphlebotomus* in Tetouan city. But, in Oued Laou village, a unimodal density distribution for species of the *Larrousius* subgenus and a bimodal seasonal distribution for species of the subgenus *Paraphlebotomus* were identified. We affirm the coexistence, in the study area, of vectors of both cutaneous and visceral leishmaniasis, namely *P. ariasi*, *P. longicuspis* and *P. perniciosus* vectors of *Leishmania infantum* and *P. sergenti* vector of *L. tropica*. However, the geographic distribution, the specific abundance, and the activity reveal significant differences between endemic and nonendemic areas in the region.

Cysticercose

Pulmonary cysticercosis: A case report of abnormal lung nodule based on chest computerized tomography.

Savigamin C, Benjacholamas V, Sriprasart T.
04-11-2022

Respir Med Case Rep.

<https://pubmed.ncbi.nlm.nih.gov/36386281/>

Pulmonary cysticercosis is one of the rare complications of cysticercosis that occurs worldwide, especially in developing countries. Its clinical presentation can range from asymptomatic, pleural effusion, and constitutional symptoms to incidental pulmonary nodule. Here, we report pulmonary cysticercosis detected as a pulmonary nodule in computed tomography. Positron emission tomography revealed that the nodule was non-FDG avidity. However, the slow-growing pattern of the nodule raised a concern to the clinician to achieve definite diagnosis by surgical biopsy. Histopathological examination revealed cysticercosis. The patient was treated with praziquantel.

Assessing the burden of *Taenia solium* cysticercosis in Burundi, 2020.

Minani S, Devleeschauwer B, Gasogo A, Ntirandekura JB, Gabriël S, Dorny P, Trevisan C.

14-11-2022

BMC Infect Dis.

<https://pubmed.ncbi.nlm.nih.gov/36376817/>

Dracunculose

Echinococcose

Peritoneal hydatidosis: An exceptional case report.

El Bakouri A, Fatine A, Eddaoudi Y, Bouali M, El Hattabi K, Bensardi F, Fadil A.

10-09-2022

Ann Med Surg (Lond).

<https://pubmed.ncbi.nlm.nih.gov/36389191/>

Temporoparietal Brain Hydatid Cyst in an Eight-Year-Old Child: A Rare Case Report.

Arega G, Merga G, Tafa G, Salah FO, Abebe G, Maru S, Ergete W.

10-11-2022

Pediatric Health Med Ther.

<https://pubmed.ncbi.nlm.nih.gov/36386041/>

Hydatidosis is a parasitic disease caused by *Echinococcus granulosus*, which affects children in many different parts of the world. It commonly affects the lungs and the liver of the children. Brain hydatidosis is an extremely rare clinical condition in the pediatric population, presenting with non-specific symptoms and signs. The diagnosis of intracranial hydatid cysts can be established by brain magnetic resonance imaging and histopathological examination of the specimen. Here, we report an 8-year-old female child diagnosed with a temporoparietal brain hydatid cyst. Brain magnetic resonance imaging showed a thin-walled cystic lesion located in the right temporoparietal lobe with significant mass effect and midline shift, with no abnormal wall or solid enhancement, and no surrounding edema. The diagnosis of brain temporoparietal hydatid cyst was made radiologically. The patient was operated on and the cyst was completely removed without rupture. The removed cyst was sent for histopathological examination; the histological sections showed a laminated acellular cyst wall with a nucleated germinal layer and no protoscolices, and the diagnosis of temporoparietal brain hydatid cyst was confirmed. The patient had a smooth postoperative course, started albendazole therapy, and was discharged with improvement.

In vitro efficacy of albendazole-loaded β -cyclodextrin against protoscolices of *Echinococcus granulosus sensu stricto*.

Bakhtiar NM, Akbarzadeh A, Ahmadpour E, Mahami-Oskouei M, Casulli A, Norouzi R, Asadi M, Ebrahimi M, Asadi N, Rodrigues Oliveira SM, de Lourdes Pereira M, Spotin A.

13-11-2022

Exp Parasitol.

<https://pubmed.ncbi.nlm.nih.gov/36384195/>

[Patient with pulmonary cysts and diagnosis of co-infection with tuberculosis and hydatidosis. Pediatric cases report].

Portillo V, Paruelo F, Olivar V, Lascano F, Squassi IRDV, Moscatelli G, Maffey A, Altchek J.

Dec-2022

Arch Argent Pediatr.

<https://pubmed.ncbi.nlm.nih.gov/36374065/>

Numerous entities in the pediatric population can present in the form of cysts or as lesions with similar characteristics. Of the pathologies that can cause these images in children, infectious diseases are the most frequent. We present the case of a native of Bolivia with recent immigration to Argentina who presented a pulmonary co-infection with tuberculosis and hydatidosis. Both infections can present with similar signs and symptoms and although this association is rarely reported in the literature, certain immunological mechanisms could intervene in the causal association of co-infection between helminth parasites and mycobacteria. Both pathologies are very prevalent infections in our region and should be taken into account among the differential diagnoses in patients with cystic or cavitary pulmonary diseases.

PMID: 36374065 Spanish.

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

Filariose lymphatique

Eosinophils in filarial infections: Inducers of protection or pathology?

Ehrens A, Hoerauf A, Hübner MP.

31-10-2022

Front Immunol.

<https://pubmed.ncbi.nlm.nih.gov/36389745/>

Filariae are parasitic roundworms, which can cause debilitating diseases such as lymphatic filariasis and onchocerciasis. Lymphatic filariasis, also known as elephantiasis, and onchocerciasis, commonly referred to as river blindness, can lead to stigmatizing pathologies and present a socio-economic burden for affected people and their endemic countries. Filariae typically induce a type 2 immune response, which is characterized by cytokines, i.e., IL-4, IL-5 and IL-13 as well as type 2 immune cells including alternatively activated macrophages, innate lymphoid cells and Th2 cells. However, the hallmark characteristic of filarial infections is a profound eosinophilia. Eosinophils are innate immune cells and

pivotal in controlling helminth infections in general and filarial infections in particular. By modulating the function of other leukocytes, eosinophils support and drive type 2 immune responses. Moreover, as primary effector cells, eosinophils can directly attack filariae through the release of granules containing toxic cationic proteins with or without extracellular DNA traps. At the same time, eosinophils can be a driving force for filarial pathology as observed during tropical pulmonary eosinophilia in lymphatic filariasis, in dermatitis in onchocerciasis patients as well as adverse events after treatment of onchocerciasis patients with diethylcarbamazine. This review summarizes the latest findings of the importance of eosinophil effector functions including the role of eosinophil-derived proteins in controlling filarial infections and their impact on filarial pathology analyzing both human and experimental animal studies.

Assessing seroprevalence and associated risk factors for multiple infectious diseases in Sabah, Malaysia using serological multiplex bead assays.

Chan YL, Patterson CL, Priest JW, Stresman G, William T, Chua TH, Tetteh K, Lammie P, Drakeley C, Fornace KM.

25-10-2022

Front Public Health.

<https://pubmed.ncbi.nlm.nih.gov/36388287/>

Microfilaria causing nephrotic syndrome: Highlighting the importance of diethylcarbamazine provocation test for diagnosis.

Lahane V, Sagar VVSS, Naik S, Shukla S, Acharya S, Kumar S.

Jul-2022

J Family Med Prim Care.

<https://pubmed.ncbi.nlm.nih.gov/36387711/>

Filarial parasite infestation not only affects the structure and function of lymphatic vessels but is also associated with extralymphatic pathology and disease. Incidence of renal involvement in microfilaria carriers has led to increased cognizance of extralymphatic presentation. Literature set forth clinical syndromes having extralymphatic manifestation of filaria. The diagnosis of filariasis is done by visualisation of microfilaria in peripheral blood smear, lymphatic tissue. Other modalities of diagnosis are Enzyme linked immunosorbent assay (ELISA), Immunochromatographic test. Diethyl carbamazone (DEC) provocation test usually is done to detect microfilaria in night blood smear due to the nocturnal periodicity of microfilaria. The drug DEC flushes the microfilaria into the peripheral circulation leading to high probability of detection. We present a case of a 59-year-old male who was diagnosed as nephrotic syndrome and after a DEC challenge we detected microfilaria in the peripheral smear confirming microfilaria-induced Nephrotic Syndrome after all other secondary conditions were excluded.

Facilitators and barriers in implementation of mass drug

administration for lymphatic filariasis elimination in India: A protocol for systematic review and qualitative meta-synthesis.

Sinha A, Mohapatra S, Pati S, Sahoo PK.

Jul-2022

J Family Med Prim Care.

<https://pubmed.ncbi.nlm.nih.gov/36387675/>

Molecular docking-based virtual screening, molecular dynamic simulation, and 3-D QSAR modeling of some pyrazolopyrimidine analogs as potent anti-filarial agents.

Ugbe FA, Shallangwa GA, Uzairu A, Abdulkadir I.

09-11-2022

In Silico Pharmacol.

<https://pubmed.ncbi.nlm.nih.gov/36387058/>

Lymphatic filariasis and onchocerciasis are common filarial diseases caused by filarial worms, which co-habit symbiotically with the Wolbachia organism. One good treatment method seeks Wolbachia as a drug target. Here, a computer-aided molecular docking screening and 3-D QSAR modeling were conducted on a series of Fifty-two (52) pyrazolopyrimidine derivatives against four Wolbachia receptors, including a pharmacokinetics study and Molecular Dynamic (MD) investigation, to find a more potent anti-filarial drug. The DFT approach (B3LYP with 6-31G** option) was used for the structural optimization. Five ligand-protein interaction pairs with the highest binding affinities were identified in the order; 23_7ESX (-10.2 kcal/mol) > 14_6EEZ (-9.0) > 29_3F4R (-8.0) > 26_6W9O (-7.7) ≈ doxycycline_7ESX (-7.7), with good pharmacological interaction profiles. The built 3-D QSAR model satisfied the requirement of a good model with R² = 0.9425, Q² LOO = 0.5019, SDEC = 0.1446, and F test = 98.282. The selected molecules (14, 23, 26, and 29) perfectly obeyed Lipinski's RO5 for oral bio-availability, and showed excellent ADMET properties, except 14 with positive AMES toxicity. The result of the MD simulation showed the great stability associated with the binding of 23 onto 7ESX's binding pocket with an estimated binding free energy (MM/GBSA) of -60.6552 kcal/mol. Therefore, 23 could be recommended as a potential anti-filarial drug molecule, and/or template for the design of more prominent inhibitors.

Mycétome

Onchocercose

Schistosomiase

Praziquantel efficacy, urinary and intestinal schistosomiasis

reinfection - a systematic review.

Aboagye IF, Addison YAA.

17-11-2022

Pathog Glob Health.

<https://pubmed.ncbi.nlm.nih.gov/36394218/>

Praziquantel (PZQ) has been extensively used as the drug of choice for the treatment of schistosomiasis on account of its safety and effectiveness against all major forms of schistosomiasis. However, low cure rate, reduced susceptibility of *Schistosoma mansoni* to PZQ and treatment failures in *S. haematobium* infections have been reported, raising concerns about its efficacy. Using the search terms, 'praziquantel efficacy, schistosomiasis, school children, reinfection' as well as defined inclusion criteria, and guided by the PRISMA guidelines, articles from 2001 to 2022 were selected from the PubMed and Google Scholar databases and reviewed to assess their importance to the research question. This review assessed the efficacy of PZQ against schistosomiasis and reinfection rates following treatment of *Schistosoma* infections in children. Majority of both intestinal and urinary schistosomiasis studies reported comparable egg reduction rates (ERRs) of 94.2% to 99.9% and 91.9% to 98%, respectively. However, ERRs suggestive of sub-optimal PZQ efficacy as well as generally high and comparable cure rates for intestinal (81.2%-99.1%) and urinary (79%-93.7%) schistosomiasis studies were reported. Schistosomiasis reinfection rates varied widely for urinary (8.1%-39.6%) and intestinal (13.9%-63.4%) studies within eight to 28 weeks following PZQ treatment. Praziquantel treatment of urinary and intestinal schistosomiasis should be accompanied by the provision of potable water, toilet, and recreational facilities to reduce reinfection and egg reduction rates and increase cure rate to expedite schistosomiasis elimination.

Pathology and molecular mechanisms of *Schistosoma japonicum*-associated liver fibrosis.

Liu Z, Zhang L, Liang Y, Lu L.

28-11-2022

Front Cell Infect Microbiol

<https://pubmed.ncbi.nlm.nih.gov/36389166/>

Schistosomiasis has been widely disseminated around the world, and poses a significant threat to human health. *Schistosoma* eggs and soluble egg antigen (SEA) mediated inflammatory responses promote the formation of egg granulomas and liver fibrosis. With continuous liver injuries and inflammatory stimulation, liver fibrosis can develop into liver cirrhosis and liver cancer. Therefore, anti-fibrotic therapy is crucial to increase the survival rate of patients. However, current research on antifibrotic treatments for schistosomiasis requires further exploration. In the complicated microenvironment of schistosome infections, it is important to understand the mechanism and pathology of schistosomiasis-associated liver fibrosis (SSLF). In this review, we discuss the role of SEA in inhibiting liver fibrosis, describe its mechanism, and comprehensively explore the role of host-derived and

schistosome-derived microRNAs (miRNAs) in SSLF. Inflammasomes and cytokines are significant factors in promoting SSLF, and we discuss the mechanisms of some critical inflammatory signals and pro-fibrotic cytokines. Natural killer(NK) cells and Natural killer T(NKT) cells can inhibit SSLF but are rarely described, therefore, we highlight their significance. This summarizes and provides insights into the mechanisms of key molecules involved in SSLF development.

Identification of Inhibitors of the *Schistosoma mansoni* VKR2 Kinase Domain.

Mathavan I, Liu LJ, Robinson SW, El-Sakkary N, Elatico AJJ, Gomez D, Nellas R, Owens RJ, Zuercher W, Navratilova I, Caffrey CR, Beis K.

5-10-2022

ACS Med Chem Lett

<https://pubmed.ncbi.nlm.nih.gov/36385939>

Schistosomiasis is a neglected tropical disease caused by parasitic flatworms. Current treatment relies on just one partially effective drug, praziquantel (PZQ). *Schistosoma mansoni* Venus Kinase Receptors 1 and 2 (SmVKR1 and SmVKR2) are important for parasite growth and egg production, and are potential targets for combating schistosomiasis. VKRs consist of an extracellular Venus Flytrap Module (VFTM) linked via a transmembrane helix to a kinase domain. Here, we initiated a drug discovery effort to inhibit the activity of the SmVKR2 kinase domain (SmVKR2_{KD}) by screening the GSK published kinase inhibitor set 2 (PKIS2). We identified several inhibitors, of which four were able to inhibit its enzymatic activity and induced phenotypic changes in *ex vivo* *S. mansoni*. Our crystal structure of the SmVKR2_{KD} displays an active-like state that sheds light on the activation process of VKRs. Our data provide a basis for the further exploration of SmVKR2 as a possible drug target.

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

A reverse vaccinology approach identifies putative vaccination targets in the zoonotic nematode *Ascaris*

Evangelista FMD, van Vliet AHM, Lawton SP, Betson M.
01-11-2022

Front Vet Sci.

<https://pubmed.ncbi.nlm.nih.gov/36387396/>

Ascariasis is the most prevalent helminthic disease affecting both humans and pigs and is caused by the roundworms *Ascaris lumbricoides* and *Ascaris suum*. While preventive chemotherapy continues to be the most common control method, recent reports of anthelmintic resistance highlight the need for development of a vaccine against ascariasis. The aim of this study was to use a

reverse vaccinology approach to identify potential vaccine candidates for *Ascaris*. Three *Ascaris* proteomes predicted from whole-genome sequences were analyzed. Candidate proteins were identified using open-access bioinformatic tools (e.g., Vacceed, VaxiJen, Bepipred 2.0) which test for different characteristics such as sub-cellular location, T-cell and B-cell molecular binding, antigenicity, allergenicity and phylogenetic relationship with other nematode proteins. From over 100,000 protein sequences analyzed, four transmembrane proteins were predicted to be non-allergen antigens and potential vaccine candidates. The four proteins are a Piezo protein, two voltage-dependent calcium channels and a protocadherin-like protein, are all expressed in either the muscle or ovaries of both *Ascaris* species, and all contained high affinity epitopes for T-cells and B-cells. The use of a reverse vaccinology approach allowed the prediction of four new potential vaccination targets against ascariasis in humans and pigs. These targets can now be further tested in *in vitro* and *in vivo* assays to prove efficacy in both pigs and humans.

Evaluation of a commercial coproantigen immunoassay for the detection of *Toxocara cati* and *Ancylostoma tubaeforme* in cats and *Uncinaria stenocephala* in dogs

Hauck D, Raue K, Blazejak K, Hanna RM, Elsemore DA, Pantchev N, Strube C.

17-11-2022

Parasitol Res.

<https://pubmed.ncbi.nlm.nih.gov/36385307/>

Coproantigen immunoassays (IDEXX Fecal Dx® antigen tests) were evaluated for their ability to identify *Toxocara cati* and *Ancylostoma tubaeforme* infections in cats and *Uncinaria stenocephala* infection in dogs. Five cats were experimentally infected with 500 embryonated eggs of *T. cati*, eight cats with 500 third-stage larvae (L3) of *A. tubaeforme* and seven dogs with 500 L3 of *U. stenocephala*. In addition to the three coproantigen tests, the course of infection was monitored by a combined sedimentation-flotation method with ZnSO₄ as flotation medium (specific gravity: 1.28-1.30) and a modified McMaster method in case of copromicroscopically positive samples. Eggs of *T. cati* were first observed between 28 and 54 days post infection (dpi) in four of the five infected cats. In these four cats, positive roundworm coproantigen signals were obtained between 16 and 44 dpi. Positive coproantigen signal always preceded egg observations, but the interval varied between 6 and 30 days. Hookworm-specific positive coproantigen signals were detected in seven of the eight *A. tubaeforme* infected cats between 10 and 52 dpi, while consecutive egg excretion was observed in three cats between day 26 and 54 pi. Of these three, coproantigen signal preceded egg observation by 12 to 24 days. Four cats had positive coproantigen results in the absence of egg excretion, and one cat never achieved a positive result for egg or coproantigen. In six of seven *U. stenocephala* infected dogs, infection was confirmed by copromicroscopy between 16 and 24 dpi as well as for hookworm coproantigen between 10 and 14 dpi. Coproantigen signal

was detected prior to egg observation by 2 to 14 days. No cross-reactions between the roundworm, hookworm and whipworm tests occurred in study animals. The results of this study demonstrate the ability of the coproantigen tests to detect the common roundworm and hookworm infections in cats and *U. stenocephala* infections in dogs as well as the ability to detect the prepatent stage of infection.

Gut bacteriome and metabolome of *Ascaris lumbricoides* in patients

Klomkiew P, Sawaswong V, Chanchaem P, Nimsamer P, Adisakwattana P, Phuphisut O, Tiphthara P, Tarning J, Payungporn S, Reamtong O.

14-11-2022

Sci. Rep.

<https://pubmed.ncbi.nlm.nih.gov/36376367/>

The most frequent intestinal helminth infections in humans are attributed to *Ascaris lumbricoides*, and there are concerns over the anthelmintic resistance of this species. The gut microbiota has essential roles in host physiology. Therefore, discovering host-parasite-microbiota interactions could help develop alternative helminthiasis treatments. Additionally, these interactions are modulated by functional metabolites that can reveal the mechanisms of infection and disease progression. Thus, we aimed to investigate bacteriomes in the gut of helminths and fecal samples of patients via next-generation sequencing. Our results showed that infection intensity was associated with the bacterial composition of helminth guts but not with the intestinal bacteriome of human hosts. Moreover, the metabolomes of *A. lumbricoides* in the heavy and light ascariasis cases were characterized using ultra-high performance liquid chromatography/time-of-flight mass spectrometry. Increased levels of essential biomolecules, such as amino acids, lipids, and nucleotide precursors, were found in the guts of helminths isolated from heavily infected patients, implying that these metabolites are related to egg production and ascariasis pathogenicity. These findings are the first step towards a more complete understanding of the mechanisms by which the bacteriome of helminth guts affect their colonization and may reveal novel and more effective approaches to parasitic disease therapy.

Gale

Surfactin secreted by *Bacillus amyloliquefaciens* Ba01 is required to combat *Streptomyces scabies* causing potato common scab

Feng RY, Chen YH, Lin C, Tsai CH, Yang YL, Chen YL.

01-11-2022

Front Plant Sci.

<https://pubmed.ncbi.nlm.nih.gov/36388520/>

Potato common scab, which is mainly caused by the bacterium *Streptomyces scabies*, occurs in key potato growing regions worldwide. It causes necrotic or corky symptoms on potato tubers and decreases the economic value of potato. At present, there is no recommended

chemical or biological control for combating potato common scab in Taiwan. It can only reduce the occurrence by cultivation control, but the efficacy is limited. Previously we found that *Bacillus amyloliquefaciens* Ba01 could control potato common scab in pot assay and in the field. The potential anti-*S. scabies* mechanism was associated with surfactin secretion, but further molecular dissection was not conducted. Thus, in this study we aimed to determine whether surfactin is the main compound active against *S. scabies* by knocking out the *srf* gene cluster in Ba01. The cloning plasmid pRY1 was transformed to Ba01 by electroporation for in-frame deletion. Two independent Δ *srf* mutants were obtained and confirmed by specific primers and mass spectrometry. The swarming ability and *S. scabies* inhibition was significantly decreased ($P < 0.001$) in Δ *srf* mutants. The swarming ability of Δ *srf* mutants could be restored by the addition of surfactin. Furthermore, we found that Ba01 formed wrinkled biofilm in MSgg liquid medium, while Δ *srf* mutants formed biofilm abnormally. Furthermore, the α -amylase, protease and phosphate-solubilizing ability of Δ *srf* mutants was decreased, and the mutants could not inhibit the growth and sporulation of *S. scabies* on potato tuber slices. In conclusion, *srf* gene cluster of *B. amyloliquefaciens* Ba01 is responsible for the secretion of surfactin and inhibition of *S. scabies*.

Exaggerated hyperkeratosis in a nursing home patient

Zhu C, Wohltmann W, Krikoriantz S, Sasaki G.

07-2022

J Family Med Prim Care

<https://pubmed.ncbi.nlm.nih.gov/36387659/>

Scabies, caused by the mite *Sarcoptes scabiei* var *hominis*, is a common infestation that presents with intense itching. Crusted scabies, also known as Norwegian scabies, is a severe variant of classic scabies that is characterized by hyperkeratotic lesions and often manifests in immunosuppressed patients. There is both a high parasitic load and high infectivity with this form of scabies because crusted scabies can look similar to many conditions including psoriasis, eczema, and seborrheic dermatitis, diagnosis can be difficult and is based on both clinical findings and microscopic detection of the scabies mite, eggs, or fecal material (scybala). We describe a case of a 64-year-old female patient diagnosed with crusted scabies.

A Clinico-Demographic Profile and Sexual Behaviour Pattern in Attendees of Designated STI/RTI Clinic Having Sexually Transmitted Infections with Special Reference to HIV Seropositivity

Datta J, Patra AC, Ghosh A, Roy S, Das NK.

May/June-2022

Indian J Dermatol.

<https://pubmed.ncbi.nlm.nih.gov/36386062/>

Morsures de serpent

Potential economic and clinical implications of improving access to snake antivenom in five ASEAN countries: A cost-effectiveness analysis.

Patikorn C, Ismail AK, Zainal Abidin SA, Othman I, Chaiyakunapruk N, Taychakhoonavudh S.

16-11-2022

PLoS Negl Trop Dis

<https://pubmed.ncbi.nlm.nih.gov/36383562/>