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ASTMH is an international society committed to equity and global impact through the treatment

ABSTRACT BOOK

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spiked a fever of 102F, and was admitted for further evaluation and treatment. He was found to have a CD4 of 76 (prior CD4 was 379 four months earlier) with an undetectable HIV viral load. Chest X ray showed bilateral infiltrates, and laboratory testing showed mild transaminase level elevation. Next-generation sequencing (NGS) of cell-free DNA was performed. Within 72 hours, the result came back with detection of *Aspergillus fumigatus*, Hepatitis B and CMV. Sputum cultures eventually grew *Aspergillus fumigatus*, and subsequent confirmatory testing revealed elevated serum aspergillus antigen and beta-D-glucan levels. Hepatitis B DNA of >100 million IU/ml and CMV of 256 IU/ml were also detected. Despite previous Hepatitis B vaccination with negative Hepatitis B surface antigen and positive surface antibody titers one year earlier, he was found to have lost his Hepatitis B immunity, and demonstrated positive Hepatitis B surface antigen, core antibody and E antigen. CT scan of the chest revealed multilobar pneumonia with a four-centimeter cavitory lesion of left lower lobe. MRI of brain revealed multiple ring-enhancing lesions likely representing abscesses from Aspergillosis. LP was unremarkable. He subsequently improved with voriconazole and micafungin treatment, and was discharged home. This case illustrated the potential utility of using NGS of cell-free DNA to rapidly diagnose multiple co-infections in severely immunocompromised HIV infected patients without the need for invasive diagnostic procedures.

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A SYSTEMATIC REVIEW OF VIRULENCE FACTORS IN THE LEISHMANIA GENUS

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Parasite-determined factors play a complementary role in the pathogenesis of leishmaniasis, a disease caused by protozoans of the genus *Leishmania* with diverse and species-specific clinical manifestations. Virulence factors (VFs), or pathogen moieties facilitating disease, can potentiate host cell damage by *Leishmania* species via increased expression, host cell invasion, stress tolerance, and modulation of the host immune system. Due to large eukaryotic genomes in *Leishmania* species, there is a wide array of VFs which contribute to different aspects of pathogenesis. Here we conduct a comprehensive, systematized review of the literature around VFs in *Leishmania* spp. and construct a complete picture of parasite-determined contributors to the pathogenesis of various clinical forms of leishmaniasis. PubMed (NCBI), MEDLINE (OVID), EMBASE (OVID), Web of Science, and LILACS (VHL) were searched from inception to July 2018 using combinations of the search terms “virulence factor*”, “*Leishmania*”, and “Leishmaniasis*”, while accounting for unique database syntax. Iterative inclusion and exclusion of search terms was employed to maximize relevant article extraction. For the systematic review, we will include primarily molecular and mechanistic pathogenesis studies in various model systems, observational studies, review studies, cohort studies, as well as clinical trials. Of 2620 articles remaining after title and abstract screening, some major VFs identified in the *Leishmania* genus are: heat shock proteins (HSP23, HSP70), cysteine peptidases (CPB), mannose phosphate isomerases (MPI), metalloproteases (GP63), and elongation factors (EF1-alpha), among many others. Data will be grouped and summarized by species, geographic region of endemicity, and VFs. This systematic compilation of mechanistic VF data will add to the large body of work in molecular pathogenesis of kinetoplastids and enhance our understanding of species and regional variations in *Leishmania* pathogenesis.

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NEW LEISHMANIA SPECIES AND ITS POTENTIAL NEW VECTOR, RESPONSIBLE FOR CUTANEOUS LEISHMANIASIS IN SOUTHEASTERN GHANA

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An outbreak of human cutaneous leishmaniasis (CL) was observed in Ho District in the Volta Region of South-eastern Ghana in 1999, which was proved to be leishmaniasis and isolated the causative protozoan from patients with skin ulcers. The study aimed at identifying the *Leishmania* species responsible for CL and their potential vectors. Aspirates from patients with cutaneous ulcers were cultured *in vitro* in *Leishmania* growth medium (Sloppy Evan's and M199). Isolates of the “yet-to-be-named” *Leishmania* species were amplified, and genomic DNA was extracted. Sequence analysis of RPL23, ITS1, RNAPolIII genes were performed with reference genomes. The Ghanaian *Leishmania* isolate clade closely with the pathogens *L. orientalis*, *L. martiniquensis*, *L. marcopodum*, belong to *Leishmania* (*Mundinia*) *enriettii* complex on the evolutionary tree. The phylogenetic analysis of Ghanaian isolates and other available sequences revealed it's a newly species. To incriminate the vector transmitting the Ghanaian isolates, two potential vectors, *Lutzomyia longipalpis* (sand fly) and *Culicoides sonorensis* (biting midge) were infected with Ghana *Leishmania* isolate and maintained for more than 10 days. Representative vectors were dissected daily to check infectivity. Heavy infections were characterised in both vectors at the blood meal stage, until the blood meals were digested. Infections in *Lu. longipalpis* decreased to 0, 3 days post-bloodmeal. Infections in the *C. sonorensis* were retained beyond 10 days to ≈80%, colonising the midgut and stomodeal valve. A newly identified human pathogenic *Leishmania* species responsible for CL in Ghana was able to heavily infected *C. sonorensis*, colonizing the midgut and stomodeal valve up to 10 days and beyond. Although most *Leishmania* spp. causing human disease are transmitted by a sand fly vector, this result leads us to hypothesize that midges could be vectors of this new *Leishmania* species in Ghana. Further proof is required to demonstrate successful transmission of the parasite by *C. sonorensis* to mammalian host.

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ACCURACY OF DIAGNOSTICS IN TEGUMENTARY LEISHMANIASIS: A SYSTEMATIC REVIEW

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Tegumentary leishmaniasis (TL) is characterized by cutaneous and mucocutaneous ulcerative skin lesions, caused by *Leishmania* parasites, that can potentially disfigure the midface. The clinical presentation of TL is similar to that of epidemiologically overlapping fungal and mycobacterial infections, thereby necessitating confirmatory diagnostics to inform appropriate treatment. Laboratory diagnostic techniques for TL include

the leishmanin skin test; microscopic identification of amastigotes from skin aspirates, biopsies and scrapings; culture; and molecular assays. We aim to determine optimal methods to accurately and efficiently diagnose TL to improve diagnostic stewardship. We searched five databases from inception to July 16, 2018 including Ovid MEDLINE, Embase, LILACS, Cochrane Library and Scopus with the following search terms: (“cut* leish*” OR “muc* leish*” OR “teg* leish*”) AND (diagnosis OR diagnostic accuracy OR sensitivity OR specificity OR stard OR test*) AND NOT (viscer*). All systematic reviews, diagnostic trials and observational studies were included. Titles, abstracts and full-texts are systematically screened by two reviewers with a tertiary arbitrator. Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) and Quality Assessment of Diagnostic Accuracy Studies (QUADAS) will be employed. 6745 papers were identified from the five databases and 1278 papers remained for abstract evaluation (3391 removed) after title screening, where non-human, non-TL, non-diagnostic and case report articles were excluded. Abstract and full-text screening will be conducted. Data will be extracted from full-texts and assessed using QUADAS for selection and information bias. Heterogeneity of the studies will be determined and meta-analysis performed as appropriate. TL cannot be distinguished from competing infectious etiologies clinically, thus necessitating confirmatory diagnostics. A knowledge synthesis of accurate diagnostic assays can provide insight into the optimal approach for TL confirmation and subsequently guide therapy.

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ETHNOPHARMACEUTICALS FOR THE TREATMENT OF OLD WORLD CUTANEOUS LEISHMANIASIS: A SYSTEMATIC REVIEW OF TOPICAL APPLICATION OF TURMERIC

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Toxicity, expense, and accessibility limit treatment success in Old World Cutaneous Leishmaniasis (OWCL), a neglected parasitic disease caused by members of the genus *Leishmania* found in the Middle East, Mediterranean basin, Arabian Peninsula, Africa as well as the Indian Subcontinent. Better drugs are urgently needed, however, drug discovery is hindered by limited funding given geographic restriction of highly endemic OWCL to LMICs. Plant-based compounds with potential anti-leishmanial effects found in and around local endemic communities present an opportunity to overcome the aforementioned therapeutic challenges, and many such interventions are supported by anecdotal evidence of efficacy. We aim to synthesize existing evidence around available ethnopharmaceuticals to promote drug discovery for the prevention and treatment of OWCL. PubMed (NCBI), Medline (OVID), Embase (OVID), Web of Science (BioSIS) and LILACS (VHL) were searched for from inception to July 26, 2018 using combinations of the search terms “cutaneous leishmaniasis” and “ethnopharmaceuticals”. Iterative inclusion and exclusion of search terms was employed to maximize relevant article extraction. The GRADE approach will be used to assess quality of studies reporting therapeutic interventions. 3057 PubMed, 2818 Medline, 4200 Embase, 3183 Web of Science and 490 LILACS articles were retrieved for title and abstract screening; after duplicate removal, 5492 remained. 550 abstracts met inclusion criteria for full-text review, of which, 241 (43.80%) abstracts pertained to Old World species, and 113 (21%) were specific to *L. donovani*. Curcuma spp. “Turmeric” was identified in 4 articles (0.7%) to date. Synthesizing the current evidence surrounding ethnopharmaceuticals for the treatment of OWCL may contribute to drug discovery pipelines and potentially lead to novel therapeutics in a field that has not seen any new drug development for over half a century, especially in the context of turmeric.

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ETHNOPHARMACEUTICALS FOR THE TREATMENT OF NEW WORLD CUTANEOUS LEISHMANIASIS: A SYSTEMATIC REVIEW OF TOPICAL APPLICATION OF PEPPER AND ALLIUM

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New World Cutaneous Leishmaniasis (NWCL) is a neglected parasitic disease caused by members of the genus *Leishmania* primarily identified in Central and South America. Better drugs are urgently needed given the toxicity, expense and accessibility limits of first-line treatment options. Plant-based compounds with potential anti-leishmanial effects found in and around local endemic communities, particularly in and around the Amazon basin, present an opportunity to overcome the aforementioned therapeutic challenges, and many such interventions are supported by anecdotal evidence of efficacy. We aim to synthesize existing evidence around available ethnopharmaceuticals to promote drug discovery for the prevention and treatment of NWCL. PubMed (NCBI), Medline (OVID), Embase (OVID), Web of Science (BioSIS) and LILACS (VHL) were searched for from inception to July 26, 2018 using combinations of the search terms “cutaneous leishmaniasis” and “ethnopharmaceuticals”. Iterative inclusion and exclusion of search terms was employed to maximize relevant article extraction. For the systematic review, we included molecular, mechanistic, and observational studies, case reports, case series, cohort studies, as well as clinical trials reporting therapeutic outcomes, if possible using the GRADE approach. A total of 13667 abstracts were retrieved, after which 7566 duplicates were removed. Of the remaining abstracts, 550 abstracts were included in the full text review, of which 176 (32%) abstracts highlighted New World species; 116 (66.0%), 33 (18.7%), and 27 (15.3%) abstracts pertained to *L. amazonensis*, members of *Viannia* subgenus, and other New World species, respectively. Of all the abstracts included in the full text review, 25 (4.5%) and 6 (1.1%) were identified for *Piper* spp. “Pepper” and *Allium* spp. “Garlic”, respectively. Synthesizing the current evidence surrounding ethnopharmaceuticals for the treatment of NWCL may contribute to drug discovery pipelines and potentially lead to novel therapeutics, particularly those targeting the *Viannia* complex, where patients often develop more severe clinical manifestations.

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AN UPDATE ON THE ROLE OF WOUND CARE IN THE MANAGEMENT OF OLD WORLD CUTANEOUS LEISHMANIASIS

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Old world cutaneous leishmaniasis (OWCL) typically presents as one or several chronic, infiltrative lesions on exposed parts of the body, and is treated pharmacologically to accelerate cure, reduce scarring, and to prevent parasite dissemination or relapse. Limited data support the role of local wound care for the management of OWCL, though the scope of such benefit and to which patient populations wound care should be applied remains undetermined due to the absence of synthesized data on the subject. We aim to synthesize the literature around the role of wound care in the management of OWCL to inform treatment guidelines and evidence-based therapeutic strategies. Medline (Ovid), Embase (Ovid), and PubMed (NCBI) were searched from inception to February 2019 without language restriction using combinations of the search terms “leishmania*” and “wound care”. The GRADE approach will be used to assess quality of studies reporting specific wound care interventions. 626 articles were identified with the initial search. After screening titles and