Joint Event

10th International Congress on

Infectious Diseases

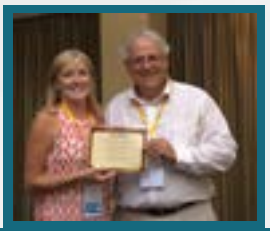
12th International Conference on

Tropical Medicine and Infectious Diseases

February 22-23, 2023

Webinar






Accepted Abstracts

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J Infect Dis Ther 2023, Volume 11

Activity of methanolic extract of Carica papaya (Caricaceae) yellow leaf against Plasmodium berghei in mice

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Statement of the Problem: Malaria still remains a public health problem in developing countries. Malaria is one of the most prevalent diseases in Nigeria and people who are infected still relay on traditional medicine as a source of treatment for the disease. Malaria causes mortality and morbidity with social economic impact in developing countries where the burden is high. Research shows that the high global health challenges is partly due to multidrug resistance by Plasmodium falciparum developed on existing and available and antimalarial drugs and that has lead to the urgent to the urgent need in search of treatment to eradicate malaria in developing countries.

Purpose of the Study: Is to evaluate the antimalarial potential of methanolic extract of Carica papaya yellow leaf on animal model.

Methodology and Theoretical Orientation: *In vivo* screening for antimalarial drug discovery is one of the recommended stream line processes for evaluating new compounds in path from drug discovery to development. The Rane's curative method is established infection was employed in vivo for assessing antimalarial activity. Swiss albino mice of both sexes weighing between 23-27 g and aged 6 weeks were infected with 1*10^-7 P. Berghei(NK-65)RBC/ml intraperitoneally and were treated with various doses (100,200 and 400 mg/kg b.wt) of C. papaya yellow leaf extract. Acute oral toxicity test was employed using OECD method.

Findings: The mice treated with 400 mg/kg b.wt of C. papaya yellow leaf extract showed significant ($p<0.05$) antimalarial activity. In acute oral toxicity studies showed that the maximum tolerated dose was found to be 5000 mg/kg body weight.

Conclusions: C. papaya yellow leaf extract showed antimalarial activity and study has validated its use by the locals in the treatment of malaria in most developing countries. Recommendations are made for the isolation and identification of bioactive substance for possible drug development.

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Association of upper respiratory tract bacteria co-infections among persons living with HIV on combined Anti-Retroviral Therapy (cART)

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Statement of the Problem: Pathogenic bacteria colonization of the upper respiratory tract can induce bloodstream infections thereby increasing disease burdens in HIV-infected persons. The goal of this study was to determine opportunistic bacteria colonization of the upper respiratory tract of people living with HIV on cART.

Methodology and Theoretical Orientation: This was across sectional study that enrolled HIV-infected persons that were on cART. The participants were selected based on persistence of pharyngitis and mouth odour from Retroviral Clinic of Enugu State University Teaching Hospital. The study adopted consecutive sampling method which involved every subject that voluntarily agreed to participate in the study. That who completed a structured questionnaire and had CD4 cells ≤ 500 cells/µl there throat swab was collected. The throat swab was analyzed bacteriologically. The data obtained were subjected to statistical analysis and significance at $P \leq 0.05$.

Findings: A total of 152 HIV-infected persons on cART were enrolled for this study. They comprised of 31.6% males (48/152) and 68.4% (104/152) females with mean age of 38.9 ± 12.9 year-olds. A prevalence rate of 68.4% (104/152) was obtained, the females accounted for 44.7% (68/152). The age group of 31-40 and 41-50 had the highest bacterial isolates of 21.7% and 19.7% respectively, while traders, teachers and healthcare workers accounted for 30.2%, 14.5% and 13.5% bacterial colonization. The bacteria colonization was more among the patients with 5-years and 6-10 years duration of cART with 35.5% and 19.1% of bacteria isolates respectively. It was observed that about 39.5% of the HIV patients that were placed on antibiotics for 3-months prior to the study had bacteria colonization. Stapylococcus aureus, Streptococcus pyogenes, coagulase-negative Staphylococcus aureus, Escherichia coli, Streptococcus pneumonia, Klebsiella pneumonia and Haemophilus influenza were the major bacteria isolates. These bacteria isolates exhibited multi-antibiotics resistant pattern and all were resistant to vancomycin and ciprofloxacin.

Conclusions: The findings in this study showed that HIV-infected persons on cART harbor opportunistic bacteria in the upper respiratory tract with limited antibiotics for treatment and/or prophylaxis.

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The spike receptor binding motif G496S substitution determines the replication fitness of SARS-CoV-2 Omicron sublineage

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The replication and pathogenicity of SARS-CoV-2 Omicron BA.2 are comparable to that of BA.1 in experimental animal models. However, BA.2 has rapidly emerged to overtake BA.1 to become the predominant circulating SARS-CoV-2 variant worldwide. Here, we compared the replication fitness of BA.1 and BA.2 in cell culture and in the Syrian hamster model of COVID-19. Using a reverse genetics approach, we found that the BA.1-specific spike mutation G496S compromises its replication fitness, which may contribute to BA.1 being outcompeted by BA.2 in the real world. Additionally, the BA.1-unique G496S substitution confers differentiated sensitivity to therapeutic monoclonal antibodies, which partially recapitulates the immunoevasive phenotype of BA.1 and BA.2. In summary, our study identified G496S as an important determinant during the evolutionary trajectory of SARS-CoV-2.

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Cyst-like structures in the life cycle of Trichomonas Vaginalis: A possible non-sexual mode of transmission

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Trichomonas vaginalis is a parasitic protozoan known to cause a non-viral sexually transmitted infection known as Trichomoniasis. The infection encompasses a broad range of symptoms in both male and female patients ranging from acute inflammation, premature labor, low birth-weight of infants, vaginitis and increased susceptibility to life-threatening Human Immunodeficiency Virus (HIV) infection, cervical neoplasia and pelvic inflammatory disease. Although most of the infected patients are asymptomatic, the annual incidences of Trichomoniasis are more than 170 million throughout the world.

Life cycle of the parasite has been traditionally described as consisting of motile and symptom causing trophozoites which are sexually transmitted. In our current research, we show the formation of viable cyst-like forms in stationary phase of *T. vaginalis* axenic culture. Like cysts from other protozoan parasites like Entamoeba histolytica and Giardia lamblia, *T. vaginalis* Cyst-Like Structures (CLS) appear spherical, immotile, uniquely stains with calcofluor white and is resistant to osmotic lysis and detergent treatments. We used calcofluor white, a stain which specifically binds to chitin and cellulose containing structures, to score for the Cyst-like structures. We demonstrate and quantitate the processes of encystation as well as excystation in vitro; thus, completing the parasite's lifecycle without any chemical/temperature alterations. We found that CLS play an important role physiologically as it is resistant to detergents, swimming pool water and also able to convert back to trophozoites.

Finally, we show that symptomatic human patient vaginal swabs have presence of both *T. vaginalis* trophozoites and CLS; thus, highlighting the role of cyst-like forms in clinical infections. The study highlights the plasticity of the pathogen and its rapid adaption when subjected to stressful environmental cues. Together, our findings suggest an important role of cysts-like structures in the parasite's life cycle, pathogenesis and transmission.

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Pediatric visceral leishmaniasis in northwest of Iran

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Leishmaniasis is one of the major health problems in Iran. Although the incidence of Visceral Leishmaniasis (VL) is reported almost everywhere, the northwestern Iran is one of the major endemic regions. To do this study, clinical, laboratory as well as disease characteristics of children admitted to Children Cure and Health Hospital, Tabriz University of Medical Sciences, were examined as the reference hospital for the treatment of VL in northwestern Iran.

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Genetic diversity and amino acids variations at vaccine target sites in rabies viruses collected from different host species in Makueni and Siaya counties, Kenya

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Background: Rabies, a viral disease that causes lethal encephalitis is endemic in Kenya and is transmitted to humans mainly by domestic dogs. Rabies kills an estimated 2000 people annually, despite there being effective vaccines for dogs and humans. This study characterized the genetic diversity of RABV obtained from brains of suspected rabid animals from Makueni county, Eastern region and Siaya county, Western Kenya and determined variances within the antigenic sites of RABV vaccines currently in use in Kenya.

Methods: Brain biopsies (165) confirmed positive for rabies with rapid kits were collected between July 2021 and August 2022 from dogs, cats, cows, sheep and goats and re-screened for RABV by qPCR. Whole Genome Sequences (WGS) and individual Nucleoprotein (N) and Glycoprotein (G) genes were used for phylogeny. The amino acid variances in the N and G genes antigenic sites were compared to three RABV vaccine sequences: Pitman-Moore L503 (PM), Challenge Virus Standard (CVS) and the Pasteur Vaccine (PV) strains.

Results: Of the 165 brain samples, 156 were positive by qPCR and 141 (74 from Makueni and 67 from Siaya) produced useable sequences. Phylogenetic lineages drawn from WGS or from individual N and G genes showed two geographical distinct lineages: The Eastern Kenya sequences overwhelmingly (n=69) clustered with the Africa 1b lineage, with only 3 in Africa 1a. In contrast, the Western Kenya sequences (n=64) clustered with Africa 1a with only 3 in Africa 1b. The nearest common ancestor of the Africa 1a traced to Sudan, while the Africa 1b traced to Tanzania. The percent amino acid homologies of the N gene to the RABV vaccines were at least 97.6% for PV, 97.8% for CVS and 98.5% for PM. The homology with the G gene was at least 93.0% for PV, 93.3% for CVS and 92.2% for PM.

Conclusions: Our data confirm geographical isolation of RABV in Eastern and Western Kenya. The data suggests limited migration, probably through wild carnivore movement or translocation of domestic dogs by humans. The observed amino acid variances RABV vaccines antigenic sites would predict good vaccine efficacy, indicating that the RABV endemicity in Kenya is due limited programmatic vaccine coverage.

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Comparison of immune response of FMD vaccine developed using different adjuvants

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Ethiopia is thought to have the most significant livestock population in Africa. The appearance of contagious diseases can excessively hinder economic development. Foot and mouth disease occurs throughout the country, with the highest incidence reported in central Ethiopia. Foot-and-Mouth Disease (FMD) is a high impact viral disease of livestock for which vaccines are extensively used in control. Despite of Vaccination campaigns, the infections is still occurring. The choice of adjuvant is a significant factor in enhancing immune responses and the efficacy of inactivated vaccines. No studied data was recorded about adjuvant in the country. This study's objective was for comparison of the immune response between Oil-based Adjuvanted, Aluminum hydroxide gel adjuvanted and FMDV vaccines in mice for the FMD. Prepared BHK-21 Cell culture (OIE Foot and Mouth 2012 Manual), The FMD virus seed ETHO38 final titrated 10^3.7 TCID50/100 µ was used for antigen preparation in a BHK21 cell line and inactivated by 1% of Formalin.

Adjuvants 50% of Oil-based Adjuvant and 2.5% of Aluminum hydroxide formulated in (V:V) with Serotype O FMD Virus were used. For the experiment 24 female BALB/c mice were grouped in to four group 6 mice in each group. Immunized the mice with 0.2 ml of the formulation FMD vaccine via intraperitoneal route and boosted at day 14 and challenged by Virulent Serotype O FMD at day 38. Serum was collected at days of 0,7,14,21,28 and 38. The results of these immunogenicity studies indicated that in mice, oil-adjuvanted vaccines led to higher and more persistent antibody titers. In contrast, aluminum hydroxide gel-adjuvanted vaccines were associated with lower antibody titers. In conclusion, mice immunized with oil-based adjuvanted vaccine showed higher antibody titer followed by Aluminum hydroxide gel adjuvanted and FMD Vaccine only respectively.