

Poster Presentations

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Echocardiographic evaluation of the cardiovascular effects of DNA vaccines containing *Trypanosoma cruzi* genes on dogs with experimental Chagas disease

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Statement of the Problem: Chagas disease (ChD) is caused by *Trypanosoma cruzi*. This Neglected Tropical Disease is also considered as an emerging disease in the USA and Europe. Two plasmids containing genes encoding a trans-sialidase protein (TcSP) and an amastigote-specific glycoprotein (TcSSP4) were studied previously as prophylactic and therapeutic vaccines. Echocardiography is a valuable tool in diagnosis and follow-up of patients with ChD. The purpose of this study is to determine the prophylactic effect of *T. cruzi* genes on echocardiographical hemodynamic parameters in chagasic dogs.

Methodology & Theoretical Orientation: Dogs were DNA-plasmid immunized and infected with metacyclic trypomastigotes. Doppler echocardiography were performed before and 7-19 months after immunization and/or infection in all dogs.

Findings: All non-vaccinated dogs had fractional shortening values decreased, suggesting an impairing in general cardiac function. Differences in the left ventricular ejection fraction values among infected and non-infected dogs were demonstrated. Left ventricular diastolic and systolic diameters were decreased in vaccinated dogs, therefore protection of progressive heart damage or heart dilation could be prevented. Systolic peak time was higher in infected and mock-vaccinated/infected groups increasing


vulnerability to malignant arrhythmias and sudden death. Left ventricular volumes were elevated in infected groups suggesting a decrease in wall thickness that might lead to increased size of the heart cavity except for the vaccinated group with the plasmid that carried the TcSP gene.

Conclusions: Experimental ChD in dogs causes cardiac dilation, poor contractibility and heart failure; the pathological process can be diagnosed by echocardiography better than other techniques in the living patient. Properties of plasmid-DNA vaccination with *T. cruzi* genes may be important in the amelioration of *T. cruzi*-induced cardiomyopathy. Using echocardiography, structural and functional changes in the chagasic heart could be monitored easily and, this should be the method of choice for characterizing the clinical stages of ChD.

Speaker Biography

Olivia Rodríguez-Morales is researcher in medical sciences at the National Institute of Cardiology, Ignacio Chávez in Mexico City, Mexico, where she conducts investigation lines related to the study of the basis of molecular pathogenesis, diagnoses, prophylaxis and therapy against *Trypanosoma cruzi*. Dr. Rodríguez-Morales is also professor in the Autonomous National University of Mexico (UNAM) where she teaches "Veterinary Cell Biology" and "Veterinary Bacteriology and Mycology" in the Faculty of Veterinary Medicine and Zootechnics. She belongs to the National System of Researchers Level 1 in Mexico.

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 Notes:

Electrolyzed oxidizing water reduces parasitemia, tissue damage, and mortality of experimentally infected BALB /c mice with *Trypanosoma cruzi*

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Background: Chagas disease or American *trypanosomiasis* caused by the protozoan *Trypanosoma cruzi* belongs to the group of Neglected Tropical Diseases. It is an endemic disease in 21 Latin American countries, and it is also considered as an emerging disease in the USA and Europe, which causes the death of 10 000 people per year worldwide. There are two clinical stages of Chagas disease: acute and chronic. Only 30% of infected patients develop cardiopathies and/or dysfunctions of the gastrointestinal tract. The remaining 70% are chronic patients without clinical manifestations but with positive serology. In the acute stage, antiparasitic treatment with any of the only two drugs on the market (Nifurtimox and Benznidazole) is effective in 80% of cases. Only a few countries treat the patient in a chronic phase with trypanocidal drugs, and most focus on controlling cardiac symptoms rather than attacking the parasite. The use of electrolyzed oxidizing water (EOW) offers a new strategy to prevent or stop the cardiac consequences of *T. cruzi* infection, as it has been reported as an innovative high-level disinfectant capable of eliminating bacteria, viruses, fungi in 30 seconds, and spores in 15 minutes. In addition, neutral pH EOWs have been shown to be innocuous orally or parenterally in rats, mice and dogs. Objective: The aim of this study was to evaluate the effectiveness of an EOW as a trypanocidal treatment that prevents the establishment of the disease or controls the progression of heart disease in a murine model infected with *Trypanosoma cruzi*.

Methods: Six-to 8-week-old female BALB/c mice were inoculated intraperitoneally with 10,000 blood trypomastigotes of H8 *T. cruzi* strain, and treated orally, intramuscularly and intravenously every 24 hours with EOW (40 ppm) at 20 days postinfection (dpi) for five days.

Parasitemia was determined, clinical signs were observed and mortality was recorded for 60 dpi. At 60 dpi euthanasia was performed and cardiac, splenic and lymph node indices were calculated. Other macroscopic alterations in the heart, spleen, esophagus, colon, intestines, skeletal muscle and nerve tissue were also registered.

Results: Intraperitoneal infection was successful in 100% of the inoculated population. In all infected groups, parasitemia was observed at 20 dpi. In treated animals, the peak of parasitemia was found earlier than in the untreated group. In addition, the quantification of parasites in blood was 2 to 5 times lower in EOW treated-mice than in non-treated ones, being the oral route with the largest difference. Moderate improvement in the physical state and health of animals treated with EOW was observed. Cardiomegaly and splenomegaly were avoided in mice receiving oral and intramuscular EOW treatment, respectively, whose cardiac and splenic indexes were very similar to the uninfected control group. Survival was 100% in the murine population receiving oral EOW treatment.

Conclusion: EOW efficiently inhibited the severity of Chagas disease in experimentally infected BALB/c mice, reducing clinical signs, parasitaemia, cardio-esplenomegaly and mortality. These outcomes may lead to the use of an effective innovative trypanocidal substance against Chagas disease.

Speaker Biography

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 Notes:

Prevalence and diversity of *Bartonella species* in ectoparasites from wild-caught rodents and domestic animals in the Northern and Northeastern regions of Thailand

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Ectoparasites are thought to be the important vectors of *Bartonella* transmission among animals, including humans. The *Bartonella* prevalence and species diversity in several types of ectoparasites (ticks, fleas, chiggers, and lice) collected from rodents and domestic animals (cats, dogs, cattle, and chickens) were investigated in this study. The surveillance study was conducted in 2 regions, 4 provinces; 2 provinces from the Northern region (Nan and Mae Hong Son) and 2 provinces from the Northeastern region (Loei and Nong Bua Lam Phu) during September 2013 to October 2014. Overall, a total of 539 pooled ectoparasites (102 fleas pools, 80 ticks pools, 6 lice pools, and 351 chiggers pools) were collected from wild-caught rodents and a total of 650 pooled ectoparasites (384 fleas pools, 213 ticks pools and 53 lice pools) were collected from domestic animals. Real-time PCR assay with TaqMan probe targeting *Bartonella*-specific *ssrA* gene was used for *Bartonella* DNA detection. Amplification of *Bartonella* *gltA* gene was confirmed using published primers, CS443f and CS1210r. Fleas were the major ectoparasites collected from domestic animals (59.0%), followed by ticks (32.8%), and lice (8.2%). Chiggers were the most common ectoparasites collected from rodents (65.1%), followed by fleas (18.9%), ticks (14.9%) and lice (1.1%). *Bartonella* DNA was detected in all ectoparasites types. Among ectoparasites collected from rodents, the

highest prevalence of *Bartonella* DNA was found in fleas pools (24.5%, 25/102), then in lice pools (16.7%, 1/6) and ticks pools (12.5%, 10/80), respectively. However, low prevalence of *Bartonella* DNA was found in chiggers pools (2.8%, 10/351). Likewise, high prevalence of *Bartonella* DNA was also found in fleas pools collected from domestic animals (14.1%, 54/381), while low prevalence was found in lice pools (5.7%, 3/53) and tick pools (6.6%, 14/213). Phylogenetic analysis of *Bartonella* *gltA* sequences (638 bp) presented the diverse range of *Bartonella* species found in ectoparasites collected from rodents including 4 *Bartonella* species in *B. elizabethae* species complex (*B. elizabethae*, *B. tribocorum*, *B. rattimassiliensis*, and *B. queenslandensis*), *B. rochalimae* and *Candidatus B. thailandensis*. However, only 2 species (*B. clarridgeiae* and *B. tamiae*) was detected in ectoparasites collected from domestic animals. Our data showed an important role of ectoparasites as potential vectors for *Bartonella* transmission among rodents and domestic animals residing in close association with humans.

Speaker Biography

Ratree Takhampunya is currently working as a Research Associate in the Armed Forces Research Institute of Medical Sciences-U.S. Army Medical Directorate in Thailand.

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 Notes:

Chytridiomycosis caused by *Batrachochytrium dendrobatidis* in Sardinia (Italy): The discovery, epidemiological study and current assessment of the role of the pathology in endemic amphibians communities decline

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In August 2005 our team detected infection with Bd in southern Sardinia on some adult specimen of sardinian newt *Euproctus platycephalus*, an endemic and threatened species. With Zoological Society of London partnering we started to map infection range all over Sardinia and describe how infection interacts with other native species. Bd infection can then be confirmed in two ways: first, by histology (sectioning skin and looking for the presence of chytrid zoosporangia within the skin) and second, by swabbing amphibians thought to be infected and testing for the presence of chytrid DNA using real-time PCR, that also allows an estimate of infection load. At the now we can report that Bd sensitivity varies significantly across the species and the species range; Bd afflicts three endemic species Sardinian newt *Euproctus platycephalus*, Sardinian painted frog *Discoglossus sardus* and Sardinian tree frog *Hyla sarda* and that infection hot spot is located in Limbara Mountain Complex in the North of the island. Our analysis in the same area confirmed that some mass die off of Sardinian painted frog were due to chytridiomycosis. In order to better know the pathogen dynamics in *Euproctus platycephalus*, our flag species, we have developed the approaches to investigate

age structure and the sensitivity at different years. Last, we have developed the molecular tools to investigate gene flow and movement patterns and have shown that source/sink dynamics vary strongly across the species range and we are currently mapping the expansion of some alien species in northern Sardinia, such as green frogs *Pelophylax* sp. and red swamp crayfish *Procambarus clarki* that are both known as chytrid vectors and represent a serious threat for endemic amphibians communities also for direct predation and habitat resources competition.

Speaker Biography

Stefano Bovero is an independent researcher at Zirichiltaggi Sardinia Wildlife Conservation NGO and his expertise includes aspects of the natural history and conservation of amphibians and freshwater fish in alpine and in Mediterranean areas. Since 1994 he devotes a particular attention to the endangered Sardinian newt *Euproctus platycephalus*. Together with his team he analyzed the distribution and the ecology of this species with attention for the conservation aspects and the identification of possible causes of population decline. Starting in 2007 he also focused attention on the serious problem of chytridiomycosis afflicting endemic amphibian species in Sardinia and his group is currently involved in a long research program in collaboration with the Zoological Society of London.

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 Notes:

Thalidomide affects macrophage activation and Leshmania

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Keywords: Leishmaniasis, thalidomide, macrophage activation, cytokines

Introduction: Leishmania parasites are the causative agents of LEISHMANIASIS, group of vector-borne parasitic diseases endemic worldwide. Once inoculated into the organism, Leishmania parasites are rapidly uptaken by macrophages. Macrophages are primary resident cells for their proliferation: they can either phagocyte or allow parasite growth. That is why proper activation of macrophages is crucial in disease fate. Macrophage activation is divided into two classes: classical (M1) and alternative (M2) that induce parasite killing and its survival, respectively. Classical activation is mediated by pro-inflammatory cytokines which cause macrophages to produce toxic molecules to kill intracellular parasites. In contrast, alternative activation is induced by anti-inflammatory cytokines that lead to parasite survival in infected cells. Thalidomide is reported to stimulate immune response and enhance cellular phagocytotic activity by selectively inhibiting M2 pathway. Here, thalidomide was examined as potential drug to have suppressive effect on intracellular replication of L.major within infected macrophages in-vitro.

Methods: To observe macrophage activation, Raw264.7 cells were cultured. After 24hr incubation of cells in 370°C, 5% CO₂ incubator, thalidomide treatment of different concentration

was done. Supernatant and pellet were collected for ELISA, RT-PCR, qPCR and WB tests. To observe pathogen survival, Raw 264.7 cells were cultured in chamber slides and infected with L. major at 1:10 ratio. After 24hr incubation, thalidomide treatment was done. Giemsa staining was applied to slides and intracellular amastigote forms of L.major were counted.

Results: In this study thalidomide's effect on proper macrophage activation and parasite survival was analyzed. It was found that thalidomide can a) up-regulate pro-inflammatory M1 macrophages (IFN- γ , TNF- α , iNOS); b) down-regulate anti-inflammatory M2 macrophages (IL-10 and Arg-1); c) decrease intracellular amastigotes of L. major. Thalidomide shows inhibitory effect on alternative activation of macrophages and induces M1 polarization of macrophages, thus making them resistant to L. major infection.

Conclusion: Results highlight thalidomide's potential contribution to a new drug development towards Leishmaniasis in the future.

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 Notes:

Aquaculture; Potential source of marine bioactives

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Marine organisms are increasingly being investigated as sources of bioactive molecules with therapeutic applications as nutraceuticals and pharmaceuticals. Marine bioactives can be derived from a vast array of sources, including marine plants, microorganisms, and sponges, all of which contain their own unique set of biomolecules. These bioactive molecules can be applied in many fields such as the drug, cosmetic, and food industries. In particular, retrieval and characterisation of these bioactive molecules from marine processing waste contribute valuable information to the vast field of marine natural product discovery (Suleria et al., 2016). All over the world, the demand for seafood has increased owing to its health promoting perspectives and also help to fight against various health-related disorder including cardiovascular disease, cancer, alzheimer's and many other major illnesses (Suleria et al., 2015). Therefore, the role of aquaculture in ensuring a consistent supply of aquatic species for human consumption and screening of valuable bioactive molecules for novel drug discoveries cannot be overstated. Moreover, several toxic compounds, called biotoxins also bioaccumulate in fish, crabs, lobster, abalone or filter-feeding bivalves (shellfish), such as mussels, oysters, scallops and clams, and cause poisoning and their potential

risks to food safety and/or market access of commercially-produced seafood are a growing concern in Australia (Murray et al., 2015; Ajani et al., 2017). Approximately 60,000 human intoxications occur per year worldwide, with an overall mortality of about 1.5% (Kantiani et al., 2010). Therefore, there should be some cost-effective food safety systems throughout the supply chain that reflect the degree of risk and to protect the health of seafood consumers. Screening and identification of marine bioactives and biotoxin can play significant role in aquaculture.

Speaker Biography

Hafiz Suleria is currently working as Honorary Fellow in the Diamantina Institute - Faculty of Medicine, The University of Queensland, Australia. Previously, he has been awarded an International Postgraduate Research Scholarship (IPRS) and Australian Postgraduate Award (APA) for his PhD research at UQ School of Medicine, the Translational Research Institute (TRI) in collaboration with Commonwealth, Scientific and Industrial Research Organization (CSIRO, Australia). His major research focus was on food science and nutrition particularly in screening of bioactive molecules - isolation, purification and characterization using various cutting-edge techniques from different plants, marine and animal sources followed by their in vitro bioactivity, in vivo, cell culture and animal modeling. He has published more than 40 peer-reviewed scientific papers in different reputed/impacted journals.

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 Notes:

Accepted Abstracts

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Report on the phylogenetic studies of diplostomatids parasites

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Introduction: *Diplostomid metacercariae* inhabit freshwater fish species as the second intermediate hosts. These parasites have been found in the eye lens, the retina, vitreous humor and the nervous system of freshwater fish. The classification of these parasitic stages to the species level using only morphology is often difficult and ambiguous. The use of molecular techniques has allowed links to be elucidated using various developmental stages of these parasites. The aim of this study was to provide a summative report on the phylogenetic tree by applying molecular biology techniques to the investigation of larval diplostomid parasites.

Materials and Methods: *Diplostomid metacercariae* were preserved in 70% ethanol prior to DNA extractions using Qiagen kit. Standard techniques for amplification of rRNA

region were followed. The DNA amplicons were sent to inqaba Biotech laboratory for sequencing and phylogenetic trees generated using software programs.

Results: The amplicons of these diplostomids had band sizes of 500 base pairs. The amplicons contained only partial regions (ITS-2). The parasitic species 28S rDNA genomic region was successfully amplified.

Conclusion: The application of molecular techniques on digenetic trematodes seems very promising and may yield great potential in future descriptions of morphologically similar parasitic species.

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A preliminary study on mitochondrial DNA of some species of family Muscidae (Diptera) of INDIA

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Flies belonging to the family Muscidae are the most cosmopolitan among the insects. This family is amply represented in all biogeographical regions with approximately 5000 described species within 170 genera (Kutty et al., 2008). They are of great importance to medicine because of their ability to transmit diseases to humans and animals. Adults of many species are passive vectors of pathogens for diseases like typhoid fever, dysentery, anthrax, cholera and African sleeping sickness (Kettle, 1995). Immature stages of many species of the Muscid flies have similar morphological characters that make their identification difficult (Benecke and Wells, 2001). To solve these problems

Deoxyribonucleic acid (DNA) based methods for species identification are used. Animal mitochondrial DNA (mtDNA) has been used extensively in studies of evolutionary and population genetics in recent years (Avice et al., 1987). The present study is designed to help us the identification for 5 species of family Muscidae. The flies were collected from various districts of Punjab during March 2016 to September 2016. The mt cytochrome oxidase subunit II (COII) has been used for this purpose. This gene has been extensively used to address phylogenetic questions in insects at different taxonomic level.

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Impact of rainfall on larval density of malaria vectors in district Baghpat, Uttar Pradesh

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Background & objective: Rainfall has been associated with mosquitoes breeding and abundance of population. It is an abiotic factor that affects the growth, development and survival of mosquito. The main objective of this study was to assess the impact of rainfall on larval density of malaria vectors in aquatic habitats.

Methods: Four study sites Katha, Khekra, Baragaon and main Baghpat were selected based on high malaria cases and availability of breeding habitats. Larval sampling was done by dipping method before and after rainfall within a period of 2-3 days. Larvae collected from the field, transported in plastic container and reared in the laboratory for adult emergence and identification. Adult mosquitoes were identified with the help of standard identification key under the dissecting microscope. The amount of rainfall (mm) was measured using a rain gauge, which was installed at Khekra study site of district Baghpat. The correlation analysis was applied for relationship between anopheline larval density and rainfall

data (mm). *Anopheles culicifacies* and *Anopheles stephensi* dominant species of malaria vectors has been reported from selected localities of district Baghpat, Uttar Pradesh.

Result: We observed that rainfall of 45.6 mm significantly reduced larval density in both permanent and temporary habitats by 8.32 and 2.16 larval density/ dip respectively. Positive co-relation ($r = 0.20$), and ($r = 0.31$) was observed between rainfall and larval density after rainfall in permanent and temporary breeding habitats respectively.

Interpretation & conclusion: The adverse effect of rainfall on larval density could be attributed to flushing out of larvae from their breeding habitats. The critical amount of rainfall required for flushing out larvae was found to be 45.6mm. *Anopheles culicifacies* and *Anopheles stephensi* emerged from collected larvae.

Keywords: Malaria vectors, rainfall, larval density, habitat.

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Bionomic of *Streblotesiva* (Lepidoptera: Lasiocampidae) a polyphagous defoliator at Bushehr, Iran

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Abstract:The Jujube lappet moth, *Streblotesiva* (Lefebvre) (Lepidoptera: Lasiocampidae), is as a polyphagous defoliator on ornamental and forest communities include *Conocarpus erectus*, *Ziziphusspina-christi* and *Acacia ampliceps* in Bushehr, Khuzestan and Hormozgan provinces of Iran. The intensification and concentration of a single plant species or variety such as *C. erectus* in ever larger and more extensive monocultures increases, the simplification of agroecosystems compared with natural ecosystems and the reduction of diversity in large crop monocultures, has long been associated with reasons for pest such as *S. siva* outbreaks. This study was conducted to determine some characteristics of the biology and ecology of the moth. The region of Bushehr was divided into three zones to study the population dynamics and biology of *S. siva*. Then, stratified random sampling was used for the range of the insect abundance and dynamism. The spatial distribution of *S. siva* larva was studied in field conditions by using regression models; Taylor's power law and Iwao's patchiness regression during 2015-2016. *S. siva* spends May to September which is very hot period in the region, as pupae in thin sturdy silk cocoons on the branches and trunk of *C. erectus*, *A. ampliceps* and *Z. spina-christi*. In early October, the adult's moths appear gradually and after mating, they start laying

eggs on leave and branches. The autumn first generation had a clear pick point. Then, the average population was gradually declined and in early November was reached to the lowest amount in the first autumn generation. Oviposition of the second autumn generation was occurred in early November and the peak number of different larva instars was observed on November 25th. After that the larval growth was started slowly and the insect population was reached to zero level on 21 January and overwintering stage began. The spring generation adults were appeared gradually since the middle of March. This larva's generation reached a population peak in the early of April and in the early of May the population of larvae reached to zero, and pupae of this generation began their over summering. The insect has three full generations in cool winters. *S. siva* has been distributed randomly throughout the province. The spatial distribution of all larvae of *S. siva* on *C. erectus* was different in generations. It was estimated as an aggregated (clumped) and random distribution by using Taylor's power law and Iwao's patchiness regression.

Keywords—*Acacia ampliceps*, *Biology*, *Conocarpus erectus*, *Ecology*, *Streblotesiva*, *Ziziphusspina-christi*

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Adulticidal susceptibility evaluation of an arbovirus vector *Aedes albopictus skuse* (Diptera: Culicidae) on Penang Island, Malaysia

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Insecticide based vector control approaches are facing challenges due to the development of resistance in vector mosquitoes. Therefore, a proper resistance surveillance programme using baseline lethal concentrations is crucial for the resistance management strategies. Currently, the World Health Organization's (WHO) diagnostic doses established for *Aedes aegypti* and *Anopheles* are being used to study the resistance status of *Aedes albopictus*. In this study we established the diagnostic doses for permethrin, deltamethrin and malathion using a known susceptible reference strain and 5 field collected populations were

screened against these doses following the WHO protocol. This study established the diagnostic dose of malathion 3.4%, permethrin 0.45% and deltamethrin 0.08%, that differs from the WHO doses. Among the insecticides tested on 5 wild populations, only deltamethrin showed high effectiveness. While, different susceptibility and resistance patterns were observed against permethrin, malathion and DDT 4%. This study may facilitate the health authorities in future to improve chemical based vector control operations in the dengue endemic areas.

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Clinical signs and symptoms of *P. falciparum* malaria infection (patent and sub-patent) in pregnant women living in an area of high seasonal transmission

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Background: Malaria in pregnancy is a major public health problem in endemic countries. However, there is a paucity of data on the signs and symptoms of clinical malaria among pregnant women. This study aimed at documenting the clinical presentation of malaria among pregnant women.

Methods: Six hundred pregnant women attending the maternity clinic of Nanoro District Hospital, Burkina Faso, were recruited, 200 with suspected clinical malaria and 400 as controls. Cases were matched by gestational age and parity with controls. Signs and symptoms were collected and a blood sample taken for rapid diagnostic test, microscopy and hemoglobin measurement. A multivariate model was used to assess the predictive value of signs and symptoms for malaria infection.

Results: The overall prevalence of malaria was 42.6%

(256/600) while anemia was found in 60.8% (365/600) women. Nearly half (49.5%) cases and 39.5% controls had a malaria infection. The most common signs and symptoms among the cases were fever (36%, 72/200), history of fever (29%, 58/200) and headache (52%, 104/200). The positive predictive value for fever was 53% (95%CI: 41-64), history of fever 58% (95%CI: 37-63) and headache 51% (95%CI: 41-61).

Conclusion: Signs and symptoms suggestive of malaria are frequent among pregnant women living in areas of intense transmission. Common malaria symptoms cannot identify all infected women. For a better management of malaria in pregnancy, active screening to early detect and treat malaria infection should be performed on all pregnant women attending a health facility

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Prevalence and morphological characterization of Myiasis causing Diptera Flies in Jeddah Saudi Arabia

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Objective: A number of dipteran flies are found in Jeddah and many of them are associated with Myiasis of livestock and humans. Although several reports are available on the Myiasis causing flies and human and animal myiasis from different parts of Saudi Arabia no literature is available on the prevalence and characterization of these flies from Jeddah Province. The objective of this work is to fill up this gap.

Methods: The survey of the adult flies was done by collecting them with the help of Malaise & bait traps and sweeping nets from different marked locations. Total number of flies were counted and different species were separated. The morphological identification was done with the help of available authentic keys.

Results: In this study 10 dipteran fly species belonging to 6 families were identified as myiasis causing on the basis

of reported cases in Saudi Arabia. The flies collected during survey were *Megaselia scellaris*, *Musca domestica*, *Fanniia canicularis*, *Sarcophaga haemorrhoidalis* (*Bercaea cruentata*); *Parasarcophaga ruficornis*, *Wohlfahrtia nuba*, *Chrysomya bezzina*, *chrysomya albicep*, *Chrysomya megacephala*, and *Oesteris ovis*. Highest number of them was of *Musca domestica* (67.6%) and the rest were other species. Most of the species were collected from Abattoirs (50%) and animal farms (39%).

Conclusion: This study would help the health and veterinary workers to identify the myiasis causing flies promptly and accurately so that the control measures can be implemented.

Key words: *Diptera, Flies, Myiasis, Morphology, Prevalence*

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Determination of the prevalence of parasitic triad infection among the Badjaos of Angeles City

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Documented reports on the health and sanitation status of Badjao are very limited to date. In view of their cultural practices, Badjaos are considered to be at high risk of acquiring the parasitic triad infections. This study focused on the determination of the prevalence of parasitic triad infection and the establishment of possible associations of each to the demographic profile of the respondents. One hundred badjao individuals were chosen as the population of the study. After stool testing which includes Direct Fecal Smear (DFS) and Formalin-Ethyl acetate concentration Technique (FECT), 100% prevalence was noted on the determination of *Ascaris lumbricoides* and *Trichuris trichuria* infections. Discrepancy of +4 Hookworm isolates was noted

during the isolation of parasite using FECT. This study was able to establish association between the manner of excreta disposal and the presence of Hookworm infection. Other associations were not obtained because of the constant response of the research population. Immediate deworming project was organized by the researchers and the local government units in response to the significant results of the study.

Keywords: Badjaos, Direct Fecal Smear, Formalin-Ethyl acetate concentration Technique, *Ascaris lumbricoides*, *Trichuris trichuria*, Hookworm

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Performance characteristics of Tortoises (*Kinixys Spp*) fed boiled Cocoyam mixed with palm oil under different watering regimes in captivity in tropical environment

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This study was carried out to determine the performance characteristics of African hinged back tortoise (*kinixys spp*) under different watering regimes. Sixteen (16) tortoises with weight ranges from 150 to 675g were randomly distributed into four treatment groups and each treatment was allotted with four tortoises. The watering regime serves as the treatment group, these were; *Ad libitum* watering (07.00-07.00hrs), 12 hour daily watering (0700-1900hrs), 6 hour daily watering (1300-1900hrs) and 12 hour night watering (1900-0700hrs) serving as treatments 1,2,3 and 4 respectively. All the animals were fed *ad libitum* the on boiled cocoyam mashed and mixed with palm oil. Parameters on feed intake, water intake, weight changes, and blood metabolites were collected and used to assess their performance. The study lasted for five weeks, however, a pre experimental period of two weeks was allowed for adaptation of the animals. The results obtained showed that the mean water consumption for the treatments 1, 2, 3 and 4 where 152mls, 179mls, 58mls, and 81mls respectively and the mean feed intake were 24.70g, 17.60g 15.80g and 25.20g respectively, revealing that the animals served water at night consumed more feed, followed by those watered 24 hour

daily. The least feed consumption was recorded for animals watered in the afternoon for only 6 hour per day. Also, the values obtained for the weight increment for the treatments were 75g, 38g, 63g and 175g for treatments 1, 2, 3 and 4 respectively. This indicates that the highest weight gain was recorded for animals under the 12 hour night watering regime followed by those under the *ad libitum* watering regime. The least weight gain was recorded in the group of animals under the 12 hour day treatment. The analysis of some blood metabolites showed the packed cell volume ranges from 23.5 to 33.5%, total serum protein 5.85 to 5.90g/dl, serum albumin 3.00 to 3.20g/dl and serum globulin 2.70 to 2.90 g/dl. Results obtained from the experiment showed that the mean feed and water intake were affected by the duration of watering that the animal was subjected to, however, the blood metabolite were not influenced by the watering regime.

Keywords: Performance, Tortoises (*Kinixys Spp*), Different Watering Regimes in Captivity

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Environmental and anthropogenic factors affecting the probability of occurrence of *Oncomegas wagneri* (Cestoda: Trypanorhyncha) in the southern Gulf of Mexico

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Understanding the environmental and anthropogenic factors influencing the probability of occurrence of the marine parasites is fundamental for determining the circumstances under which they can act as bioindicators of environmental impact. The aim of this study was to determine whether physicochemical variables and polyaromatic hydrocarbons affect the probability of occurrence of the larval cestode *Oncomegas wagneri*, which infects the shoal flounder, *Syacium gunteri*, in the southern Gulf of Mexico. The study included 162 sampling sites, where sediments, water and the shoal flounders were collected. We used the boosted generalized additive models (boosted GAM) to examine the potential statistical relationships between the contaminants and physicochemical variables from the water and sediments, and the probability of the occurrence of this parasite. The boosted GAM accurately predicted the

probability of the occurrence of *O. wagneri*. The variables with the highest frequencies of appearance in the models (proxies for the explained variability) were the polyaromatic hydrocarbons of high molecular weight (PAHH, 95 %). The PAHH, together with N and P, are carried by rivers that discharge into the ocean, which enhances the growth of bacteria and intermediate hosts. Our results suggest that sites with PAHL/PAHH ratio values up to 1.89 promote transmission based on the high values of the prevalence of *O. wagneri* in the study area. In contrast, PAHL/PAHH ratio values ≥ 1.90 were apparently harmful for the parasite transmission. Overall, the results indicate that the PAHs affect the probability of occurrence of *O. wagneri* in the southern Gulf of Mexico.

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