vector surveillance and control. Human antibody response to mosquito salivary antigens is emerging as a relevant additional tool to directly assess vector-human contact, monitor efficacy of control interventions and evaluate the risk of arboviral transmission. Recently, we showed that IgG responses to the *Ae. albopictus* 34k2 salivary protein (al34k2) appear suitable to evaluate seasonal and spatial variations of human exposure to *Ae. albopictus* in conditions of natural exposure in a non-endemic area of Italy. The aim of this study was the validation of the al34k2 antigen in epidemiological settings with ongoing arboviral transmission maintained by *Ae. albopictus*. ELISA were used to measure human IgG responses to the al34k2 in adults from an area of Reunion Island where *Ae. aegypti* is absent and *Ae. albopictus* represents the unique vector of chikungunya. In addition, to check the specificity and/or cross-reactivity of this biomarker, we also analyzed the IgG responses i) of the same individuals from Reunion Island to the orthologous 34k2 salivary protein from *Ae. aegypti* (ae34k2) and ii) of Bolivian subjects, only exposed to *Ae. aegypti*, to both al34k2 and ae34k2. A group of French individuals, not exposed to either *Ae. albopictus* and *Ae. aegypti*, was used as control group. Individuals from Reunion showed significantly higher IgG responses to al34k2 than to ae34k2 validating this antigen as a good and specific marker of human exposure to *Ae. albopictus* in an endemic area. In contrast, IgG responses to the ae34k2 showed in both areas a low specificity and yielded a relatively high background, even in unexposed controls. These results provided a clear evidence that IgG responses to al34k2 may represent a suitable marker of human exposure to *Ae. albopictus*. On the contrary, the *Ae. aegypti* orthologue ae34k2 does not appear suitable as marker of human exposure to *Ae. aegypti* due to the unspecific IgG response and a high background.

0114

PRELIMINARY BLOOD MEAL ANALYSIS OF CULICOIDES SPECIES IN LEISHMANIA (MUNDINIA) ENRIETTII COMPLEX-ENDEMIC REGION IN GHANA

Godwin Kwakye-Nuako[1], Priscilla Abena Ankamaa Opare[1], Mba-Thissommah Mosore[2], Seth Offei Addo[2], Mary E. Wilson[3]

[1]University of Cape Coast, Cape Coast, Ghana, [2]Department of Parasitology, U.S. Naval Medical Research Unit No. 3, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Accra, Ghana, [3]University of Iowa, Departments of Internal Medicine, Infectious Diseases, Microbiology and Immunology, and the Veterans' Affairs Medical Center, Iowa City, IA, USA, Iowa City, IA, United States

Cutaneous leishmaniasis (CL), since 1992, has been endemic in the south-eastern part of Ghana. During the periods 2002 and 2003, a total of 8876 human leishmaniasis were recorded in this endemic focus. The *Leishmania* parasites have long been known to be transmitted by female phlebotomine sand fly vectors. However, in recent laboratory models of infection studies, the new species of *Leishmania* belonging to the *Leishmania* (*Mundinia*) *enriettii* complex found in Ghana does not survive in sand flies but rather, multiply and develop successfully in *Culicoides* species. *Culicoides* species are distributed worldwide and are capable of transmitting several infectious agents including parasites. In this study we analyze the hosts feeding preferences of *Culicoides* found in the leishmaniasis endemic foci in Ghana to expedite the study of a member of *Leishmania* (*Mundinia*) *enriettii* complex transmission routes and vector implication. The biting midges were collected in August to December 2019 at two weeks intervals using CDC light traps and sweep nets. A total of 185 midges were collected, pooled together in groups of ten and subjected to DNA extraction. Molecular analyses were conducted using the universal mammalian primers (Mammal-F, Mammal-R) in the meantime. PCR revealed that 34.7% of flies collected fed on mammalian hosts. The primers amplified the 772bp band size which is the identical to the size of the mammalian amplified product. This result indicates that the *Culicoides* analyzed so far prefer mammalian host for blood meal. The preliminary results obtained indicate the host preferences of some *Culicoides* species feed on mammals. We conclude that *Culicoides* species collected in the CL endemic communities can potentially serve as a vector for the novel *Leishmania* species found in Ghana. Keywords: Ghana, *Leishmania* (*Mundinia*) *enriettii* complex, *Culicoides* species

0115

INCRIMINATING CULICOIDES BITING MIDGES AS VECTORS OF HUMAN CUTANEOUS LEISHMANIASIS IN GHANA AND VALIDATION OF STANDARD LIGHT TRAPS AGAINST EXPLICIT HUMAN BITING RATES

Priscilla Abena Ankamaa Opare[1], Godwin Kwakye-Nuako[1], Marion England[2]

[1]University of Cape Coast, Cape Coast, Ghana, [2]The Pirbright Institute, Surrey, United Kingdom

Human cutaneous leishmaniasis (CL) is a neglected tropical disease endemic to some communities in Ghana and is caused by a newly identified species of *Leishmania* belonging to the *L. enriettii* complex. The vector(s) responsible for transmitting human CL in Ghana remain unknown as very few sandflies have been collected in the various endemic foci in Ghana. Previous laboratory investigations have shown that the new species of *Leishmania* colonized and replicated successfully within the gut of *Culicoides* biting midges. In this study, we validated CO_2-baited CDC light traps against human landing catches (HLC) for *Culicoides* and sandflies caught in the endemic Ho district of Ghana and characterised the *Culicoides* fauna to incriminate species of *Culicoides* as vector candidates responsible for CL in Ghana. *Culicoides* biting midges and sandflies were collected from May 2020 to August 2020 using CO_2-baited CDC light traps and filtered mechanical aspirators for HLCs. Light traps and human volunteers were rotated around four collection locations using a Latin square design. A morphological key was developed for the identification of *Culicoides* midges collected. Statistical analyses were carried out using R to determine whether CO_2- baited light traps could be accurately used as a proxy for human biting rates. Significantly, more *Culicoides* were collected by HLCs than by the traps ($p<0.001$) showing that CO2-baited CDC traps do not accurately reflect biting rates of Culicoides on humans. *Culicoides grahami* (98.5%) were the predominant species identified from both CDC traps and HLCs. Other species were identified in very small numbers (1.5%) and included *C. imicola*, *C. inornatipennis*, and *C. leucostictus* . Therefore, *C. grahami* is proposed as the putative vector of *Leishmania* in the Ho District of Ghana.

0116

UTILITY OF MALDI-TOF MS IN SPECIES IDENTIFICATION AND BLOOD MEAL ANALYSIS

Jonathan K. Karisa, Kelly Ominde, Martin Rono, Philip Bejon, Joseph Mwangangi, Maureen Laroche, Marta Maia

KEMRI-Wellcome Trust Research Programme, Kilifi, Kenya

Jonathan Karisa[1,2,3], Kelly Ominde[3], Martin Rono[1,2,3], Philip Bejon[3,4], Joseph Mwangangi [1,3], Maureen Laroche[3], Marta Maia[3,4]

[1]Pwani University, Department of Biological Sciences, [2]Pwani university Bioscience Research Centre (PUBReC), [3]KEMRI-Wellcome Trust Research Program, Bioscience department, [4]University of Oxford, Centre for Global Health and Tropical Medicine, Oxford, UK

Protein profiling using MALDI-TOF MS is a promising technology in the field of medical entomology. Studies have shown its ability to rapidly identify mosquito species and their associated blood meal sources. The technology overcomes challenges posed by the current methods used for entomological surveillance. The purpose of this study was to test the discriminative power of MALDI-TOF MS to distinguish between members of *An. gambiae* complex collected in coastal Kenya and their trophic preferences. Template mosquitoes obtained from the field and insectary were characterized using gold standard approaches. Proteins were extracted from legs and abdomens of individual mosquitoes for spectra acquisition and ClinProTools software was used for preprocessing and database creation. A total of 167 *An. gambiae* produced quality spectra

that were subsequently used for database creation and validation (query). These comprised of *An. merus* (143), *An. arabiensis* (n=34) and a pool of 45 *An. gambaie* s.s. (Kilifi strain) mosquitoes from the insectary were also processed. MALDI-TOF MS provided accurate identification of members of *An. gambiae* complex collected in the field including *An. arabiensis* (31/31) and *An. merus* (139/139) and insectary (*An. gambaie* s.s) (40/40). Analysis of abdominal proteins of blood fed mosquitos provided accurate identification of host sources. Majority of the samples had fed on Goat (n=63), Bovine and Human (n=6) and the rest (n=3) had fed goat-bovine. This study provides further evidence on the utility of MALDI-TOF MS approach for entomological surveillance by accurately identifying *An. gambiae* sibling species and their associated blood meals.

0117

SPOTLIGHT REPORTS: TICKS AND TICK-BORNE DISEASE THREATS IN ETHIOPIA

Rachel Wofford[1], Graham Matulis[1], David Pecor[2], Alexander Potter[2], Michael von Fricken[1], Bersissa Kumsa[1], Dawn Zimmerman[3], Yvonne-Marie Linton[2]

[1]George Mason University, Fairfax, VA, United States, [2]Walter Reed Biosystematics Unit (WRBU), Suitland, MD, United States, [3]Smithsonian's National Zoological Park and Conservation Biology Institute, Washington, DC, United States

Tick-borne diseases are a rising health concern across Africa. Understanding the geographic distribution of ticks at the country level can inform Ethiopian and international stakeholders about potential pathogens in circulation. Over 6,000 peer-reviewed articles from 1901-2020 were systematically screened for data meeting our inclusion/exclusion criteria. A total of 116 articles met final inclusion criteria with data extraction and geo-referencing, before being combined into a single database. Tick species identified came from seven different genera including five hard ticks (Amblyomma, Haemaphysalis, Hyalomma, Ixodes, and Rhipicephalus) and two soft tick genera (Argas and Ornithodoros). Fifteen species of Rhipicephalus ticks were reported, followed by 11 different species of Hyalomma ticks. The most commonly survey tick species was Amblyomma variegatum (Fabricius, 1794) with approximately 64% of articles detecting this species; with Rhipicephalus decoloratus Koch, 1844 and Rhipicephalus evertsi s.l. in 61% and 57% of studies, respectively. A total of 28 pathogens were reported in Ethiopian ticks, including medically important genera: Anaplasma, Borrelia, Coxiella, Ehrlichia, Haemoplasma, Rickettsia, Theileria, and Trypanosoma, along with four viruses (Congo, Dugbe, Jos and Thogoto). Amblyomma and Rhipicephalus ticks were the most commonly reported genera with identifiable pathogens. The data collected from this systematic review provides valuable information on historic high-risk areas for transmission of tick-borne disease, as correlated with tick vector distributions, and can be used to enhance ongoing surveillance and targeted sampling efforts.

0118

STUDY OF RED MEAT ALLERGY USING A MOUSE MODEL WITH BITES OF THE LONE STAR TICK, AMBLYOMMA AMERICANUM

L. Paulina Maldonado-Ruiz, Gunavanthi D. Boorgula, Yoonseong Park

Kansas State University, Manhattan, KS, United States

Recent studies have provided strong evidence supporting the Lone star tick bites as a cause of red meat allergy (RMA) in humans. RMA is caused by an increase of Immunoglobulin E (IgE) antibody production against galactose-alpha-1,3-galactose (aGal), which is a common glycan in mammals with the exceptions of old word monkey and human. The main factor causing the RMA, the lone star tick (*Amblyomma americanum*), is broadly distributed throughout the East and Midwest of the United States, which is also a vector of a wide range of human and animal pathogens. We previously found that the salivary glands of male and female ticks contained high levels of aGal epitopes after feeding on bovine blood. In our current work, we aimed to test whether the ticks mediate the transmission of the aGal sensitizer, acquired from non-human blood to humans through salivary secretions. In the course of tick feeding in the field, intrastadial host switches in completely fed ticks could occur as an episode of transmission of the aGal sensitizer. To test this hypothesis, we used an alpha-galactosyltransferase knockout mutant mouse (aGT-KO) model system, where untreated ticks (unfed) and pretreated ticks (partially fed with bovine blood) were placed. Using the enzyme-linked immunosorbent assay (ELISA), we measured the IgE and IgG levels, the total and specific antibody against aGal, after tick feedings with the pretreated ticks. Our results showed that aGT-KO mice significantly responded to tick feedings and injections of aGal (Galα1-3Galβ1-4GlcNAc) conjugated to human serum albumin or mouse serum albumin (aGal-HAS or aGal-MSA) by increased total IgE and aGal-specific IgE compared to those in C57BL/6 control mice. All the treatments by tick feedings with pretreated and untreated ticks functioned as sensitizer for increased specific IgE against aGal with large individual variations. This study confirmed that the aGT-KO mouse can be used as the model for RMA study while more study is required for understanding the individual variations in the immune responses to aGal.

0119

SPOTLIGHT REPORT: TICKS AND TICK-BORNE DISEASE THREATS IN CHAD: A CASE FOR INCREASED SURVEILLANCE

Stephanie Mitchell[1], Graham Matulis[2], Alexander Potter[3], David Pecor[4], Michael von Fricken[5], Alec Richardson[6], Katherine Mertes[7], Dawn Zimmerman[8], Yvonne-Marie Linton[9]

[1]a.) University of California, Berkeley b.) Smithsonian's National Zoological Park and Conservation Biology Institute Global Health Program, a.) Berkeley b.) Washington D.C, CA, United States, [2]George Mason University, Manassas, VA, United States, [3]a.) Walter Reed Biosystematics Unit (WRBU), Smithsonian Institution Museum Support Center b.) Department of Entomology, Walter Reed Army Institute of Research c.) Smithsonian Institution–National Museum of Natural History, a.) Suitland B.) Silver Spring C.) Washington D.C, MD, United States, [4]a.) Walter Reed Biosystematics Unit (WRBU), Smithsonian Institution Museum Support Center b.) Department of Entomology, Walter Reed Army Institute of Research c.) Smithsonian Institution–National Museum of Natural History, A.) Suitland B.) Silver Spring C.) Washington D.C, MD, United States, [5]a.) George Mason University, College of Health and Human Services b.) Smithsonian's National Zoological Park and Conservation Biology Institute Global Health Program, a.) Fairfax b.) Washington D.C, VA, United States, [6]a.) Walter Reed Biosystematics Unit (WRBU), Smithsonian Institution Museum Support Center b.)Department of Entomology, Walter Reed Army Institute of Research c.) Smithsonian Institution–National Museum of Natural History, a.) Suitland b.) Silver Spring c.) Washington D.C, MD, United States, [7]Conservation Ecology Center, Smithsonian's National Zoological Park and Conservation Biology Institute, Front Royal, VA, United States, [8]a.) Smithsonian's National Zoological Park and Conservation Biology Institute Global Health Program b.) Department of Epidemiology of Microbial Disease, Yale School of Public Health, a.) Washington b.) New Haven, DC, United States, [9]a.) Walter Reed Biosystematics Unit (WRBU), Smithsonian Institution Museum Support Center b.) Department of Entomology, Walter Reed Army Institute of Research c.) Smithsonian Institution–National Museum of Natural History, a.) Suitland b.) Silver Spring c.) Washingto D.C., MD, United States

Ticks and their associated pathogens pose a significant risk to animal and human health in the Sahel, where pastoralist lifestyles increase the interface and possibility of zoonotic spillover. To augment our surveillance activities in Chad, to develop effective risk assessments for tick-borne diseases of humans and livestock, additional high-quality surveillance data is needed to better document the distribution and pathogen-association of ticks in Chad. A systematic literature review was conducted to compile tick surveillance data from peer-reviewed literature. In this systematic review, terms were searched within titles and abstracts in PubMed, CABI, Web of Science, Scopus, with date limits of 1901–2020 in languages limited to English and French. Reported surveillance findings were standardized using