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ACL-clinical forms: ADCL and BDCL, both due to *L. (L.) amazonensis* and with negative DTH⁽⁻⁾, five cases of each; LCL due to *L. (L.) amazonensis*, divided into two groups: five cases with negative DTH⁽⁻⁾ and three with positive DTH⁽⁺⁾; and eight cases of LCL due to *L. (V.) braziliensis*, all with positive DTH⁽⁺⁾. Paraffin-embedded biopsies of cutaneous lesions were carried out for immunohistochemical analysis of immunostained cells (CD11c⁺), using rabbit anti-human CD11c McAb (ab52632 Abcam). A Zeiss image analysis system was used to quantify dDCs⁺ in 5–8 fields per histological section (400×). dDC expression was analyzed by Mann-Whitney test using Biostat 5.0 ($P < 0.05$). The dDC⁺ cell density showed an increased expression from the central LCL^(DTH+/++) due to *L. (V.) braziliensis* to the sub-polar BDCL^(DTH-) and polar ADCL^(DTH-) due to *L. (L.) amazonensis*: LCL/L.b.^(DTH+/++) = 358 cells/mm² → LCL/L.a.^(DTH+/++) = 244 cells/mm² → LCL/L.a.^(DTH-) = 310 cells/mm² → BDCL/L.a.^(DTH-) = 517 cells/mm² → ADCL/L.a.^(DTH-) = 674 cells/mm², thus revealing more significant expression ($P < 0.05$) in the BDCL and ADCL compared to that of LCL. These results strongly suggest that, although dDC is regarded as the main activator cell of innate and adaptive immune responses, the species-specific *Leishmania*-antigens within the subgenera *Viannia* and *Leishmania* are determinant for modulating the T-cell immune response-type; i.e., the role of dDC depends on the *Leishmania*-antigenic environment in which it is interacting.

DISCLOSURE Nothing to disclose.

PSI.133

***P. papatasi*: does it prefer it hot?**

R. M. Ali, N. F. Loutfy and O. M. Awad

Tropical Health Department, High Institute of Public Health, Alexandria University, Alexandria, Egypt

A longitudinal entomological survey was carried out in four demographically different provinces at West of Alexandria governorate, Egypt from May to November 2010. Standardized sampling with oiled paper 'sticky traps' was employed during the breeding season to determine monthly trends in species composition, density and sex ratio. Temperature and relative humidity were recorded by manual thermo-hygrometer once per month in each province, during application of sticky traps. *Plebotomus papatasi* was the only anthropophilic species found. One hundred and 43 *P. papatasi* were collected; the highest prevalence was 44.8% in Al-Hawareya, followed by 29.4% in Al Agamy then 25.8% in old King Mariout while Marakya was free of sandflies, with male to female sex ratio 1:1.6 and two peaks of abundance in both July and September. Of the collected sandflies, 51.7% were from interior traps while 48.3% were from exterior traps. Adult sandflies showed increased activity during months of high humidity and relatively high temperature; the highest number of sandflies was recorded in both July and September at a temperature of 29–30°C and RH ranging from 60% to 73%, while the lowest monthly abundance of sandfly was in November at a temperature of 23–25°C and RH ranging from 55% to 60%. The monthly population densities of sandflies in west Alexandria were calculated; the average internal density was highest at 11% in July and lowest at 2% in November. The average external density was highest at 9% in July and lowest at 2% in October. The number of sandflies per trap was greatest (10) in July and lowest (2.75) in November; and the number of sandflies per square meter was highest with 83.3 in July and lowest with 22.9 in November.

KEYWORDS *P. papatasi*, Sticky traps, Internal and external densities, Temperature and Humidity.

DISCLOSURE Nothing to disclose.

PSI.134

Arginase activity in lesions of acute and chronic cases of cutaneous leishmaniasis due to *Leishmania tropica* and *Leishmania major*

P. Sadeghipour¹, H. Mortazavi², Y. Taslimi³, S. Habibzadeh³, F. Zahedifard³ and S. Rafati³

¹Iran University of Medical Sciences, Tehran, Iran; ²Department of Dermatology, Razi Hospital, Tehran University of Medical Sciences, Tehran, Iran; ³Pasteur Institute of Iran, Tehran, Iran

INTRODUCTION *Leishmania* (L) species are human pathogens that infect more than 12 million people worldwide. The disease can present with a wide range of clinical syndromes that may be cutaneous or visceral. Cutaneous leishmaniasis (CL) is one of the most important vector-borne disease in Iran and is highly endemic. CL in Iran is caused by *L. major* and *L. tropica*. Activation of macrophages is an important step for killing of intracellular pathogens and they produced two key enzymes that regulate the killing ability of macrophages, inducible nitric oxide synthase (iNOS) and arginase.

METHODS AND MATERIALS In the present study, we evaluated the arginase activity in the lesion, PBMC, PMN and sera of 32 cases of acute (<3 years), 11 cases of chronic CL (more than 3 years) and 11 cases of healthy controls. All CL samples were first diagnosed by Nested PCR and determined the causing *Leishmania* strain.

RESULTS The arginase activity in the acute lesion of CL samples was higher than chronic samples and significantly higher than healthy control. There are no significant differences in arginase activity of the lesion between *L. tropica* and *L. major* as causing agent. There are no significant differences between the numbers of lesions. The assessed arginase activity levels in PBMC and sera of both acute and chronic patients were not statistically increased and no differences with healthy controls. In contrast, PMN of both acute and chronic cases showed higher levels of arginase activity in comparing to PBMC and sera. **CONCLUSIONS** These results suggest that increased arginase expression in the lesion might contribute to persistent disease in patients presenting with cutaneous leishmaniasis. There is a hope by therapeutic intervention through regulating the arginase activity might be useful in the treatment of cutaneous leishmaniasis.

DISCLOSURE Nothing to disclose.

PSI.135

Proteome analysis reveals expression profile differences in elongation factors and the trypanothione reductase – peroxidase system between *Crithidia fasciculata* and *Leishmania infantum*

A. M. Alonso, P. J. Alcolea, F. García-Tabares and V. Larraga

Centro de Investigaciones Biológicas (CSIC), Madrid, Spain

Differences species of culicids are hosts of the monogenetic trypanosomatid parasite *Crithidia fasciculata*. They are non-pathogenic to mammals and comparison with evolutionary close species of trypanosomatids that develop digenetic life cycles and cause chronic severe sickness to millions of people worldwide is of outstanding interest. First, the growth kinetics is slightly faster

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in *C. fasciculata* than in *Leishmania* spp. Second, as *L. major* and *L. infantum* promastigotes are able to agglutinate with peanut lectin (PNA) and non-agglutinating parasites are more infective, the PNA agglutination properties were evaluated in *C. fasciculata*, what revealed that choanomastigotes of *C. fasciculata* are able to agglutinate with PNA and a non-agglutinating subpopulation can also be isolated. Consequently, the behavior in the presence of the lectin is similar. Finally, proteome analysis has revealed substantial differences in abundance of proteins involved in catabolism, redox homeostasis, intracellular signalling, and gene expression regulation. Logarithmic phase choanomastigotes of *C. fasciculata* over-express CACK, enzymes involved in redox homeostasis (TDR1, TryP, catalase and Fe-SOD), the translation factors eIF5a, EF1 β and EF2 and most of the glycolytic enzymes catalyzing irreversible reactions and the enzymes of the non-oxidative phase of the pentose-phosphate pathway. The abundance of the translation factors (EF1 α instead of EF1 β) and of the enzymes involved in redox homeostasis (TryR instead of TDR1) increases again in the PNA⁻ subpopulation, as a difference with *L. infantum*. These changes in abundance may have a role in growth in the nutrient rich environment at the logarithmic phase and a role in differentiation in the minor PNA⁻ subpopulation within the population in stationary phase.

DISCLOSURE Nothing to disclose.

PS1.136

Spatial analysis of malaria distribution in the Union of Comoros

A. Attoumane¹, R. Silai², A. Bacar², C. Révillon¹, E. Cardinale³, G. Pennober¹ and V. Herbreteau¹

¹UMR ESPACE-DEV (IRD, UM2, UR, UAG), Saint-Pierre, Réunion; ²Programme Nationale de Lutte Contre le Paludisme, Ministry of Public Health, Moroni, Comoros; ³CIRAD, UMR 15 CMAEE, Sainte Clotilde, Réunion

BACKGROUND Malaria remains endemic in Comoros. In 2006, malaria was the leading cause of mortality, morbidity and consultation in hospitals. The Government of the Union of the Comoros is committed in the fight against malaria through the establishment of a National Strategic Plan in 2007 that was later updated for the period 2012–2016. The results of these efforts show that the disease is in a pre-elimination phase. Despite a clear decline of malaria several aspects of its epidemiology should be clarified including the identification of endemic areas. **METHODS** Monthly cases, as reported by the 'Programme National de lutte Contre le paludisme' (PNLP) from 2010 to 2014, were geo-referenced in each island at the sanitary district level. The incidence of malaria by district was calculated using population data from the National Census. We completed the spatial database with data on environmental and social factors including meteorology, physical geography, land use (analyzed by remote sensing of SPOT 5 satellite images), population characteristics, and health care facilities. We performed statistical analyzes to show the relationships between the variables and the prevalence of malaria.

RESULTS The mapping of malaria incidence between 2010 and 2014 shows its heterogeneity among the 17 sanitary districts. Five districts (Hambou, Centre, Fomboni, Mutsamudu and Pomoni) reveal a high endemicity. Also we have highlighted the spatial relationships between malaria incidences and environmental and socio-demographic variables.

CONCLUSION This work is the first spatial analysis of the epidemiology of malaria in Comoros. It contributes to a better

understanding of the spatial dynamics of malaria to help the Ministry of Health to eradicate malaria by 2016.

KEYWORDS malaria; incidence; spatial analysis; GIS; Union of Comoros.

DISCLOSURE Nothing to disclose.

PS1.137

Systematized review on spatial analysis of environmental risk factors of malaria transmission

T. Canelas, H. Ribeiro and C. Castillo-Salgado

School of Public Health at University of Sao Paulo, Sao Paulo, Brazil

Malaria is still the major parasitic disease in the world, with approximately 600 000 deaths in 2013. Environmental risk factors of malaria have been widely studied, however, there are discrepancies on the results about their influence on malaria transmission. Recently, manuscripts have been published about spatial analysis of environmental risk factors of malaria, in order to explain why malaria varies from place to place. Our primary objective was to identify the environmental variables most used in the spatial analysis of risk factors of malaria. The secondary objective was to identify geo-analytic methods and techniques, as well as geo-analytic statistics commonly related to environmental risk factors and malaria. To assess the current state of knowledge, we conducted a systematized review of articles published from January 2004 to March 2015, within Web of Science, Pubmed and Scielo databases. Initially 676 articles were found in these databases, after inclusion and exclusion criteria, were selected 41 manuscripts. Among these selected studies, precipitation, vegetation and temperature were the most frequent variables related to malaria, among others. As for geo-analytic methods, Bayesian geostatistical models were the most applied. On the other hand, Kriging interpolations, as well as Kulldorff's spatial scan, were the techniques more widely used. The main objective of many studies was to use these methods and techniques to create risk maps, showing their importance. In recent years, spatial analysis performed with satellite images and geo-referenced data are increasing in relevance due to the use of remote sensing and Geographic Information System (GIS). The combination of these new technologies identifies more accurately environmental risk factors, and the use of Bayesian geostatistical models allows a wide diffusion of malaria risk maps. It is known that precipitation, temperature and vegetation play a critical role in malaria transmission; however, other environmental risk factors have also been identified. Risk maps have a tremendous potential to enhance the effectiveness of malaria-control programs.

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PS1.138

Land use, an environmental risk factor for very high malaria transmission

A. D. M. Sovi and M. C. Akogbéto

Centre de Recherche Entomologique de Cotonou, Cotonou, Benin

INTRODUCTION The goal of the study was to investigate if local agricultural practices have an impact on malaria transmission in four villages located in the same geographical area within a radius of 15 kilometers in southern Benin. Among