PP-002-57 Relevance of genotype I in congenital toxoplasmosis in Brazil: Analysis of *Toxoplasma gondii* surface antigen 2 gene (SAG2)

R. S. Vaz[1], V. Thomaz-Soccol[2]. [1]*Faculdades Pequeno Principe, Curitiba-Parana, Brazil,* [2]*Universidade Federal do Parana, Curitiba-Parana, Brazil*

Toxoplasmosis is one of the most disseminated infections throughout the world, and generally asymptomatic in immunocompetent individuals, except in pregnant women, and depending of the pregnancy trimester, parasitic burden and *T. gondii* strain, can lead to severe sequelae to the fetus. Early antenatal diagnosis is of outmost importance in order to establish antiparasitic therapy to avoid and minimize parasitemia and transplacental infection. In Europe, only a few clonal genotypes (I, II and III) seem to be responsible for the majority of toxoplasma infections. Surface antigen 2 gene (SAG2) has been used for genotyping *T. gondii* isolates in amniotic fluid. The analysis of this locus shows that in Europe an many Anglophonic countries, human congenital toxoplasmosis isolates are mainly type II, whereas *T. gondii* isolated from domestic and wild animals are both type II and III. Since immune response depends on specific genotype, it seems relevant to characterize parasites producing congenital toxoplasmosis in different geographical areas. The majority of information about *T. gondii* genotypes prevalence in Brazil are mostly related to domestic animals. This is the first report of genetic characterization of *T. gondii* isolates from clinical samples from pregnant women and neonates in Southern Brazil. All the samples analyzed are related to SAG2 type I isolates, and differ from classic SAG2 type I by genetic polymorphisms. This study demonstrates the very few available information on *T. gondii* in Brazil, and indicates that SAG2 type I, rather than II, parasites are a frequent cause of congenital toxoplasmosis.

PP-002-58 Molecular detection of *Leishmania* antigen within natural infected sand flies collected in Iran

H. Nekouie, M. Razavi. *Pasteur, Tehran, Islamic Republic of Iran*

The surveillance of prevalent *Leishmania* and sand fly species in endemic areas is important for prediction of the risk and expansion of leishmaniasis. In this study, we developed a semi nested PCR assay for detection of *Leishmania* minicircle DNA within individual natural infected sand flies and compared with culture and Dot blot immunoassay methods. Cutaneous *leishmaniasis* is endemic in parts of Iran. Natural infections of *Phlebotomus* species with *Leishmania* parasites in Abardej one of endemic areas were analyzed. A total of 4379 *Phlebotomus papatasi* were captured during summer 2008 and analyzed. One hundred and forty four blood fed females *Phlebotomus papatasi* were examined by PCR, Culture and Dotblot for detection *leishmania* antigen. It was found that 41.7%, 45.8% and 46.52% were positive by Culture, Dot blot and PCR respectively. The infectivity of *P. papatasi* with *Leishmania* was consistent with the infection rates reported from other areas of the world.

PP-002-59 Strain-specific and strain-transcending immune responses against *Plasmodium vivax* Merozoite Surface Protein-1p42 in Sri Lanka

S. Dias, T. Wickramarachchi, P. V. Udagama-Randeniya. *Department of Zoology, Faculty of Science, University of Colombo, Colombo 3, Sri Lanka*

Diversity in the surface antigens of malaria parasites is an immune evasion mechanism that leads to 'strain-specific' protective immunity, that hinders vaccine development. Amino acid sequences of P. vivax MSP-1p42 in 72 Sri Lankan parasite isolates were aligned with the homologous host antibody (IgM + IgG) responses, assayed against recombinant proteins p42 and p19 representing the Belem strain by ELISA.

Two clear groups of anti-p42 antibody responders were observed to PvMSP-1p42 sequence homology of 99.7-96.7% and 93.8-91.4% compared with the Belem strain, where the two groups manifested 1-11 and 21-29, amino acid substitutions, respectively. A majority of individuals (68%) assembled in the latter group. Anti-p42 antibody prevalence of a 100%, evident to the 99.4-96.7% homology group of parasite isolates may suggest strain-specific immune responses. Of the amino acid sequences of the other homology (93.8-91.4%) group, that those with 98.5% and 99.1% homology to the Salvador I strain, and those with 93.8- 91.7% homology to the Belem strain both recording a 100% anti-p42 antibody prevalence, may imply strain-transcending (cross reactive) immune responses.

Though, all 72 parasite amino acid sequences were identical to the p19 recombinant protein, only 64.7% individuals screened positive for anti-p19 antibodies. The 35.3% that did not respond to p19 may reflect other genetic factors of the host, such as HLA polymorphism of individuals, immunological tolerance and immunosupression/ immunodepression.

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PP-002-60 Serum insulin-like growth factor-I [illegible] evolution of *Leishmania (L.) chagasi* infection

H. Goto[1], C. M. V. Vendrame[2], B. L. Lima[3], S. M. B. [illegible]
de Medicina Tropical de Sao Paulo, Universidade de [illegible] Paulo, Brazil, [2]*Instituto de Medicina Tropical de Sao [illegible] de São Paulo, Sao Paulo, Brazil,* [3]*Dep. Bioquimica, [illegible] do Rio Grande do Norte, Natal, Brazil*

In endemic areas for visceral leishmaniasis (VL), [illegible] *chagasi*-infected individuals progresses to disease [illegible] known. We have shown that insulin-like growth factor-I [illegible] the development of cutaneous leishmaniasis lesion in [illegible] 95:13211,1998) and increases arginase activity in *Leish* SJI, 66:287,2007). To address its role in human leish[illegible] IGF-I and its binding protein IGFBP-3 serum concentration[illegible] nescent assay in individuals from endemic area in [illegible] (N = 19) and cured (N = 31) visceral leishmaniasis patients [illegible] DTH positive (N = 39) and DTH negative (N = 50) [illegible] different age range between groups, data were analyzed [illegible] to median reference value of the corresponding age. [illegible] cantly lower in active VL (0.41 + 0,26, mean + standard [illegible] pared with cured VL (0.92 + 0.59), DTH positive (0.89 + 0,47) negative (0.89 + 0,47) individuals. IGFBP-3 index was [illegible] (0.72 + 0.42) than in DTH negative (1.07 + 0.36) individuals. IGFBP-3 levels were positively correlated to parameters [illegible] globin and albumin serum levels. Since interferon gamma [illegible] IGF-I production, IGF-I level may reflect activation status [illegible] with interferon gamma been highly produced in lymphocytes [illegible]

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PP-002-61 Differences in insulin-like growth [illegible] (IGF-I)-induced and constitutive arginase activity [illegible] *Leishmania braziliensis* may relate to diverse [illegible] tegumentary leishmaniasis

C. M. V. Vendrame[1,2], L. D. Souza[3], K. Salgado[1], E. M. Carvalho[1], H. Goto[3]. [1]*Universidade Federal [illegible] Brazil,* [2]*Instituto de Medicina Tropical de São Paulo, [illegible]* [3]*Instituto de Medicina Tropical de São Paulo, São [illegible]*

Introduction: In Brazil, American tegumentary leishmaniasis [illegible] caused by *Leishmania (Viannia) braziliensis* and cutaneous [illegible] (ML) and disseminated (DL) forms of the disease are [illegible] pathogenic processes are poorly understood. IGF-I [illegible] and is present in the skin and inside macrophages. [illegible] exacerbates the lesion development in mouse cutaneous [illegible] et al PNAS 95:13211,1998) and increases arginase activity [illegible] *L. amazonensis* strain (Vendrame et al, SJI, 66:287,2007).

Objectives: Since arginase activity has been related to [illegible] ment, we studied constitutive and IGF-I induced [illegible] *L. braziliensis* isolated from CL, ML or DL patients from [illegible]

Methods and Results: Stationay phase *L. braziliensis* [illegible] from CL, ML or DL patients were cultured with or without [illegible] studied proliferation index and arginase activity [illegible] observed that isolates from ML presented higher basal [illegible] (mean ± SD = 30,9 ± 9,7 mU arginase/10^7 parasites) [illegible] clinical forms of ATL (mean ± SD = 9,3 ± 0,8). Upon IGF-I [illegible] sented different behavior and the isolates from DL (DL [illegible] reached the arginase activity (mean ± SD = 28 ± 15) [illegible] from ML.

Conclusion: These results suggest that differences [illegible] influence disease outcome with high arginase activity [illegible] evolution to mucosal form in patients with *L. braziliensis*.

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PP-002-62 Immune response to *Plasmodium* [illegible] study in the Central China

K. Jangpatarapongsa[1,2], H. Xia[3,4], Q. Fang[3,4], J. Sattabongkot[5], L. Cui[7], B. Li[8], R. Udomsangpetch[9,2]. [1]*Department of Microbiology, Faculty of Medical Technology, Mahidol University, Bangkok, Thailand,* [2]*Center of Excellence for Vector Diseases, Faculty of Science, Mahidol University,* [3]*Department of Parasitology, Bengbu Medical College,* [4]*Anhui Key Laboratory of Infection and Immunity, Bengbu College, Anhui, China,* [5]*Department of Entomology, Military Component, Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand,* [6]*Jiangsu Institute of Parasitic Diseases, China,* [7]*Department of Entomology, The Pennsylvania State University, State College, PA, United States,* [8]*Department of Pathology, Medical School, Anhui, China,* [9]*Department of Pathobiology, Science, Mahidol University, Bangkok, Thailand*

P. vivax infection possesses a characteristic of relapse [illegible] re-infection by previously hidden parasites in the host [illegible] can lead to activation of memory T cells pool which may [illegible]