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ESTUDO DA OCORRÊNCIA DE FILARIOSE BANCROFTIANA NO MUNICÍPIO DE GUAJARÁ MIRIM, RONDÔNIA, BRASIL.

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Introdução: Guajará-Mirim (RO), nunca constou como área de ocorrência de transmissão ativa de filariose bancroftiana no Brasil, ao contrário de outras cidades amazônicas como Manaus e Belém que já foram focos de transmissão. O único estudo relatado sobre a prevalência de filariose bancroftiana em Rondônia na região de Guajará-Mirim, data de 1953, por RACHOU, sendo que o único caso encontrado era alóctone. Objetivos: a-) verificar a ocorrência de filariose bancroftiana em Guajará Mirim, b-) determinar a infecção natural de mosquitos da espécie Culex quinquefasciatus por W. bancrofti em Guajará Mirim-RO, utilizando a Reação em Cadeia da Polimerase (PCR) Materiais e Métodos: a-) em humanos: pesquisa hemoscópica pelo método da gota espessa, na população de área de risco da cidade de Guajará Mirim, realizadas das 22 às 01 h. b-) em mosquitos: captura de mosquitos por xenomonitoramento nas áreas de risco das 07 às 10 horas e determinação da infecção dos mosquitos por W. bancrofti pela técnica da PCR. **Resultados:** até a presente data foram realizadas pesquisas hemoscópicas em 169 pacientes no Bairro Triângulo (de um total de 320 pessoas residentes), não sendo encontrado paciente portador de filariose. Na pesquisa de vetores foram capturados e já processados pelo método da PCR um total de 299 mosquitos fêmeas, sendo 281 Culex quinquefasciatus e todos negativos. **Conclusão:** pelos dados apresentados, podemos afirmar, até o momento, que não há a ocorrência de filariose bancroftiana na cidade de Guajará Mirim. O estudo deve-se ampliar para a abordagem de 1.000 habitantes, incluindo outros bairros e a captura de 3.000 mosquitos. Apoio: FAPESP 2007/00848-9

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ASEPTIC MENINGITIS ASSOCIATED WITH PARVOVIRUS B19 INFECTION IN PATIENTS FROM BELÉM, BRAZIL.

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Introduction: The parvovirus B19 was discovered in the England by Cossart et al. (1975). After its discovery, seroepidemiology studies were developed in temperate and tropical climate countries, showing its worldwide dispersion across age groups and in both sexes. Studies related to its pathogeny showed that the virus is associated with erythema infectiosum, an exanthematous disease that affects mainly children less than 10 years old. In addition, this virus causes transient aplastic crisis, particularly in patients suffering from hemolytic chronic anemia, arthropathy, hepatitis, meningitis, and meningoencephalitis in immunossupressed individuals and intrauterine infections leading to hydrops fetalis and even fetal death. In this study, the main objective was to assess the possible association between parvovirus B19 infections and aseptic meningitis. Material and methods: The clinical samples (LCR) were collected in the Health Basic Unit of Pedreira district, Secretary of Public Health, Para State. The samples were examined by ELISA to the capture of detect IgM and IgG antibodies. With regards to the molecular biology, was utilized the polymerase chain reaction (PCR)/nested PCR to detect parvovirus B19 DNA. Results: A total of 144 clinical samples were examined with 49.3% (71/144) of samples belonging to patients with symptoms suggestive of aseptic meningitis, including fever, headache, vomits, neck stiffness. There were 73 (50.7%) out of 144 samples which belonged to the control group, including patients with symptoms other than those typical of aseptic meningitis. The rate of parvovirus B19 recent infection (antibody IgM positive and/or DNA detection) was of 11.3% (8/71) among patients with symptoms and signs suggestive of aseptic meningitis and of 1.4% (1/73) those patients assigned to the control-group. There was a significant difference between these two groups: 11.3% (8/71) and 1.4% (1/73) [P=0.01] for patients with aseptic meningitis and controls, respectively. Other viruses, bacteria, parasite and fungi were ruled out as potential etiological agents. Conclusion: Although preliminary, our data strongly suggest that parvovirus B19 may play a role as a cause of aseptic meningitis in the Amazon region and serve as an alert for health professionals.

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THE "PRESSURE PAN" EVOLUTION OF HUMAN ERYTHROVIRUS B19 IN THE AMAZON, BRAZIL.

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Introduction: The erythrovirus B19, a human-associated member of the family Parvoviridae, is the only known human pathogenic erythrovirus and has been detected globally in human populations. This virus causes a wide spectrum of clinical conditions, mainly erythema infectious in children and arthropathy/arthralgia in adults. **Objective**: To understand the evolutionary dynamics of human parvovirus B19, analyzing VP1 and VP2 gene sequences of B19 sampled from Belém (Amazon), the city of São Paulo, Brazil and globally. **Material and Methods**: Viral DNA was extracted from serum samples by the phenol-chloroform method. The PCR and seminested PCR were performed and positive samples were sequenced by the dideoxy chain termination method. To compare B19 from different regions we inferred maximum likelihood phylogenetic trees using PAUP, using the best-fit evolutionary model, as determined by Modeltest 3.7. To determine the selective pressures acting on B19 virus we performed the Tajima\'s D statistic and rates of nonsynonymous (dN) and synonymous (dS) substitutions per site (ratio dN/dS) using the MEGA v3.1 package. We also inferred site-specific dN and dS using both the CODEML and HyPhy programs. To estimate rates of evolutionary change of B19 in both Brazilian populations we employed the Bayesian-Markov Chain-Monte Carlo (MCMC) method available in the BEAST v1.3 package. **Results**: Our results support the hypothesis of multiple and independent introductions of genotype 1 lineages into the Amazon region. The analysis revealed strikingly different patterns of evolutionary change for those viral lineages introduced in Belém, which exhibited a higher rate of nonsynonymous substitutions compared to those viruses sampled from other locations. We propose that such a difference is due to the high prevalence of B19 in Belém (up to 85%) compared to other locations (prevalences of approximately 50%), which imposes a more intense selection pressure. **Conclusion**: Hence, those B19 lineages introduced in Belém experienced an elevated rate of amino acid change, driven by positive selection, in order to generate serial re-infections in a small web of transmission, which can be thought of as an evolutionary "pressure pan".

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MOLECULAR CHARACTERIZATION OF HUMAN ERYTHROVIRUS B19 STRAINS OBTAINED FROM PATIENTS WITH SEVERAL CLINICAL PRESENTATIONS IN THE AMAZON REGION OF BRAZIL.

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Introdution: Human erythrovirus B19, endemic in the Amazon region since 1990, is associated with a wide spectrum of clinical presentations. **Objectives**: To assess the prevalence of erythrovirus B19 infection and the relative frequency of erythrovirus B19 genotypes in patients in the Amazon region with various clinical presentations. **Material and Methods**: A total of 487 clinical samples obtained from patients with symptoms suggestive of erythrovirus infection were tested using specific IgM and IgG antibody assays (ELISA) and PCR for viral DNA detection. Partial VP1 and VP2 regions were sequenced and genotyped by phylogenetic reconstruction. **Results**: B19 DNA was detected in 117 (24%) of 487 samples. Of these, 106 (91%) isolates were genotype 1 and 11 (9%) were genotype 3. No genotype 2 was found. Genotype 1 had three clusters (A1, A2 and B) and all genotype 3 sequences were subtype 3b. All patients with hematological disorders within cluster B of genotype 1 were infected by the same B19 lineage, suggesting that this lineage of B19 may have been transmitted via transfusion of blood products. **Conclusion**: We reported two genotypes, 1 and 3b, with three genotype 1 clusters co-circulating in the Amazon region during the past 10 years.