company provides ~5000 travel consultations per year and the tools are saving ~2500 working hours/year, both health professionals and travelers. In 2023 there were 61k travelers, 17% going to risk locations, and 2% needed additional medical assistance during travel.

Conclusion: Technology for measuring disease risk is relevant to meet demands of an outbreak. Technologies available on the market that display the risks, have been demonstrated to be effective to help health professionals but may need business customization to be user centric. To achieve desired results on customer journey it is recommended to evaluate interface and define indicators to ensure you promote and protect worker health.

Keywords: Travel health, Infectious disease, Technology.
Conflicts of interest: There was no conflicts of interest.
Ethics and financing: No financial support.

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DOENÇAS CAUSADAS POR PROTOZOÁRIOS E HELMINTOS

CAN THE RS2234246 POLYMORPHISM IN THE TREM-1 GENE BE RELATED TO THE CLINICAL COURSE IN INDIVIDUALS INFECTED WITH PLASMODIUM VIVAX IN AN ENDEMIC AREA OF THE BRAZILIAN AMAZON?

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Introduction: Plasmodium vivax is the most widely distributed species of malaria in the world. In Brazil, this parasite is responsible for around 90% of cases. Infections caused by P. vivax can generate a variety of symptoms, such as fever, chills, headache, nausea, vomiting and anemia. The immune response directly influences the individual's clinical evolution. The TREM-1 receptor is an important molecule that acts by recognizing the pathogen and amplifying inflammation. Polymorphisms in the gene encoding this protein have been linked to the severity of malaria.

Objective: We investigated the association between the SNP rs2234246 (C>T) in the TREM-1 gene and the development of nausea and vomiting in individuals infected with P. vivax in an area of the Brazilian Amazon.

Methodology: We analyzed 76 patients with a microscopic and molecular diagnosis of P. vivax and 114 controls from the municipality of Oiapoque in Amapá state, Brazil, on the border with French Guiana. The clinical signs of the individuals were assessed by a nurse. Genomic DNA was extracted from blood samples and the SNP rs2234246 was genotyped by qPCR. The occurrence of nausea and vomiting symptoms was adjusted for the SNP using Logistic Regression. Variables such as: occurrence of anemia, gender, age, length of residence in the study area, number of previous episodes of malaria and period of the last malaria were inserted as adjustment variables for the logistic regression. All analysis was carried out with a 5% significance level.

Results: Among the 76 patients, 44.7% reported experiencing nausea and vomiting. As for SNP rs2234246 genotyping, CC = 15, CT = 42 and TT = 19. In the association between the SNP and symptoms, it was observed that infected individuals with the TT mutant genotype for the TREM-1 rs2234246 C>T SNP were 90% less likely (OR = 0.1; 95% CI = 0.0 - 0.6; p = 0.013) to develop nausea and vomiting than wild-type CC individuals. The reduced risk of developing these symptoms may provide relevant insight into the human parasite-host relationship in the population studied, which may suggest a possible protective role for the homozygous mutant allele (TT). Case highlighting characteristics malaria vivax infection, necessitating close clinical and laboratory correlation.

Conclusion: Our results aim to help the global public develop a comprehensive understanding of malaria in Brazilian-French Guiana, thereby contributing to malaria control and elimination.

Keywords: Immunological Factors, Malaria, Polymorphism, Genetic, Signs and Symptoms.
Conflicts of interest: There was no conflicts of interest.
Ethics and financing: Declarations of interest: None.

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INTERVENÇÃO EDUCATIVA E AÇÕES EM SAÚDE PARA A PREVENÇÃO DAS PARASITOSES INTESTINAIS ENTRE CRIANÇAS CARENTES

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Introdução: As enteropatias parasitárias são doenças comuns em indivíduos de todo o mundo, mas principalmente aqueles expostos a condições de vida precárias e em vulnerabilidade social, sendo, portanto, mais prevalentes em países subdesenvolvidos, a exemplo do Brasil. Crianças em idade escolar estão entre as mais suscetíveis, já que possuem um sistema imune menos desenvolvido, uma higiene pessoal deficiente e o hábito de brincar em terra poluída. Logo, localidades com déficit de salubridade propagam a contaminação principalmente entre os menores. Dessa maneira, compreende-se a relevância desse tema. Posto isto, este projeto de intervenção teve como objetivos transmitir educação em saúde em relação às parasitoses intestinais nas crianças, analisar em laboratório os parasitológicos de fezes e verificar a prevalência das parasitoses, iniciar práticas educativas, prevenir e educar a comunidade.

Materiais e métodos: As práticas de educação em saúde foram realizadas com crianças de 2 a 14 anos de idade,

residentes da comunidade de baixa renda São João do Cazumbá em Feira de Santana - Bahia. Em suma, apresentou-se o projeto para a comunidade e foram recolhidas as assinaturas dos Termos de Assentimento do Menor e do Consentimento Livre e Esclarecido das famílias interessadas. Ainda foi realizado um questionário de dados de cada família, abrangendo: condições de moradia e saúde, ambiência residencial e contexto familiar. Após, foi armazenado em cooler as amostras de fezes entregues pelos pais e responsáveis. Por fim, utilizou-se recursos de um laboratório para análise dos parasitológicos de fezes e, com os resultados foi feito um levantamento das parasitoses mais prevalentes nessa comunidade infantil, para elaboração de panfletos educativos.

Resultados: Posterior a análise laboratorial, foi detectado, por ordem de mais prevalentes: Ascaris lumbricoides, Giardia lamblia, Trichuris trichiura, Entamoeba histolytica, Ancilostomídeos, Taenia sp. e Enterobius vermicularis. Com isso, estudantes de medicina elaboraram panfletos para promover uma conscientização dos habitantes dessa comunidade em relação a tais parasitoses. CONCLUSÃO Com a execução do projeto e após as análises laboratoriais, os panfletos elaborados foram de importância ímpar para a educação dessa parcela da população feirense, inclusive, porque foi realizado com olhar atencioso para os menores em idade escolar, possuindo grande interferência sobre o crescimento e estado nutricional desses.

Palavras-chave: Enteropatias Parasitárias, Pré-Escolar, Promoção da Saúde.

Conflitos de interesse: Não houve conflito de interesse.

Ética e financiamentos: Declarações de interesse: Nenhum.

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POLYMORPHISMS IN THE CYP-450 GENE AND MALARIA: A GENOTYPIC AND PHENOTYPIC RELATIONSHIP WITH THERAPEUTIC FAILURE

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Introduction: Therapeutic failure in patients with malaria can occur due to various factors and polymorphisms in enzymes of the Cytochrome P450 (CYP450) family, responsible for around 90% of the metabolization of chloroquine and primaquine, can generate individuals who are low, intermediate or fast metabolizers of antimalarial drugs.

Objective: We evaluated the relationship between these polymorphisms and the biometalization of antimalarial drugs worldwide through a systematic review using the PRISMA statement.

Methodology: The research question was structured in the PICO format (Population = people infected with Plasmodium vivax; Intervention = people without vivax malaria; Comparison = polymorphisms in the CPY450 gene; Outcome = biometabolization of antimalarial drugs is influenced by polymorphisms in the CYP450 gene). The investigation in the databases (Medline through Pubmed, Google scholar, Science direct and Scopus) was carried out by grouping descriptors (DECs/Mesh) with Boolean operators (AND/OR). Duplicate articles were excluded, as well as those with in vitro research, which did not meet the objective of the study and which, when applying the Joanna Briggs Institute questionnaire, had ≤ 50% "yes" answers.

Results: Of the 187,935 articles retrieved, only 12 were selected for this review, adding up to 2050 individuals. The majority (75%) of the articles reported an interaction between polymorphisms in the CYP2A6, CYP2D6, CYP2B6, CYP3A4 and CYP3A5 genes in individuals infected with Plasmodium falciparum and interference in drug metabolization. As for Plasmodium vivax (25%), the SNP in the CYP2D6 gene was the most frequently reported cause of therapeutic failure. As for the phenotype regarding biometabolization, 65% were normal, 25% low, 5% fast and 5% null metabolizers. Conclusions: It is important to develop measures aimed at profiling genetic biomarkers and their respective phenotypes in populations from endemic areas, in order to prevent relapses from P. vivax and treatment failure for both plasmodia; important for establishing malaria prevention and control measures.

Keywords: Molecular Epidemiology, Pharmacogenetics, Plasmodium, Public Health.

Conflicts of interest: There was no conflicts of interest.

Ethics and financing: Declarations of interest: None.

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WORLDWIDE GENETIC POLYMORPHISM OF CIRCUMSPOROZOITE PROTEIN IN PLASMODIUM VIVAX SEQUENCES: A SYSTEMATIC REVIEW

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The Circumsporozoite Protein of Plasmodium vivax (PvCSP) is an immunodominant antigen expressed on the surface of the sporozoite. PvCSP consists of a central repetitive region (CRR), capable of stimulating both T and B lymphocytes. The CRR is flanked by two non-repetitive regions, N-terminal (RI) and