

2387

**HLA FREQUENCIES AND DIFFERENTIAL REGIONAL INCIDENCE OF COVID-19 IN BRAZIL: A POPULATION STUDY BASED IN A LARGE BONE MARROW DONORS BANK DATASET**

CATEGORIA DO TRABALHO: PESQUISA

Juliano André Boquett, Fernanda Sales Luiz Vianna, Nelson Jurandi Rosa Fagundes, Lucas Schroeder, Márcia Helena Barbian, Marcelo Zagonel-oliveira, Tiago Finger Andreis, Luis Cristóvão de Moraes Sobrino Pôrto, José Artur Bogo Chies, Lavínia Schüller-faccini, Patricia Ashton-prolla, Clevia Rosset  
HOSPITAL DE CLÍNICAS DE PORTO ALEGRE  
UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL

Introduction: Coronavirus disease 2019 (COVID-19) rapidly spread all over the world causing high morbidity and mortality. Even though all Brazilian regions and states have reported a high number of cases, mortality rates varies among them. Environmental and genetic factors may influence the immune response towards SARS-CoV-2. The Brazilian population is highly heterogeneous, with different colonization and immigration histories in each region resulting in different genetic backgrounds, including a high variability in genes that influence in immune response. In this line, we tested if specific Human Leukocyte Antigen (HLA) haplotypes, which are responsible for antigen recognition, are associated with COVID-19 incidence and mortality in different Brazilian states. Methods: HLA data was obtained The Brazilian Voluntary Bone Marrow Donors Registry (REDOME) which harbors data more than four million individual donors all Brazilian states, and COVID-19 data was retrieved epidemiological bulletins issued by State Health Secretariats via the Ministry of Health of Brazil until November 2020. We tested the association between the most frequent HLA haplotypes in Brazil and COVID-19 incidence and mortality using Spearmans correlation analysis. The study was approved by the research ethics committee of Hospital de Clínicas de Porto Alegre (number 2020-0361). Results: No correlation between HLA haplotypes and COVID-19 rates was found when we analyzed data the 26 states and Federal District. Significant negative correlation (suggestive of protection) between COVID-19 mortality and haplotypes HLA-A01~B08~DRB103, HLA-A29~B44~DRB107 and HLA-A02~B44~DRB104 was found when analyzing data cities with at least 50 deaths registered in the entire country, but no differences between haplotypes frequencies were found among the Brazilian states. Conclusions: Our results do not support an association of specific HLA haplotypes with an increased risk of contracting SARS-CoV-2 or dying COVID-19 in different states Brazil. Nevertheless, using bone marrow donor registries for testing for associations between HLA variation and COVID-19 outcomes may represent an additional tool for health policymakers in the fight against COVID-19.

2403

**COVID-19 NA ERA PRÉ-VACINAL EM PACIENTES COM DOENÇAS RARAS DA AMÉRICA LATINA: RELATO DE 75 CASOS**

CATEGORIA DO TRABALHO: PESQUISA

Ana Paula Pereira Scholz de Magalhães, Dévora Natalia Randon, Thiago Oliveira Silva, Carolina Fischinger Moura de Souza, Lília Farret Refosco, Fabiano de Oliveira Poswar, Lavínia Schüller-faccini, Natalya Gonçalves Pereira, Dafne Dain Gandelman Horovitz, Maria Denise Fernandes Carvalho de Andrade, Louise Lapagesse de Camargo Pinto, Emerson de Santana Santos, Raquel Tavares Boy da Silva, Ida Vanessa Doederlein Schwartz  
UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL  
HOSPITAL DE CLÍNICAS DE PORTO ALEGRE

Introdução: Pouco se sabe sobre o impacto direto e indireto da infecção por SARS-CoV-2 em pacientes com doenças raras. A pesar de serem individualmente raras, estas condições afetam em conjunto até 10% da população e podem representar um grupo de risco especial para o desenvolvimento de complicações graves. Objetivo: Avaliar os determinantes e o impacto da COVID-19 em uma amostra de pacientes latino-americanos com doenças raras. Métodos: Estudo observacional, transversal, com estratégia de amostragem por conveniência. Os dados foram coletados a través de formulário divulgado entre médicos especialistas da América Latina. Setenta e cinco indivíduos de diferentes regiões do Brasil (sul n=33, sudeste n=22, nordeste n=10, norte n=5, e centro-oeste n=4) e da Argentina (n=1) foram identificados como tendo COVID-19 (femininos = 48.6%). A idade média no momento da inclusão foi de 26,7±17,7 anos (6 meses-64 anos). CAAE 30767320.7.00005327 Resultados: Quarenta diferentes doenças raras foram relatadas, 36 (90,0%) de origem genética, sendo 23 (63,9%) erros inatos do metabolismo. Nenhum paciente havia sido vacinado contra COVID-19 antes de contrair a