afirmam também que a correta aplicação da profilaxia com uso do anti-D é resolutiva e com potencial para reduzir os casos de aloimunização. **Conclusão:** O correto seguimento dos protocolos de exames de pré-natal, aliados ao atendimento e reconhecimento da DHPN nas maternidades ou serviços de parto auxiliam a prevenção e manejo da afecção. A redução dos números de internamento, ano após ano, apontam para melhorias na condução do pré-natal, mas ainda há muito a ser feito para que fetos deixem de padecer desse problema, que, nos casos mais graves, podem evoluir para óbito.

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COVID-19 - HEMATOLOGIA GERAL

FREQUENCY OF POLYMORPHISMS IN THE HFE GENE (H63D, C282Y E S65C) IN PATIENTS WITH COVID-19

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Objectives: Coronavirus disease 2019 (COVID-19) is caused by a novel beta-coronavirus (SARS-CoV-2) and is characterized by a diverse clinical severity. The infection process of SARS-CoV-2 leads to a substantial increase in pro-inflammatory cytokines, contributing to damage of lung epithelial cells. Hereditary hemochromatosis (HH) is a disease characterized by excessive iron in the blood, and individuals with polymorphisms in the *HFE* gene (*H63D*, *C282Y* e *S65C*) have alterations in iron metabolism, which further exacerbate the inflammatory process. This study aims to investigate the association between *HFE* gene inheritance and the severity of the disease in patients with COVID-19. **Methodology:** Blood samples were collected from 87 adults diagnosed with COVID-19 and categorized based on disease severity, mild, moderate and severe. Molecular analysis was conducted to confirm the presence of mutations in the *HFE* gene (*H63D*, *C282Y* e *S65C*) using the PCR-RFLP method. Statistical analyses were performed using IBM SPSS Statistics 20 software, with a significance level set at 0.05. Associations between COVID-19 severity and biological sex were assessed using Fisher's exact test. The associations between homozygous wild-type, heterozygous, and homozygous mutant genotypes for each polymorphism were tested using the Chi-square test. To investigate the relationship between sex and *HFE* gene mutations with the severity of COVID-19, ANOVA was performed. **Results:** The group comprised 53 women (60.9%) and 34 men (39.1%) with ages ranging from 18 to 61 years, and a mean and standard deviation of 30.4 ±12.96. Among these, the majority of mild COVID-19 cases were observed in females (49.4%), while most moderate cases were found in males. Severe cases were exclusively identified in males, indicating a significant association between COVID-19 severity and gender ($p < 0.05$). A total of 522 alleles were evaluated for the *HFE* gene mutations. For the *H63D* mutation, were found 22 wild-type homozygous genotypes, 64 heterozygous and 1 mutant homozygous. For the *C282Y*, 78 wild-type homozygous, 7 heterozygous and 2 mutant homozygotes were found. For the *S65C*, 73 wild-type homozygous, 13 heterozygous and 1 mutant homozygous were found. Statistically significant differences were observed between genotypes for polymorphisms ($p < 0.05$). The covariate gender and the variables severity of the disease and presence or absence of *HFE* gene polymorphisms did not show significant differences. However, when comparing the severity of COVID with the *H63D* polymorphism, a statistically significant association was observed ($p < 0.01$). **Discussion:** The higher occurrence of moderate and severe COVID cases in males suggests a more severe disease course in this population group. The prevalence of the *H63D* mutation was more frequent in this group and associated with COVID-19 severity. The relatively low incidence of homozygous mutant alleles can be explained by the admixture of the Brazilian population. The *C282Y* and *S65C* genotypes exhibit low expressiveness, which is insufficient to establish a significant relationship. **Conclusion:** The *H63D* genotype exhibits a higher frequency of heterozygotes and is associated with increased clinical severity of COVID-19, especially in males. Further investigations are warranted to characterize the *HFE* gene and develop strategies for managing exacerbated COVID-19 symptoms.

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MARCADORES INFLAMATÓRIOS ASSOCIADOS A SEQUELAS NA SÍNDROME PÓS-COVID-19 AGUDA: UMA REVISÃO DE SISTEMÁTICA

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Introdução: A Síndrome Pós-COVID-19 Aguda (PASC) está relacionada a sintomas que persistem por mais de 12 semanas. A fisiopatologia da PASC ainda é pouco elucidada em relação a marcadores hematológicos e inflamatórios. **Objetivos:** Avaliar pacientes que tiveram sequelas e correlacionar com marcadores inflamatórios, alterações hematológicas meses após a resolução da doença aguda do COVID-19 por meio de uma revisão sistemática. **Material e métodos:** Foram selecionados ensaios clínicos e estudos observacionais publicados em inglês, entre 2021 e 2023, tendo como referência as bases de dados MedLine, Web of Science, Embase e Scopus, com as seguintes palavras chaves e suas respectivas variações no DeCS/MeSH: *long-COVID; Post-Acute Sequelae of COVID; biomarkers; inflammatory, complications*. Foram incluídos estudos que continham exames laboratoriais e avaliaram pacientes que se recuperaram da COVID-19 com no mínimo três meses após a fase aguda. Foram encontrados 316 estudos e após aplicação dos critérios de inclusão e exclusão somente quatro foram selecionados. **Resultados:** Foram avaliados 252 pacientes. O D-dímero pode prever sequelas pulmonares ou associado a gravidade da doença ($p < 0,05$). Foram observados que a elevação de alguns biomarcadores durante a fase crítica