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POLIMORFISMO DE LOS GENES APO-A Y APO-B Y EL PERFIL LIPÍDICO DE PACIENTES CON COVID-19: UNA REVISIÓN INTEGRATIVA

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ABSTRACT

Objective: to analyze the influence of polymorphisms of APOA and APOB genes with the lipid profile of patients with COVID-19.

Method: the research was carried out in the databases Scholar Google, Biblioteca Virtual em Saúde - BVS, Portal de Periódicos CAPES, and PubMed, using the descriptors "Apo-B polymorphism AND SARS-Cov-2 AND COVID-19" and "Apo-A polymorphism AND Covid-19". We selected studies from 2020 that were compatible with the objective of the study.

Results: an association was found between the polymorphism of Apo A-1 -75G/A (rs670) and lower levels of triglycerides (TG) in patients with COVID-19, whereas the polymorphism of Apo B (rs693) was associated with reduced levels of TG only when and codominance with SNP -75G/A (rs670).

Conclusion: the polymorphisms of Apo A-1 and Apo B play a significant role in the prognosis and development of COVID-19, added to this is of paramount importance the investment in studies for so, the development of new therapeutic intervention strategies based on the patient's genetic profile, in order to optimize treatment and increase survival of individuals in a critical state.

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Keywords: Apolipoprotein B. Apolipoprotein A-1. Obesity. COVID-19. Genetic Polymorphism.

RESUMO
Objetivo: analisar a influência dos polimorfismos dos genes APOA e APOB com o perfil lipídico de pacientes com COVID-19.

Metodologia: realizou-se a pesquisa nas bases de dados Scholar Google, Biblioteca Virtual em Saúde – BVS, Portal de Periódicos CAPES, e PubMed, utilizando os descritores “Apo-B polymorphism AND SARS-Cov-2 AND COVID-19” e “Apo-A polymorphism AND Covid-19”. Foram selecionados estudos a partir de 2020 e que fossem compatíveis com o objetivo do estudo.

Resultados: foi encontrada a associação entre o polimorfismo da Apo A-1 -75G/A (rs670) e níveis mais reduzidos de triglicerídeos (TG) em pacientes com COVID-19, já o polimorfismo da Apo B (rs693) teve associação a redução dos níveis de TG apenas quando e codominância com o SNP -75G/A (rs670).

Conclusão: os polimorfismos da Apo A-1 e Apo B desempenham um papel significativo no prognóstico e desenvolvimento da COVID-19, somado a isso é de suma importância o investimento em estudos, para assim haver o desenvolvimento de novas estratégias terapêuticas de intervenção baseadas no perfil genético do paciente, a fim de otimizar o tratamento e aumentar a sobrevida de indivíduos em estado crítico.

Palavras-chave: Apolipoproteína B. Apolipoproteína A-1. Obesidade. COVID-19. Polimorfismo Genético.

RESUMEN
Objetivo: analizar la influencia de los polimorfismos de los genes APOA y APOB con el perfil lipídico de pacientes con COVID-19.

Método: se realizó la búsqueda en las bases de datos Scholar Google, Biblioteca Virtual en Salud - BVS, Portal de Periódicos CAPES, y PubMed, utilizando los descriptores "Apo-B polymorphism AND SARS-Cov-2 AND COVID-19" y "Apo-A polymorphism AND Covid-19". Se seleccionaron estudios a partir de 2020 que fueran compatibles con el objetivo del estudio.

Resultados: se encontró la asociación entre el polimorfismo de Apo A-1 -75G/A (rs670) y niveles más reducidos de triglicéridos (TG) en pacientes con COVID-19, ya que el polimorfismo de Apo B (rs693) tuvo asociación com la reducción de los niveles de TG solo cuando codominancia con el SNP -75G/A (rs670).

Conclusión: los polimorfismos de Apo A-1 y Apo B juegan un papel significativo en el pronóstico y desarrollo del COVID-19, sumado a esto es de suma importancia la inversión en estúdios, para así tener el desarrollo de nuevas estrategias terapéuticas de intervención basadas en el perfil genético del paciente, con el fin de optimizar el tratamiento y aumentar la supervivencia de los individuos en estado crítico.

Palabras clave: Apolipoproteína B. Apolipoproteína A-1. Obesidad. COVID-19. Polimorfismo Genético.

1 INTRODUCTION

COVID-19 is an infectious disease caused by the SARS-CoV-2 RNA virus (Costa *et al*., 2024), which first emerged in 2019 in Wuhan, China, and quickly spread, becoming a global pandemic (Galvão; Roncalli, 2020). Known to cause from asymptomatic patients to death, this disease was responsible for 714,379 deaths in Brazil until December 2024 in Brazil (Ministry of Health, 2024).

Considering that obesity promotes a chronic inflammatory state, in addition to endocrine and metabolic disruption, it is classified as one of the comorbidities that can increase the risk of severity in COVID-19 cases (Hutten *et al*., 2024). The study by Carra *et al.* (2024) evaluated the impact of obesity on the outcomes of patients hospitalized due to SARS-CoV-2, revealing that obesity is present in up to 30% of patients hospitalized with COVID-19 (Carra *et al*., 2024).

Among the pathophysiological mechanisms involved in severe cases, changes in lipid metabolism stand out, such as reduced levels of high-density cholesterol (HDL-c) and increased levels of total cholesterol (TC), triglycerides (TGs), and low-density cholesterol (LDL-c) (Makarova *et al.,* 2023). These changes are observed due to the alteration that the SARS-CoV-2 virus causes in the lipid metabolism of the host cell in order to ensure its replication (Makarova *et al.,* 2023).

Other relevant factors for the outcome of COVID-19 are apolipoproteins, which are proteins responsible for directing lipoproteins to target organs and tissues. They are essential for lipid metabolism, as they have 4 essential functions: they play a structural role in lipoprotein, act as ligands for lipoprotein receptors, guide the formation of lipoproteins, and participate in the process of activation and/or inhibition of enzymes (Feingold; Grunfeld, 2024).

The main apolipoproteins involved in changes in the lipid profile of patients with COVID-19 are Apo A-1 and Apo B (Costa *et al.,* 2024). Apo A-1 is the apolipoprotein constituent of HDL, it is responsible for helping HDL to develop its functions, such as reverse cholesterol transport (CRT), that is, the transport of excess cholesterol from peripheral tissues to the liver, one of its main activities (Lent-Schochet; Jialal, 2023).

Apo B can be divided into two variations: Apo B-48, constituent of the Chylomicrons (Lent-Schochet; Jialal, 2023); and Apo B-100, a constituent of very low-density lipoprotein (VLDL), intermediate-density lipoprotein (IDL), and LDL. Through the binding of Apo B-100, LDL is able to perform its function, characterized as a pro-atherogenic molecule (Costa *et al.,*

2024).

Once it has been identified that changes in the lipid profile of patients with COVID-19 influence their prognosis (Golin *et al.,* 2021), the importance of studying the genetic changes of the apolipoproteins involved in the patient's lipid profile, in this case Apo A-1 and Apo B, becomes evident.

Thus, the objective of this study was to analyze studies that address the influence of polymorphisms of *the APOA* and *APOB* genes on the lipid profile of patients with COVID-19. Specifically, it seeks to:

a) To analyze whether there are changes in the parameters of the lipid profile of patients with COVID-19 in the selected studies.
b) To verify whether there is an association between *Apo A-1* and *Apo-B polymorphisms* as a predictive factor of worse prognosis of patients with COVID-19 in the selected studies.

2 THEORETICAL FRAMEWORK

2.1 COVID-19: EPIDEMIOLOGY

COVID-19 is an infectious disease that is caused by SARS-CoV-2, a positive sense-positive single-stranded RNA virus (RNAfs+) (Costa *et al.,* 2024). It first emerged in Wuhan, China, in December 2019 and quickly spread around the world, becoming a pandemic and public health emergency (Galvão; Roncalli, 2020).

From the beginning, this disease was characterized by having heterogeneous clinical manifestations, ranging from asymptomatic individuals, with mild or moderate symptoms, to severe ones with risk of death (Costa *et al.,* 2024). Despite infecting people of different age groups, studies indicate that advanced age can be a risk factor and a worse prognosis for severe cases of COVID-19. One of the hypotheses is that older people tend to have more comorbidities, which predispose them to severe outcomes of the disease (Galvão; Roncalli, 2020).

SARS-CoV-2 belongs to the β-coronavirus family. Like it, there are other coronaviruses capable of infecting humans, as well as HCoV229E, HCoV-OC43, HCoV-NL63, HKU1, SARS-CoV, MERS-CoV (Costa *et al.,* 2024). Both SARS-CoV and SARS-CoV-2 have a relevant genetic proximity, sharing the same receptor for cell entry, angiotensin-converting enzyme 2 (ACE2) (Goyal *et al.,* 2022).

In Brazil, by the beginning of January 2025, 39,113,560 cases had been confirmed, and 714,535 deaths, with the Southeast region having the highest incidence, about 344,795 deaths (Ministry of Health, 2025).

2.2 OBESITY AS A RISK FACTOR FOR COVID-19

Obesity is a chronic disease that is defined as the excessive accumulation of fat that leads to damage to health. According to the World Health Organization (WHO), one in eight people in the world lives with obesity (Pan American Health Organization, 2024).

The pathophysiological mechanisms involved in the development of obesity are multifactorial, including genetic, hormonal, social, psychological, and other factors. Among its complications, it is worth highlighting insulin resistance and the activation of pro-inflammatory pathways, which makes obesity a risk factor for other clinical conditions, such as type 2 diabetes mellitus, cardiovascular diseases, hypertension, and dyslipidemias (Gallo *et al.,* 2024).

It is believed that obesity, as a disease that results in endocrine and metabolic disruption and has a chronic inflammatory state, can increase the risk of severity of COVID-19 cases (Hutten *et al.,* 2024). In fact, some studies point out that obesity is present in up to 30% of patients hospitalized with COVID-19 and that it could be associated with a worse prognosis, especially in younger patients (Carra *et al.*, 2024) (Hutten *et al.*, 2024).

2.3 APOLIPOPROTEINS

Apolipoproteins are essential proteins for lipid metabolism, they are responsible for directing lipoproteins to their target organs and tissues through plasma, in addition to participating in the process of activation or inhibition of enzymes (Feingold; Grunfeld, 2024).

The classification of lipoproteins is based on lipid content, density and type of apolipoprotein present, so it is verified that: Chylomicrons that carry triglycerides and cholesterol and have Apo B-48 as apolipoprotein, VLDL (very low-density lipoprotein) that carries triglycerides and cholesterol and have Apo B-100, IDL (intermediate-density lipoprotein) that carries triglycerides and cholesterol and have Apo B-100, LDL (low-density lipoprotein) that carries cholesterol A has Apo B-100 and HDL (high-density lipoprotein) that carries phospholipids and cholesterol and has Apo A-1 (Lent-Schochet; Jialal, 2023).

When there is an increase in plasma lipids associated with lipoproteins containing Apo B or a decrease in lipids associated with lipoproteins containing Apo A-1, we define these changes in metabolism as dyslipidemias (Costa *et al.,* 2024). Dyslipidemias can be of two

origins, primary in which it is associated with mutations and genetic polymorphisms and secondary, when it is associated with external factors such as diet, lifestyle, age, among others (Mosca *et al.,* 2022).

Currently, cardiovascular diseases are among the main causes of death in Brazil. Thus, studies suggest that cardiovascular risk assessments should be made with the concentrations of apolipoproteins Apo A-1 and Apo B as an alternative in order to improve the prediction of cardiovascular risk compared to traditional biomarkers (Păunică *et al.,* 2023).

Finally, several studies that have investigated the role of apolipoproteins in lipid metabolism indicate that the ApoB/ApoA-1 ratio is a highly significant way of determining cardiovascular risk. Thus, the importance of Apo A-1 and Apo B in the risk assessment of patients is observed (Yaseen *et al.,* 2021).

2.4 COVID-19 AND LIPID METABOLISM ALTERATIONS

In the context of the pathophysiology involved in COVID-19, where its main mechanisms are: endothelial cell injury; tissue fibrosis; dysregulation of the immune response; and induction of cytotoxicity in cells that express angiotensin-converting enzyme (ACE2), the propensity of organs that express this enzyme to the virus is remarkable (Beyerstedt *et al.,* 2021).

Among the affected systems, the cardiovascular system is one of the systems with the highest risk of being the target of the disease, considering that this is a tissue that has high expression of the ACE2 enzyme, and because it is responsible for the transport of nutrients, oxygen, defense cells, any alteration that affects several organs together, being associated with a risk of more severe cases (Costa *et al.,* 2024) (Rezaei *et al*., 2020).

Among the mechanisms that lead to serious adverse events in COVID-19, related to the cardiovascular system, it is important to highlight the alterations in lipid metabolism, which lead the body to a pro-atherogenic and pro-thrombotic state, which favors the destabilization of atheromatous plaques, thrombus formation, and vasoconstriction, which can culminate in acute myocardial infarction during infection, or post SARS-CoV-2 infection (Makarova *et al.,* 2023).

2.5 POLYMORPHISMS ASSOCIATED WITH *APOA-1* AND *APOB*

Genetic polymorphisms are defined as genetic variations that occur in more than 1% of the population of the same species. These alterations can occur in coding and non-coding

areas of DNA, and can generate qualitative or quantitative effects of the protein's activity (Wong *et al.*, 2022). Among the types of polymorphisms, single nucleotide polymorphisms (SNPs) are the most frequent in the population. They are characterized by the replacement of only one nucleotide in any region of the human genome (Meneses, 2023).

The gene responsible for encoding Apo A -1 is located on the long arm (q) of chromosome 11, in band 23.3 (11q23.3) (Costa *et al*., 2024). One of its most studied polymorphisms is the *rs670 SNP*, in which there is the replacement of a cytosine (C) by thymine (T), and data suggest that it leads to an increase in the gene's promoter function and may be associated with changes in the size and antioxidant action of high-density lipoprotein (HDL) (Al-Bustan *et al*., 2013; Meneses, 2023).

The gene responsible for encoding Apo B-48 and Apo B-100 is located on the short arm (p) of chromosome 2 band 24.1 (2p24.1) (Alves *et al*., 2020). Among the polymorphisms that can cause changes in the lipid profile and bring the most significant risk for heart disease we have the SNP *rs693*, in which it is possible to identify the alteration 7545C>T. This is considered a silent alteration because there is no alteration of the resulting amino acid (Wong *et al*., 2022).

Thus, it is possible that genetic alterations in the *APOB* and *APOA* genes may alter the outcome of COVID-19, which demonstrates the relevance of genotyping these patients for better risk prediction. However, it is possible to observe a clear gap in this area, since there are few studies that verify the association between the genetic polymorphisms of *APOA* and *APOB* with the SARS-CoV-2 virus.

3 METHODOLOGY

3.1 SEARCH STRATEGY AND SELECTION CRITERIA

This integrative review included studies that presented relevant data on the polymorphisms of the *APOA* and *APOB* genes. Articles published from 2020 onwards were selected, of the clinical trial, cross-sectional, case-control and cohort type, which had the full text freely available online and were written in Portuguese or English. Studies that did not meet the defined criteria, as well as those that did not contain complete data, or were duplicates, were excluded.

The survey was conducted from November 2024 to July 2025. The databases used were Google Scholar, Virtual Health Library – VHL, CAPES Journal Portal, and PubMed. The assembly of the research descriptor was done through the PECO strategy, where

P(population)= patients with COVID-19, E(exposure)= presence of the Apo A-1 and/or Apo B polymorphism, C(comparison)= patients with COVID-19 with the presence of any of the Apo A-1 and/or Apo B polymorphisms and patients with COVID-19 without the presence of Apo A-1 and/or Apo B polymorphisms, O(outcome)= alteration in the lipid/biochemical profile that has an impact on the evolution of the disease. The descriptors used were "Apo-B polymorphism AND SARS-Cov-2 AND COVID-19" and "Apo-A polymorphism AND COVID-19", combined by the Boolean operator "AND".

3.2 SELECTION OF STUDIES AND DATA EXTRACTION

The pre-selection phase of the studies was carried out with the collaboration of two reviewers (AB and DM) in a double-blind manner, in which the search was carried out and the studies were delimited according to their eligibility. Independently, with the aid of the Rayan® software, the title, abstract, and context of each study were analyzed.

In the second phase, the AB reviewer cataloged the selected studies according to common criteria, where they would be analyzed: author, year of publication, country, study objective, population sample, results, and P value. This phase was carried out with the help of the Microsoft Office Excel software.

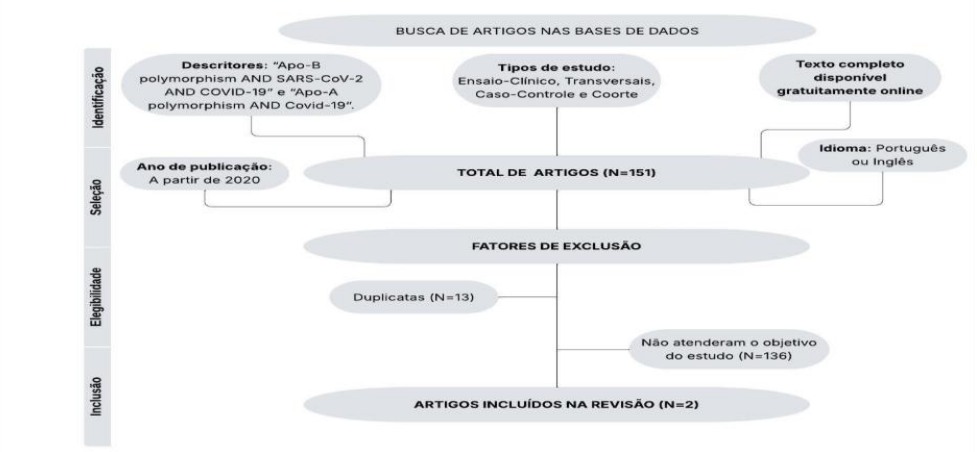
In the third phase, the DM reviewer evaluated all the items in the table, making corrections and answering questions when necessary.

3.3 SEARCH AND SELECTION OF STUDIES

At first, 151 articles were identified in the chosen databases (Figure 1). There were 13 duplicates and only 138 were selected for the analysis of the title and abstract, observing the previously established inclusion and exclusion criteria. Of the remaining articles, 136 were excluded because they did not fit the selection criteria, either by year of publication, type of study, type of approach, or because they were not publicly accessible. Thus, 2 articles were included in this review.

Figure 1

Flowchart with the steps adopted in the selection of studies



Source: authorship, based on PRISMA (2025).

4 RESULTS AND DISCUSSIONS

The studies that were analyzed involved populations from Croatia and Brazil, with publication years of 2022 and 2024, respectively. Both studies were cross-sectional and were conducted with patient samples from the first semester of 2021. Regarding the characteristics of the demographic profile of the participants, adults over 18 years of age, of both sexes, were recruited.

They were divided into two groups, COVID-19 patients diagnosed through reverse transcription followed by quantitative polymerase chain reaction (RT-qPCR) and healthy patients. Table 1 shows the data collected from the articles in a reduced form.

Table 1

Comparison of the studies resulting from the selection carried out

Author	Year	Title	Country	Goal	Sample	Laboratory test	Findings	P value
Costa *et al.*	2024	Single nucleotide polymorphisms in apolipoprotein A-1 (rs670) and B (rs693) associated with serum lipoproteins and endothelial activation in	Brazil	To evaluate the association of Apolipoprotein A-1 (rs670) and B (rs693) polymorphisms with serum lipoproteins and	N= 167 (86 COVID-19 outpatients and 81 healthy subjects)	qPCR	An association was found between the dominance of the rs670 SNP A allele and lower TG levels in outpatients with COVID-19; on the	0.012 (rs670) 0.024 (RS693 & RS670)

		COVID-19 outpatients		endothelial activation in patients with COVID-19 treated at a Sentinel Unit in the city of Fortaleza-Ceará/Brazil			other hand, the T allele of the SNP rs693 was associated only when in codominance of the A allele (rs670)	
Lapic *et al.*	2022	Association of polymorphisms in genes encoding prothrombotic and cardiovascular risk factors with disease severity in COVID-19 patients: A pilot study	Croatia	To conduct a comprehensive analysis covering a selection of polymorphisms in genes encoding prothrombotic and atherosclerotic risk factors in COVID-19 patients and to assess their possible association with disease severity	N= 79 (30 patients with a severe form of COVID-19 and 49 patients with non-severe COVID-19)	qPCR	No association was found between the ApoB R3500Q polymorphism genotype in severe and non-severe COVID-19 patients	1.000

Source: authorship (2025).

In the study by Costa et al. (Costa *et al.*, 2024) an association was found between the polymorphism of Apo A-1 -75G/A (*rs670*) and lower TG levels in patients with COVID-19. However, in the case of the Apo B polymorphism (*rs693*), an association of the T allele was found only when in codominance with the A allele of the *rs670* polymorphism, resulting in a greater TG reduction.

In the study by Lapic et al. (Lapić *et al.*, 2022), no association was found between the Apo B *R3500Q polymorphism* in severe and non-severe patients with COVID-19.

Data show that lipid mediators are involved in the process of controlling inflammation, so the exacerbated inflammatory reaction of infectious diseases such as COVID-19 can alter the production of these molecules (Carvalho *et al*., 2023). Recently, the effect of inflammation and infection on lipids and lipoproteins has revealed that in several inflammatory and infectious disorders, alterations in lipid levels can often be found, the most relevant of which are increased TG levels, reduced HDL-c, increased small and dense LDL, and increased lipoprotein A (in cases of inflammation) (Feingold; Grunfeld, 2025).

In this sense, it is possible that variations in the lipid profile may be one of the factors that influence the outcome of COVID-19 (Golin *et al.*, 2021). In line with this data, another study analyzed the association between lipid profile and clinical outcomes in patients with COVID-19, and identified that patients with higher HDL-c levels may have a higher chance of survival (Ochoa-Ramírez *et al*., 2024).

Therefore, studying in depth the lipid variations that occur in patients affected by COVID-19 is essential to improve knowledge about the prognosis.

One of the most studied polymorphisms involving the *APOA1 gene* is the SNP -75G/A (*rs670*), in which there is the replacement of a guanine (G) by an adenine (A) in exon 75 of chromosome 11 (Muheeb *et al.,* 2022). This variant influences gene transcription, and can increase *ApoA1* levels and, therefore, HDL. Due to the antioxidant, anti-inflammatory, and antithrombotic functions associated with HDL, this polymorphism is known for its antiatherogenic properties, acting as a protective factor against cardiovascular disease (Muheeb *et al*., 2022) (Meneses, 2023).

In the case of *APOB,* one of the most studied polymorphisms is the Xbal SNP (*rs693*), where there is a replacement of a cytosine (C) by a thymine (T) in exon 26 of chromosome 2, (ACC >ACT), however, there is no change in the amino acid sequence (Souza *et al.,* 2024). This polymorphism affects the metabolization of cholesterol, which causes an increase in serum levels of TC and LDL-c, which ends up contributing, as well as other risk factors, to the development of cardiovascular disorders, such as atherosclerosis (Souza *et al.,* 2024).

Currently, researchers indicate the *ApoB/ApoA-1* ratio as a more accurate way to assess cardiovascular risk (Nurtazina *et al.*, 2020) (Behbodikhah *et al.,* 2021). An increase in the *ApoB/ApoA-1* ratio indicates that there is an imbalance in lipid metabolism, i.e., the concentration of pro-atherogenic molecules such as Apo B (LDL and VLDL) is being higher than antiatherogenic molecules, in this case Apo A-1 (HDL) (Meneses, 2023). This means that a patient who has an increase in this ratio is more likely to develop various cardiovascular conditions, such as atherosclerosis, when compared to patients with a balanced lipid metabolism (Păunică *et al.,* 2023).

Once the importance that Apo A-1 and play in lipid metabolism has been identified, it is essential to study its genetic variations, in view of the possibility of identifying which groups of patients are at higher risk of developing severe COVID-19 outcomes, thus helping to improve a better prognosis (Golin *et al.,* 2021).

In this review, two articles were analyzed, the first by Costa *et al*. (Costa *et al.*, 2024), which aimed to evaluate the association of Apolipoprotein A-1 (*rs670*) and B (*rs693*) polymorphisms with serum lipoproteins and endothelial activation in patients with COVID-19, found that the prevalence of the polymorphic A allele in the *rs670* SNP was associated with reduced triglyceride levels. On the other hand, the polymorphic T allele of the *rs693 SNP* was only associated with a reduction in triglyceride levels when in codominance with the A allele of the *rs670 SNP* (Costa *et al.*, 2024).

In disagreement with the above, a Brazilian study analyzed the association of *the XbaI* polymorphism (*rs693*) with increased cholesterol in children and adolescents. It was revealed that people with the polymorphic T allele had a higher chance of having an increase in serum cholesterol levels when compared to individuals of the ancestral C allele (Souza *et al.,* 2024).

The second article, by Lapic *et al.* in 2022 (Lapić *et al.,* 2022), aimed to conduct a comprehensive analysis covering a selection of polymorphisms in genes encoding prothrombotic and atherosclerotic risk factors in COVID-19 patients. Its objective was to evaluate a possible association with disease severity. However, no association was found between the Apo B *R3500Q polymorphism genotype* (*rs5742904: G>A*) in severe and non-severe patients with COVID-19.

Also in contradiction with this finding, another study conducted with a population of southern Brazil of European descent identified that the polymorphism of Apo B *R3500Q* (*rs5742904: G>A*) is a risk factor for increased total cholesterol (TC) levels regardless of age and gender (Gasparin *et al.,* 2024). Such findings suggest that different populations may lead to different influences of the polymorphism regarding the outcome analyzed.

With respect to Apo A-1 alterations, a Ukrainian study was able to conclude that serum Apo A-1 levels in COVID-19 patients were significantly lower compared to healthy people. In addition, COVID-19 patients were found to have higher levels of Apo B and ox-LDL than healthy people (Pushkarev *et al.,* 2021).

Similar results were corroborated by several studies, which found a positive influence on the presence of COVID-19 and changes in lipid metabolism, especially regarding the lowest serum levels of Apo A-1. In addition, it was found that lower serum levels of Apo A-1 are associated with a worse prognosis of COVID-19 (Zhu *et al.,* 2021) (Li *et al.,* 2021) (Ulloque-Badaracco *et al.,* 2021).

Thus, although it is clear the relevance that Apo A-1 and Apo B have on the lipid profile of patients affected by COVID-19, there are gaps in the literature on the impact that the

polymorphisms of these apolipoproteins can cause in these patients, evidenced by the scarcity of material addressing genetic variations and the context of COVID-19.

Thus, it is essential that there are more studies addressing the topic of lipid metabolism in the face of COVID-19, however, bringing to light the relevance and impact of genetic variations in this context, as evidenced by their importance in predicting the risks of severe cases and prognosis.

5 CONCLUSION

This research observed that, in patients with COVID-19, the *rs670 polymorphism* was associated with the polymorphic A allele with a reduction in TG levels, suggesting a possible association witha cardiovascular risk predictor. In the rs693 polymorphism, there was an association of the polymorphic T allele only when in codominance with the A allele of the *rs670 SNP.The* rs5742904 *polymorphism* showed no statistically significant changes in COVID-19 patients. In addition, a gap in the relevant literature was observed in relation to genetic variations in the lipid profile of patients with COVID-19, showing that further studies will be needed in the context of the genetic background of patients with the SARS-CoV-2 virus.

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