




Carrageenan-amino acid interaction as a tool for understanding atherosclerotic process initiation

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Citation: Chiconi de Picoli PM, Araújo Soares T, Marques Gonçalves A, Trovatti E. Carrageenan-amino acid interaction as a tool for understanding atherosclerotic process initiation. *Electron J Gen Med.* 2024;21(3):em590. <https://doi.org/10.29333/ejgm/14652>

ARTICLE INFO

Received: 09 Dec. 2023

Accepted: 05 May 2024

ABSTRACT

Atherosclerosis is the primary trigger for severe pathologies. The atherosclerotic inflammatory process is well known after low-density lipoprotein (LDL) adhesion in blood vessel walls, however, limited information exists regarding LDL penetration into subendothelial layers. Here, we propose for the first time, to the best of our knowledge, the pathway for the initial trajectory of the lipid molecules internalization into the arterial endothelial tissue. The investigation shows a computational model analyzing molecules involved in the atherosclerotic process, specifically LDL and molecules of the vascular endothelium. The theoretical model was experimentally tested using carrageenan to simulate the anionic counterparts of vascular tissue and amino acids from apolipoprotein B-100. The molecular interactions were analyzed by conductimetric titration, FTIR, and rheology. The computational model identified potential amino acids involved in the process, and the experimental results demonstrated the interaction between lysine and polymer, as the mechanism of adhesion, confirming the model.

Keywords: atherosclerosis, apolipoprotein B-100, lysine, low-density lipoprotein, dermatan sulfate

INTRODUCTION

Atherosclerosis is a pathology characterized by the gradual accumulation of fatty plaques in arterial endothelial tissue over years [1-5]. If undiagnosed, the growth of lipid plaques interrupts the blood flow, leading the affected area to necrosis [6, 7]. Atherosclerosis affects 10% of the global population [8, 9] and is the primary trigger for pathologies such as acute myocardial infarction, ischemic stroke and peripheral arterial disease (PAD), among others [10-13]. Acute myocardial infarction accounts for 15 million annual deaths worldwide [14], with 80% occurring within the first 24 hours after disease manifestation [15]. Ischemic stroke is a leading cause of death and neurological sequelae [16, 17], with a 40% mortality rate within the first year of disease onset. Diagnosis and treatment within the first 4.5 hours are crucial, as delayed intervention often results in irreversible damage [18]. PAD is the major predictor of amputations, with 87% of global amputations attributed to this pathology. Early diagnosis is challenging, as 70% of cases are asymptomatic, leading to clinical progression and increased amputation rates [19].

Atherosclerosis starts with vascular endothelial dysfunction, predominantly in areas of arterial bifurcations, branches, or angulations [20]. In these sites the blood flow generate turbulence because of the anatomy, increasing the chances of tissue injuries [21]. The literature provides a detailed description of the atherosclerotic process after low-density lipoprotein (LDL) molecules adhere to the internal

blood vessel walls generating the atheroma plaques [22-24]. In short, atherosclerosis is an inflammatory process in specific artery regions [25-27]. Injured endothelial cells express cytokines and chemokines [28-30] such as tumor necrosis factor-alpha and interleukins 1, 6, and 8 [31-33], attracting immune mediators like monocytes and T cells to the arterial endothelial surface through selectin and integrin expression [34-37]. The injured endothelial surface exhibits negative charges from proteoglycans [38], molecules based on the proteinaceous core of aggrecan. Anionic glycosaminoglycan chains, dermatan sulfate, and chondroitin sulfate covalently bind to the protein core through serine residues in the central protein skeleton [39-41]. In this sense, LDL molecules in the bloodstream are attracted by dermatan sulfate and chondroitin sulfate molecules on the surfaces of injured arteries [42]. Additionally, LDL molecules adhering to arterial tissue are endocytosed, along with macronutrients, by endothelial cells, in an endocytosis process independent of LDL receptors [43], which are not expressed because there is no need of LDL molecules for cell metabolism at that moment. These LDL molecules are then released into the extracellular space in the subendothelial layer inside the arterial vessel wall, where they are attracted by glycosaminoglycans at the cell interstices [44]. Besides glycosaminoglycans, elastin and collagen fibers at the subendothelial layer, also contribute to keep LDL in artery walls [45, 46]. LDL molecules are oxidized by myeloperoxidase and NADPH oxidase enzymes and oxygen reactive species at the subendothelial layer [47-50]. The oxidative process leads LDL molecules to be recognized by

scavenger receptors at the surface of macrophages [51-54]. Macrophages remove LDL molecules from artery walls [55]. Thus, oxidized LDL molecules are identified, phagocytosed by macrophages, and transformed into foam cells [56-59]. Foam cell aggregation results in atheroma plaques [60-62].

As described above, the inflammatory process and the formation of the atheroma plaque after internalization of LDL are very well described in the literature, however, little information is available about the process by which LDL molecules penetrate the endothelial layers. For internalization, LDL certainly interacts with the molecules at the surface of the endothelial cells, a crucial process that needs to be deeply understood to elucidate the beginning of plaque formation.

Hence, based on the information from the literature, this work aims to contribute to elucidating the starting point of the atherosclerotic process, namely, the initial steps of the molecular interactions between LDL molecules and the vessel walls. In this sense, the chemical structure of LDL and the surface molecules of the endothelial cells were studied. Then, we have proposed a lipid adhesion model, which predicts the electrostatic interaction between LDL molecules and endothelial tissue cells. The model anticipates that this interaction only occurs in injured tissue after the initiation of an inflammatory process, and to the best of our knowledge, it is not described in the literature. The model employed the polymer carrageenan and the primary amino acids lysine, serine or arginine. Carrageenan displays a pendent sulphate group at its surface and was used to simulate the pendent sulphate group from dermatan sulphate available at the surface of the epithelial cells. It was also used because it displays only sulphate and hydroxyl groups in its structure, available for hydrogen bonds or electrostatic interactions. The primary amino acids were those available at the surface of apolipoprotein B-100. The model aims to predict the interfacial adhesion between them, possibly by electrostatic interactions, which can lead to the adhesion of LDL to the surface of the epithelial cells.

METHODOLOGY

Molecular Modeling & Docking

The protonation state of dermatan sulphate was estimated at 7.4 pH, using MarvinSketch (v.21.2) software. Dermatan sulphate was constructed with Discovery Studio Visualizer (v.20.1) [63]. The tridimensional structures were optimized using the semi-empirical method PM7 in MOPAC (v.2016) [64] with graphical interface of Mercury CSD software (v2020.1) [65]. The optimization commands MMOK, XYZ and CHARGE (depending on the charge of each molecule at 7.4 pH).

Since APOB-100 protein does not have a solved 3D structure, I-TASSER was used to model a 355 amino acid length sequence of the protein structure. The chosen region was based on studies pointing to residues important for the apo-B100 interaction. The 355 amino acid sequence was retrieved from the apo-B100 human protein (Uniprot ID P04114) from residues 3186 to 3540.

For docking studies hydrogen atoms were added to .pdb file with GOLD software (v.2020.1). The same software was used to perform the rigid docking, using L3391 coordinates of the modeled structure as the center of the 10 Å search radius. The method was applied using 100 runs, and GoldScore function.

Conductimetric Titration

For the conductimetric titrations, solutions of the amino acids lysine, arginine, and serine (1 mM) were first prepared at room temperature, along with the carrageenan polymeric solution (0.1 mol/L) at 60 °C. Subsequently, the pH of the solutions was adjusted to 7. A 3 mL aliquot of the carrageenan polymeric solution was placed in a beaker. A conductimetric cell (Analyzer 650MA conductometer) was immersed in the solution for analysis. The polymeric solution was titrated with different amino acids—lysine, arginine, and serine—under constant stirring, with the conductance value recorded after each addition of titrants at 25 °C. Following each addition, a waiting period of approximately one minute was observed for stabilization before each reading.

Chemical Characterization by FTIR

The chemical characterization of the lysine, arginine, and serine amino acid solutions, carrageenan polymer, and carrageenan-amino acid solutions was performed using FTIR (with ATR accessory) on a Perkin Elmer Spectrum 100 spectrometer at a resolution of 4 cm⁻¹, with 16 scans in the range of 4,000 to 600 cm⁻¹. The amino acid solutions (lysine, arginine, and serine) and carrageenan solution used for FTIR analysis were the same as those prepared for the conductimetric titration analysis. Carrageenan-lysine, carrageenan-arginine, and carrageenan-serine solutions were prepared by mixing 0.5 mL of the carrageenan solution with 0.5 mL of the amino acid solutions at room temperature. Aliquots of the carrageenan-amino acid solutions were dried in an oven at 45 °C, and the analysis was then carried on the dried samples.

Rheology

The samples used in the rheological analysis, polymeric solution, and polymeric-amino acid solutions, were the same solutions prepared and used in the conductimetric titration and FTIR analysis. Rheological analyses of the carrageenan, carrageenan-lysine, carrageenan-arginine, and carrageenan-serine samples were performed using an Anton Paar MCR92 rheometer. To ensure result accuracy, a specific configuration was adopted, employing a 50 mm parallel plate geometry during the tests. The main objective was to evaluate viscosity concerning the reaction time of the samples under study. To maintain test consistency and uniformity, the following experimental parameters were defined: a 0.25 mm gap between the plates, controlled temperature of 25 °C, and an angular deformation rate of 0.01 rad/s over a period of 240 seconds. Choosing a low shear rate during the analysis was crucial to ensure that the deformation process did not interfere with the viscosity response of the material.

RESULTS

Molecular Modeling & Docking

The results of dermatan sulphate docking using the modeled apo-B100, permitted the prediction of interactions that may be important in the binding process. The ligand formed mainly hydrogen bond with residues S(serine)3343, K(lysine)3345, S(serine)3346, R(arginine)3392 and N(asparagine)3421. An ionic interaction between dermatan sulphate carboxyl oxygen and amidine nitrogen of R3392 was also predicted (**Figure 1**), where Nitrogen atoms are shown in

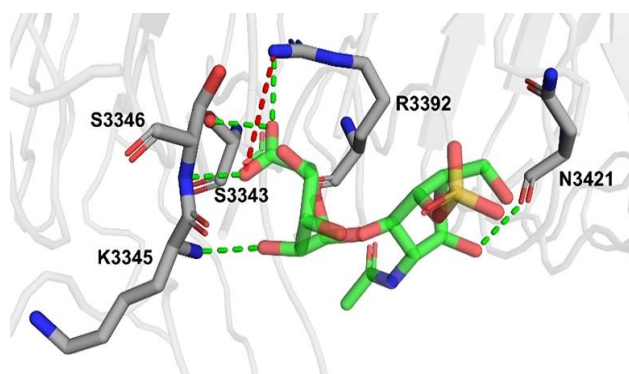


Figure 1. Best docking pose of dermatan sulphate & predicted interactions with apo-B100 modeled structure (Source: Authors' own elaboration)

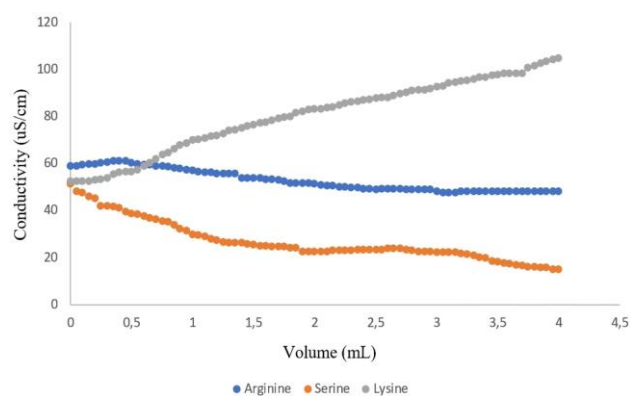


Figure 2. Conductimetric titration: Carrageenan & amino acids (Source: Authors' own elaboration)

blue, oxygen atoms in red, carbon atoms in gray (protein) or green (ligand), hydrogens were omitted for clarity. Molecular interactions are shown as dotted lines: hydrogen bonds in green and ionic interactions in red.

Conductimetric Titration

Figure 2 shows the conductimetric titration curves of carrageenan polymeric solution with titrants, specifically lysine, arginine, and serine solutions. The conductance curve of lysine exhibits an increasing trend, whereas the curves for arginine and serine demonstrate remarkably similar decreasing values.

Figure 2 describes the conductometric curves of amino acids: the increasing curve of lysine is depicted in gray, the decreasing curve of arginine in blue, and the decreasing curve of serine in orange.

Chemical Characterization by FTIR

FTIR spectra of carrageenan, amino acids, and carrageenan-amino acid samples are shown in **Figure 3**. The carrageenan spectrum shows a broad absorption band at $3,380\text{ cm}^{-1}$ attributed to the axial deformation of OH groups and an absorption band at $1,050\text{ cm}^{-1}$ corresponding to $\text{O}=\text{S}=\text{O}$ bonds. The absorption band at 1630 cm^{-1} corresponds to the angular deformation of OH groups from residual water molecules present in the polysaccharide [66]. The lysine spectrum displays double strong bands at $1,620\text{ cm}^{-1}$ and $1,558\text{ cm}^{-1}$ typical of the stretching of COO^- and the stretching and bending vibrations of NH bonds, respectively [67]. The carrageenan-lysine mixture spectrum shows a shift in the band

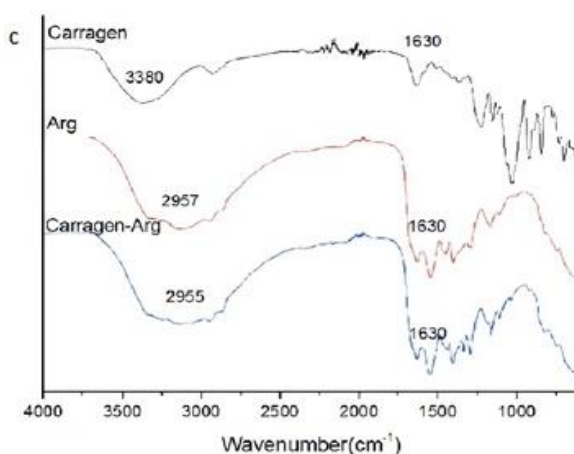
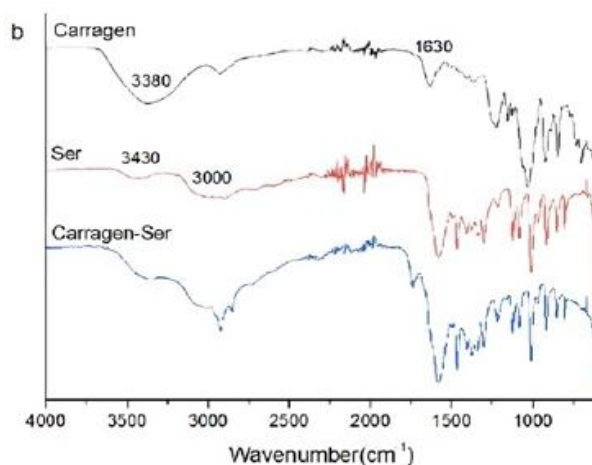
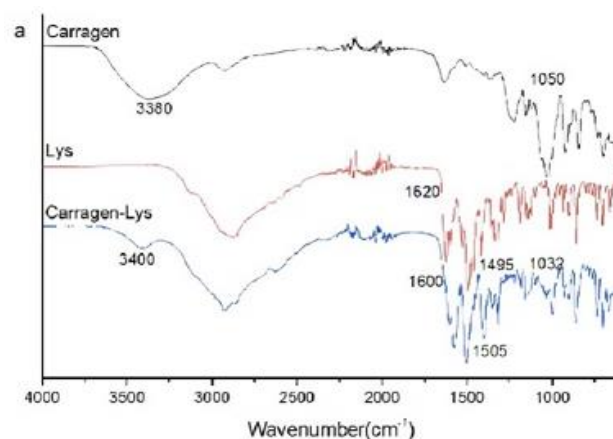


Figure 3. FTIR spectrum-carrageenan, amino acid, & carrageenan-amino acids: (a) FTIR spectrum in blue carrageenan bands, in black lysine bands, in red carrageenan-lysine bands; (b) FTIR spectrum in black carrageenan bands, in red serine bands, in blue carrageenan-serine bands; & (c) FTIR spectrum in black carrageenan bands, in red arginine bands, in blue carrageenan-arginine bands (Source: Authors' own elaboration)

at $3,380\text{ cm}^{-1}$ to $3,400\text{ cm}^{-1}$, indicating the interaction of the polymer with the amino acid via the OH groups from carrageenan.

The analysis also indicates the shift of the band related to the axial deformation of COO^- at $1,620\text{ cm}^{-1}$ in the amino acid to $1,600\text{ cm}^{-1}$ in the mixture, and the shift of the NH bending

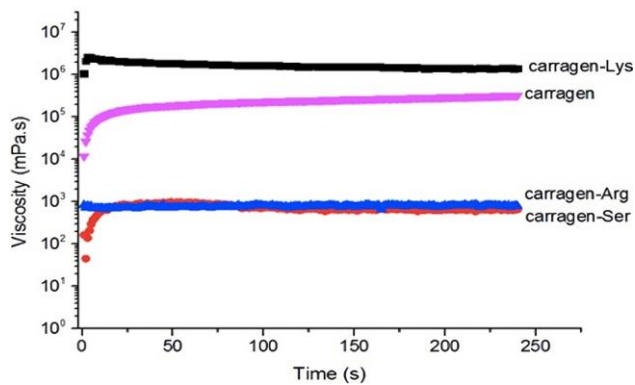


Figure 4. Rheological results of the viscosities of carrageenan, carrageenan-lysine, carrageenan-arginine, & carrageenan-serine (Source: Authors' own elaboration)

from $1,495\text{ cm}^{-1}$ on the amino acid to $1,505\text{ cm}^{-1}$ on the mixture [68]. These band shifts in the carrageenan-lysine spectrum indicate the molecular interaction between the polymer and the amino acid.

This result is in total agreement with the theoretical model in which the OH from the carrageenan polymer (showed in green in the model), interacts with the amino group from lysine (K3345) by hydrogen bond.

The serine spectrum showed an absorption bands at $3,430\text{ cm}^{-1}$ attributed to the axial deformation of NH_2 , at $3,000\text{ cm}^{-1}$ attributed to the stretching of the OH of carboxylic acid [69], and its typical fingerprinting bands, below $1,100\text{ cm}^{-1}$.

The carrageenan-serine mixture spectrum shows absorption bands at $3,430\text{ cm}^{-1}$, $3,196\text{ cm}^{-1}$, and at $2,940\text{ cm}^{-1}$ [68], indicating the overlapping of the amino acid and carrageenan bands at this region. These results suggest no molecular interaction between the polymer and the amino acid.

Typical stretching frequencies of arginine are NH bond of the amine at $2,957\text{ cm}^{-1}$ and C=O of the carboxyl group at $1,630\text{ cm}^{-1}$ [70]. The carrageenan-arginine spectrum did not show shifts when compared to the polymer or the isolated amino acid. The resulting spectra is the overlapping of the polymer and the amino acid spectrum, indicating no molecular interaction.

Rheology

Figure 4 shows the viscosity of the analyzed samples, including carrageenan, carrageenan-lysine, carrageenan-arginine, and carrageenan-serine, where viscosity curves in lilac carrageenan polymer, in black carrageenan-lysine solution, in blue carrageenan-arginine solution, in red carrageenan-serine solution.

Viscosities remained relatively constant during the analysis. Comparing the viscosity of carrageenan with the viscosities of carrageenan-amino acid mixtures, it was observed that the viscosity of the carrageenan-lysine sample exceeded the viscosities of the polymer and the carrageenan-arginine or carrageenan-serine samples, indicating a greater molecular interaction between lysine and the polymer.

Figure 5 displays the photographs of the carrageenan, amino acids, and carrageenan-amino acid solutions before the rheological analysis. The formation of a gel-like precipitate in the carrageenan-lysine sample is evident.



Figure 5. Samples of carrageenan, amino acids, & carrageenan-amino acid solutions: (a) Carrageenan solution, lysine solution, & carrageenan-lysine solution; (b) carrageenan solution, arginine solution, & carrageenan-arginine solution; & (c) carrageenan solution, serine solution, & carrageenan-serine solution (Source: Authors' own elaboration)

Figure 5 describes the physical state of the solutions used in rheological analysis, in sequence: polymeric solution, amino acid solution and polymer-amino acid solution.

DISCUSSION

Since there are no solved structures for apo-B100, our results originate a model, which may help to understand dermatan sulphate interactions with the referred protein. It is important to notice that it does not show the mechanism of action but brings insights on how they may work.

To better understand the process, it would be necessary to elucidate protein structure, which is a difficult task, based on its mass and complexity. In this sense, our model was constructed based on a small sequence of 355 amino acids, therefore, it does not represent the full structure of the protein. The amino acids sequence was chosen according to [38], which identified as apo-B100 binding site for proteoglycans.

Although it is a small model, we found that the main interactions occur in accordance with previous results in other works. In fact, the results show interactions with L (leucine) residue by hydrogen bond and that other residues such as S (serine), R (arginine), K (lysine) and N (asparagine) seem important for ligand/protein interaction.

Another important finding is the predicted electrostatic interaction between R (arginine) and dermatan sulphate, showing the importance of positive interaction in ligand target bonding [38]. In spite of predicting important interactions the binding region was modelled similar to random coils, which may influence docking results.

For instance, L (leucine) 3391, a known important residue did not show interactions with dermatan sulphate. On the other hand, the model was able to predict possible mechanisms of interactions, considering the characteristics of

amino acid residues and dermatan sulphate. The apolipoprotein B-100 molecule contains 4.536 amino acid residues with several interaction sites.

It was explored some of these sites found that the site composed by the 3359- 3369 residues, specifically the amino acids arginine 3362, lysine 3363, and arginine 3364 can promote the interactions between LDL molecules and the glycosaminoglycans from the arterial endothelial tissue [38]. When replacing these amino acids by acidic amino acids such as glutamic acid or aspartic acid, the interaction of LDL molecules with glycosaminoglycans was disrupted, mainly when the lysine residue 3363 was replaced by glutamic acid [38]. Based on these studies, a computational model was designed here, to investigate the amino acids involved in the molecular interaction process that starts the plaque formation in the arterial vessels tissues, namely, the adhesion of the lipids (from LDL) to the epithelial tissues.

The experimental investigation was carried out using the carrageenan polymer, as it displays sulfated groups and free hydroxyls in its molecular structure, and the absence of carboxyl groups. The tested amino acids were lysine, arginine, and serine, present at the surface of the apolipoprotein B-100 molecule, as suggested by the computational model.

In summary, the literature describes that in lesions in injured arterial endothelial tissues, the immune system cells express the glycosaminoglycans (dermatan sulfate and chondroitin sulfate) on their surface [71, 72]. These molecules have negative charges in their structure, which are available on the surface of arterial endothelial cells, forming a high-density network of negative charges. Our results suggest that these negative charges attract LDL molecules to the injured region, initiating the adhesion process of LDL to the endothelial tissue. Electrostatic attraction occurs between the electronegative groups present in the glycosaminoglycan molecules of endothelial tissue and the electropositive amino acid residues on the surface of apolipoprotein B-100 molecules of LDL.

Regarding the carrageenan solution, it is highly stable under neutral or alkaline pH [73]. The conductimetric titration experiment was carried out at pH 7, close to the physiological environment (pH 7.4). At this pH, carrageenan is negatively charged, its sulphate and hydroxyl groups are both deprotonated. Lysine displays a secondary amino group in its side chain and a secondary amino group in its main chain, both protonated at pH 7. Its hydroxyl group is deprotonated. Arginine, featuring a guanidinium group, displays ionizable side chains in its molecular structure, from its protonated amine and deprotonated hydroxyl group. Serine displays one protonated amine and one deprotonated hydroxyl group [74]. These features may have an important role in interactions between dermatan sulphate and apo B-100.

The conductimetric titration of carrageenan with lysine showed an ascending curve, which may be attributed to the increase in ions available in solution arising from the positive charge of the lysine's structure. At the beginning, the curve shows a stable profile, followed by an increase in conductivity as the result of the addition of lysine. This result can be correlated to the neutralization of the carrageenan hydroxyl groups by free lysine amine groups, followed by the excess of free amine in solution, resulting in increased conductivity [75].

The conductimetric titration curve of carrageenan with arginine or serine displayed a very similar behavior, with a slightly decrease in the conductivity values. The guanidine side

chain from arginine provide a positive delocalized charge, resulting from its conjugated system between double bonds and hydrogen atoms [76]. The system's conductance decreases because the molecular interactions of the terminal amine group of arginine and the negative charges from the polymer, with no excess of positive charges. This behavior is similar for serine in which its single amine protonated group interacts with the negative charges from the polymer, and no excess of positive charges. In these cases, the positive charges (amino group) was mobilized to neutralize the polymer's charges, and the negative charge (hydroxyl), which did not interact with the polymer was responsible for the system's conductivity.

As shown in **Figure 4** and **Figure 5**, the mixture of carrageenan with amino acids leads to interesting results, mainly the formation of a gel when mixing carrageenan with lysine, and the break of the viscous state of carrageenan when mixing with arginine or serine. Viscosity is directly associated with molecular interactions; the greater the intermolecular forces, the higher the viscosity of the system [77]. Several natural systems are formed and structured by electrostatic complexes between proteins and polysaccharides. The interactions of these systems depend on the electric charges of the polymers, pH, and ionic strength. They can be incompatible or compatible [78]. Incompatible interactions between similarly charged molecules, result in electrostatic repulsion [78]. Compatible interactions result from attraction between molecules with opposite electric charges. Compatibility interactions occur in a pH range located between the protein's isoelectric point (pI) and the polysaccharide's pKa. Under these conditions, molecules are attracted to each other, leading to the formation of precipitates [78], such as gels [79]. In these gels, the interaction force is proportional to the number of charged groups; the more charged molecules, the stronger the precipitates, and the ionic strength of the mixture influences gel stability [80]. The nature of the electrically charged group also influences the strength of interactions. Certain proteins interact more strongly with polysaccharides containing sulfonic groups than polysaccharides with only carboxylic groups [77]. Most proteins have some lysine residues; the amino groups of lysine are usually exposed on the protein's surface and are highly reactive when protonated. The high reactivity of carrageenan with lysine is due to the strong electrostatic interaction between the negatively charged groups of carrageenan and the positively charged side chain of lysine. Interactions between carrageenan and lysine can be observed by the gelation of the solution [77]. Arginine has a guanidine group and an end terminal amine group, which carries a positive charge under physiological conditions because of their intrinsic pKa; although the guanidine group is protonated, its positive charge is delocalized due to the presence of the conjugated double bonds between carbon and nitrogen atoms [68]. Thus, the moderate interaction between arginine and carrageenan is attributed to the guanidinium group in the amino acid's side chain, which has six π electrons in bonding orbitals and is protonated with a positively charged delocalized form at neutral pH [76]. Serine is a neutral amino acid and its interaction with carrageenan is the result of the interaction of its only amine end group with the negative charges of polymer [76]. All these data are in total agreement with FTIR results and with the proposed theoretical model.

The results and the proposal of this adhesion model are described here for the first time, to the best of our knowledge. It is a preliminary proposal, however it shows important

results, obtained from simple experiments, that can be useful to future studies and aim to present the issue to the scientific community and sparking interest, encouraging the development of more in-depth studies.

CONCLUSIONS

Herein we presented experimental results aligned with a theoretical model of interaction, using the carrageenan molecule, due to its similarity to dermatan sulfate and amino acids, specifically those present on the surface of apolipoprotein B-100 molecules.

The results of the conductometric titration, with carrageenan as the titrated polymer and lysine, arginine, and serine as titrants, showed that all three amino acids interacted with the polymer. The rising titration curve of lysine demonstrated a greater availability and mobility of lysine ions in the system. Rheological analysis addressed molecular interactions through viscosity. All three amino acid solutions showed interaction with carrageenan, and the formation of a gelatinous precipitate in the carrageenan-lysine solution highlighted a greater molecular interaction of lysine with the polymer. FTIR analysis depicted the polymer-amino acid interaction through band shifts, visible in all three spectra. These analyses indicated that among the investigated amino acids, lysine exhibited a greater molecular affinity with the polymer.

The results support the hypotheses addressed in the theoretical model of lipid adhesion, suggesting that the molecular interaction between LDL molecules and the injured vascular tissue occurs through lysine residues present in apolipoprotein B-100. Based on the findings outlined in this study, it is anticipated that these results may help the development of further research projects aimed at advancing in this particular matter. It is also expected that this lipid adhesion model will assist in the development of new drugs, devices, and effective technologies for the control and prevention of atherosclerotic pathologies; reflecting a reduction in atherosclerotic cases, as well as a decrease in mortality rates and sequelae caused by these diseases.

Author contributions: **PMCP:** research protocol design, literature search, data extraction, draft manuscript, & data interpretation; **TAS & AMG:** analysis, interpretation, draft manuscript, & data interpretation; & **ET:** conception & design, acquisition, analysis, interpretation, draft manuscript, & data interpretation. All authors have agreed with the results and conclusions.

Funding: This study was supported by São Paulo Research Foundation under Grant 2017/18782-6.

Ethical statement: The authors stated that the study did not involve testing on animals/humans. The authors further stated that approval by an ethics committee was not required for the study.

Declaration of interest: No conflict of interest is declared by the authors.

Data sharing statement: Data supporting the findings and conclusions are available upon request from the corresponding author.

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