

Basic Study

SARS-CoV-2 proteins show great binding affinity to resin composite monomers and polymerized chains

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Specialty type: Medicine, research and experimental**Provenance and peer review:** Invited article; Externally peer reviewed.**Peer-review model:** Single blind**Peer-review report's classification****Scientific Quality:** Grade B**Novelty:** Grade B**Creativity or Innovation:** Grade B**Scientific Significance:** Grade B**P-Reviewer:** Arumugam EAP**Received:** March 10, 2024**Revised:** October 3, 2024**Accepted:** October 30, 2024**Published online:** March 20, 2025**Processing time:** 291 Days and 0.9 Hours**Pedro Henrique Sette-de-Souza, Moan Jéfter Fernandes Costa**, Faculdade de Odontologia, Universidade de Pernambuco-campus Arcoverde, Arcoverde 56503-146, Pernambuco, Brazil**Pedro Henrique Sette-de-Souza**, Programa de Pós-Graduação em Saúde e Desenvolvimento Socioambiental, Universidade de Pernambuco-campus Garanhuns, Garanhuns 55294-902, Pernambuco, Brazil**Moan Jéfter Fernandes Costa**, Programa de Pós-Graduação em Biologia Celular e Molecular Aplicada, Universidade de Pernambuco-campus Santo Amaro, Recife 50100-130, Pernambuco, Brazil**Boniek Castillo Dutra Borges**, Department of Odontologia, Universidade Federal do Rio Grande do Norte, Natal 59056-000, Rio Grande do Norte, Brazil**Boniek Castillo Dutra Borges**, Programa de Pós-Graduação em Ciências Odontológicas, Universidade Federal do Rio Grande do Norte, Natal 59056-000, Rio Grande do Norte, Brazil**Corresponding author:** Pedro Henrique Sette-de-Souza, DDS, MSc, PhD, Full Professor, Faculdade de Odontologia, Universidade de Pernambuco-campus Arcoverde, Rua Cícero Monteiro de Melo, s/n-São Cristóvão, Arcoverde/PE, Arcoverde 56503-146, Pernambuco, Brazil.pedro.souza@upe.br**Abstract****BACKGROUND**

Due to saliva and salivary glands are reservoir to severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2), aerosols and saliva droplets are primary sources of cross-infection and are responsible for the high human-human transmission of SARS-CoV-2. However, there is no evidence about how SARS-CoV-2 interacts with oral structures, particularly resin composites.

AIM

To evaluate the interaction of SARS-CoV-2 proteins with monomers present in resin composites using in silico analysis.

METHODS

Four SARS-CoV-2 proteins [*i.e.* main protease, 3C-like protease, papain-like protease (PLpro), and glycoprotein spike] were selected along with salivary amylase as the positive control, and their binding affinity with bisphenol-A glycol

dimethacrylate, bisphenol-A ethoxylated dimethacrylate, triethylene glycol dimethacrylate, and urethane dimethacrylate was evaluated. Molecular docking was performed using AutoDock Vina and visualised in Chimera UCSF 1.14. The best ligand-protein model was identified based on the binding energy (ΔG -kcal/mol).

RESULTS

Values for the binding energies ranged from -3.6 kcal/mol to -7.3 kcal/mol. The 3-monomer chain had the lowest binding energy (*i.e.* highest affinity) to PLpro and the glycoprotein spike. Non-polymerised monomers and polymerised chains interacted with SARS-CoV-2 proteins *via* hydrogen bonds and hydrophobic interactions. Those findings suggest an interaction between SARS-CoV-2 proteins and resin composites.

CONCLUSION

SARS-CoV-2 proteins show affinity to non-polymerised and polymerised resin composite chains.

Key Words: Composite resins; COVID-19; SARS-CoV-2; Dental restorations; Molecular docking simulation; Dentistry

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Core Tip: The severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) may interact with monomers of resin composites; triethylene glycol dimethacrylate has the smallest affinity with SARS-CoV-2 among monomers; bisphenol-A glycol dimethacrylate and bisphenol-A ethoxylated dimethacrylate show a remarkable affinity mainly with papain-like protease.

Citation: Sette-de-Souza PH, Fernandes Costa MJ, Dutra Borges BC. SARS-CoV-2 proteins show great binding affinity to resin composite monomers and polymerized chains. *World J Exp Med* 2025; 15(1): 94022

URL: <https://www.wjgnet.com/2220-315x/full/v15/i1/94022.htm>

DOI: <https://dx.doi.org/10.5493/wjem.v15.i1.94022>

INTRODUCTION

Saliva and salivary glands are a significant reservoir for severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) [1]. Aerosols and saliva droplets are primary sources of cross-infection and are responsible for the high human-human transmission of SARS-CoV-2[2,3]. Once saliva wets oral tissues, tooth structures, and dental restoratives present in the oral cavity, SARS-CoV-2 can bind to them, thereby increasing the permanence of microorganisms in the mouth.

Among dental restoratives, resin composites are widely used to restore decayed teeth[4] due to their aesthetic properties and capacity to preserve healthy tooth tissues. Such materials contain organic monomers such as bisphenol A glycol dimethacrylate [bisphenol-A glycol dimethacrylate (Bis-GMA)], bisphenol A ethoxylated dimethacrylate [bisphenol-A ethoxylated dimethacrylate (Bis-EMA)], triethylene glycol dimethacrylate (TEGDMA), and urethane dimethacrylate (UDMA), along with inorganic filler particles[5]. Those monomers present chemical components such as hydroxyl, oxygen, and nitrogen that affect intermolecular interactions with substrates[6,7]. It has been demonstrated that, aside from taking shelter on dental biofilms, SARS-CoV-2 can interact with oral tissues and tooth structures[8,9]. However, it remains unclear whether SARS-CoV-2 proteins interact with resin composites.

Knowing the sites within the mouth that can harbour SARS-CoV-2 is essential for understanding its spread once saliva is not the only oral harbour for viruses[9]. However, the mechanism by which SARS-CoV-2 colonises dental biofilm remains unclear. At the same time, the acquired pellicle (AP) may form on any exposed surface, including dental materials, through the selective adsorption of proteins[10]. Thus, SARS-CoV-2 proteins may interact with dental materials and collaborate in the formation of AP.

Given the above, *in silico* analyses play a remarkable role in investigations involving cellular and molecular processes [11,12]. The molecular docking method, which entails searching for probable interactions between microorganisms' proteins and substrates, has been used worldwide as the first step to understanding probable interactions with SARS-CoV-2[13]. That computational approach is an essential tool due to the urgent need to better understand SARS-CoV-2's effects on human health.

Against that background, in our study we evaluated the possible interaction of SARS-CoV-2 proteins with monomers and polymers present in resin composite *in silico*. The null hypothesis tested was that an interaction between the SARS-CoV-2 proteins and the monomers and other proteins would not occur.

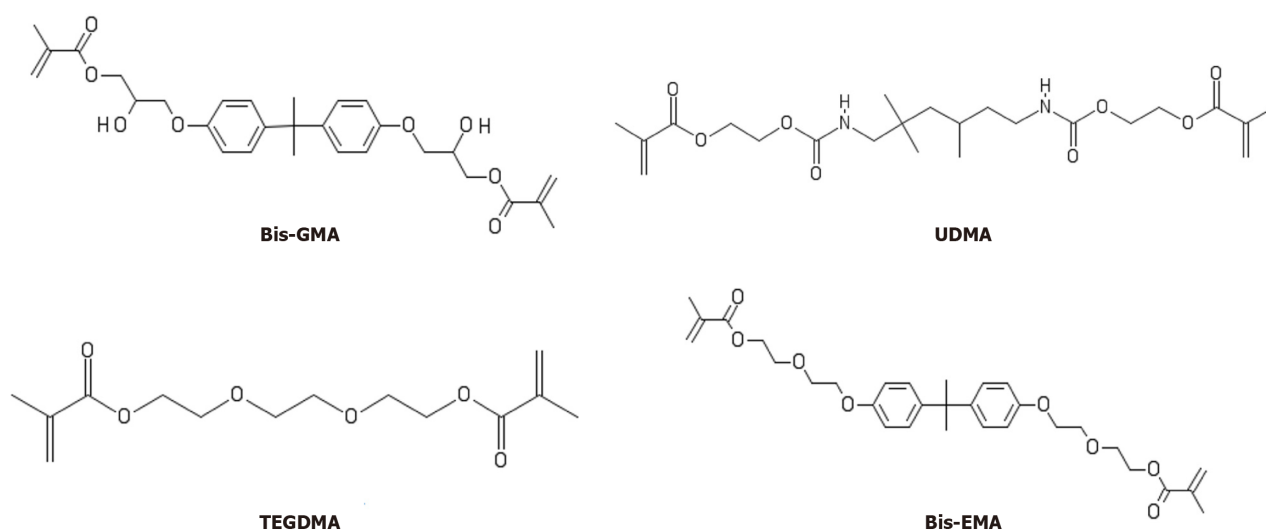


Figure 1 Chemical structure of the tested monomers: Bisphenol-A glycol dimethacrylate, bisphenol-A ethoxylated dimethacrylate, triethylene glycol dimethacrylate, and urethane dimethacrylate. Bis-EMA: Bisphenol-A ethoxylated dimethacrylate; Bis-GMA: Bisphenol-A glycol dimethacrylate; UDMA: Urethane dimethacrylate; TEGDMA: Triethylene glycol dimethacrylate.

MATERIALS AND METHODS

Protein selection and structure preparation

SARS-CoV-2 has some proteins involved in biological processes related to coronaviruses[14]. Thus, to simulate a whole new coronavirus, four different SARS-CoV-2 protein groups—the main protease (Mpro) (PDB: 6LU7), 3C-like protease (3CLpro) (PDB: 6M2N), papain-like protease (PLpro) (PDB: 6W9C), and glycoprotein spike (PDB: 6VYB)—were selected in light of previous studies[15–17]. For a positive control, we used salivary amylase (PDB: 3BLP) because it is involved in AP formation on multiple surfaces[10].

The crystal structures of SARS-CoV-2 proteins were obtained from the GenBank National Center for Biotechnology Information (RRID: SCR_002760). The AutoDock (RRID: SCR_012746) was used to delete duplicated chains, heteroatoms, and water molecules, as well as add polar hydrogens atoms and the charge of all atoms in the protein structure. Gasteiger charges were computed, and the structure was saved as a PDBQT file for the docking studies.

Ligand selection and structure preparation

The monomers Bis-GMA ($C_{29}H_{36}O_8$, PubChem CID: 15284), TEGDMA ($C_{14}H_{22}O_6$, PubChem CID: 7979), UDMA ($C_{23}H_{38}N_2O_8$, PubChem CID: 170472), and Bis-EMA ($C_{31}H_{40}O_8$, PubChem CID: 92523) were used in this study. Their chemical structures appear in Figure 1.

After retrieving SMILE codes from the National Center for Biotechnology Information's chemical structure library (RRID: SCR_004284), we constructed multiple chains through monomer combination using PubChem Draw (RRID: SCR_021249). We also linked the individual chains to simulate the natural polymerised resin composite. Next, we simulated various polymerised chains linking the monomer methacrylate regions during polymerisation, after which we transformed the new SMILE code in a PDB file in Chimera UCSF 1.14 (RRID: SCR_004097).

The rotatable bonds of the ligands were defined using AutoDock, and the structures were saved as PDBQT files for use in the docking studies.

Docking procedure

The Autogrid algorithm created the three-dimensional grids to generate the grid parameter files (RRID: SCR_015982). Each grid map was set to the centre of chain A, docking parameters were set according to the protein (Table 1), and all analyses were performed with a/an exhaustiveness value of 8.

Molecular docking was performed using AutoDock Vina (RRID: SCR_011958), and the best ligand–protein model was identified based on the binding energy (ΔG -kcal/mol)[18].

Docking visualisation

The results obtained through the docking procedure were visualised in Chimera UCSF 1.14 (RRID: SCR_004097). The two-dimensional interactions of the complex protein–ligand structure, including hydrogen bonds and bond lengths, were analysed in LigPlot+ (RRID: SCR_018249) for all interactions[19]. The step-by-step methodological approach that we followed is depicted in Figure 2.

Table 1 Binding energy (ΔG -kcal/mol) and standard deviation of the interaction between the severe acute respiratory syndrome-coronavirus 2 proteins and resin composite

Chain	Binding energy (ΔG -kcal/mol)				
	6LU7 ¹	6M2N ¹	6W9C ¹	6VYB ¹	3BLP ¹
3-monomer-chain	-4.95 ± 0.53	-5.28 ± 0.65	-5.46 ± 0.83	-5.15 ± 0.49	-5.63 ± 0.48
2-monomer-chain	-4.71 ± 0.72	-4.93 ± 0.71	-4.78 ± 0.83	-4.85 ± 0.56	-5.17 ± 1.30
Monomers	-5.05 ± 0.66	-5.28 ± 0.47	-5.25 ± 1.10	-5.03 ± 0.53	-5.05 ± 0.76
Hydroxyapatite	-4.2	-4.6	-5.1	-4.9	-4.8
PO ₄	-3.3	-3.2	-3.6	-3.6	-3.7

¹Severe acute respiratory syndrome-coronavirus 2.

6LU7: Main protease; 6M2N: 3C-like protease; 6W9C: Papain-like protease; 6VYB: Glycoprotein spike; 3BLP: Salivary amylase.

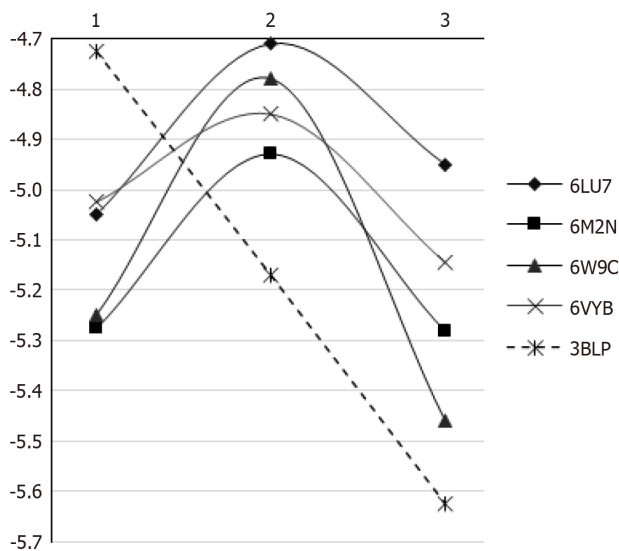


Figure 2 Binding energy between severe acute respiratory syndrome-coronavirus 2 proteins and resin composite chains. 1: Monomer; 2: Two-monomer chain; 3: Three-monomer chain.

RESULTS

Binding energy evaluation

Binding energies ranging from -3.1 kcal/mol to -8.0 kcal/mol were found. The 3-monomer chain had the lowest binding energy (*i.e.* highest affinity) to PLpro, the glycoprotein spike, and salivary amylase (Table 1). For all tested proteins, the 2-monomer chain demonstrated the highest binding energy.

Interaction analyses

To observe the specific interactions between monomers and proteins, we used LigPlot*. The central oxygen and nitrogen atoms from monomers were involved in hydrogen bonds with amino acid residues, and some alkene groups of monomers presented hydrophobic interactions with the residues. Those interactions were also observed in the polymerised chains.

Non-polymerised monomers and polymerised chains interacted with SARS-CoV-2 proteins *via* hydrogen bonds and hydrophobic interactions (Figure 3). Beyond that, any SARS-CoV-2 protein may have interacted with many non-polymerised and polymerised chains simultaneously (Figure 4).

DISCUSSION

The null hypothesis tested in our study—that an interaction between the SARS-CoV-2 proteins and the monomers and polymers would not occur—was rejected because the binding affinity between all monomers and polymers and all proteins (*i.e.* Mpro, 3CLpro, PLpro, and the glycoprotein spike) was observed.

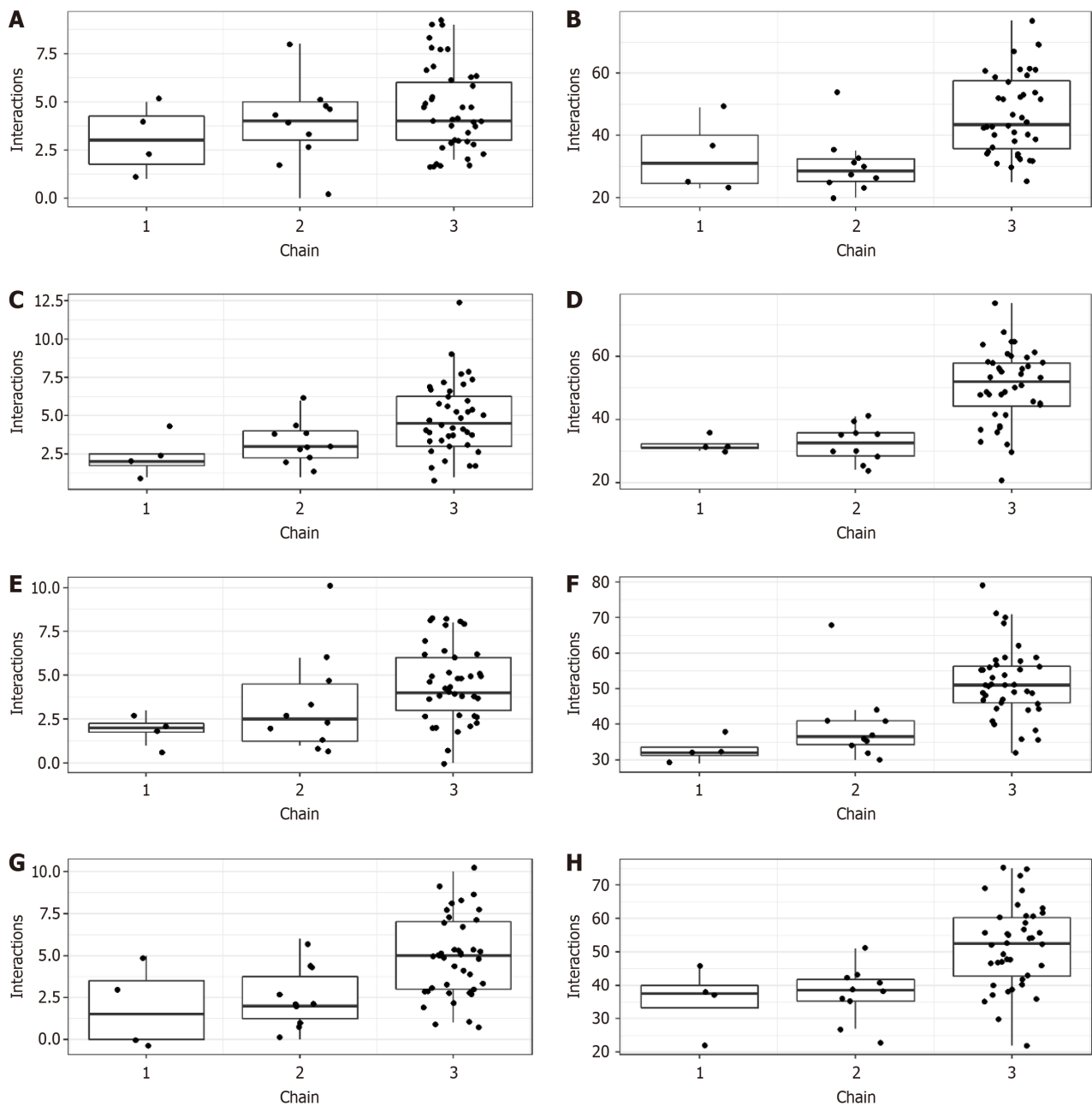


Figure 3 Interactions between severe acute respiratory syndrome-coronavirus 2 proteins and resin composite. A: Hydrogen bond between 6LU7 and resin composite; B: Hydrophobic interactions between 6LU7 and resin composite; C: Hydrogen bond between 6M2N and resin composite; D: Hydrophobic interactions between 6M2N and resin composite; E: Hydrogen bond between 6VYB and resin composite; F: Hydrophobic interactions between 6VYB and resin composite; G: Hydrogen bond between 6W9C and resin composite; H: Hydrophobic interactions between 6W9C and resin composite.

Among other results, Bis-GMA and Bis-EMA showed remarkable binding energy with all tested proteins, with ΔG values equal to or less than -5.0 kcal/mol. Such affinity relates to the number of interactions presented (*i.e.* hydrogen bonds and hydrophobic interactions) such that hydrogen bonds are more potent than hydrophobic interactions[20]. A higher number of oxygen atoms and a central, highly hydrophobic group present in Bis-GMA and Bis-EMA formed hydrogen bonds with hydroxyl radicals of polar amino acid residues and hydrophobic interactions with nonpolar amino acid residues. The fact that Mpro showed the highest binding energy to UDMA can be due to many interactions, primarily hydrogen bonds. A highly hydrophobic central area of Bis-EMA promoted many hydrophobic interactions with residues of PLpro, which was responsible for promoting the highest binding energy. Meanwhile, the highest binding energy (*i.e.* lowest affinity) obtained between TEGDMA and all proteins tested related to its having the smallest area of the monomers, which decreased the number of interactions with amino acid residues.

We evaluated binding energy values and interactions between SARS-CoV-2 proteins and non-polymerised methacrylate monomers and polymerised chains of resin composites. The growth of polymeric chains occurs when monomers are linearly connected by converting double $C=C$ bonds into $C-C$ bonds from different terminal methacrylate groups [21]. Monomers, especially Bis-GMA, may also be cross-linked *via* hydrogen bonds between hydroxyl groups and nitrogen or oxygen[22]. Thus, because hydrogen bonds and hydrophobic interactions between each non-polymerised

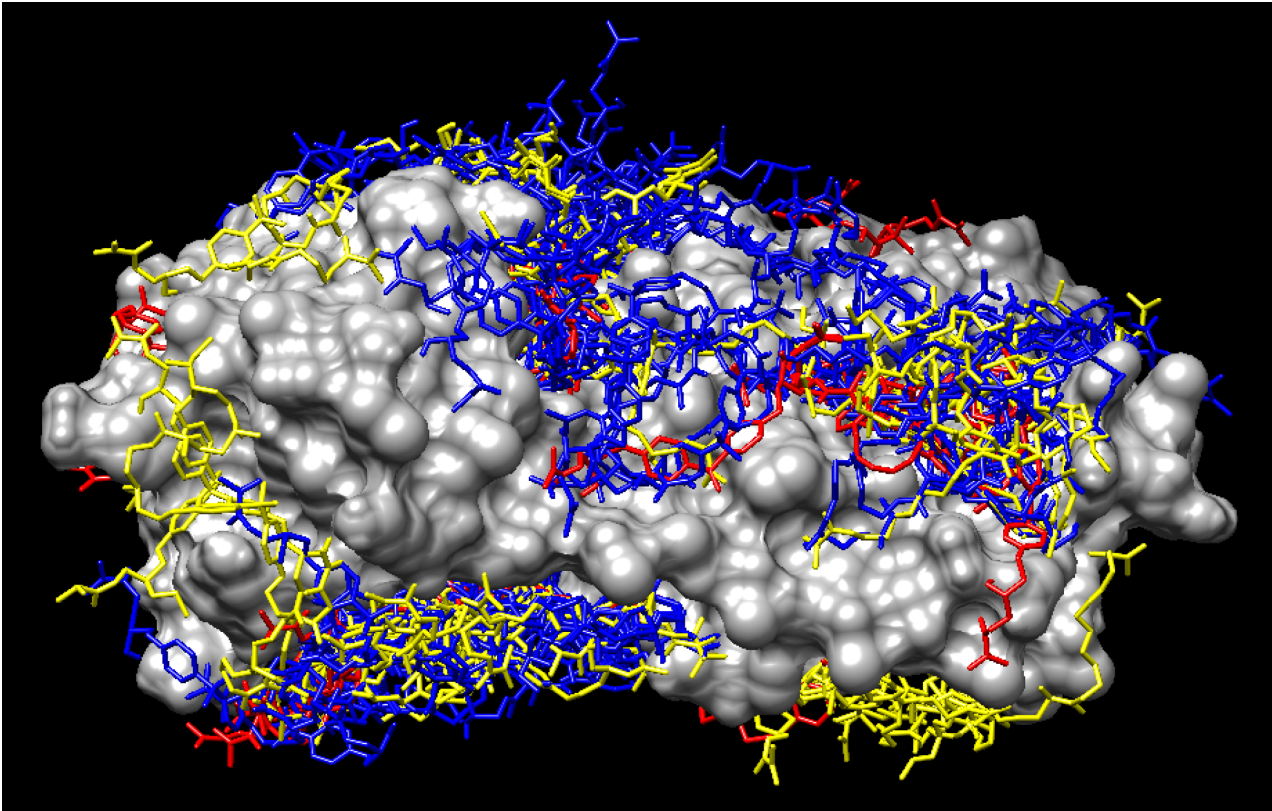


Figure 4 Graphical interaction between unpolymerised chain (red), 2-monomer chain (yellow), 3-monomer polymerised chain (blue), and the severe acute respiratory syndrome-coronavirus 2 protein.

monomer and SARS-CoV-2 proteins did not involve terminal methacrylate groups or hydroxyl groups in Bis-GMA, it was probable that similar binding between SARS-CoV-2 proteins and a polymerised chain would occur. Our results validate that assumption.

In a tooth preparation restored with resin composite, polymer chains of polymerised monomers and filler particles are likely present[21]. In general, resin composite restorations are polished in clinical conditions in order to achieve adequate smoothness and aesthetic properties and expose filler particles[23]. Thus, further investigations should evaluate the binding affinity of SARS-CoV-2 proteins to different filler particles. If a high binding affinity between them were found, then an increase the number of microorganisms might increase in resin composite restorations, and all implications highlighted by our results might increase. At the same time, another study[10] has shown that salivary amylase interacts with resin composites and collaborates in AP formation in filled resin composites. Thus, given our results, we believe that SARS-CoV-2 may also collaborate in AP formation.

In our computational study of a new microorganism, evidence to compare and corroborate our findings was inadequate. In response, *in vitro* and *in vivo* analyses need to be performed to validate our findings. Further research should also be conducted to clarify the mechanisms of interaction observed in our study. Despite those limitations, the chief strength of our work lies in its being the first to provide data about a possible interaction between resin composites and SARS-CoV-2. Besides that, due to concerns about the degradation of the resin–dentin interface[24], further studies could be performed to determine whether the virus will adhere to resin and collaborate in the resin–dentin degradation in dental adhesive systems.

CONCLUSION

SARS-CoV-2 proteins (*i.e.* Mpro, 3CLpro, PLpro, and the glycoprotein spike) showed an affinity to non-polymerised and polymerised resin composite chains.

FOOTNOTES

Author contributions: Sette-de-Souza PH, Fernandes Costa MJ and Dutra Borges BC designed, performed the experiments, acquired, analyzed, and interpreted the data; all of the authors wrote the manuscript and approved the final version of the article.

Supported by The Coordenação de Aperfeiçoamento de Pessoal de Nível Superior-Brasil (CAPES), No. 001.

Conflict-of-interest statement: All authors declare no conflict of interest in publishing the manuscript.

Data sharing statement: Request to the corresponding author.

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S-Editor: Luo ML

L-Editor: A

P-Editor: Zheng XM

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