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Article

Analysis of Molecular Mimicry between Antigens of the SARS-CoV-2 and Dengue Viruses: Implications for Cross-Reactivity

Carolina Prieto Silva [1], Marlon Munera [2,*] and Andres Sanchez [2]

[1] Department of Bacteriology and Clinical Laboratory, Faculty of Health, University of Pamplona, Pamplona 543050, Colombia

[2] Department of Health, Corporación Universitaria Rafael Nuñez (Ginumed), Caratgena 130001, Colombia

[*] Correspondence: marmunera@gmail.com

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Abstract: The co-circulation of dengue virus (DENV) and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in endemic regions poses significant immunological challenges, particularly in the context of cross-reactivity and vaccine design. Leveraging an in-silico pipeline, this study sought to identify conserved antigenic determinants between DENV serotype 1 (DENV-1) and SARS-CoV-2 that may underlie molecular mimicry and immunological cross-reactivity. Viral protein sequences were obtained from UniProt, structurally modeled via SWISS-MODEL, and aligned using PRALINE. Conserved regions were mapped and visualized using PyMOL to identify accessible surface-exposed epitopes. Strikingly, up to 42% sequence identity was observed between DENV-1 polyproteins and SARS-CoV-2 proteins, including the nucleoprotein (N), spike (S), and nonstructural proteins NS7a and NS7b. Several conserved patches displayed surface accessibility, reinforcing their potential to elicit cross-reactive B or T cell responses. These findings highlight a critical concern in co-endemic settings: pre-existing DENV immunity could alter the outcome of SARS-CoV-2 infection or vaccination through heterologous immune responses, potentially contributing to antibody-dependent enhancement (ADE) or atypical inflammatory profiles. From an immunotherapeutic perspective, the identification of shared epitopes underscores the need for precision design in vaccines and monoclonal antibody therapies to avoid unintended immunopathology. While this bioinformatic study provides a foundational framework for predicting cross-reactive epitopes, experimental validation using serological assays, neutralization tests, and T cell activation studies are imperative. Ultimately, a deeper understanding of DENV–SARS-CoV-2 molecular mimicry may inform the development of safer and more effective immunotherapeutic strategies in regions burdened by both pathogens.

Keywords: Molecular Mimicry; Cross-Reactivity; Dengue Virus; SARS-CoV-2; Immunotherapy; Epitope Conservation

1. Introduction

In recent decades, the geographical expansion of dengue and the emergence of new SARS-CoV-2 variants have posed significant challenges to global public health. According to estimates by the World Health Organization (WHO), between 100 and 400 million dengue infections are reported each year, with approximately 100 million symptomatic cases and around 22,000 deaths. Meanwhile, coronavirus disease 2019 (COVID-19), caused by the SARS-CoV-2 virus, has infected more than 640 million people worldwide and resulted in over 6.6 million deaths globally, based on WHO data through December 2022 [1,2].

From a genomic and proteomic perspective, dengue virus (DENV) is a flavivirus with a single-stranded, positive-sense RNA genome of approximately 10.7 kilobases (kb). This genome encodes a polypeptide of about 3,400 amino acids that is processed into three structural proteins (C, prM/M, and E) and seven non-structural proteins (NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5). On the other hand, SARS-CoV-2 belongs to the Coronaviridae family and has a single-stranded, positive-sense RNA genome of about 30 kb, making it one of the largest known RNA viruses. Its structural proteins include S, E, M, and N, while its non-structural proteins derive from the processing of two large polyproteins (ORF1a and ORF1b) [3,4].

Cross-reactivity between DENV and SARS-CoV-2 presents a considerable challenge in the specific diagnosis of viral diseases, especially in regions where both infections co-circulate endemically or epidemically. The presence of antibodies and T cells capable of recognizing common epitopes in different pathogens can lead to false-positive or false-negative serological results, hindering the accurate identification of active infections. This phenomenon not only complicates clinical decision-making—making differential diagnoses more difficult—but also impacts epidemiological surveillance and the evaluation of public health interventions [5–7]. Consequently, developing highly specific diagnostic methods and gaining a detailed understanding of cross-reactivity mechanisms are crucial for improving diagnostic accuracy and ultimately optimizing the management and control of both diseases.

Moreover, the potential impact of cross-reactivity on vaccine development is another critical consideration. The presence of shared epitopes between DENV and SARS-CoV-2 could influence the immune response elicited by vaccine formulations designed for one virus or the other, potentially leading to atypical immune reactions or suboptimal efficacy. Understanding these molecular phenomena and their relevance to immunogenicity is an essential step in designing vaccines that can induce protective, specific responses while minimizing the risk of adverse events associated with inducing cross-reactive antibodies or T cells [7].

In this context, bioinformatics has become an essential tool for studying epitopes and antigens. Computational analysis enables the rapid and systematic processing of large volumes of genomic and proteomic data, making it easier to identify conserved and potentially immunogenic sequences [8]. By using epitope prediction algorithms and protein-antibody interaction modeling, it is possible to evaluate the likelihood of cross-reactive immune responses and prioritize those segments with greater clinical relevance for subsequent in vitro and vivo studies [9]. In the present work, we employed various bioinformatic tools to identify and characterize protein regions potentially shared between DENV and SARS-CoV-2. Our goal is to provide evidence of the immunological interaction between these two viruses, as well as to lay the foundation for developing more specific diagnostic, therapeutic, and vaccine strategies for immunotherapy. By delving into the molecular mechanisms underlying cross-reactivity, we hope to contribute to a deeper understanding of these two diseases and, ultimately, to support their control on a global scale.

2. Materials and Methods

2.1. Retrieval of Viral Antigens

Protein sequences corresponding to DENV-1 and SARS-CoV-2 were retrieved from the UniProt and NCBI databases [10]. For DENV-1, we prioritized full-length, well-annotated genome polyproteins (UniProt IDs: B5AGU1, P17763, P27909) because dengue virus encodes a single polyprotein that is proteolytically processed into all structural proteins (C, prM/M, E) and non-structural proteins (including NS1–NS5). Consequently, immunogenic antigens such as NS1 and E were not omitted; they are inherently represented within the selected polyprotein sequences. Using three independent polyprotein entries reduces isolate-specific bias and increases the robustness and reproducibility of conservation estimates in molecular mimicry screening. For SARS-CoV-2, 23 proteins were identified, including structural (S, E, M, N), non-structural, and accessory proteins. Several proteins shared common UniProt accessions due to polyprotein processing, especially for SARS-CoV-2 (e.g., P0DTC1 and P0DTD1).

Selection criteria for inclusion were: (i) complete or near-complete sequence length with clear annotation; (ii) reference-quality entries widely used in molecular databases; and (iii) suitability for downstream comparative alignment and structural modeling workflows.

2.2. Homology-Based Structural Modeling

All 3D structure models from SARS-CoV-2 were retrieved from SWISS-MODEL repository reported online. Web consulted: https://swissmodel.expasy.org.

2.3. Identification of Conserved Sequences

Sequence alignments were conducted using PRALINE [11], a multiple sequence alignment tool, to identify conserved regions between SARS-CoV-2 and DENV-1 proteins. Alignments were assessed for regions with ≥ 30% identity, considered potentially relevant for immunological cross-reactivity. Conservation percentages ranged up to 42% between selected protein pairs (e.g., NS7b and DENV polyproteins).

Protein pairs were initially prioritized using a pragmatic sequence-identity filter (≥30%) as a coarse screening step to reduce the search space. This threshold was not intended to imply immunological cross-reactivity; rather, it served to enrich candidates for downstream epitope-level analyses. Candidate pairs were subsequently evaluated using epitope-focused criteria, including the presence of conserved contiguous segments and structural mapping of conserved, surface-accessible patches in the modeled proteins.

We did not conduct phylogenetic or functional experiments to support evolutionary or functional convergence between ORF7a and prM/M; thus, the reported similarities should be interpreted as antigenic/structural hypotheses requiring validation.

2.4. Structural Mapping of Conserved Epitopes

Using PyMOL [12], conserved amino acid residues identified via PRALINE were mapped onto the three-dimensional structures of the SARS-CoV-2 proteins. This allowed the visualization of surface-exposed antigenic patches, which were considered potential cross-reactive B or T cell epitopes. Attention was given to residues forming accessible clusters or antigenic patches on proteins such as NS7a, Nucleoprotein (N), and Spike (S).

3. Results

3.1. Selection and Characterization of Viral Antigens

A total of 3 polyproteins from Dengue virus serotype 1 (DENV-1) (UniProt IDs: B5AGU1, P17763, P27909) and 23 proteins from SARS-CoV-2, including structural, non-structural, and accessory proteins, were selected for analysis. Due to the derivation of multiple proteins from the same precursor (e.g., ORF1ab), these were grouped into 12 distinct UniProt accession numbers for downstream processing (**Table 1**).

Table 1. List of antigens derived from SARS-CoV-2 and Dengue virus.

SARS-CoV-2			
Antigen	**Access Number**	**Aminoacid**	**Mass (Da)**
2'-O-ribose methyltransferase (nsp16)	P0DTD1	7096	794,058
3C-like proteinase (3CL-PRO)	P0DTC1	4405	489,989
Envelope small membrane protein (E protein)	P0DTC4	75	8,365
Guanine-N7 methyltransferase (ExoNnsp14)	P0DTD1	7096	794,058
Helicase (nsp13)	P0DTD1	7096	794,058
Host translation Inhibitor nsp1 (nsp1)	P0DTC1	4405	489,989
Membrane Protein (M protein)	P0DTC5	222	25,147
Non-structural protein 2 (nsp2)	P0DTC1	4405	489,989
Non-structural protein 4 (nsp4)	P0DTC1	4405	489,989
Non-structural protein 6 (nsp6)	P0DTC1	4405	489,989
Non-structural protein 7 (nsp7)	P0DTC1	4405	489,989
Non-structural protein 8 (nsp8)	P0DTC1	4405	489,989
Non-structural protein 9 (nsp9)	P0DTC1	4405	489,989
Non-structural protein 10 (nsp10)	P0DTC1	4405	489,989
Nucleoprotein (NC)	P0DTC9	419	45,626
orf1ab polyprotein	A0A6B9V049	7096	794,058
ORF10 protein	A0A663DJA2	38	4,449
Papain-like proteinase (PL-PRO)	P0DTC1	4405	489,989
Protein 3a	P0DTC3	275	31,123
Protein 7a	P0DTC7	121	13,744
Protein non-structural 7b (ns7b)	P0DTD8	43	5,18
Protein non-structural 8 (ns8)	P0DTC8	121	13,831
RNA-directed RNA polymerase (PolRdRp)	P0DTD1	7096	794,058
Spike protein S1	P0DTC2	1273	141,178

Table 1. *Cont.*

SARS-CoV-2			
Antigen	**Access Number**	**Aminoacid**	**Mass (Da)**
Antígenos de Dengue Virus Tipo 1			
Genome polyprotein	B5AGU1	3392	378,532
Genome polyprotein	P17763	3392	378,702
Genome polyprotein	P27909	3392	378,905
Proteinas No Estructurales DENV-1 NS3	P27909	3392	378,905

3.2. Structural Modeling of Viral Proteins

Homology models of the viral proteins were retrieved from SWISS-MODEL repository. Proteins exhibited fold expected for each family protein they belong to (Supplementary Materials).

3.3. Sequence Alignment and Epitope Conservation

Multiple sequence alignments using PRALINE identified conserved regions between DENV-1 and SARS-CoV-2 proteins. The following identity percentages were observed between DENV-1 polyproteins and selected SARS-CoV-2 proteins (**Table 2**): Up to 42% identity with NS7b (P0DTD8), 36% with protein 7a (P0DTC7), 34% with nucleoprotein (N) (P0DTC9), 30% with spike protein (S) (P0DTC2). Alignments with less than 30% identity were excluded from downstream analysis.

Table 2. Identification of the percentage identity obtained from the alignment of protein sequences of SARS-CoV-2 and Dengue Virus Type 1 using PRALINE.

SARS-CoV-2	UniProt	DENV-1	UniProt	% Identity	*p* Value
3C-like proteinase (3CL-PRO) Proteínas no estructurales: (nsp1) (nsp2)-(nsp4)-(nsp6)-(nsp7)-(nsp8)-(nsp9)-(nsp10)	P0DTC1	Genome polyprotein	B5AGU1	0.24	0.03
Papain-like proteinase (PL-PRO)					
Envelope small membrane protein (E protein)	P0DTC4			0.32	0.002
Membrane Protein (M protein)	P0DTC5			0.30	0.004
Nucleoprotein (NC)	P0DTC9			0.34	0.06
Protein 3a	P0DTC3			0.32	0.001
Protein 7a	P0DTC7			0.36	0.002
Protein non-structural 7b (ns7b)	P0DTD8			0.23	0.02
Protein non-structural 8 (ns8)	P0DTC8			0.33	0.006
Spike protein S1	P0DTC2			0.29	0.03
3C-like proteinase (3CL-PRO) Proteínas no estructurales: (nsp1) (nsp2)-(nsp4)-(nsp6)-(nsp7)-(nsp8)-(nsp9)-(nsp10)	P0DTC1	Genome polyprotein	P17763	0.23	0.06
Papain-like proteinase (PL-PRO)					
Envelope small membrane protein (E protein)	P0DTC4			0.35	0.001
Membrane Protein (M protein)	P0DTC5			0.31	0.002
Nucleoprotein (NC)	P0DTC9			0.34	0.06
Protein 3a	P0DTC3			0.33	0.002
Protein 7a	P0DTC7			0.35	0.03
Protein non-structural 7b (ns7b)	P0DTD8			0.42	0.001
Protein non-structural 8 (ns8)	P0DTC8			0.27	0.02
Spike protein S1	P0DTC2			0.30	0.002
3C-like proteinase (3CL-PRO) Proteínas no estructurales: (nsp1) (nsp2)-(nsp4)-(nsp6)-(nsp7)-(nsp8)-(nsp9)-(nsp10)	P0DTC1	Genome polyprotein	P27909	0.23	0.04
Papain-like proteinase (PL-PRO)					
Envelope small membrane protein (E protein)	P0DTC4			0.32	0.001
Membrane Protein (M protein)	P0DTC5			0.31	0.003
Nucleoprotein (NC)	P0DTC9			0.34	0.002
Protein 3a	P0DTC3			0.36	0.002
Protein 7a	P0DTC7			0.34	0.04
Protein non-structural 7b (ns7b)	P0DTD8			0.42	0.01
Protein non-structural 8 (ns8)	P0DTC8			0.33	0.02
Spike protein S1	P0DTC2			0.30	0.003

3.4. Structural Mapping of Conserved Antigenic Regions

3.4.1. Protein 7a (SARS-CoV-2) vs. DENV-1 B5AGU1

Structural alignment revealed a conserved segment from Met44 to Glu294, with 43 aligned residues and 36% identity. PyMOL modeling identified two antigenic patches on the surface of protein 7a: Patch A (green): 82Arg, 83Gly, 103Thr, 159Cys, 206Gln, 236Leu, 243Leu. Patch B (blue): 66Leu, 106Leu, 121Gly, 124Pro, 152Ala, 201His (**Figure 1**).

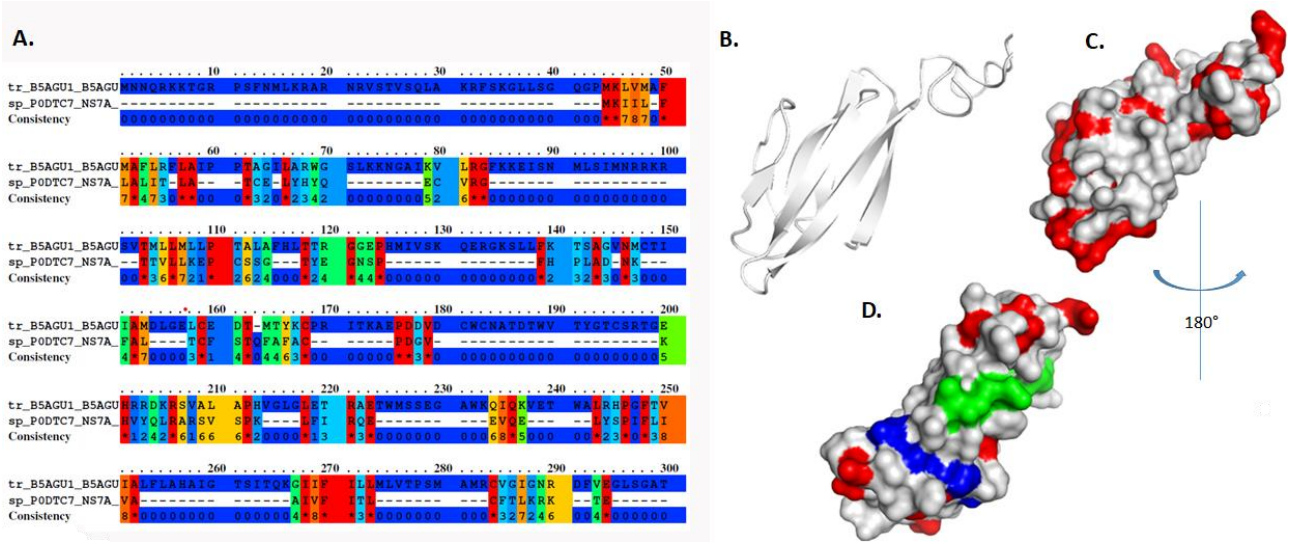

Figure 1. SARS-CoV-2 protein 7a with identification of conserved regions compared to the B5AGU1 polyprotein of DENV-1.

3.4.2. Nucleoprotein (SARS-CoV-2) vs. DENV-1 B5AGU1

The alignment revealed 141 conserved amino acids (34% identity) between residues Asn1339 and Asp2145. PyMOL-based structural mapping showed two prominent surface-exposed clusters: Cluster 1 (green): 1891Gly, 1903Arg, 1904Arg, 1914Gly, 1915Pro, 1916Glu, 1933Gln. Cluster 2 (green): 1666Thr, 1672Pro, 1673Gly, 1674Ser (**Figure 2**).

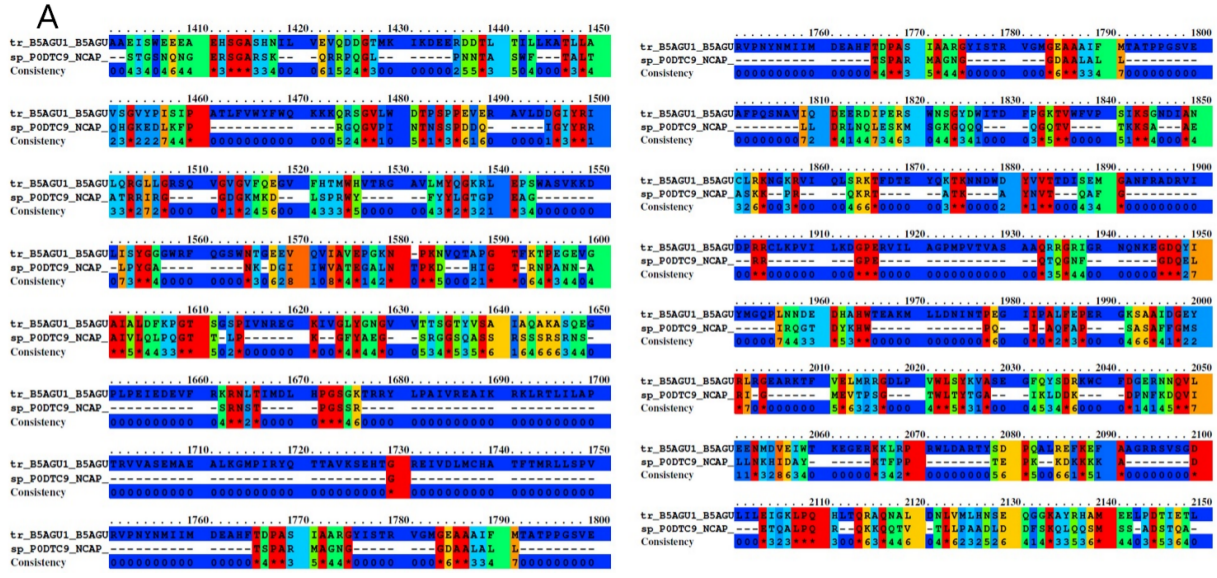

Figure 2. *Cont.*

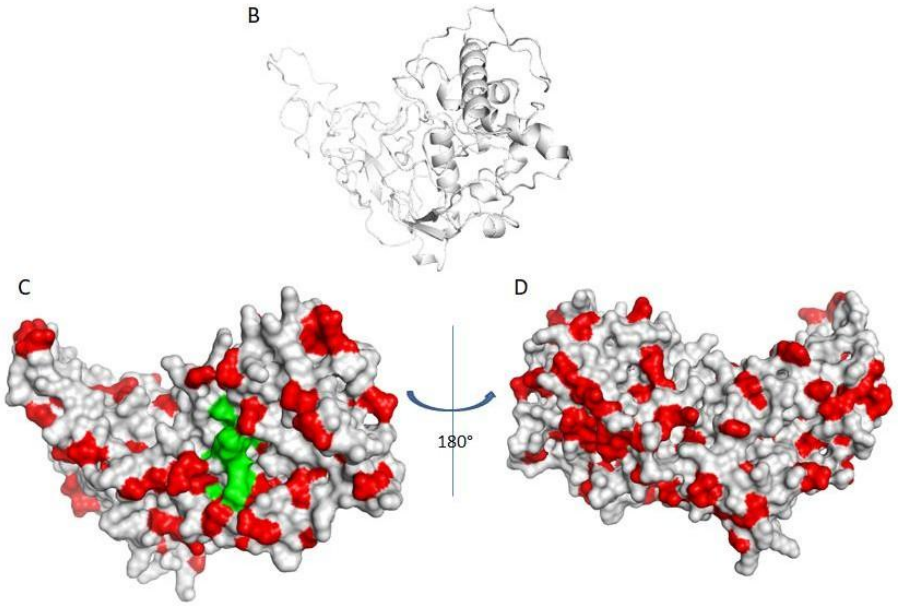

Figure 2. Conserved regions in PRALINE alignment of the SARS-CoV-2 nucleoprotein against the B5AGU1 polyprotein of DENV-1, with conserved regions highlighted in red.

3.4.3. Spike Protein (SARS-CoV-2) vs. DENV-1 Polyproteins P17763 and P27909

Spike protein showed ~30% identity with the P17763 and P27909 polyproteins of DENV-1, polyproteins, with 381 and 384 conserved amino acids respectively (**Figure 3**). Structural modeling was limited to residues 553–984, where several conserved, surface-exposed residues were mapped: Patch A (magenta): 617Pro, 629Asn, 633Ile, 634Thr, 648Asn. Patch B (green): 683Phe, 685Ala, 686Thr, 692Trp, 849Asn, 955Arg, etc. Additional clusters: 770Tyr, 777Ala, 778Asp, 779Ser, 862Lys, 867Val, 868Gly, 877Gly (**Figure 4**).

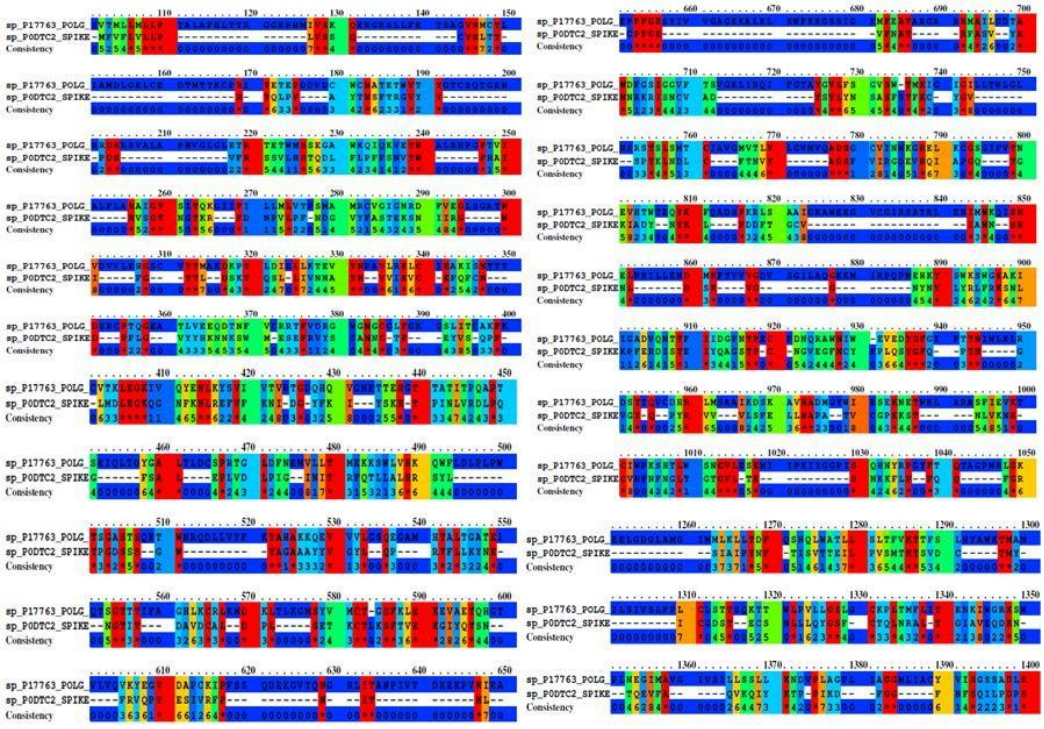

Figure 3. *Cont.*

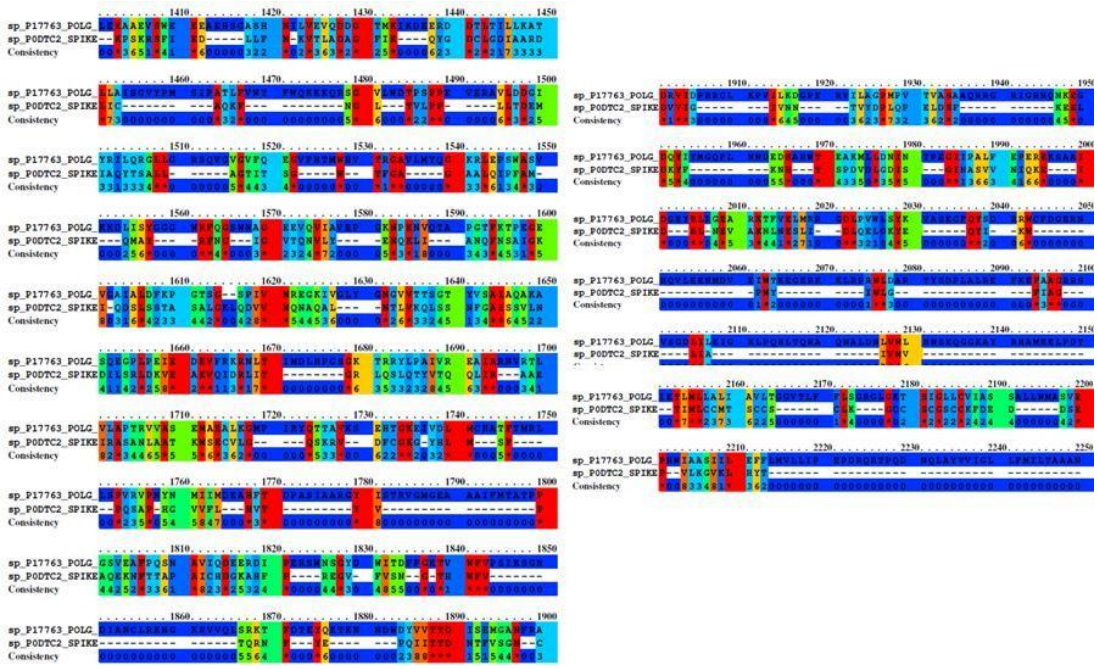

Figure 3. Conserved regions in PRALINE alignment of the SARS-CoV-2 spike protein against the P17763 polyprotein of DENV-1.

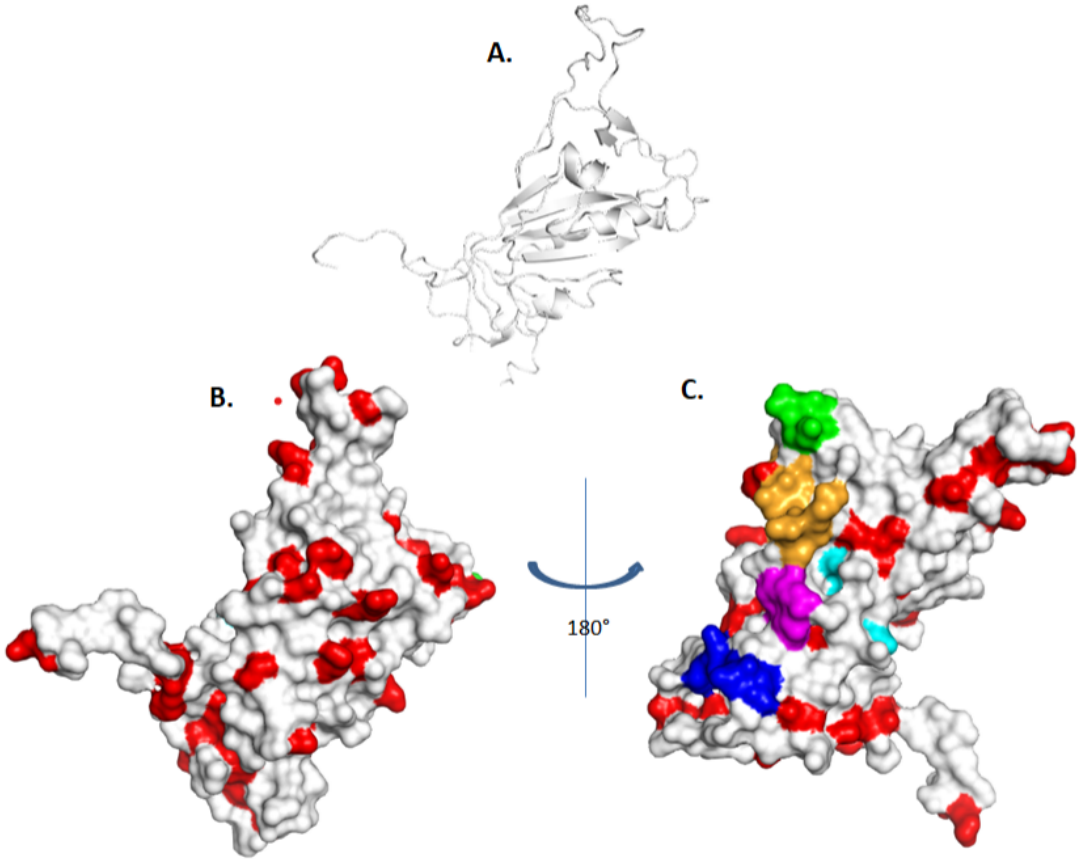

Figure 4. SARS-CoV-2 Spike protein with identification of conserved regions against the P17763 polyproteins of DENV-1.

3.4.4. NS7b (SARS-CoV-2) vs. DENV-1 Polyproteins P17763 and P27909

This protein pair showed the highest identity (42%) among all alignments. Although only 11 of the 18 conserved residues could be visualized due to template constraints, a hydrophobic epitope patch was clearly identified: Patch (green): 2973Ala, 2975Phe, 2976Leu, 2978Phe, 2981Leu (**Figure 5**).

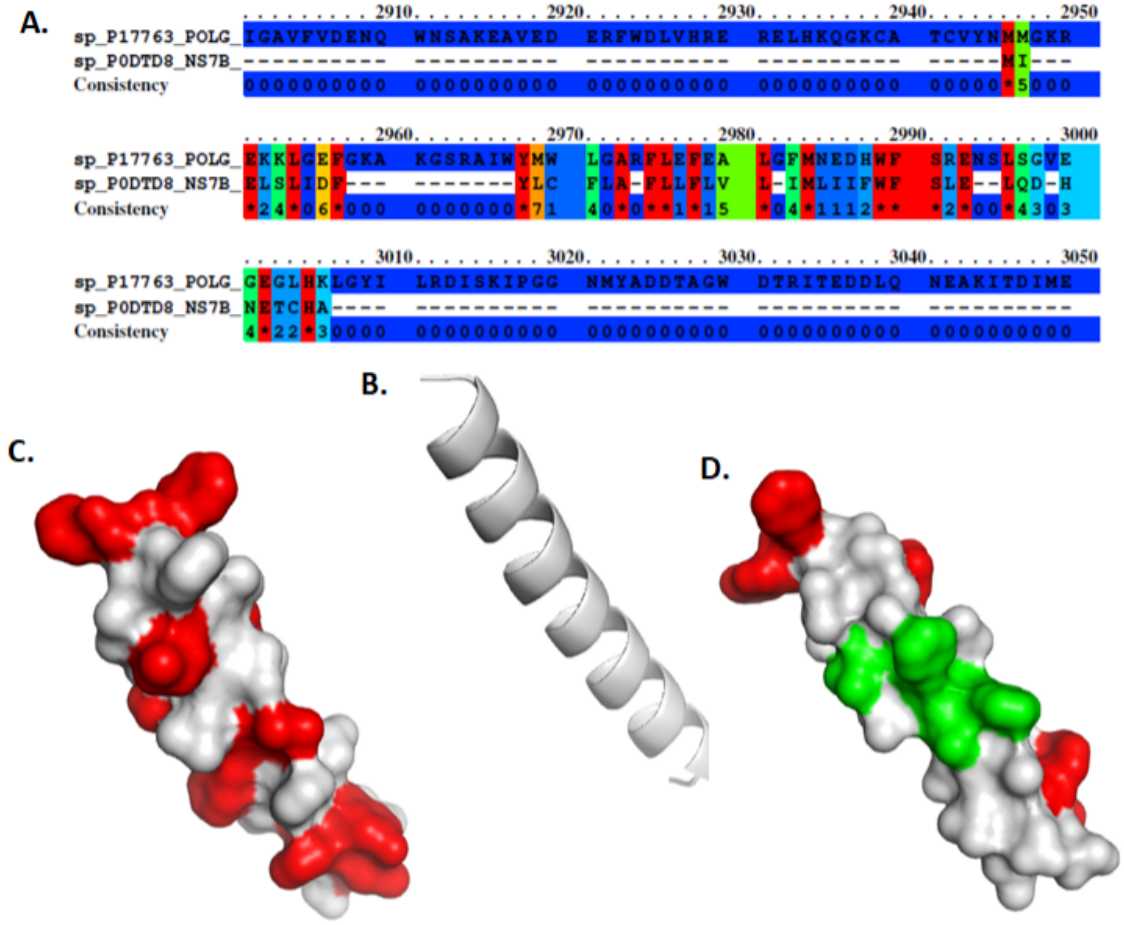

Figure 5. SARS-CoV-2 NS7b protein with identification of conserved regions against the P17763 polyprotein of DENV-1.

4. Discussion

The geographic co-circulation of Dengue virus (DENV) and SARS-CoV-2 in endemic regions poses serious public health challenges, especially regarding diagnostic accuracy and immune response modulation in previously exposed individuals [13–15]. Cross-reactivity arising from structurally conserved epitopes between both viruses has been documented and may contribute to misdiagnosis, immune interference, and atypical clinical presentations [16–18]. This study identified conserved antigenic regions, most notably between DENV-1 polyproteins and SARS-CoV-2 proteins such as NS7a, NS7b, nucleoprotein (N), and spike protein (S). NS7b exhibited up to 42% sequence identity, and structural modeling revealed accessible antigenic patches that may act as targets for B and T cell responses.

The spike protein, a major immunogen in current SARS-CoV-2 vaccines, shared 30% identity with DENV-1 polyproteins. Conserved residues mapped on the protein surface could represent cross-reactive epitopes, potentially explain false-positive serological results or alter immune responses in individuals with prior DENV infection [19]. Similar concerns were identified with the SARS-CoV-2 nucleoprotein, which shares 34% identity with DENV-1 NS3—an immunodominant antigen in flavivirus infections [20–23]. Furthermore, the structural similarity between SARS-CoV-2 protein 7a and DENV-1 prM/M suggests possible convergence in immune eva-

sion strategies, given their roles in viral maturation and modulation of host responses [19–22]. These findings raise concerns about antibody-dependent enhancement (ADE), a phenomenon previously reported in DENV and theoretically plausible in SARS-CoV-2 under cross-reactive conditions [18]. Our alignments showed 30–42% sequence identity between DENV-1 polyproteins and SARS-CoV-2 proteins such as spike, nucleoprotein, and ORF7 family members. While overall identity at this level does not guarantee functional cross-reactivity, the mapping of these conserved segments onto surface-exposed, immunodominant domains (notably spike RBD patches and nucleoprotein clusters) overlap with regions previously implicated in antibody binding in both viruses. These conserved, accessible epitopes are the most relevant candidates for generating cross-reactive, non-neutralizing antibodies, which are mechanistically associated with antibody-dependent enhancement (ADE) in flaviviruses. Thus, our data suggest that 30–42% identity is not just a background similarity but corresponds to regions of immunological importance where ADE-like mechanisms could plausibly occur, warranting experimental validation through neutralization and Fc-receptor–mediated uptake assays.

Spike (S) conserved patches fall around aa 617–648 and the S1/S2 junction (≈681–692), and into S2 (≈770–955). These segments overlap known immunodominant linear B-cell epitopes: multiple cohorts identified strong responses immediately N-terminal to the furin site (657–671) and at the S1/S2 and S2′ proteolytic sites (which include 681–686)—sites repeatedly mapped as serodominant in convalescent plasma and animal models. Several studies also report antibodies to adjacent S2 regions (including sites near 770–790 and within the central helix/HR1 corridor), though these are generally less potently neutralizing than RBD/NTD epitopes. Together, this supports that your S-region matches sit within known immunodominant/cleavage-proximal epitopes associated with functional antibody responses [21]. For Nucleocapsid (N), conserved N clusters map to the central linker/CTD half of N (per your alignment window), which independent studies consistently identify as serodominant linear epitope zones in humans (rich diagnostic targets, robust IgG binding across variants). While N-directed antibodies are typically non-neutralizing, these regions are immunodominant and highly reactive, matching the intent of your cross-reactivity argument [21]. ORF7 family (7a/7b) reports the highest conservation with 7b (≈42%) and accessible patches on 7a. Although neutralizing epitopes are classically defined on S, serology papers show that ORF7a/7b elicits measurable antibody responses and contains CD8/CD4 T-cell epitopes in patients; thus, your mapped, surface-exposed sites fall within documented immunogenic regions (antibody/T-cell), even if they are not established neutralizing sites [22,23]. For ADE context (DENV), the dengue epitopes most linked to ADE are prM and the E protein fusion loop (EDII 98–110); these are immunodominant, often non-neutralizing targets that mediate Fc-receptor uptake. Your cross-virus conservation does not claim identical ADE epitopes, but locates immunodominant, surface-exposed SARS-CoV-2 sites were cross-reactive, non-neutralizing antibodies (a mechanistic prerequisite for ADE) could arise in DENV-immune individuals—hence the call for Fc-mediated uptake/neutralization assays [24,25].

We acknowledge that selecting a global sequence-identity threshold (e.g., ≥30%) is a heuristic and does not provide immunological proof of cross-reactivity. In practice, cross-reactivity depends on epitope-level determinants, including the conservation of critical residues within the epitope, their spatial arrangement, and, for B-cell epitopes, structural similarity and surface accessibility rather than overall linear identity. Accordingly, in our workflow the ≥30% identity filter was used only to prioritize candidates for deeper analysis and was not interpreted as sufficient evidence of cross-reactivity. Our main inferences rely on epitope-oriented observations, particularly the identification of conserved contiguous regions and the localization of conserved residues into surface-exposed patches in the structural models, which are more directly relevant to plausible antibody accessibility and molecular mimicry.

The identification of conserved, surface-exposed epitopes supports the hypothesis that molecular mimicry may influence vaccine efficacy and safety in co-endemic regions. Vaccines targeting spike or nucleoprotein domains that overlap with DENV-1 antigens could inadvertently trigger pre-existing memory responses or non- neutralizing antibodies, increasing the risk of immunopathology. Therefore, epitope-level screening should be integrated into the early stages of vaccine and monoclonal antibody development. Immunotherapeutic candidates must be designed to avoid cross-reactive regions, especially in populations with high DENV seroprevalence. Similarly, diagnostic tools must discriminate between virus-specific and shared epitopes to ensure test accuracy in dengue-endemic settings. This in silico study provides a robust framework for predicting conserved immunogenic regions; however, it must be complemented with in vitro and in vivo validation. Functional assays to assess antibody binding, T cell activation, and potential for ADE are essential to confirm the immunological relevance of these findings. The novelty of

our work lies in demonstrating that the 30–42% sequence identity is not random but corresponds to structurally exposed clusters within immunodominant proteins (spike, nucleoprotein, ORF7a/7b). By integrating sequence conservation with structural accessibility, we identify concrete epitope patches that may underlie antibody cross-reactivity and potential ADE. This adds granularity beyond previous reports by pinpointing specific candidate regions that should be prioritized for experimental validation in co-endemic populations.

Future work should explore broader DENV serotypes, other coronaviruses, and structural refinements of predicted epitopes. This knowledge will enhance the rational design of next-generation vaccines and therapeutic platforms with improved specificity and safety profiles in the context of overlapping endemic viruses. A limitation is that we did not include immunoinformatic epitope predictions (e.g., NetMHCpan/NetMHCIIpan, BepiPred), which could further prioritize candidates and support HLA-restricted presentation hypotheses; this will be addressed in future work.

5. Conclusions

This study demonstrates that DENV-1 and SARS-CoV-2 share structurally conserved antigenic regions with the potential to elicit cross-reactive immune responses. Through bioinformatic analyses and structural modeling, we identified accessible epitope patches on key viral proteins—such as spike, nucleoprotein, and NS7b—that may contribute to immunological interference in co-endemic areas. These findings have important implications for the development of vaccines, diagnostic tools, and immunotherapies. Incorporating epitope-level specificity into the design of immunological interventions is essential to avoid unintended cross-reactivity, reduce the risk of antibody-dependent enhancement (ADE), and ensure efficacy and safety, particularly in populations with pre-existing flavivirus immunity. Future experimental validation will be critical to translate these insights into clinically relevant strategies for the prevention and management of viral co-infections. Overall, our findings identify conserved, surface-accessible candidate regions consistent with potential antigenic overlap; however, their immunodominance, neutralizing relevance, and any role in ADE require dedicated experimental validation.

Supplementary Materials

The supporting information can be downloaded at https://ojs.ukscip.com/files/TI-1375-Supplementary-Materials.docx.

Author Contributions

Conceptualization, C.P.S. and M.M.; methodology, C.P.S.; software, A.S.; validation, C.P.S., A.S. and M.M.; formal analysis, C.P.S.; investigation, C.P.S.; resources, M.M.; data curation, C.P.S.; writing—original draft preparation, C.P.S.; writing—review and editing, M.M.; visualization, A.S.; supervision, M.M.; project administration, M.M.; funding acquisition, M.M. All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement

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Informed Consent Statement

Not applicable.

Data Availability Statement

All data used in this study is public database such as Uniprot.

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Conflicts of Interest

The authors declare no conflict of interest.

AI Use Statement

The authors used ChatGPT 5.4 solely for grammar checking, sentence structure refinement, and improving the readability of the English text in this manuscript. The authors take full responsibility for all academic content, including all ideas, data, analyses, and conclusions presented herein. The use of AI was thoroughly reviewed and supervised by the authors.

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