

Repurposing plant-derived substances as antivirals against sars-cov-2

Redirecionando substâncias derivadas de plantas como antivirais contra Sars-cov-2

DOI:10.34119/bjhrv4n2-156

Recebimento dos originais: 18/02/2021 Aceitação para publicação: 18/03/2021

Luiza Eduarda Costa Silva

discente do curso de Biomedicina Universidade Estadual de Santa Cruz Rodovia Jorge Amado, km 16, s/n, Salobrinho, Ilhéus, Bahia, Brazil E-mail: luieduarda013@gmail.com

Eanes Pereira de Sousa

discente do curso de Biomedicina Universidade Estadual de Santa Cruz Rodovia Jorge Amado, km 16, s/n, Salobrinho, Ilhéus, Bahia, Brazil E-mail: eanessouza@gmail.com

Aline Oliveira da Conceição

Doutora em Biologia (Université du Québec a Montréal, 2010) Universidade Estadual de Santa Cruz Departamento de Ciências Biológicas, Rodovia Jorge Amado, km 16, s/n, Salobrinho, Ilhéus, Bahia, Brazil E-mail: aoconceicao@uesc.br

ABSTRACT

The urgent need for effective treatments for COVID-19 has developed, encouraging pharmaceutical companies to develop or redirect substances against SARS-CoV-2. Among them, substances used against worms, malaria, or bacteria were targeted to combat the virus. Such substances have been used in clinical trials and evaluated in vitro and in silico regarding the action on viral proteins, pharmacodynamics and toxicity of drugs. In this study, we conducted a systematic review of peer-reviewed articles involving molecules of plant origin with potential antiviral action on SARS-CoV-2. Reports containing the combinations of key words herbal, medicinal plants, natural products, and SARS-CoV-2 available from 01-01-2019 to 28-08-2020 in the Pubmed Central and World Wide Science sites were selected. A total of 677 items were retrieved. Of these, 170 were excluded because they were not complete, peer reviewed, freely, or related to vegetable products. Of the remaining, 345 were review articles, 23 were discussions, 4 were clinical trials, 14 showed in vitro experiments, and 121 were in silico studies. The proteins of SARS-CoV-2 considered as the therapeutic targets for the molecular docking were the structural spike glycoprotein (S protein), membrane protein Mpro, papain-like protease (PLpro), and RNA-dependent RNA polymerase (RdRp). Also, some studies have addressed the cell receptor ACE2 and natural products interaction. From in silico tests, therefore, 149 isolated plant molecules were identified with binding affinity to SARS-CoV-2 Mpro. Also, pharmacokinetic properties and bioavailability of some products were investigated highlighting the products nimbolide, withaferin-A, caffeic acid derivatives, rhamnetin, delta d-Viniferin, myri-citrin, chrysanthemin, myritilin,



taiwanhomoflavone A, lactucopicrin 15-oxalate, nympholide A, afzelin, biorobin, herperidin and phyllaemblicin B, glycyrrhizic acid, and rutin. As reported, rutin may influence viral functional protein assembly and host inflammatory suppression. Its affinity for Mpro and toll like receptors (TLRs) besides in vivo results render rutin a potential novel therapeutic anti-coronavirus strategy. This study highlights the in silico diversity of plant metabolites with high potential of antiviral activity against SARS-CoV-2 as alternatives in the repurposing course against COVID-19 as well as other viral pandemics that may arise.

Keywords: Coronavirus, Natural products, Medicinal plants, *in silico*.

RESUMO

No último ano, com o advento da pandemia pela COVID-19, doença causada pelo novo coronavírus associado à síndrome respiratória aguda (SARS-CoV-2), houve a necessidade urgente do desenvolvimento de tratamentos eficazes e a agilidade da indústria farmacêutica em desenvolver ou redirecionar substâncias utilizadas contra outros agentes para o combate do SARS-CoV-2. Entre essas substâncias, as empregadas no tratamento anti-helmíntico, anti-malária e antimicrobiano conhecidas foram utilizadas em ensaios clínicos e avaliadas in vitro e in silico em relação à ação sobre proteínas virais, farmacodinâmica e toxicidade de drogas. Entretanto, até o momento não existe um tratamento em uso, eficaz com ação direta sobre o vírus o que faz com que a busca de novas substâncias com ação seletiva sobre o SARS-CoV-2 continue necessária. Desta feita, neste estudo, realizou-se revisão sistemática de publicações científicas revisadas por pares envolvendo moléculas de origem vegetal com ação antiviral potencial sobre o SARS-CoV-2. Foram selecionados relatos contendo as combinações de palavras-chave herbal, medicinal plants, natural products e SARS-CoV-2 disponíveis de 01-01-2019 a 28-08-2020 nos sites Pubmed Central e World Wide Science. Na busca, foram recuperados 677 itens. Destes, 170 foram excluídos porque não estavam completos, não eram revisados por pares, não eram de acesso livre, ou não eram originados de plantas. Dos restantes, 345 eram artigos de revisão, 23 eram discussões, quatro eram ensaios clínicos, 14 mostravam experimentos in vitro e 121 eram estudos in silico. As proteínas do SARS-CoV-2 consideradas como alvos terapêuticos para o acoplamento molecular foram a glicoproteína estrutural spike (proteína S), proteína de membrana Mpro, protease papaína-like (PLpro) e RNA polimerase dependente de RNA (RdRp). Além disso, alguns estudos abordaram a interação entre o receptor celular ACE2 e produtos naturais. A partir de testes in silico, portanto, 149 moléculas vegetais isoladas foram identificadas com afinidade de ligação a Mpro do SARS-CoV-2. Também foram investigadas as propriedades farmacocinéticas e a biodisponibilidade de alguns produtos, destacando-se os produtos nimbolide, withaferin-A, derivados de ácido cafeico, ramnetina, delta d-Viniferina, mircitrina, crisantina, mirtilina, taiwanhomoflavona A, lactupicrina 15oxalato, ninfolfe A, afzelina, biorobina, herperidina e filaemblicina B, ácido glicirrízico e rutina. Destaca-se a rutina por sua ação tanto na montagem da proteína funcional viral como na supressão da inflamação do hospedeiro. Além disso, sua afinidade com a Mpro, com os receptores toll-like (TLRs) além de resultados in vivo tornam a rutina candidata à terapêutica anti-coronavírus. Este estudo destaca a diversidade dos metabólitos vegetais com alto potencial de atividade antiviral contra o SARS-CoV-2 identificados in silico como alternativas no redirecionamento contra a COVID-19, bem como outras pandemias virais que possam surgir.

Palavras-chave: Coronavírus, Produtos naturais, Plantas medicinais, in silico



1 INTRODUCTION

The year 2020 has been marked by the emergence of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative agent of coronavirus disease-19 (COVID-19). The virus has been spread all over the world and caused a high number of cases and death, becoming one of the most reliable events that affected humanity in the last few decades (Dutra et al., 2020; Lauxmann et al., 2020).

In order to restrain the pandemia, efforts have been made worldwide to efficiently control this health crisis through public health policies such as lockdown, border control, early virus detection, hands hygiene, and face protection usage (WHO, 2020). Meanwhile, although the results of population protection are not conclusive, novel health products such as vaccines against SARS-CoV-2 have been released as a public health emergency measure (WHO, 2021).

At clinical and hospitalization level controversial treatments were put into question and the focus is mainly on supportive care and symptomatic treatment (Song et al., 2020). Clinical trials have not demonstrated therapeutic advantages over the toxicological risks of the drugs used so far, which demonstrates the need to investigate new therapeutic alternatives (Oroojalian et al., 2020).

Thus, in the search for redirection of substances with antiviral action, researchers have suggested the metabolites of vegetal origin already identified and reported in the literature as an alternative (Azim et al., 2020; Ghosh et al., 2020; Rolta et al., 2020). The molecules of vegetal origin deserve attention in this area since they present molecular structures with great variety and versatility of interactions with other molecules or biological fonctions (Shahzad et al., 2020).

For this, one must take into consideration peculiar characteristics of the new coronavirus that were important in pathogenesis, interspecies infection and in the triggering of the pandemic, such as the large positive sense, single stranded RNA genome and the presence of envelope (Malik, 2020). In addition, there are other viral structures that are also relevant when seeking therapeutic alternatives after infection in individuals in the critical phase of the disease, from which one can highlight the main protein (M), also called 3C-like protease, that is not recognized by any host protease (Mazzini et al., 2020).

Thus, from a networked database available for both substances of plant origin and therapeutic targets, the interaction between the elements is observed. Using virtual tools and empirical rules, information such as degree of interaction, pharmacokinetics,



pharmacodynamics and possible toxicological risks are obtained. Thus, in a short period of time, substances with good affinity score and biological potential can be selected to be tested in vitro, in vivo and in clinical trials, if they already have previous results in vivo for other agents or even viruses.

2 OBJECTIVE

In this context, the objective of the present study was to conduct a systematic review based on peer-reviewed articles containing molecules of plant origin with potential antiviral action on SARS-CoV-2.

3 METHODOLOGY

3.1 DATABASE

Two international databases were used to search scientific publications: PubMed and WorldWide Science. Natural products, medicinal plants, SARS-CoV-2, and herbal were chosen. In order to validate the keywords, they were checked at Medical Subject Headings (MeSH) controlled vocabulary thesaurus used for indexing articles for PubMed.

The search was conducted combining the keywords in the following order: "SARS-CoV-2 and herbal"; "SARS-CoV-2 and medicinal plants"; "SARS-CoV-2 and natural products". In the sequence, each individual search was unified and duplication was verified.

Search filters included date of publication, peer revision, language and type of text available. Thus, peer-reviewed scientific articles retrieved in English between January 1st, 2019 and August 26th, 2020. A date before SARS-CoV-2 notification was established to include reports with other coronaviruses such as SARS-CoV and MERS-CoV or, in the case of WorldWide Science, only the filter 'year' was available. Finally, the articles whose methodology contained in silico analysis were selected for the most thorough analysis.

4 RESULTS AND DISCUSSION

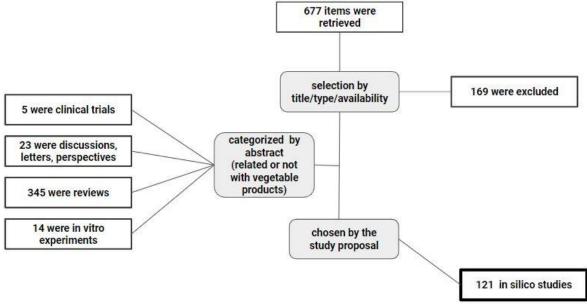
The initial search showed 677 articles which were downloaded and organized into categories, according to table 1 and figure 1. Among these, 57 were repeated, as they were found in two or even all the researches performed for each unit.



Table 1. Scientific reports classified by type retrieved from PubMed and WorldWide Science between January 1st, 2019 and August 26th, 2020.

Article type	SARS-CoV-2 and Herbal	SARS-CoV-2 and Medicinal plants	SARS-CoV-2 and Natural products
Meta-Analysis	1	0	0
Review	64	35	74
In vitro	4	3	7
In silico	40	58	24
Discussion, letter, perspectives	5	11	7
Clinical Trial	2	2	1
Not related to natural products	40	31	33
Total	227	213	237

Figure 1. Flowchart of search in PubMed and WorldWide Science and number of articles found by category.



Retrieving *in silico* studies, 121 reports were then selected and throughout analysed. The current pandemic scenario has accelerated the scientific race, so that more agile and economically viable researches, such as *in silico* studies, have been crucial for a possible direction of more costly investigations with greater promise of positive results. The *in silico* methods have advantages in view of the fact that they comprehend computational simulation that aims to model a phenomenon that occurs naturally; it is an alternative for research models that use animal experimentation (Herrman et al., 2019;



Madden et al., 2020); or facilitate rational strategies for drug repurposing and the detection of side effects (Cheng et al., 2018).

In this context, articles retrieved showed simulation of molecular affinity of isolated natural products to molecules involved in SARS-CoV-2 infection. Prediction took into consideration optimal binding temperatures and if the binding strength would be enough to determine the viability or not of these substances as future antivirals. Thus, the natural products with high affinity to molecules involved in SARS-CoV-2 infection tagged in silico studies are shown in Table 2.

Table 2. Natural products with high affinity to molecules involved in SARS-CoV-2 infection tagged in silico studies.

Products	Molecules	N	References
withaferin A	ACE2/M ^{pro}	3	AZIM et al, 2020; MAURYA et al, 2020; SUDEEP et al, 2020.
caffeic acid derivatives	M ^{pro}	1	KUMAR et al, 2020.
rhamnetin	M ^{pro}	1	FISCHER et al, 2020.
d-Viniferin	M ^{pro}	1	JOSHI et al, 2020.
myricitrin	M ^{pro}	4	CHIKHALE et al, 2020; GOSH et al, 2020; JOSH et al, 2020; MAHMUD et al, 2020.
taiwanhomoflavone A	M ^{pro}	1	JOSHI et al, 2020.
lactucopicrin 15-oxalate	M ^{pro}	1	JOSHI et al, 2020.
nympholide A	M ^{pro}	1	JOSHI et al, 2020.
afzelin	M ^{pro}	1	JOSHI et al, 2020.
biorobin	M ^{pro}	1	JOSHI et al, 2020.
hesperidin	M ^{pro} /ACE2/ S protein/RdRp	7	BALMEH et al, 2020; DAS et al, 2020; CHIKHALE et al, 2020; GOSH et al, 2020; KODCHAKORN et al, 2020; KOULGI et al, 2020; PANDEY et al, 2020.
phyllaemblicin B	M ^{pro} /ACE2	1	JOSHI et al, 2020.
glycyrrhizic acid	M ^{pro} /ACE2/NSP1/ RdRp/S protein	3	SHARMA et al, 2020; SINHA et al, 2020; VARDHAN and SAHOO, 2020.
rutin	M ^{pro}	5	ALAMRI et al, 2020; DAS et al, 2020; GOSH et al, 2020; HU et al, 2020; XU et al, 2020.

N - number of articles retrieved; M^{pro} - main protein; ACE2 - angiotensin-converting enzyme type II; RdRp - RNA polymerase RNA dependent; S protein - Spike protein



Between SARS-CoV-2 molecules most studied by this technique were a) the Main protease (M^{pro}) that acts indirectly through the cleavage of polyproteins in smaller structures (He et al., 2020); the external Spike (S) protein related to the virus entry events in the host cell (Huang et al., 2020); and the RNA polymerase RNA dependent (RpRd), an important enzyme for viral RNA synthesis (Aftab et al., 2020).

Besides the molecules mentioned above, some human receptors have also been considered as the target of antiviral action in in silico analysis. Here, we highlight the angiotensin-converting enzyme type II (ACE2), a specific cellular receptor that has presented a direct relation with SARS-CoV-2 infection (AZIM et al., 2020; MAURYA et al., 2020; BALMEH et al., 2020).

From the analyzed results, the multiple action of the substances hesperidin and glycyrrhizic acid on both the S (Sinha et al., 2020) and the RpRd proteins of the virus and on the ACE receptor stands out. On the other side, the virus M^{pro} proved to be an excellent target of antiviral therapy by natural products with amplitude of molecules with good score in the compounds sizes, ability to fit into the protein binding pocket and to reach the catalytic dyad (Mazzini et al., 2020), for example.

Another substance that draws attention is rutin. For this dietary polyphenol there are reports of a good affinity score only with M^{pro} (Das et al., 2020) and Toll-like cell receptors involved in the host's cellular inflammatory response (Hu et al., 2020). In addition, rutin has been widely used as an antioxidant in the food processing industry. Therefore, as suggested by Hu et al. (2020), it would be easy to ingest it in daily meals as well as through complex vitamin-based supplements.

5 CONCLUSION

From the systematic review carried out, it can be concluded that in silico studies involving products of plant origin reveal a diversity of metabolites with high antiviral potential against SARS-CoV-2.

It is noted that the molecule rutin stands out as a promising antiviral agent. It has potential to act in viral assembling, in suppressing the inflammatory process in the host, and is easily found in food products.

And, finally, the plant substances constitute an excellent alternative in the race to redirect substances with action on SARS-CoV-2, as well as other viral diseases that may arise in the future.



REFERÊNCIAS

AFTAB, S.O et al. Analysis of SARS-CoV-2 RNA-dependent RNA polymerase as a potential therapeutic drug target using a computational approach. J Transl Med 18, p. 275, 2020. https://doi.org/10.1186/s12967-020-02439-0.

ALAMRI, Mubarak et al. Structure-based virtual screening and molecular dynamics of phytochemicals derived from Saudi medicinal plants to identify potential COVID-19

therapeutics. Arabian Journal of Chemistry, 13 (9): p. 7224-7234, 2020.

AZIM, Kazi Faizul et. al. Screening and druggability analysis of some plant metabolites against SARS-CoV-2: An integrative computational approach. Informatics in Medicine Unlocked, v. 20, 2020.

BALMEH, Negar. Predicted therapeutic targets for COVID-19 disease by inhibiting

SARS-CoV-2 and its related receptors. Informatics in Medicine Unlocked, v. 20, 2020.

CHENG, F., Desai, R.J., Handy, D.E. et al. Network-based approach to prediction and population-based validation of in silico drug repurposing. Nat Commun 9, 2691. 2018. https://doi.org/10.1038/s41467-018-05116-5

CHIKHALE, RV et. al. Identification of potential anti-TMPRSS2 natural products through homology modelling, virtual screening and molecular dynamics simulation studies. Journal of Biomolecular Structure and Dynamics, p. 1-16, 2020 Aug 02.

DAS, Sourav et al. An investigation into the identification of potential inhibitors of SARS-CoV-2 main protease using molecular docking study. Journal of Biomolecular Structure and Dynamics. 2020 May 13.

DUTRA, M et al. Estimated number of deaths, confirmed cases and duration of the COVID-19 Pandemic in Brazil Braz. J. Hea. Rev., Curitiba, v. 3, n. 4, p. 10266-10284 jul./aug.. 2020.

FISCHER, André et al. Potential Inhibitors for Novel Coronavirus Protease Identified by Virtual Screening of 606 Million Compounds. International Journal of Molecular Sciences, v. 21 (10), 2020.

GHOSH, Kalyan et. al. Chemical-informatics approach to COVID-19 drug discovery: Exploration of important fragments and data mining based prediction of some hits from natural origins as main protease (Mpro) inhibitors. Journal of Molecular Structure, v. 1224, 2020.

HE, Jun. Potential of coronavirus 3C-like protease inhibitors for the development of new anti-SARS-CoV-2 drugs: Insights from structures of protease and inhibitors. International Journal of Antimicrobial Agents, v. 56, 2020.

HERRMAN, K., PISTOLLATO, F., STEPHENS, M.L. Beyond the 3Rs: Expanding the use of human-relevant replacement methods in biomedical research. ALTEX -Alternatives to animal experimentation, 36(3), pp. 343-352. 2019 Jul 19. doi:



10.14573/altex.1907031.

HU, Xiaopeng et al. Possible SARS-coronavirus 2 inhibitor revealed by simulated molecular docking to viral main protease and host toll-like receptor. Future Virology, 2020 Jun 12.

HUANG, Y et al. Structural and functional properties of SARS-CoV-2 spike protein: potential antivirus drug development for COVID-19. Acta Pharmacol Sin, v. 41, p. 1141– 1149, 2020.

JOSHI, Rakesh et al. Discovery of potential multi-target-directed ligands by targeting host-specific SARS-CoV-2 structurally conserved main protease. Journal of Biomolecular Structure and Dynamics. Online ahead of print. 2020 May 5.

KODCHAKORN, Kanchanok et. al. Molecular modelling investigation for drugs and nutraceuticals against protease of SARS-CoV-2. Journal of Molecular Graphics and Modelling, v. 101, 2020.

KOULGI, Shruti, et. al. Drug repurposing studies targeting SARS-CoV-2: an ensemble docking approach on drug target 3C-like protease (3CLpro). Journal of Biomolecular Structure and Dynamics, p. 1-21, 2020 Jul.

KUMAR, Vipul et al. Withanone and caffeic acid phenethyl ester are predicted to interact with main protease (Mpro) of SARS-CoV-2 and inhibit its activity. Journal of biomolecular structure & dynamics, p. 1-13, 2020 Jun 1.

LAUXMANN, Martin Alexander et al. The SARS-CoV-2 Coronavirus and the COVID-19 Outbreak. International braz j urol, 46(Suppl. 1), p. 6-18, 2020.

MADDEN, JC et al. A Review of *In Silico* Tools as Alternatives to Animal Testing: Principles, Resources and Applications. Altern Lab Anim. 48(4):146-172. 2020 Jul. doi: 10.1177/0261192920965977. Epub 2020 Oct 29.

MAHMUD, Shafi et al. Molecular docking and dynamics study of natural compound for potential inhibition of main protease of SARS-CoV-2. Journal of biomolecular structure & dynamics, p. 1-9, 2020 Jul 24.

MALIK, YA. Properties of Coronavirus and SARS-CoV-2. Malays J Pathol. Apr;42(1):3-11. 2020.

MAURYA, Vimal K. et. al. Structure-based drug designing for potential antiviral activity of selected natural products from Ayurveda against SARS-CoV-2 spike glycoprotein and its cellular receptor. Virus Disease, v. 31, p. 179-193, 2020.

MAZZINI, S et al. Putative SARS-CoV-2 Mpro Inhibitors from an In-House Library of Natural and Nature-Inspired Products: A Virtual Screening and Molecular Docking Study. Molecules 2020, 25, 3745. https://doi.org/10.3390/molecules25163745

OROOJALIAN, F et al. Novel insights into the treatment of SARS-CoV-2 infection: An overview of current clinical trials. International Journal of Biological Macromolecules, 165 (A): 18-43, 2020, https://doi.org/10.1016/j.ijbiomac.2020.09.204.



PANDEY, Preeti et al. Targeting SARS-CoV-2 spike protein of COVID-19 with naturally occurring phytochemicals: an in silico study for drug development. Journal of Biomolecular Structure Dynamics, 1-11. doi: and 2020. 10.1080/07391102.2020.1796811

ROLTA, Rajan et al. In silico screening of hundred phytocompounds of ten medicinal plants as potential inhibitors of nucleocapsid phosphoprotein of COVID-19: an approach to prevent virus assembly. Journal of biomolecular structure & dynamics, p. 1-18, 2020 Ago 28.

SHAHZAD, F et al. The Antiviral, Anti-Inflammatory Effects of Natural Medicinal Herbs and Mushrooms and SARS-CoV-2 Infection. Nutrients.12(9):2573. 2020 Aug 25. doi: 10.3390/nu12092573.

SHARMA, Abhishek et al. Computational search for potential COVID-19 drugs from FDA approved drugs and small molecules of natural origin identifies several anti-virals and plant products. Journal of biosciences. vol. 45 (1): 100, 2020.

SINHA, Saurabh K et al. Identification of bioactive compounds from Glycyrrhiza glabra as possible inhibitor of SARS-CoV-2 spike glycoprotein and non-structural protein-15: a pharmacoinformatics study. Journal of biomolecular structure & dynamics, p. 1-15, 2020 Jun 18.

SONG, Y et al. COVID-19 treatment: close to a cure? A rapid review of pharmacotherapies for the novel coronavirus (SARS-CoV-2). Int J Antimicrob Agents. 2020 Aug;56(2):106080. doi: 10.1016/j.ijantimicag.2020.106080. Epub 2020 Jul 4.

SUDEEP, HV et al. Molecular docking analysis of Withaferin A from Withania somnifera with the Glucose regulated protein 78 (GRP78) receptor and the SARS-CoV-2 main protease. Bioinformation v. 16.5, p. 411-417, 2020.

VARDHAN, S and SAHOO, SK. In silico ADMET and molecular docking study on searching potential inhibitors from limonoids and triterpenoids for COVID-19. Computers in Biology and Medicine, v. 124, 2020.

WORLD HEALTH ORGANIZATION (WHO). Transmission of SARS-CoV-2: implications for infection prevention precautions. Scientific brief. Available at <WHO/2019-nCoV/Sci_Brief/Transmission_modes/2020.3>. Accessed in <Feb, 16th,</p> 2021 > .

XU, Chi et. al. Systemic In Silico Screening in Drug Discovery for Coronavirus Disease (COVID-19) with an Online Interactive Web Server. Journal of Chemical information and modeling, v. 60 (12), p. 5735-5745, 2020.