In Silico Molecular Docking and ADMET analysis of compounds isolated from *Neocarya macrophylla* against three targets of SARS CoV-2 coronavirus

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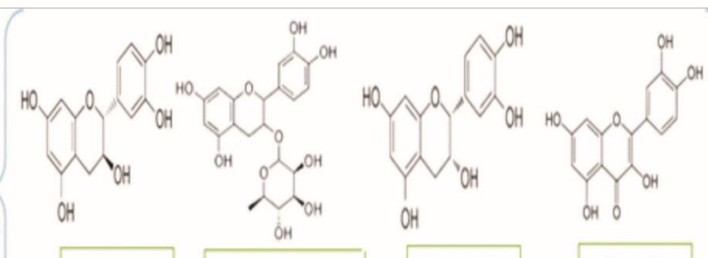
Introduction

The novel corona virus disease (COVID-19) which emerged in China is a highly transmittable and pathogenic viral infection caused by the SARS-CoV-2; the disease has been declared by WHO as a public health emergency of international concern. The unavailability of approved therapeutic agents or vaccines is of great concern. The aim of this study was to perform molecular docking and ADMET analysis of some compounds isolated from *Neocarya macrophylla* against three targets of SARS CoV-2 proteins (3C-like protease, spike protein and papain-like protease).

Materials and Methods

Isolation



Ligand preparation: SDF files of the compounds were retrieved from PUBCHEM (https://pubchem.ncbi.nlm.nih.gov/). The structures were prepared and converted to PDB format using Chimera 1.14 [1]

Protein preparation

Crystallography structure of the SARS CoV-2 main protease (PDB: 6LU7), spike protein (PDB ID: 6LZG) and papain-like protease (PDB: 6W9C) were retrieved from the protein data bank (https://www.rcsb.org) and prepared using Chimera 1.14 [1].

Molecular docking

Molecular docking was performed using AutoDock tools in PyRx software and post docking analysis was conducted using the BIOVIA Discovery studio visualizer 2020 and Chimera 1.14 [1].

***In silico* ADMET and drug-likeness prediction**

Main protease

conducted using swissADME and pkCSM ADMET descriptors algorithm protocol [2-3]. The drug-likeness properties of the compounds were predicted using Molinspiration Cheminformatics free web services (https://www.molinspiration.com/cgi-bin/properties) by inserting the Canonical SMILES of the compounds.

Results and Discussion

Molecular docking

The four compounds (catechin, catechin-3-rhamnoside, epicatechin and quercetin)isolated from *N. macrophylla* were screened against three important protein targets of SARS CoV-2 including main protease, spike protein and papain-like protease by conducting a molecular docking analysis using AutoDock Vina tools in PyRx. The docking scores and interactions of the four ligands at the active site of the three proteins are shown in Table 1 and Figures 1 – 3. The ADMET and drug-likeness results indicated that all the compounds have satisfied the limitations and drug-likeness.

Table 1: Docking scores of the compounds against three targets proteins of SARS CoV-2

		Docking scores (kcal/mol)		
Compound name	Compound ID	Main protease	Spike protein	Papain-like protease
Catechin	9064	-7.0	-6.6	-6.4
Catechin-3-rhamnoside	21626704	-8.0	-7.1	-6.9
Epicatechin	72276	-6.9	-6.3	-7.1
Quercetin	528043	-6.9	-6.7	-7.0

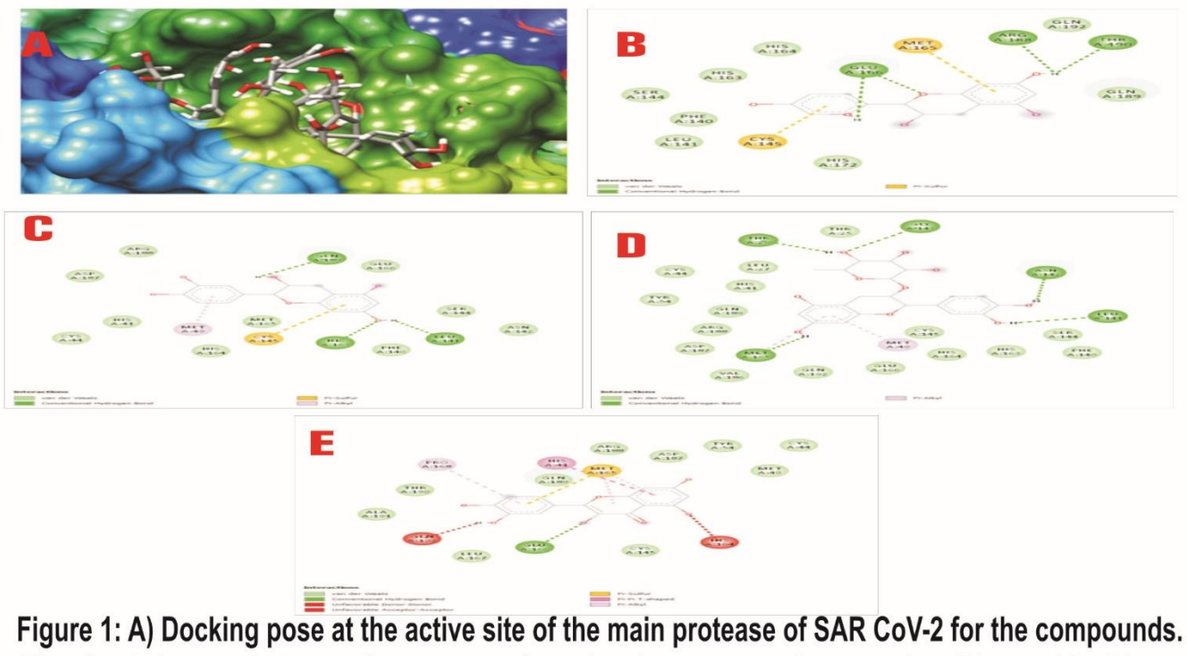


Figure 1: A) Docking pose at the active site of the main protease of SAR CoV-2 for the compounds. 2D animated poses between the compounds and main protease of coronavirus B) catechin, C) epicatechin, D) catechin-3-rhamnoside, E) Quercetin

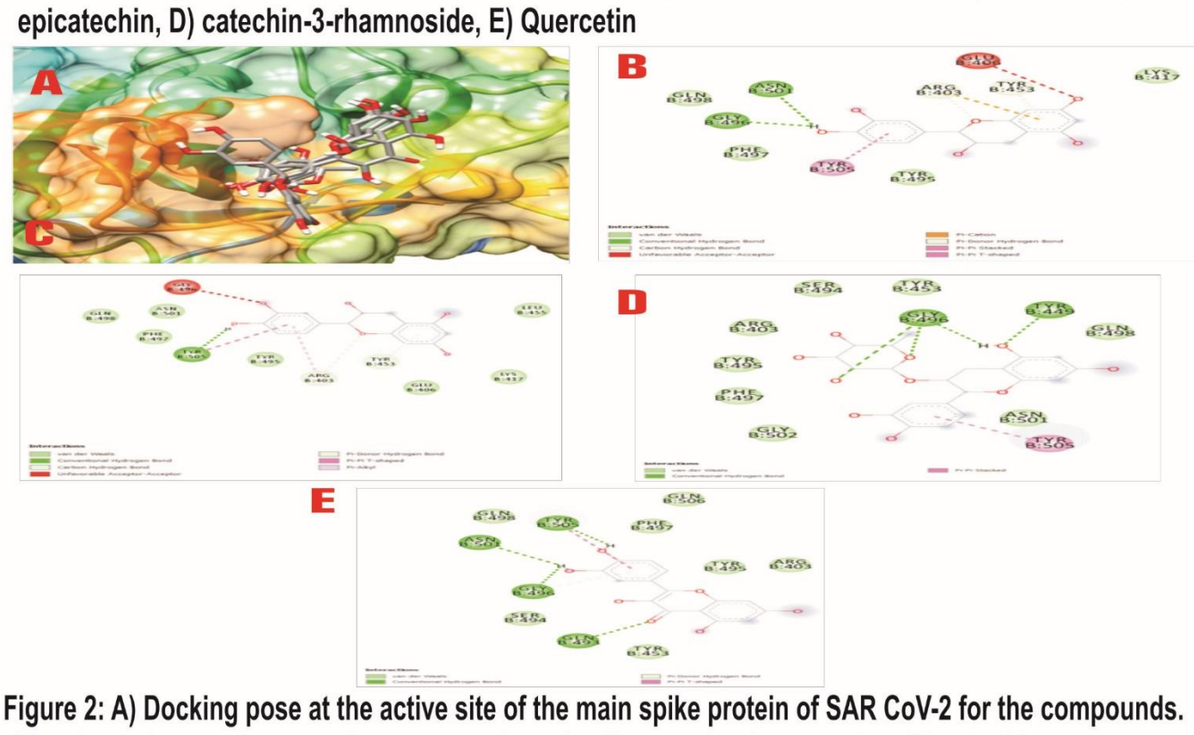


Figure 2: A) Docking pose at the active site of the main spike protein of SAR CoV-2 for the compounds. 2D animated poses between the compounds and spike protein of coronavirus B) catechin, C) epicatechin, D) catechin-3-rhamnoside, E) Quercetin

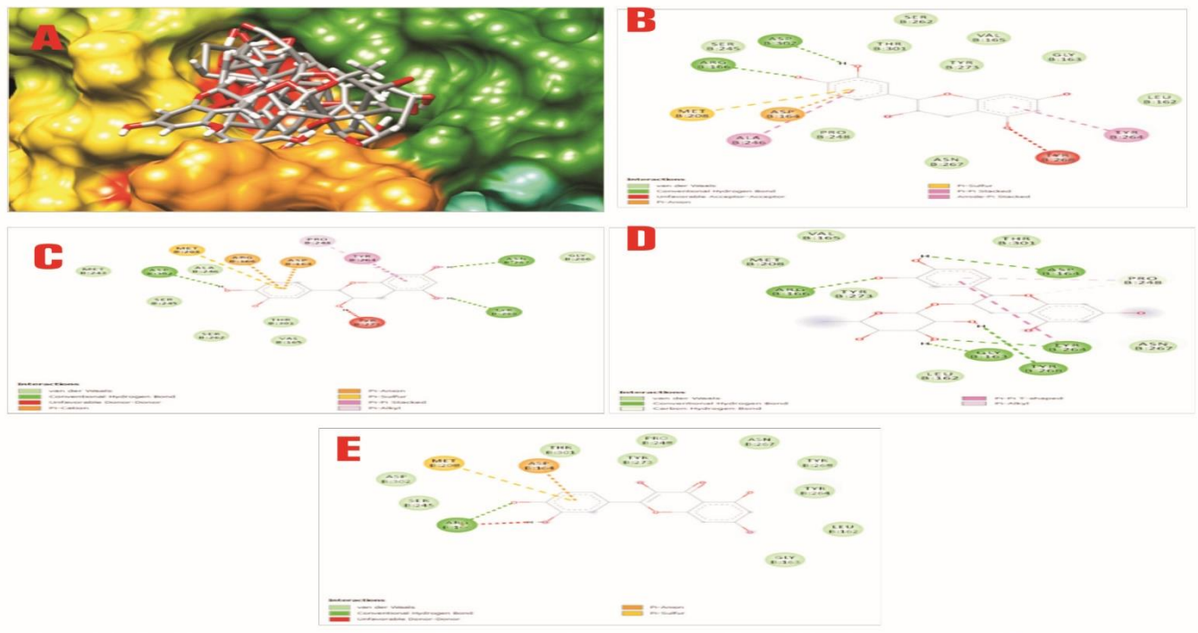


Figure 3: A) Docking pose at the active site of the papain-like protease of SAR CoV-2 for the compounds. 2D animated poses between the compounds and spike protein of coronavirus B) catechin, C) epicatechin, D) catechin-3-rhamnoside, E) Quercetin

Conclusion

In *conclusion*, we have screened four compounds (catechin, catechin-3-rhamnoside, epicatechin and quercetin) isolated from *N. macrophylla* using molecular docking, *in silico* ADMET and drug-likeness prediction. The findings of this study have shown that, the plant *N. macrophylla*may contain potential leads for SARS CoV-2 inhibition and thus, should be studied further for development as effective therapeutic agents against COVID-19.

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Some References

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