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Computational Screening of Toxicity, Drug-like Molecule, and Bioactivity from Green Tea Phytochemical as Antiviral Candidate

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ABSTRACT

Viruses are obligate intracellular parasites because they can infect cells and hijack the gene expression process in host cells for the replication of viral genetic material. The mechanism of the viral life cycle is generally divided into three stages such as viral entry, genome replication, budding, and release. Several viruses can inhibit interferon signaling through the JAK/STAT pathway such as human cytomegalovirus (HCMV), HIV-1, murine hepatitis virus (MHV), severe acute respiratory syndrome coronavirus (SARS-CoV-2), & vaccinia virus (VACV). Antiviral drugs can be developed by

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studying how viruses evade the immune response, several drugs have been discovered but most of them are synthetic compounds that produce the use effect. Screening of drug candidate compounds can be carried out on a specific natural ingredient such as green tea used in this study. Scientific evidence of compounds from green tea as an antiviral agent is very little, this study is important because it is to screen the potential of compounds from green tea as an antiviral agent through computational approach. Green Tea phytochemical compounds are predicted to be antiviral based on *in silico* analysis. Antiviral candidate are EGCG, ECG, EGC, EC, & Catechin, they are drug-like molecules and have positive probabilities as antiviral agents.

Keywords: Antiviral, Computational Screening, Bioactivity, Green Tea, Phytochemical

INTRODUCTION

Viruses are obligate intracellular parasites because they can infect cells and hijack the gene expression process in host cells for the replication of viral genetic material $1/2$. The mechanism of the viral life cycle is generally divided into three stages such as viral entry, genome replication, budding, and release $3,4$. Virus replication begins with viral entry through an attachment mechanism with target receptors on the surface of the host cell, then the virus penetrates to the cytoplasm and carries out the genome replication stage^{5,6}. When specific proteins and viral genomes have been formed, they will undergo assembly to form new virions and undergo maturation and then released out of the cell to infect other host $cells^{7,8}$. The viral life cycle process also involves activities to evade the body's immune response, the virus can produce a protein to inhibit the recognition of immune cells or prevent host cells from releasing specific cytokines for natural antiviral activation responses such as interferon^{9,10}.

Viral infections are viral pathogen-associated molecular patterns (PAMPs) recognized by immune cells through host pattern recognition receptors (PRRs) $11,12$. PAMPs are present in viruses and not in host cells, thus enabling cells to carry out an immune response during infection 13 . Several types of PRRs to detect viral infections consist of RIG-I-like receptors (RLRs), Toll-like receptors (TLRs), and DNA sensors for the detection of proteins and nucleic acids from viruses $14,15$. These three proteins can be activated and then trigger transcription factors for the regulation of IFN expression. IFN can inhibit viral replication in host cells and trigger apoptotic signaling to reduce virus spread to other cells^{16,17}. Several viruses can inhibit interferon signaling through the JAK/STAT pathway such as human cytomegalovirus (HCMV), HIV-1, murine hepatitis virus (MHV), severe acute respiratory syndrome coronavirus (SARS-CoV-2), &

vaccinia virus (VACV)^{18,19}. Antiviral drugs can be developed by studying how viruses evade the immune response, several drugs have been discovered but most of them are synthetic compounds that produce the use effect.

Screening of drug candidate compounds can be carried out on a specific natural ingredient such as green tea used in this study. Compounds in green tea consist of catechin, epigallocatechin-3-gallate (EGCG) CID, (−) epicatechin-3-gallate (ECG) CID, (−)-epigallocatechin (EGC) and (−)-epicatechin (EC)²⁰. Previous research has shown that green tea compounds have the potential to treat diseases such as diabetes, cancer, autoimmune disease, and others 21 . Scientific evidence of compounds from green tea as an antiviral agent is very little, this study is important because it is to screen the potential of compounds from green tea as an antiviral agent through an in silico approach.

METHOD

Compound retrieval

Green tea compounds such as catechin, (−) epigallocatechin-3-gallate (EGCG), (−)-epicatechin-3 gallate (ECG), (−)-epigallocatechin (EGC) and (−) epicatechin (EC) for ligand preparation was obtained from the PubChem database [\(https://pubchem.ncbi.nlm.nih.gov/\)](https://pubchem.ncbi.nlm.nih.gov/). The information obtained from PubChem consists of Canonical SMILE and the 3D structure of the target compound. Visualization of the 3D structure of green tea compounds was carried out using PyMol v2.5 software with structural selection and atomic coloring techniques^{22,23}.

Druglikeness and toxicity prediction

Computational Screening of Toxicity, Drug-like Molecule, and Bioactivity from Green Tea Phytochemical as Antiviral Candidate

Table 1. Green tea compound drug-like molecule

The ability of candidate compounds from green tea and the degree of similarity to drug molecules when triggering activity in the body were predicted on the Lipinski Rule of Five server [\(http://www.scfbio](http://www.scfbio-iitd.res.in/software/drugdesign/lipinski.jsp)[iitd.res.in/software/drugdesign/lipinski.jsp\)](http://www.scfbio-iitd.res.in/software/drugdesign/lipinski.jsp).

Parameters for the determination of drug-like molecules on the server consists of molar refractivity, hydrogen acceptors & donors, molecular mass, and high lipophilicity²⁴. Toxicity prediction on query compounds from green tea was carried out via the ProTox-II server [\(https://tox-new.charite.de/protox_II/\)](https://tox-new.charite.de/protox_II/). Prediction is done by referring to the LD50 value or the dose where 50% of the test subjects die after administration of the query compound^{25,26}.

Antiviral identification

Identification of compounds from green tea as an antiviral was done through the Wy2Drug PASSOnline server [\(http://www.pharmaexpert.ru/passonline/\)](http://www.pharmaexpert.ru/passonline/). Prediction works with Canonical SMILE data input and confidence score then the antiviral candidate compound with positive prediction results is obtained with activation probability (Pa)> inhibition probability $(Pi)^{27,28}$.

RESULT AND DISCUSSION

Revealing of drug-like molecule and toxicity

The parameters used in this study in determining druglike molecules by referring to the Lipinski Rule of Five, this rule refers to the hydrogen bond donor (HBD), high lipophilicity (LogP), molecular weight (MM), hydrogen bond acceptor (HBA), & molar refractivity (MR), query compounds with drug-like molecule properties must follow at least two Lipinski rules^{29,30}. Lipinski's rule consists of molar refractivity should be between 40-130, molecular mass less than 500 Dalton, less than 5 hydrogen bond donors & 10 for hydrogen bond $acceptors^{31,32}$. Drug candidate compounds that follow the Lipinski Rule of Five are predicted to be able to pass through selectively permeable membranes, affect charge movement, and trigger passive transport 33,34 . Bioactive compounds from Green Tea consisting of EGCG, ECG, EGC, EC, & Catechin, were obtained from PubChem, then 3D visualization was performed using PyMol v2.5 software with color selection (Figure 1). All bioactive compounds in this study were predicted as drug-like molecules because all compounds follow more than two of Lipinski's rules (Table 1).

Table 2. The results of compound toxicity prediction

Toxicity tests were carried out on compounds from green tea via the ProTox-II server. Toxicity is determined by the LD50 or median lethal dose meaning the dose at which 50% of test subjects die upon exposure to a compound. LD50 values are classified into class I: fatal if swallowed (LD50 5), class II: fatal if swallowed (5 < LD50 50), class III: toxic if swallowed (50 < LD50 300), class IV: harmful if swallowed (300 < LD50 2000), class V: may be harmful if swallowed (2000 < LD50 5000) & class VI: nontoxic (LD50 > 5000)^{35,36}. ProTox-II incorporates machinelearning, propensities, molecular similarity, frequent features, based a total of 33 models for the prediction of various toxicity endpoints such as acute toxicity, carcinogenicity, hepatotoxicity, cytotoxicity, mutagenicity, immunotoxicity, & Tox21 pathways and toxicity targets 37 . The results of the prediction of the

toxicity of the Green Tea compound showed that the LD50 value of all compounds was 1000 mg/kg with toxicity class IV – VI (Table 2). The toxicity of Green Tea compounds is classified as safe for use or consumption because in low doses.

Figure 1. Molecular visualization of Green Tea compounds. (A) EGCG (B) ECG (C) EGC (D) EC & (E) Catechin.

The probability of antiviral candidate

Antiviral probability prediction on drug-like compounds from Green Tea is done through the PASSOnline server. This prediction aims to determine the antiviral probability by referring to the value of probability activation (Pa) and probability inhibition (Pi) 38 . Antiviral probabilities with medium confidence (Pa>0.3) were used in the study. Probability with medium confidence (Pa>0.3) was chosen to screen the potential of a bioactive compound with scientific evidence through a

computational approach or based on data mining³⁹. Predicted results of bioactivity as antiviral showed EGCG, ECG, EGC, EC, & Catechin is predicted as a candidate antiviral agent because it has Pa>0.3 (Table 3). Antiviral candidate compounds with Pa>0.3 should be re-selected through literature studies, it is for additional scientific evidence.

Table 3. The results of antiviral probability

Green tea catechins (GTCs) are reported to play an important role in the treatment of various diseases such as viruses. GTCs can be antiviral agents in cases of infection with HBV, HSV, EBV, Adenovirus, HIV, Influenza, DENV, JEV, TBEV, ZIKV, CHIKV, HTLV, Rotavirus, EBOV, PRRSV, & EV71⁴⁰. The mechanism of GTCs triggers antiviral effects by inhibiting and decreasing the activity of the protein coding for the replication of the target virus. Based on the results of the literature study, compounds from Green Tea with Pa>0.3 which have potential as antiviral agents are EGCG, ECG, EGC, EC, & Catechin, these compounds can be recommended for further analysis.

CONCLUSION

Green Tea phytochemical compounds are predicted to be antiviral based on *in silico* analysis. Antiviral candidate are EGCG, ECG, EGC, EC, & Catechin, they are drug-like molecules and have positive probabilities as antiviral agents. We recommend these three compounds for further analysis such as molecular docking, dynamic simulation, target identification, and biological pathway simulations for additional scientific evidence.

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