Abstract

Coronavirus disease 2019 (COVID-19) has become a worldwide pandemic disease and is brought by another type of coronavirus named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The SARS-CoV-2 infection is thought to spread between people mainly through respiratory droplets generated during coughing. Ginger (*Zingiber officinale*) is a rhizome plant that is very popular as a spice and medicine ingredient and there is also turmeric (*Curcuma longa*) that has long been used in Ayurvedic medicine to treat inflammatory disease. Especially in Indonesia, ginger and turmeric are usually consumed as a traditional medicine known as jamu. This study aims to assess and evaluate several bioactive compounds in *Zingiber officinale* and *Curcuma longa* can be candidates for drug design to treat COVID-19. The crystals structure of the SARS-CoV-2 main protease (Mpro) with the PDB ID: 6WTT was taken from the protein sequence database, which is Protein Data Bank (PDB). The bioactive compounds of *Zingiber officinale* (4-Gingerol, 6-Gingediol, 6-Gingerol, 6-Shogaol, 8-Gingediol, 8-Gingerol, 10-Gingerol, Gingerdione, Methyl-6-Gingerol, Methyl-6-Shogaol, and Zingerone) and *Curcuma longa* (α-Thujene, β-Phellandrene, Carvacrol, Cyclocurcumin, Limonene, M-Cymene, Menthol, Piperitone epoxide, Piperitone, Thymol, and Vanillic acid) were analyzed using The PASS SERVER to achive the expected biological activity profile. The molecular docking analysis was performed using PyRx, and the interaction between the SARS-CoV-2 M pro and the active compounds from *Zingiber officinale* as well as *Curcuma longa* was analyzed by performing molecular dynamics simulation using CABSFLEX2. Based on QSAR properties, it was discovered that all of the chemicals are predicted to have antiviral or 3C-like protease inhibitor activity. In this regard, the leads were further screened using molecular docking and molecular dynamics methods. Based on the results of the further screening, 4-Gingerol and Cyclocurcumin were chosen as the best compounds to inhibit 3C-like protease.

Keywords: COVID-19, *Curcuma longa*, Mpro, Molecular Docking, *Zingiber officinale*