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MOLECULAR CHARACTERIZATION, PHYTOCHEMICALS SCREENING, AND MOLECULAR DOCKING OF CARDAMOM (*Wurfbainia compacta*), AND SAMBILOTO (*Andrographis paniculata*) AGAINST COVID-19

Karakterisasi Molekuler, Uji Fitokimia dan *Molecular Docking* Kapulaga (*Wurfbainia compacta)* dan Sambiloto (*Andrographis paniculata) terhadap COVID-19*

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ABSTRACT

Cardamom and Sambiloto are phytopharmaceutical plants that produce phytochemical compounds that have the potential to be used to increase immunity against COVID-19. because they contain carotenoids, phenols, anthocyanins, saponins, alkaloids and steroids. This research aims to obtain the molecular characteristics of Cardamom and Sambiloto plants from the Gunungpati area, Semarang by ITS primer, testing phenolic phytochemicals, tannins, flavonoids, saponins and alkaloids followed by molecular docking tests with the 6WX4 protein. SARS-CoV-2. Molecular characterization results show that Cardamom and Sambiloto are similar to Wurfbainia compacta MF802556.1 (100%) and Andrographis paniculate LC646073.1 (84.47%). The results of the phytochemical test screening showed that both plants contain flavonoids. Molecular docking tests were carried out with the compounds Quercetin, Avicularin, Naringenin, 5-hydroxy-7,8,2',5' tetramethoxyflavone, and Retinoic Acid. Retinoic Acid as a test ligand has the greatest potential in inhibiting the 6WX4 protein in the SARS-CoV-2 virus with a binding affinity value of -7.28 and RMSD 0.00.

Keywords: *Phytopharmaceutical, Phytochemical, Cardamom, Sambiloto, Molecular Docking*

ABSTRAK

Kapulaga dan sambiloto merupakan tanaman fitofarmaka yang menghasilkan senyawa fitokimia yang berpotensi meningkatkan imunitas melawan COVID-19. karena mengandung karotenoid, fenol, anthosianin, saponin, alkaloid, dan steroid. Penelitian ini bertujuan untuk memperoleh karakter molekuler tanaman Kapulaga dan Sambiloto dari daerah Gunungpati, Semarang dengan pemetaan daerah ITS, uji fitokimia fenolik, tannin, flavonoid, saponin dan alkaloid yang dilanjutkan dengan uji penambatan molekuler dari beberapa senyawa yang terdapat pada kedua tanaman dengan protein 6WX4 SARS-CoV-2. Hasil karakterisasi molekuler menunjukkan Kapulaga dan Sambiloto memiliki kemiripan dengan *Wurfbainia compacta* MF802556.1 (100%) dan *Andrographis paniculate* LC646073.1 (84.47%). Hasil skrining uji fitokimia menunjukkan bahwa kedua tanaman tersebut memiliki kandungan flavonoid. Uji penambatan molekuler dilakukan dengan senyawa Quercetin, Avicularin, Naringenin, 5-hydroxy-7,8,2’,5’ tetrametoxyflavone, dan Retinoic Acid. Retinoic Acid sebagai ligan uji memiliki potensi paling besar dalam menghambat protein 6WX4 pada virus SARS-CoV-2 dengan nilai binding affinity -7,28 dan RMSD 0.00.

Kata kunci: *Fitofarmaka, Fitokimia, Kapulaga, Sambiloto, Molecular Docking*

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INTRODUCTION

The corona virus outbreak began to be reported in December 2019 as a severe acute respiratory disease syndrome corona virus-2 (SARS-CoV-2). On February 11, 2020, WHO officially announced the official name of the disease caused by 2019-nCoV as Coronavirus Disease 2019 or what is often referred to as COVID-19 (Alzaabi et al, 2022). SARS-CoV-2 can be a complicated disease and have a risk of death if it attacks people who have inherited diseases such as cancer, diabetes, cardiovascular disease and chronic respiratory disease. Common symptoms of COVID-19 are fever, shortness of breath, cough and dyspnea, whereas in severe cases SARS-CoV-2 infection can cause severe acute respiratory syndrome, pneumonia, organ failure and even death (Wang et al, 2020). SARS-CoV-2 has *non-structural polyprotein protease* which processed by 2 protease, main protease (Mpro) and papain like protease (PLpro) (Alfaro et al, 2020).

PLpro is responsible for cleaving in the sequence nsp1 to nsp4. Mpro is encoded to cleave on the polyprotein at 11 sites further after PLpro. Inhibition of PLpro and Mpro will have an impact on the inhibition of the replication process of the SARS-CoV-2 virus (Calleja et al, 2022). Both of their activities are important in the viral replication process, therefore Mpro and PLpro are the main drug target proteins in SARS-CoV-2 (Alfaro et al, 2020). The FDA has approved the use of drugs that interfere with viral replication, such as Molnupiravir and Remdesivir (Calleja et al, 2022). However, screening for the potential for protease inhibition of SARS-CoV-2 using naturally-available phytochemicals is still needed to create an immunomodulator with low side effects.

Cardamom (*Wurfbainia compacta)* is a phytopharmaceutical plant originating from the Zingiberaceae family which has ± 1,300 species spread from Asia to Australia (Alkandhari et al, 2021). *W. compacta* has various types ranging from Javanese cardamom, Sebrang cardamom, and cardamom originating from India. *W. compacta* has pharmacological abilities such as overcoming digestive problems, carminative, breath freshener, and aphrodisiac (Praditha et al, 2020). Bioactive compounds in plants such as polysaccharides, lectins, tannins, flavonoids, feolate, peptides, and terpenoids are able to inhibit and treat disease, increase immunity as well as anti-inflammatory and anti- cancer (Alkandhari et al, 2021). Therefore, *W. compacta* contributes greatly to drug discovery (Praditha et al, 2020).

Sambiloto (*Andrographis paniculata*) is one of the herbal plants that are commonly found in areas of Indonesia such as Java and Sumatra (Prihatini et al, 2010). Sambiloto belongs to the plant of the Acanthaceae family. Sambiloto is widely used in several countries such as Hong Kong, Malaysia, India, Pakistan, China, Philippines, Indonesia, Bangladesh and Thailand. The phytochemical content in bitter plants that can be used as herbal medicines includes diterpenoids, diterpene glycosides, glycosides, lactones, and flavonoids. Sambiloto has effects as anti- inflammatory, antibacterial, anti-microbial, antioxidant and immunomodulatory (Hossain, 2014).

There are quite a lot of types of Cardamom herbal plants in Indonesia, so molecular characterization is needed to determine the species of the plant. De Boer et al. (2018) and Kaewsri & Sangvirotjanapat (2022) conducted morphological and molecular phylogenetic studies on Wurfbainia because they found several types of Cardamom. Furthermore, Hande et al, 2022 have used several genetic markers, namely rbcl, matK, ITS and psbA to identify Andrographis species and found that ITS was the best marker.

The ITS molecular markers is one of the most commonly used molecular markers to identify species to the species level (Cheng et al, 2016). ITS markers contain ITS1, 5.8S rDNA and ITS2 genes which can be amplified using the Polymerase Chain Reaction (PCR) method (Wu et al, 2013). The ITS region has a high degree of variation compared to other regions in small and large rDNA subunits. The ITS region has a fairly short size of ±700 bp and has a large number of copies in the core genome. This causes the ITS area to be easy to isolate, amplify and analyze (Baldwin et al, 1995).

Molecular characterization of phytopharmaceutical plants using ITS markers will provide information related to the

genetic character of cardamom and sambiloto from Indonesian region. Phytochemical screening research, and molecular docking of Cardamom and Sambiloto are significantly needed to determine their inhibitory potential against SARS-CoV-2 protease with the advantage of low side effects. Thus, the purpose of this study is to conduct molecular characterization, phytochemical testing and molecular docking of cardamom and sambiloto plants.

MATERIALS AND METHODS

Materials

The samples used were cardamom leaf samples, cardamom seeds and Sambiloto leaf samples as shown on Fig 1. was collected from Gunungpati district, Semarang, Central Java. Each 400 mg of *W. compacta* and *A. paniculata* leaf samples, CTAB buffer, Tris-Base solution, ddH2O, NaCl, Tris Acetate EDTA (TAE), sterile distilled water, NaOH, Ethanol, DNA ladder, PCR Kit (My TaqTM HS Red Mix), agarose gel, Primer ITS4 and ITS5, loading dye, Alcohol 70%, DNA ladder 100 bp, Florosafe DNA Strain, tissue, chloroform, ammonia, H2SO4 2N, Mayer reagent, Wagner reagent, Dragendrof reagent, HCl, ethanol, Mg powder, ether, 50% methanol, 5% FeCl and 1% FeCl3.

DNA isolation

DNA isolation was carried out using the Doyle and Doyle (1987) method with slight modifications (Kamilah et al, 2022). The CTAB buffer was incubated at 65°C, the plant leaf samples were weighed as much as 0.4 g, the samples were crushed using mortar and pestel. The CTAB buffer was added in 5 mL increments. The sample was then transferred to a new microtube of 1 mL. Samples were incubated in a water bath at 65°C for 1 hour. The CIA solution was added 500 µL and vortexed for approximately 1 minute. The sample was centrifuged at 8000 rpm for 10 minutes. The supernatant layer was collected to a new microtube. Isopropanol was added as much as 500 µL. The samples were then incubated at -20°C overnight. Samples were centrifuged at 8000 rpm for 10 minutes. The pellet was air-dried until the supernatant solution was completely evaporated. The dried pellets were washed using 200 µL 70% alcohol. Alcohol was aspirated and the pellet was dried and then 50 µL of TE buffer was added.

Figure 1. Sambiloto leaf, Cardamom leaf, Sambiloto and Cardamom plants

PCR (Polymerase Chain Reaction)

The process of amplification of plant DNA in the ITS rDNA area was carried out by making a PCR mix solution with a volume of 50 µL consisting of a mixture of 25 µL of the My Taq™ HS Red Mix PCR kit, 2 µL of ITS4 primer (10 pmol), 2 µL of ITS5 primer (10 pmol), 2 µL extract of plant DNA genome as template and 19 µL ddH_2O. ITS4 primer pair as reverse primer (5`– TCC TCC GCT TAT TGA TAT GC – 3`) and ITS5 primer as forward primer (5` – GGA AGT AAA AGT CGT AAC AAG G –3`) (White et al, 1990). DNA amplification was carried out for 35 cycles with the following steps: pre-denaturation at 94°C for 3 minutes, denaturation at 94°C for 30 seconds, annealing at 54°C for *W. compacta* samples and 54°C for *A. paniculata* samples for 20 seconds, Extension at 72°C for 1 minute, post extension at 72°C for 7 minutes and storage temperature at the final stage of 4°C (Kusumaningrum et al, 2018).

Phytochemical Test

Screening of phytochemical compounds was carried out by several tests, namely alkaloid, saponin, phenolic, tannin, and flavonoid testing. Alkaloid testing was carried out with 4 g of plant extract, 5 mL of chloroform, 10 mL of ammonia, and 10 mL of chloroform were added. The solution was filtered into a test tube and added with 10 drops of 2N H_2SO_4 filtrate. The solution was homogenized, then left for a few minutes to form 2 layers. The first layer was transferred into 3 test tubes 1 mL each then each test tube added with Mayer, Wagner, and Dragendorf reagents respectively. Mayer's reagent will form a white precipitate, Wagner's reagent will form a brown precipitate, and Dragendrof's reagent will form an orange precipitate (Farnsworth, 1996).

The flavonoid compound test was carried out with a sample of leaves that were grounded until they were finely powdered as much as 200 mg. The sample was extracted using 5 mL of ethanol and heated for 5 minutes in a test tube then concentrated HCl was added. Magnesium powder was added as much as 0.2 g (Harborne, 1996). The flavonoid test will show positive results if a dark red, yellow or orange color is formed for 3 minutes (Harborne, 1996; Syaputra, 2021).

The saponin test was carried out with 2 g of a sample of plant leaf powder put into a test tube, added with distilled water until the sample was submerged, the solution was heated for 2-3 minutes and cooled and then homogenized. A positive result on the saponin test will form a stable foam (Farnsworth, 1966).

The phenolic compound test was first carried out by continuous sample extraction using a Soxhlet apparatus with ether as a solvent. Samples were extracted with 50% methanol. The test was continued by adding 1 ml of 5% FeCl into the methanol extract. The positive result if there is a color change from brownish yellow to brown orange which indicates the presence of phenolic compounds (Dai and Mumper, 2010).

The tannin compound test was carried out with a sample of 20 mg of plant powder added with ethanol until the plant sample was completely submerged in ethanol and 2-3 drops of 1% $FeCl_3$ solution were added. A positive result from the tannin test will form a bluish black or green color (Siquera et al, 2012). The addition of $FeCl_3$ will cause the tannin to be condensed with the ethanol solution in it so that after the solution is added with $FeCl_3$ it will change color to blackish green.

Molecular Docking

The molecular docking process is carried out using Autodock 4.0 and Autogrid 4.0 software. AutoGridFR (AGFR) is a software tool facilitating the calculation of affinity maps that greatly speed up the docking process (Zhang et al, 2019). Before docking, the COVID-19 receptor protein (PDB ID: 6WX4) were downloaded on the PDB RSCB website for its 3D structure the ligand, as part of the study. Furthermore, ligand and receptor preparation were carried out using the discovery studio. The value of binding affinity, RMSD and bonding residues formed on the test compounds were used as the main parameters to determine the potential effectiveness of the test compounds as immunomodulators and the success of the docking process.

The Molecular docking process was carried out using the 6WX4 receptor protein which is part of the SARS-CoV-2 PLpro (Papain Like Protease) protein structure with

the original peptide or ligand inhibitor being the VIR251 compound. The test compounds used in this study were flavonoid compounds including 5-Hydroxy-7,8,2',5' tetramethoxyflavone, Naringenin, Quercetin, Avicularin and Retinoic acid. The selection of flavonoid compounds was due to the results of phytochemical tests showing that all plants were positive for flavonoids. Alzaabi et al. (2021) explained that flavonoids are one of the secondary metabolites in plants that have pharmacological functions such as antioxidants, anti-cancer, anti-inflammatory, anti-bacterial and anti-virus.

RESULTS AND DISCUSSION

DNA qualitative and quantitative test results

The quality and quantity tests were carried out using Nanodrop ND2000. The results of measuring the quality and quantity of DNA in *W. compacta* samples obtained a concentration of 767.1 ng/µL and a purity of 2.01. The sample of *A. paniculata* had a concentration of 1961.8 ng/µL and a purity of 1.71. According to Sambrook and Russel (2001) the range of DNA purity numbers required for molecular analysis is 1.80-2.0.

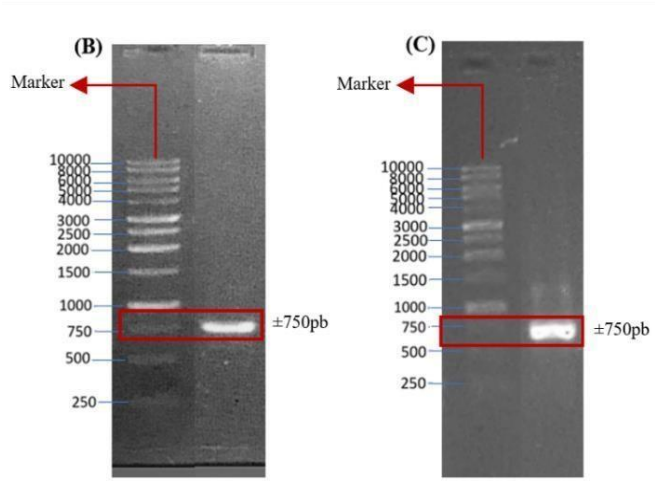

Figure 2. Electrophoresis Results of *W. compacta* and *A. paniculata*

Based on the results of visualization using a UV transluminator as illustrated in Fig. 2. The results of DNA bands on samples of *W. compacta* and *A. paniculata* were thick and clear and had a size of ±750 bp. The visible bands are the result of DNA amplification of *W. compacta* with annealing temperature of 54°C and *A. paniculata* with annealing temperature of 53°C. Xia et al. (2004) performed DNA amplification of *W. compacta* in the ITS area using an annealing temperature of 54°C to obtain a DNA length of ITS area of 606 bp. The results of visualization of DNA bands conducted by Xiong et al. (2021) in the ITS area obtained a DNA band length of ±700 bp. Mamedov et al. (2008) stated that the optimal annealing temperature is influenced by the G-C content contained in the template DNA.

Sequencing Result Analysis

The results of the PCR product sequencing from the *W. compacta* sample showed that the amplified partial size in the reverse sequence was 639 bp and the forward sequence was 639 bp. While the alignment results obtained contiq with a length of 648 bp. To determine the characteristics of the *W. compacta* sample from the Gunungpati area, Semarang, Central Java, an alignment was carried out with *W. compacta* MF802556.1 contained in the GenBank. *W. compacta* sample with accession number OL774795.1 did not show any difference in nucleotide bases. The ITS area is able to distinguish *W. compacta* species at the interspecies level with a percent identity distance ranging from 0% to 0.62% while at the intraspecies level with a percent identity distance of 6.11% to 9.21%.

The results of DNA sequence analysis for *A. paniculata* samples obtained DNA sequence lengths of 721 bp for forward and 727 bp for reverse. Alignment results showed a contiq length of 264 bp. Characteristics of the *A. paniculata* sample were identified by aligning it with other *A. paniculata* in the GenBank data. The BLAST results of the GenBank data showed that the *A. paniculata* sample had the same nucleotide base, 223 of the 264 nucleotide bases, with *A. paniculata* LC646073.1 with a percent identity value of 84.47% with a difference of 15.53%. *A. paniculata* from Gunungpati, Central Java is a different species from *A. paniculata* LC646073.1.

Phytochemical Screening

Table 1. Phytochemical Screening Result

Screening Compund	BK	DS
Flavonoid	+	+
Saponin	+	-
Tanin	-	+
Fenolik	+	-
Alkaloid	+	+
Mayer	+	+
Wagner	+	+
Dragendorff	+	+

BK: Cardamom seeds, DS: Sambiloto leaf

The results of the phytochemical screening of cardamom seeds showed a positive result of flavonoids, saponins, phenolics and alkaloids (Table 1). Sambiloto leaf samples showed positive results in the flavonoid, tannin and alkaloid test. This phytochemical screening was carried out with the aim of providing an explanation of the class of compounds found in *W. compacta* and *A. paniculata* plants. The method used in the phytochemical screening is the detection of color changes that occur in the sample after being added with a reagent.

The results of the BK and DS flavonoid test showed positive results, supported by the results of the research of Septiana et al. (2017); Syaputra et al. (2021) and Nurkholis et al. (2022). The results of the saponin test on BK are in accordance with the results of research conducted by Chismirina and Aulia (2016) and Nurkholis(et al. (2022). The results showed that the DS sample did not contain saponins, this is in accordance with the research of Septiana et al. (2017) and Fardiyah et al. (2020). The positive results on the tannin testing of the DS sample are supported by the research of Fardiyah et al. (2020). The tannin testing of the BK sample is different from the results of Khusnul (2019). This is possible because of the difference in the use of solvent compounds. The positive results of the phenolic test in the BK sample are supported by Embuscado (2015).

which explains that the phenolic content in cardamom seeds is high. The negative phenolic results of the DS sample were different from the results of Nagajothi et al. (2018) this is possible due to the use of a different test solution, namely Folin-Ciocalteu and in the research of Nagajothi et al. (2018) used the DPPH test method. Testing for alkaloids on both samples obtained positive results. The BK sample alkaloid test was in accordance with the research results of Ajit et al. (2020); Komala and Maulana (2020). The results of the DS sample alkaloid test are in accordance with the research of Septiana et al. (2017) using n-hexane, ethyl acetate and 70% ethanol.

Molecular Docking

The selection of flavonoid compounds was due to the results of phytochemical tests showing that all plants were positive for flavonoids as anti-virus. The results of the screening in the table 2. show that retinoic acid has the best binding energy value of -7.18 Kcal/Mol to the 6WX4 receptor followed by avicularin, 5- hydoxy-7,8,2',5' tetramethoxyflavone, naringenin, and quercetin.

Table 2. Molecular Docking of 6WX4 with samples test

No.	Bioactive compounds	Chemical formula	Binding Energy (Kcal/Mol)	Cluster RMSD
1.	Ligan *Native*	VIR251	-5.42	0
2.	5-hydroxy-7,8,2',5'- tetrametoxyflavone	C19H18O7	-5,03	0
3.	Quercetin	C15H10O7	-4,56	0
4.	Naringenin	C15H12O5	-4,58	0
5.	Avicularin	C20H18O11	-5,19	0
6.	Retinoic acid	C20H28O2	-7,28	0

Vitamin A had a lot of impact on immunity because it is a key regulator of the functions of various innate and adaptive immune cells and promotes immune-homeostasis. Vitamin A (syn. retinol) can exist in the transcriptionally active form as retinoic acid (Vollenberg et al, 2022). Retinoic acid was the most biologically active and all-trans-RA (ATRA) its main derivative, comparing with retinol and retinal (Midha et al, 2021). Several type of flavonoid contained in the Sambiloto plant consist of 5-Hydroxy-7,8,2',5'tetrametoxyflavone (Chao et al, 2021; Liaqat et al, 2021), quercetin (Fardiyah et al, 2020) and retinoic acid (Intharuksa et al, 2022). Cardamom contain high flavonoid content, particularly quercetin (Choockong et al, 2024).

The negative binding energy value of retinoic acid in this research indicates that the docking results have good stability between the ligand and the receptor molecule. This is one of the important characteristics in determining the effectiveness of a drug (Afriza et al, 2018). Binding energy is a value that describes the strength of the interaction of two or more molecules (Kastritis and Bonvin, 2013). The greater the binding energy value, the smaller the binding energy between the receptor and the ligand, and vice versa. Saputri et al. (2016) explained that the comparative affinity value of the test compound which was lower than the native ligand showed that the binding affinity between the ligand and the aldose reductase receptor was also getting lower and it was predicted that the next test results would not be better for the target protein used.

The result of the research showed that RMSD (Root Mean Square Deviation) value obtained from the four test ligands shows a value of less than 2 which means that the docking method used is appropriate. Saputri et al. (2012) explained that RMSD is the result of docking that is aligned with the native ligand and expresses the closeness of the 3D conformation of the native ligand. Furthermore, Ramírez and Caballero (2018) stated that the docking method can be said to be good if the RMSD value obtained ≤ 2.0 Å. The size of the RMSD value serves as a comparison for shifts or changes in molecular conformation during the docking process.

The molecular docking results showed that only one test compound obtained a lower binding affinity value than the test ligand, namely retinoic acid. The results of this study obtained docking data from the SARS-Cov2 PLpro 6WX4 protein with the test ligand having an RMSD value of 0.00 which indicates that all test ligands have no conformation or shift in the docking process with PLpro 6WX4 protein and indicates that the docking method used is correct. The results of molecular docking analysis show that sambiloto plays a greater role in increasing immunity against COVID-19 compared to cardamom due to the retinoic acid as flavonoid substances in sambiloto flavonoids.

Further analyzation through protein and ligand interactions showed that protein-ligand interaction of 6WX4 receptor with protein residues will facilitate the discovery, design, and development of sambiloto and cardamom as medicinal ingredients for COVID-19. Protein as a biological macromolecule will perform its function through binding with itself or other molecules (Du et al, 2016). Based on the Table 3, there is a comparison between the amino acid residues in 6WX4 with the amino acids from bioactive compounds attached to the test ligand in the Conventional Hydrogen Bond. Pitsillou et al., (2021) carried out molecular docking by making a grid on the 6WX4 receptor with protein residues as markers, these residual

proteins include Pro248, Asp164, Tyr273, Gly163, Tyr112, Cys111, Asn109, Trp106, Met208, Pro247, Thr301, Leu 162, His272, Cys270, Gln169, Tyr268, Tyr264, Gly271. Furthermore, in the study of Alfaro et al. (2020) Tyr 268, Tyr264, Tyr273, Asp 164, Met208, Pro248, Pro247, Thr301 are amino acid residues found in the 6WX4 receptor protein and are considered as active sites that can inhibit protein replication.

Table 3. Formed bonds from docking results of 6WX4 with samples test

Bioactive Compounds	Residual Amino Acid on Hydrogen Bond	Type of bond	Residual Amino Acid of 6WX4
VIR251	TYR D:264, GLY D:163, ASP D:164, TYR D:268, TRP D:106, GLY D:271	-OH	
5-hydroxy-7,8,2',5'-tetrametoxyflavone	TYR D:268	-OH	Met208, Pro247, Thr301, Pro248, Asp164, Tyr273,Gly163, Tyr112, Leu 162, Cys111, Asn109, Trp106, His272, Cys270, Gln169, Tyr268, Tyr264, Gly271
Quercetin	GLY D:163, LEU D:162, TYR D:273	-OH	
Naringenin	LEU D:162	-OH	
Avicularin	TYR D:273, GLY D:163, GLY D:271, TYR D:268, LEU:162	-OH	
Retinoic Acid	GLY D:163, CYS D:111	-OH	

All test ligands from bioactive compounds in this study have a bond with one of the amino acid residues 6WX4. The bond between the test ligand and the amino acid residue 6WX4 indicates activity against the target molecule. One of the parameters in determining the similarity of interaction and similarity of activity in the test ligand can be seen from the presence of hydrogen bonds with the same residue amino acids as the ligand. Hydrogen bond is an interaction that can facilitate, enhance and stabilize the ligand bond with the receptor (Chen et al, 2016). According to Nursamsiar et al. (2020) if there is a similar interaction between the test ligand and amino acid residues, then there is a similar type of interaction that describes the similarity of activity.

Molecular characterization, phytochemical and molecular docking analysis shows that flavonoid compounds from *W. compacta* and *A. paniculata* have the potential to be used to increase immunity against COVID-19. Nevertheless, Sambiloto has better potential because of its retinoic acid binding affinity.

CONCLUSION

The molecular character of the cardamom plant has similar genetic characteristics with *W. compacta* MF802556.1 with 100% identity. Sambiloto plant has similar characteristics with *A. paniculata* LC646073.1 with a percent identity of 84.47%. The phytochemical screening of cardamom were negative for saponins, while the Sambiloto leaf samples were negative for tannins and phenolics. Both plants were positive in having flavonoid. The result of the molecular docking test is that the Retinoic acid compound from Sambiloto has the best binding affinity value of -7.28 with an RMSD value of 0.00.

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