Review: Bioavailability and Activity Prediction of Bioactive Compounds of Red Fruit (*Pandanus conoideus* Lam.) and Pandan Grape (*Sararanga sinousa* Hemsley) by *in silico* Method

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Abstract. Red Fruit (RF) and Pandan grape (PG) contained bioactive compounds that good for health. The structure influenced the availability and activity, including the interaction with another in the body. It needs time and financial consumption, whereas bioinformation technology offers the solution. The research aims to predict the availability and activity of RF and PG compounds by *in silico* method based on the SAR. Fourteen RF and PF phenolics were evaluated for availability, antioxidant, and antiglycation activity during binding to HSA. The flavonoids showed Pa>0,7 for antioxidant in general, free radical scavenging, and lipid peroxidase inhibitor activity. The availability was shown by the ligand's capability to bind to HSA. The order of affinity energy from the largest to the smallest was RF flavonoid > PG anthocyanin > GP phenolic acids. Taxifolin and Quercetin still had antioxidant activity during binding because there are free hydroxyl groups. PG chlorogenic acid and RF flavonoids play as an anti-diabetic through antioxidant mechanism and HSA glycation disturbance. Based on this review, *in silico* method is effective as an analysis tool for the activity and mechanism prediction of food bioactive compounds.
Keywords: Prediction, Bioavailability, Activity, Bioactive Compounds, *In-Silico* Method

1. Introduction

Fruits and vegetables are well known rich in nutrition and bioactive compounds, including Red Fruit (*Pandanus conoideus* Lamk.) or known with local name as *Buah Merah* and Pandan Grape or Pandan Anggur (*Sararanga sinousa* Hemsley). Both fruits are endemic Papua region, Indonesia. Red Fruit is part of a daily meal for Papuan and traditional medicine. Pandan Grape is more served as table fruit, although less popular than RF [1]. Food

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bioactive compounds can be consumed daily including polysaccharides, glycosides, flavonoids, phenols, xanthones, alkaloids, and some saponins [2]. Red Fruit contained phenols and flavonoids [3,4,5,6,7], alkaloid [8,9], terpenoid [8,9,10], and triterpenoid saponin [8,9,11], and steroid [8,9,4]. PG contained vitamin C [1,12], phenolic acids [13,14], and anthocyanins [15].

The absorption and metabolism of a bioactive compound will affect the functionality of the compound in the human body [16]. Glycoside, aglycon, and conjugated phenolic are distributed in the blood after digestion, absorption, and metabolism in the intestinal [17,18] and then distributed to its target tissue. The compound that is found in high concentration may less available and have low activity intracellularly, because of the interactions after digestion and distribution [19,20] although it depends on the structure [20]. It was affected by the affinity of the compound to blood protein [20]. Human serum albumin is a major binding protein in the blood serum [21,22] that plays like a "metabolite sponge" [21]. It binds and transports phenolic compounds and their metabolites to different tissue of the human body where the compounds show the functional effects [21]. Then, the intramolecular interaction between bioactive compounds and HSA may determine the availability and functional effect of the compounds intracellularly.

In vitro and or *in vivo* methods are usually utilized to evaluate the availability and activity of some compounds. Those methods need more time and adequate financial support. Whereas *in silico* method offers more practical and economic analysis than *in vitro* or *in vivo* method. in silico is a term used in bioinformatics analysis. Bioinformatics analysis use methods and tools (software) for understanding biological system. Bioinformatics combines biology science with the computer, mathematics, and statistical science and techniques to analyse and then interpret the data [23]. This method may evaluate treatments on specific diseases or some different conditions targeted. The model is representative of human diseases or bioactivity [24], which conventional techniques had a limitation. There is increasing attention in research to associate human health and foods bioactive compounds, then involving bioinformatics analysis techniques in foodomics [23]. The detail of *in silico* analysis for prediction of bioactive compounds availability and activity intracellularly will be described in this paper.

2. Bioactive Compounds in Red Fruit (RF) and Pandan Grape (PG)

Previous studies showed that RF and PG contained many compounds classified as phenolic. The flavonoids are identified in methanol and ethyl acetic extract of the RF-short red, consisting taxifolin, quercetin, and quercetin 3'glucoside (Q3G) [6]. Quercetin is the main flavonoid in RF. The green PG was the raw fruit. The Papuans usually eat the orange-red and red ones. The orange-red fruit has been mature but is not completely ripe [12]. Phenols found in PG that identified as phenolic acids and anthocyanin. The phenolic acids consisted of hydroxybenzoic acid and hydroxycinnamic acid derivatives [14]. Hydroxycinnamic derivatives include 2-hydroxycinnamic acid, Caffeic acid, Sinapinic acid, Chlorogenic acid, Caffeic acid, and Ferulic acid. The concentration of phenolic acids decreased as maturity increased significantly. Galic acid, caffeic acid, ferulic acid and coumaric acid (354.67$\pm$9.41, 290.88$\pm$4.71, 266.16$\pm$ 8.33, 244.05$\pm$7.37 mg/100g, respectively) are the main phenolic acids in ripe PG [15]. Ripeness influenced the anthocyanin content of PG. The ripe contained 108.15$\pm$6.79 mg/100mg. The green contained 44.71$\pm$5.94 mg/100mg. The orange red contained (91.12$\pm$6.52 mg/100mg [15]. Those were described in Table 1 below.

Table 1. Anthocyanin Profile of *Pandan Grape* at Three Ripening Stage*

The Anthocyanins	Anthocyanin Content at Three Ripening Stage (mg/100g wb)		
	Raw (green fruit)	Mature (orange-red)	Ripe (red)
Pelargonidin 3-glucoside	12.57±1.66 [a]	22.57±1.67 [b]	27.25±1.72 [b]
Pelargonidin 3-rutinoside	11.19±1.47 [a]	21.61±1.51 [b]	23.88±1.58 [b]
Pelargonidin 3-arabinoside	7.57±1.04 [a]	15.93±1.11 [b]	19.42±1.05 [c]
Cyanidin 3-malonyl-glucosyl 5-glucoside	7.59±0.97 [a]	11.27±0.70 [b]	13.72±0.85 [b]
Cyanidin 3-glucoside	nd	9.39±0.74 [b]	11.36±0.74 [c]
Cyanidin 3-rutinoside	nd	6.56±0.50 [b]	7.98±0.56 [c]
Pelargonidin 3,5-diglucoside	nd	3.78±0.29 [c]	3.41±0.22 [b]
Pelargonidin 3-galactoside	2.20±0.31 [c]	nd	1.14±0.10 [b]
Pelargonidin 3-malonyl glucoside	2.69±0.37	nd	nd
Cyanidin 3-malonyl glucoside	0.89±0.11	nd	nd

nd= not detected
value in the same row followed by different letters is significantly different at $p < 0.05$ by Tukey's test
*[15]

3. Activity Prediction of RF and GP Bioactive Compounds

Activity prediction is the important step for beginning the *in silico* analysis. The prediction is usually based on the chemical structure of the compounds that well known as Structure-Based Relationship (SAR) analysis. Several online programs are available for SAR activity prediction, such as PASS online (http://www.pharmaexpert.ru/passonline/) [25] and Swiss-Target-Prediction (http://www.swisstargetprediction.ch/). The structure can be prepared as a canonical SMILE or molecular structure. The SMILE can be retrieved from the PubChem Compound database.

PASS online program will present the predicted activities that rank from the highest until the lowest the Pa value. The Pa (Probability to be active) and Pi (Probability to be inactive) values range from 0.0000 to 1.0000. The higher Pa value is the higher probability of the compound showing the pharmacology activity *in vitro* and or *in vivo* analysis. The cut-off is Pa value more than 0.7 [26]. Since PASS online program cannot support activity prediction for charged molecules like anthocyanins, then a prediction can be performed by the Swiss Target Prediction program. The program will show the probability estimation of a macromolecular target for each tested bioactive compound. This is assumed as bioactivity. [27].

Table 2. Antioxidant Activities Prediction of The *Red Fruit* and *Pandan Grape* Bioactive Compounds

Bioactive Compounds	Biology Activities and Probability to be Active (Pa) Value			
	Antioxidant	**Free radical scavenger**	**Lipid peroxidase inhibitor**	**Reductor**
RED FRUIT*				
Taxifolin	0,945	0,883	0,915	-
Quercetin	0,878	0,816	0,813	-
Quercetin 3'Glucoside	0,917	0,978	0,976	-
PANDAN GRAPE				
Hydroxycinnamic Acids**				
Ferulic acid	0,540	0,731	0,618	0,714
Isoferulic acid	0,540	0,731	0,618	0,714
p-coumaric acid	0,553	0,627	0,529	0,758
o-coumaric acid	0,523	0,613	0,533	0,684
Caffeic acid	0,611	0,670	0,570	0,781
Chlorogenic acid	0,785	0,856	0,855	0,555

*[7], **[16]

Table 2 above showed that RF has more potential as an antioxidant source than PG. All RF flavonoids gave Pa value > 0.7 for antioxidant in general (0.878-0.945), free radical scavenging (0,816-0.978), and lipid peroxidase inhibitor activity (0.813-0.976). The value means that it will show at least 70% of the activity when tested used *in vitro* and or *in vivo* [26,28] had proved that RF had high free radical scavenging activity. RF methanol and ethyl acetic extracts at concentration 300 ppm inhibited DPPH (40.7$\pm$0.72 and 74.92$\pm$1.33%) and ABTS radical (80.89$\pm$0.84 and 99.23$\pm$0.16%, respectively) significantly. These extracts contained high taxifolin, quercetin and quercetin 3-glucoside. PG extracts from each stage of maturity showed good inhibition for DPPH radicals. The IC50 values were 12.49 ± 0.35, 17.62 ± 3.49, and 12.23 ± 0.46 mg/ml fresh weight for the raw, mature, and ripe PG fruit, respectively [12]. It proved that *in silico* prediction is valid and relates to the chemical analysis result.

Tables 3 and 4 showed that RF and PG bioactive compounds had less potent as antidiabetic, except as NADPH oxidase inhibitors. Only quercetin and Q3G had Pa value > 0.7. Bioactivity prediction using Swiss Target Prediction online program gave a similar result for anthocyanin (Table 4.). Aldose reductase and NADPH oxidase are the most probable target for anthocyanin in the antidiabetic mechanism, but the probability values are very low. It needs further analysis using molecular interaction.

Table 3. Prediction of Activities Related Antidiabetic from Bioactive Compounds of The *Red Fruit* and *Pandan Grape*

Bioactive Compounds	Biology Activities and Probability to be Active (Pa) Value				
	Antidiabetic	Oligo 1,6-glucosidase inhibitor	Alpha-amylase inhibitor	Aldose reductase inhibitor	NADPH oxidase inhibitor
RED FRUIT*					
Flavonoids					
Taxifolin	0,462	0,340	0,146	0,152	0,339
Quercetin	0,195	0,210	0,069	0,466	0,928
Quercetin 3'Glucoside	0,661	0,673	0,468	0,592	0,731
PANDAN GRAPE					
Hydroxycinnamic Acids**					
Ferulic acid	0,274	0.153	0.260	0.138	0.198
p-coumaric acid	0,370	0.270	0.362	-	0.157
o-coumaric acid	0,365	0.217	0.349	0.119	0.163
Caffeic acid	0,385	0.238	0.357	-	0.171
Chlorogenic acid	0,289	0.210	0.190	-	-

*[7], **[16]

Table 4. Prediction of The Most Probable Macromolecular Targets Related to Diabetic of *Pandan Grape* Anthocyanin

Bioactive Compounds	Probability for Molecular Targets related to Diabetic			
	Oligo 1,6-glucosidase inhibitor	Alpha-amylase inhibitor	Aldose reductase	NADPH oxidase
PANDAN GRAPE				
Anthocyanins*				
Pelargonidin 3-glucoside	-	-	0.1430	0.1349
Pelargonidin 3-rutinoside	-	-	0.0743	0.0743
Pelargonidin 3-arabinoside	-	-	0.1044	0.0956
Pelargonidin 3-Galactoside	-	-	0.1430	0.1349
Cyanidin 3-glucoside	-	-	0.1044	0.0956
Cyanidin 3-rutinoside	-	-	0.0822	0.0822

*[16]

4. Bioavailability Prediction of RF and GP Bioactive Compounds by Molecular Interaction with Human Serum Albumin

Albumin is a major soluble protein in human blood serum [29]. Albumin can transport and distribute various compounds to human tissue, making them present or available [30,31,32]. The high affinity of quercetin on serum albumin is the reason for the higher presence of quercetin in the tissue [21]. It makes the ability to bind on albumin is useful for bioavailability prediction.

The molecular interaction was analyzed using AutoDock Vina in the PyRx 0.8 (http://pyrx.sourceforge. net) [33]. RF and PG bioactive compounds as ligands will be attached to HSA as a protein target. This ligation was blind-rigid docking; the ligands were

free and flexible molecules then were subjected to HSA as a rigid molecule in the maximal grid box. The result is expressed in binding affinity or energy (kcal/mol) in a negative value. The most favourable interaction is presented as bound energy scores at a root-mean-square deviation (RMSD) value of less than 1.0A [33]. The higher and negative binding affinity is the lower energy for binding.

Table 5. Molecular Interaction and Binding Affinity of RF and PG Bioactive compounds on Human Serum Albumin (HSA)

Ligand	Pubchem CID	Binding affinity on HSA (kcal/mol)	Hydrophilic (H-bond) and Hydrophobic (HI) Interaction
RED FRUIT			
Flavonoids*			
Taxifolin	439533	−8.2	H-bond: Ser216(3.03)
			HI: Lys223; Leu262, Leu284; Ile314; Arg281; Ala285, Ala315; Ser311; Tyr174
Quercetin	5280343	−8.2	H-bond: Ser216(3.03)
			HI: Lys223; Leu262, Leu284; Ile314; Arg281; Ala285, Ala315; Ser311; Tyr174; Glu177
Quercetin 3-Glucoside	5280804	-7.5	H-bond: Ala315(3.28), Glu316(2.98); Ser478(2.89), Asp475(3.15); Trp238 (3.15); Arg242(2.91); Cys472(2.96), Pro471(3.29)
			HI: Lys219, Lys223; Leu222
PANDAN GRAPE			
Hydroxycinnamic Acids			
Ferulic acid**	445858	-6,0	H-bond: Asp108(2,91;3,04); Asn429 (2.95)
			HI: His146, Pro147, Lys190, Ala194, Asn429, Gln459
Chlorogenic acid**	1794427	−8.1	H-bond: Tyr150, Ser192, Gln196, Arg257(2), Ala291, Glu292
			HI: **Lys195, Lys199**; Leu219, Leu234, Leu238, Leu260; Ile290; Glu153, Glu154; His242; Phe223
Caffeic acid**	689043	−6.3	H-bond: Ser192(2), Gln196, Arg222(2), Ala291
			HI: **Lys195, Lys199**; Leu238; Glu153; His242; Tyr150
p-coumaric acid***	689043	−6.6	H-bond: **Lys199**(3); Ala291(3.05); Arg222(3.05;3.22)
			HI: Leu238, Leu260; Ile264, Ile290; Ala261; Arg257
o-coumaric acid***	689043	−6.6	H-bond: **Lys199**(2.9); Ala291(2.88); Arg222(3;3.23), Arg257(3.08;3.08); Tyr150(3.08)
			HI: Leu238, Leu260; Ile264

Table 5. *continued*

Ligand	Pubchem CID	Binding affinity on HSA (kcal/mol)	Hydrophilic (H-bond) and Hydrophobic (HI) Interaction
Anthocyanins***			
Pelargonidin 3-glucoside	443648	-7.9	H-bond: Pro96(2,97), Asn99(3,26), Glu100(2,78), Thr243(3,13), His247 (2,99;2,99)
			HI: Leu103, Gln104, Leu203, Gln204
Pelargonidin 3-rutinoside	44256626	-9.2	HL: Leu115(3,02), Val116(2,59), Arg117(3,14), Arg186(2,83)
			HB: Arg114, Pro118, Met123, Lys137, Tyr138, Arg145, His146, Tyr161, Leu182, Leu185, Lys190
Pelargonidin 3-arabinoside	44256694	-8,3	HL: Phe206(3,01;3,13), Arg209 (3,06), Ala210(3,13), Asp324(3,03), Ser480(2,7), Leu481(2,88), Val482 (2,98)
			HB: Ala213, Leu327, Ala350
Pelargonidin 3-Galactoside	16218556	-8,1	HL: Arg114(2,81;3,14;3,26), Leu115 (2,80), Val116(2,89), Tyr138(2,87)
			HB: Arg117, Met123, Ile142, Phe157, Leu185, Arg186, Gly189
Cyanidin 3-glucoside	12303220	-8,4	HL: Arg114(3,09), Arg117(2,84), Tyr138(2,99), Arg186(3,18;3,32)
			HB: Leu115, Ile142, Arg145, His146, Tyr161, Leu182, Leu185, Lys190
Cyanidin 3-rutinoside	29231	-8,8	HL: Arg114(2,80), Arg117(2,98), His146(2,87;2,97)
			HB: Leu115, val116, Met123, Tyr138, Ile142, Arg145, Arg186, Gly189, Lys190

*[7], **[15], ***[16]
Residues with red color are important for the glycation process

All RF and PG bioactive compounds are bound to HSA (Table 5), which mean all are available intracellularly. The anthocyanin structure had the highest binding affinity [(-) 7.9-(-)9.2 kcal/mol], followed by the flavonoid [(-)7.5-(-)8.2 kcal/mol] and then the hydroxycinnamic acid [(-)6.0-(-)8.1 kcal/mol]. It means anthocyanin is the most available bioactive compound. It may be due to the high solubility of anthocyanins in water. Flavonoids are not easily absorbed. Only some flavonoids can pass through the intestinal wall passively [35]. The number of hydroxyl groups on rings A and B influences the binding of flavonoids to HSA. The increase of the hydroxyl groups enhances the affinity. Glycosylation reduces the affinity of the flavonoid [20]. Those explained why taxifolin and quercetin had a higher binding affinity to HSA [(-)8.2 kcal/mol] than Q3G [(-)7.5 kcal/mol] (Table 5).

5. Bioactivity Prediction of RF and GP Bioactive Compounds

In general, antioxidant capacity depends on the phenolic compound structure. The number and position of free hydroxyl groups and other substituents will affect the antioxidant activity [36]. The presence of free hydroxyl groups at C5 and C7 on ring A, C3 on ring C and C4' and C5' on ring B. determine the antioxidant activity of flavonoids [37]. The presence of hydroxyl group on ring B determines the reactive oxygen radical scavenging capability of

flavonoid [38]. Flavonoid-protein interaction may cover the antioxidant activity of flavonoids [39,40]. Figure 3 showed the position of hydrogen bonding on HSA and free hydroxyl group in RF flavonoid structures. Q3G had Pa value for radical scavenging higher than taxifolin and quercetin (Table 2), but binding to HSA made Q3G have less free hydroxyl groups compared to taxifolin and quercetin (see the red arrow in Figure 3). It reduced Q3G scavenging capacity. Based on this data, we predict that taxifolin and quercetin are responsible for the strong radical scavenging activity of RF extracts [7]. We can also predict that the antioxidant activity *in vivo* of the extract will be lower than the chemical analysis.

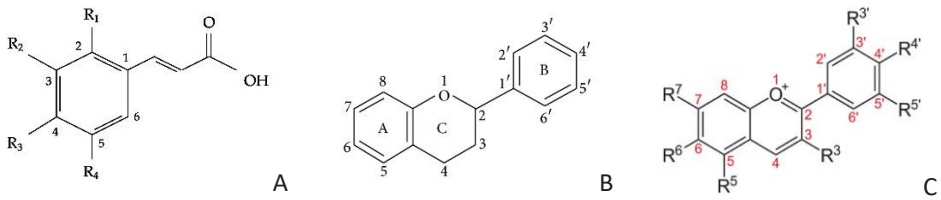


Fig 1. The basic structure of Hydroxycinnamic Acid (A), flavonoid (B), and anthocyanin (C)

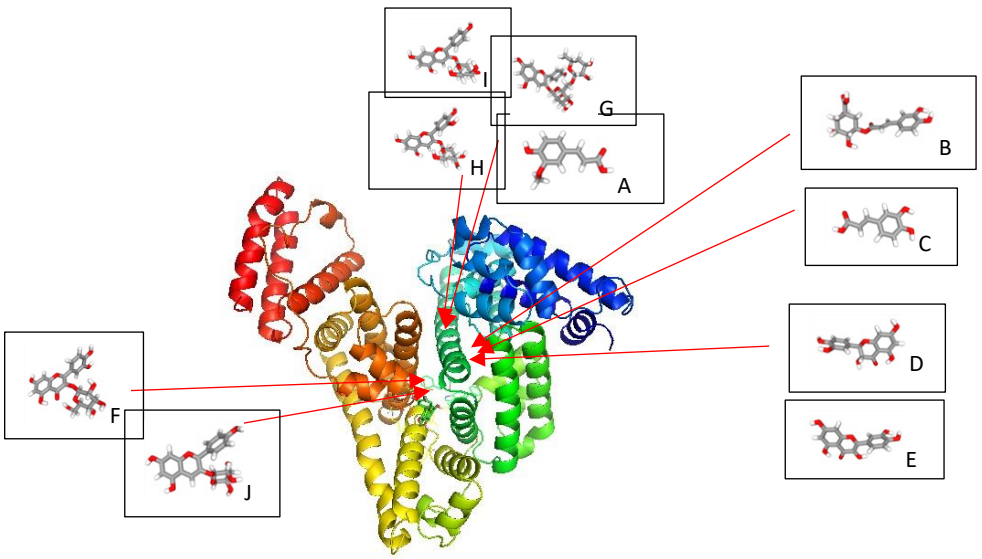


Fig 2. Docking Position of RF and PG Bioactive Compounds on HSA
A: ferulic acid, B: chlorogenic acid, C: caffeic acid, D: taxifolin, E: quercetin, F: Q3G, G: pelargonidin-3-rutinoside, H: pelargonidin-3-galactoside, I: cyanidin-3-glucoside, J: Pelargonidin-3-arabinoside [7,14,15]

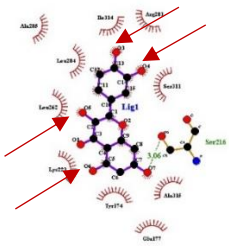
Anthocyanin has a flavonoid structure basic (Figure 1, B and C) [2], but C3 on ring C bound sugar moiety. The similarity makes anthocyanin have a similar mode of activity action to flavonoid. Figure 2 showed that chlorogenic acid and caffeic acid share the same site to HSA (FA7 site) with taxifolin and quercetin. This site is a major drug-binding pocket that preferentially binds the heterocyclic compounds. Residue Lys199 on this site is nucleophilic that withdraw many electron-donating compounds [32] including flavonoid and phenolic acid. PG anthocyanins share the FA9 site with ferulic acid, whereas Q3G and Pelargonidin-3-arabinoside are on FA8. FA8 site forms like an open ring because of the residues Lys195,

Lys199, Arg218, Asp451, and Ser454 [32]. It makes the site is more hydrophilic and suitable for Q3G and pelargonidin-3-arabinoside.

The antioxidant capacity of anthocyanin depends on the presence of free hydroxyl groups on ring A or B. Figure 3 showed that only anthocyanin with cyanidin structure (cyanidin 3-glucoside and cyanidin 3-rutinoside) that had free hydroxyl groups on ring B (see the red arrow on that figure) during attached to HSA. The free hydroxyl groups in PG hydroxycinnamic acids were higher than in the anthocyanins. The number and position of free phenolic hydroxyl groups influenced the ability of free radical scavenging. Phenolic acids had a higher number of phenolic hydroxyl groups show higher antioxidant activity [35]. Chlorogenic acid played as the main antioxidant in PG. It related to antioxidant prediction data in Table 2, where chlorogenic acid had the highest Pa value (0.775 for antioxidant in general; 0.856 as free radical scavenger; and 0.855 as lipid peroxidase inhibitor). Chlorogenic acid had free catechol moiety that is important for the antioxidant activity of phenolic acid [35,41]. The CH_2COOH in hydroxycinnamic acid is a weak electron-donating group. It increases the free radical scavenging ability of hydroxycinnamic acid [35]. Anthocyanins do not involve in the antioxidant activity of PG extract. Food anthocyanin may be absorbed and metabolized as phenolic acids [2]. The acidity of gastric may hydrolyse the glycosidic and ester bonds in anthocyanins and produce "phenolic acids" [36]. For example, cyanidin 4-glucoside has metabolite product protocatechuic acid. That acid inhibits nitric oxide (NO) production. The red or ripe PG fruit that has the highest anthocyanin content showed the best inhibition of DPPH radical (IC50 values = 12.23 ± 0.46 mg/ml fresh weight).

The phenolic structure determines the anti-diabetic activity of the phenolic. The number and position of hydroxyl groups, the presence of double bonds and the C-4 ketonic group are important structural characteristics for anti-diabetic activity [36]. The presence of hydroxyl groups on C5 and C7 of the ring A and C3' and C4' of the ring B enhance the inhibition of flavonoids on a-glucosidase and a-amylase activity [20]. That positions are also important for antioxidant activity, so there is a strong relation between antioxidant and anti-diabetic activity based on the chemical structure of bioactive compounds [2].

The glycation in human serum albumin is done by glucose [42,43,45]. The glycated-HSA may involve advanced glycation end-products (AGE). It plays a complication in diabetic patients [43,45]. The disturbance in the glycation process in HSA can play as anti-diabetic activity. The antioxidants and radical scavengers can inhibit glycation and AGE formation. The compound that has a combination of antioxidant and antiglycation activity is more effective for inhibition of AGE formation [43].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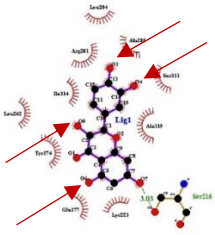
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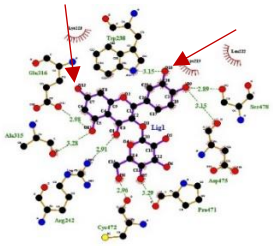
HSA-Q3G

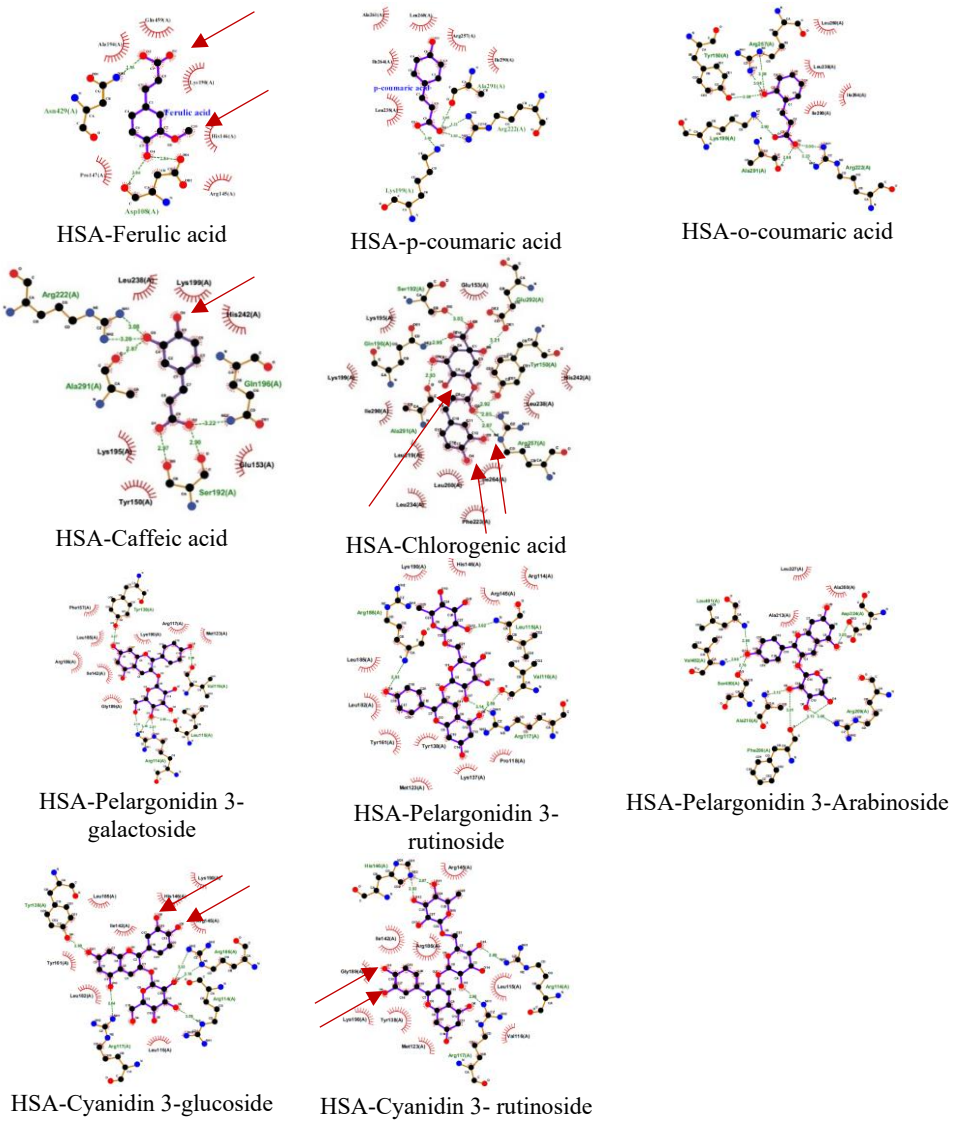

Fig 3. Hydrogen Bonding Position of RF and PG Bioactive Compounds on HAS. The red arrow pointed to the position of the hydroxyl group that play in antioxidant activity [7,14,15]

The glycation usually happened on residues Arg197, Lys199, Lys233, Lys276, Lys281 and Lys525 [46]. They are taken place in FA7 site or subdomain IIA called Sudlow's site I [32]. The residue Lys199 and Lys195 are the gates for early HSA glycation [47]. Table 5 and Figure 3 showed that only hydroxycinnamic acids especially coumaric acids that directly bound on Lys195 and Lys 199. It means coumaric acids have strong anti-diabetic activity. They compete with sugar for binding to HSA. Chlorogenic acid and caffeic acid did not bind directly on the lysine residues but had hydrophobic interaction with Lys195 and Lys 199. It makes them still have the potency to disturb the HSA glycation. RF taxifolin and quercetin did not bind directly to Lys195 and Lys 199 (Table 5), but they share in the same site of HSA ligation with chlorogenic acid and caffeic acid (Figure 2.). It means RF taxifolin and quercetin has the same potency as chlorogenic acid and caffeic acid as anti-diabetic. The PG

anthocyanin did not bind to the important residues for HSA glycation. The glycosylation of Q3G and the anthocyanin decrease antidiabetic activity [20]. Since anthocyanin can be metabolized as phenolic acids, it means the anthocyanin play as anti-diabetic through its metabolite's activity.

A strong inhibitor for lipid peroxidation may act as an antidiabetic [2,43]. Membrane lipid peroxidation and glycation are the main processes in diabetes development [43]. Free radical from lipid membrane oxidation increase HSA glycation [43]. The AGE formation inhibition positively correlated to radical scavenging activity [48]. PG chlorogenic acid and RF flavonoids showed the highest on lipid peroxidase inhibition and free radicals scavenging prediction (Table 2.). On the other side, they showed the lowest antidiabetic activity prediction (Table 3). Anthocyanin can decrease free radical concentration [2]. Those data explained that PG phenolic acids and RF flavonoids play as antidiabetic through the antioxidant mechanism and HSA glycation disturbance. The macromolecule target for their activity is albumin.

6. Conclusion

Based on the activity prediction, RF and PG bioactive compounds had a high Pa value for antioxidant activity but a low Pa value for antidiabetic activity. All ligands bound on human serum albumin (HSA) mean are available in the human body, but the affinity energy was RF flavonoid > PG anthocyanin > GP phenolic acids. The molecular interaction between the bioactive compounds made the activities revealed. The antioxidant activity of the compounds depended on the presence and position of the free hydroxyl group during binding to HSA. The compounds play as antidiabetic through the antioxidant mechanism and HSA glycation disturbance. Those are chlorogenic acid and flavonoid (flavonol). RF and PG fruit were rich in the compounds, so can be used in diabetic treatment. This proved that in silico method can analyse for the activity and mechanism of food bioactive compounds.

7. Reference

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