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Theoretical Evaluation of the Interaction of a Series of Chalcone Derivatives on CK2 Protein Surface

Figueroa-Valverde Lauro ^{1,*(1)}, Rosas-Nexticapa Marcela ^{2,*(1)}, Cervantes-Ortega Catalina ^{2,1)}, López-Ramos Maria ^{1,1)}, Díaz-Cedillo Francisco ^{3,1)}, Alvarez-Ramirez Magdalena ^{2,1)}, Mateu-Armad Maria Virginia ^{2,1)}

- Laboratory of Pharmaco-Chemistry, Faculty of Chemical Biological Sciences, University Autonomous of Campeche, Av. Agustín Melgar s/n, Col Buenavista C.P. 24039 Campeche, Camp., México
- Nutrition Laboratory, Faculty of Nutrition, Veracruzana University, Médicos y Odontologos s/n C.P. 91010, Unidad del Bosque Xalapa Veracruz, México
- Laboratory Organic Chemistry, National School of Biological Sciences, National Polytechnic Institute. Prol. Carpio y Plan de Ayala s/n Col. Santo Tomas, México, D.F. C.P. 11340
- * Correspondence: lfiguero@uacam.mx (F.L.); rosasnm@yahoo.com (R.M.);

Scopus Author ID 55995915500

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Abstract: Several studies suggest that chalcone derivatives can produce a broad spectrum of biological activities such as antibacterial, antiulcer, antiviral, insecticidal, antiprotozoal, anti-cancer, and antifungal. Besides, other reports suggest that chalcone derivatives exert changes in the cardiovascular system; however, its site of action is not very clear; perhaps this phenomenon could be to differences involved in the chemical structure of chalcone derivatives. This research aimed to carry out a theoretical study on the interaction of a series of chalcone analogs (compounds 1 to 20) on casein kinase 2 (CK2) protein using 3fl5 protein and quinalizarine drug as theoretical tools in a theoretical model (DockingServer). The results showed that chalcone derivatives (compounds 2, 9, 11, and 19) could have a higher affinity for the 3fl5 protein surface translated as greater CK2 inhibition than quinalizarine. These data open the possibility that chalcone derivatives can produce changes in the biological function of CK2, resulting in a decrease in heart failure.

Keywords: chalcone; derivatives; theoretical study; docking.

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1. Introduction

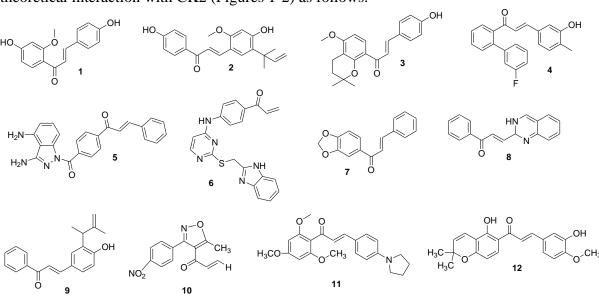
For several years, chalcone derivatives have been used in organic chemistry and pharmaceutical industry fields [1-4]. It is noteworthy that chalcone analogs are α - β -unsaturated ketones [5, 6], which can produce different biological activity against Parkinson's [7] cancer [8], gastric ulcer [9], malaria [10], antiviral [11-14], antibacterial [15], antifungal [16, 17]. Besides, some studies indicate that chalcone derivatives may exert changes in the cardiovascular system [18]; for example, difluoro-chalcone derivative protects cardiomyocytes from hyperglycemia-induced injuries through ROS (reactive oxygen species) and NF-kB (nuclear factor- κ B) inhibition [19]. Other reports showed that a chalcone derivative can inhibit inflammation of human aortic smooth muscle cells through increased expression of peroxisome proliferator-activated receptor gamma [20]. Furthermore, a study shows that trans-chalcone inhibits transforming growth factor- β 1 in rat heart connective tissue [21]. Recently, a report indicated that hesperidin methyl chalcone produces a cardioprotective through lipid peroxidation inhibition in vitro [22].

On the other hand, different theoretical models have been used to characterize the molecular mechanism involved in the biological activity produced by chalcone derivatives in the cardiovascular system. In this way, a theoretical study showed that some chalcone derivatives could produce a biological effect through interaction with HMG-CoA (β -hidroxi- β -metilglutaril-coenzima A) reductase using CASTp software [23]. Other data indicate that 3,5-disubstituted thiazolidinedione chalcone may interact with PPAR- γ (peroxisome proliferator-activated receptor gamma) using AutoDock-4.2 software [24]. In addition, a report displayed that dihydrospirochalcone-A could have an affinity to the eNOS enzyme (endothelial nitric oxide synthase) using a docking model [25]. All these data suggest that chalcone derivatives could produce changes in the cardiovascular system; however, there is no information on the effect produced by chalcone derivatives on protein kinases, specifically on CK2, which has been involved in heart failure patients [26-28]. Analyzing these data, this study aimed to conduct a theoretical study on the interaction of twenty chalcone analogs with Casein Kinase 2 (CK2) protein using Docking Server software [29].

2. Materials and Methods

2.1. General methodology.

A series of chalcone derivatives previously reported [30] were used to evaluate their theoretical interaction with CK2 (Figures 1-2) as follows:



- $\mathbf{1} = 1 (4 \text{Hydroxy-2-methoxy-phenyl}) 3 (4 \text{hydroxy-phenyl}) \text{propenone}.$
- 2 = 3-[5-(1,1-Dimethyl-allyl)-4-hydroxy-2-methoxy-phenyl]-1-(4-hydroxy-phenyl)-propenone.
- **3** = 3-(4-Hydroxy-phenyl)-1-(5-methoxy-2,2-dimethyl-chroman-8-yl)-propenone.
- 4 = 1-(3'-Fluoro-biphenyl-2-yl)-3-(3-hydroxy-4-methyl-phenyl)-propenone.
- **5** = 1-[4-(3,4-Diamino-indazole-1-carbonyl)-phenyl]-3-phenyl-propenone.
- $\mathbf{6} = 1 \{4 [2 (1 + Benzoimidazol 2 ylmethylsulfanyl) pyrimidin 4 ylamino] phenyl\} propenone.$
- 7 = 1-Benzo[1,3]dioxol-5-yl-3-phenyl-propenone.
- ${\bf 8}=3\hbox{-}(2,3\hbox{-Dihydro-quinazolin-}2\hbox{-yl})\hbox{-}1\hbox{-phenyl-propenone}.$
- $\mathbf{9} = 3\text{-}[3\text{-}(1,2\text{-}Dimethyl\text{-}allyl)\text{-}}4\text{-}hydroxy\text{-}phenyl]\text{-}1\text{-}phenyl\text{-}propenone.}$
- $\mathbf{10} = 1$ -[5-Methyl-3-(4-nitro-phenyl)-isoxazol-4-yl]-propenone
- 11 = 3-(4-Pyrrolidin-1-yl-phenyl)-1-(2,4,6-trimethoxy-phenyl)-propenone.
- 12 = 1 (5 Hydroxy 2, 2 dimethyl 2H chromen 6 yl) 3 (3 hydroxy 4 methoxy phenyl) propenone.

Figure 1. Structure chemical of chalcone derivatives (1-10).

13 = 3-[3-(2-Hydroxy-phenyl)-3-oxo-propenyl]-1H-quinolin-2-one.

14 = 6-Acryloyl-2-methyl-3H-quinazolin-4-one.

15 = 3-(3-Oxo-3-phenyl-propenyl)-1H-quinolin-2-one.

 $\textbf{16} = 1 - \{3 - [(2,3 - \text{Dihydroxy-benzylidene}) - \text{amino}] - 4 - \text{methoxy-phenyl}\} - 3 - (3,4,5 - \text{trimethoxy-cyclohexyl}) - \text{prope-none}\} - 3 - (3,4,5 - \text{trimethoxy-cyclohexyl}) - 3 - (3,4,5$

17 = 1,3-Bis-(2-chloro-phenyl)-propenone.

18 = 1,2,3-Trimethyl-4-(1-m-tolyl-ethyl)-benzene.

19 = 3-[3-(1,2-Dimethyl-allyl)-4-hydroxy-phenyl]-1-phenyl-propenone.

20 = 1-(3-Hydroxy-phenyl)-3-(4-trifluoromethyl-phenyl)-propenone.

Figure 2. Structure chemical of chalcone analogs (6-20).

2.2. Pharmacophore model.

3D pharmacophore model for chalcone derivatives was evaluated using LigandScout 4.08 software [28, 29].

2.3. Ligand-protein interaction.

The interaction of chalcone derivatives with the CK2 protein surface was evaluated using 3fl5 protein as a theoretical model [30]. In addition, to evaluate the types of binding energy involved in the interaction of chalcone derivatives with the 3fl5 protein surface [33], the DockingServer software was used [29].

2.4 Pharmacokinetics parameter.

Pharmacokinetic parameters were determined using the SwissADME software [34, 35].

3. Results and Discussion

Several studies indicate that chalcone derivatives can affect the cardiovascular system differently [36-39]; however, the interaction with some biological molecules is unclear. Analyzing this data, in this investigation, the theoretical activity of a series of chalcone derivatives on the CK2 protein was evaluated as follows:

3.1. Pharmacophore model.

For several years, various theoretical methods have been developed to design new drugs for treating different diseases. For example, the pharmacophore model provides a new perspective on the design of new compounds useful for developing new drugs. Based on these data, in this study, the LigandScout software [17, 18] was used to design a pharmacophore model to evaluate the possible chemical interactions of chalcone derivatives (compound 1-20) with some biomolecules such as CK2 protein. The results showed differences in functional

groups involved in the chemical structure of the chalcone derivatives, which could interact through hydrophobic or hydrogen bonds with CK2 protein (Figures 3 and 4; Table 1).

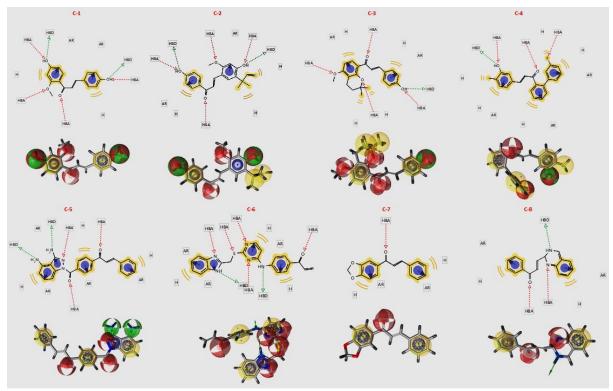


Figure 3. Pharmacophore was developed for chalcone derivatives (compounds **1** to **8**) using the LigandScout software. Hydrogen bond acceptors (HBA, red) and hydrogen bond donors (HBD, green).

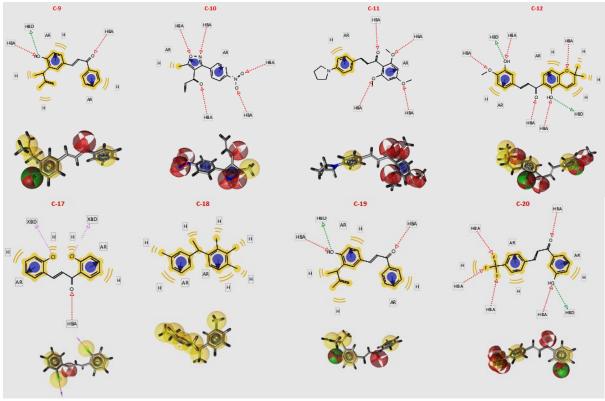


Figure 4. Pharmacophore was prepared to chalcone derivatives (compounds 9 to 20) using the LigandScout software. Hydrogen bond acceptors (HBA, red) and hydrogen bond donors (HBD, green).

Table 1. Physicochemical parameters of chalcone derivatives (Compounds 1 to 20).									
Compound	Concensus Log	HBA	HBD	Molar refracty	TPSA				
	$P_{ m o/w}$				Å				
Quinalizarin	1.38	6	4	67.94	115.06				
1	2.55	4	2	76.79	66.76				
2	3.93	4	2	100.39	66.76				
3	3.85	4	1	98.57	55.76				
4	3.85	3	1	98.63	37.30				
5	3.39	3	2	114.52	104.00				
6	3.60	4	2	111.96	108.86				
7	3.17	3	0	72.31	35.53				
8	2.46	2	1	95.39	41.46				
9	4.95	2	1	91.99	37.30				
10	1.87	5	0	70.25	88.92				
11	3.69	4	0	110.37	48.00				
12	3.60	5	2	100.91	75.99				
13	3.03	3	2	86.40	70.16				
14	1.76	3	1	61.86	62.82				
15	3.23	2	1	84.38	49.93				
16	3.01	8	2	129.61	106.81				
17	4.50	1	0	76.27	17.07				
18	5.30	0	0	80.57	0.00				
19	4.48	2	1	91.99	37.30				
20	3.96	5	1	73.27	37.30				

Table 1. Physicochemical parameters of chalcone derivatives (Compounds 1 to 20)

3.2. Interaction theoretical evaluation.

Several theoretical methods have been used to predict some ligands' interaction with proteins and enzymes [40, 41].

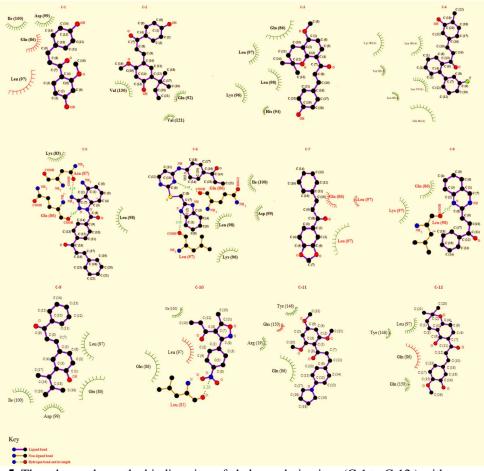


Figure 5. The scheme shows the binding sites of chalcone derivatives (C-1 to C-12) with some amino acid residues involved on the protein kinase surface (3FL5). The visualization was carried out using DockingServer software.

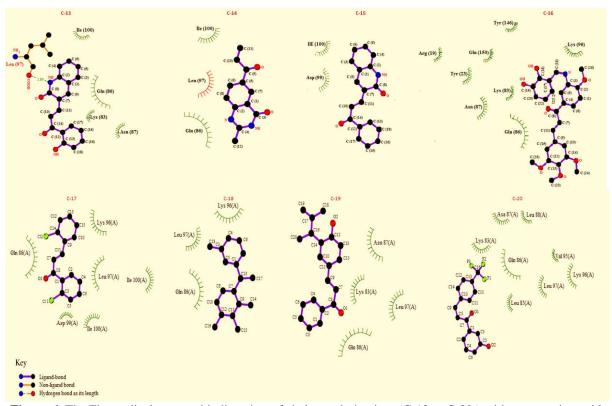


Figure 6. The Figure display some binding sites of chalcone derivatives (C-13 to C-20) with some amino acid residues involved on *the* protein kinase surface (3FL5). The visualization was carried out using DockingServer software.

Notably, the molecular recognition of protein-ligand interactions is essential to understand some biological activities, which can be of great importance for designing and developing new compounds with pharmacological activity [42]. Besides, it is important to mention that the drug quinalizarine was used as a control because some reports indicate that this drug can produce changes in the biological activity of CK2 [28, 43]. The results showed different amino acid residues involved in the interaction of chalcone derivatives with 3f15 protein surface compared with quinalizarin (Figures 5 and 6; Table 2); this phenomenon could be due to differences in their chemical structure (Figures 1 and 2).

Table 2. Aminoacid residues involved in the interaction of chalcone derivatives (1 to 20) and quinalizarin with 3fl5-protein surface.

Compound	Aminoacid Residues				
Quinalizarin	Gly ₈₆ , Leu ₉₇ , Ile ₁₀₀				
C-1	Gln ₈₆ , Leu ₉₇ , Asp ₉₉ , Ile ₁₀₀				
C-2	Arg ₁₃ , Tyr ₂₃ , Asn ₈₇ Tyr ₁₄₆ ,				
	Gln ₁₅₈				
C-3	Gl ₈₆ , Lys ₉₆ , Leu ₉₇ , Leu ₉₈				
C-4	Leu ₈₅ , Gln ₈₆ , Val ₉₆ , Lys ₉₆ ,				
	Leu97, Leu98				
C-5	Lys ₈₃ , Gln ₈₆ , Asn ₈₇ , Leu ₉₈				
C-6	Gly86, Lys96, Leu97, Leu98,				
	Asp ₉₉ , Ile ₁₀₀				
C-7	Gln ₈₆ , Lys ₉₆ , Leu ₉₇				
C-8	Gln ₈₆ , Leu ₉₇ , Asp ₉₉				
C-9	Gln ₈₆ , Leu ₉₇ , Asp ₉₉ , Ile ₁₀₀				
C-10	Gln ₈₆ , Gln ₈₆ , Leu ₉₇ , Ile ₁₀₀				
C-11	Arg ₁₉ , Gln ₈₆ , Tyr ₁₄₆ , Gln ₁₅₀				
C-12	Gln ₈₆ , Leu ₉₇ , Tyr ₁₄₆ , Gln ₁₅₀				
C-13	Lys ₈₃ , Gln ₈₆ , Asn ₈₇ Leu ₉₇ , Ile ₁₀₀				
C-14	Glu ₈₆ , Leu ₉₇ Ile ₁₀₀				
C-15	Asp ₉₉ , Ile ₁₀₀				

Compound	Aminoacid Residues
C-16	Arg19, Tyr23, Lys83, Gln86,
	Asn ₈₇ , Lys ₉₆ , Tyr ₁₄₆ , Gln ₁₅₀
C-17	Gln ₈₆ , Lys ₉₆ , Leu ₉₇ , Asp ₉₉ ,
	Ile ₁₀₀
C-18	Gln ₈₆ , Lys ₉₆ , Leu ₉₇ , Ile ₁₀₀
C-19	Lys ₈₃ , Gln ₈₆ , Asn ₈₇ , Leu ₉₇
C-20	Lys ₈₃ , Leu ₈₅ , Gln ₈₆ , Asn ₈₇ ,
	Leu88, Val95, Lys96, Leu97

3.3 Bond energies.

Some studies suggest that different thermodynamic factors could be involved in the drug-protein interaction, such as i) binding free energy, which involves the energy level produced by ligand-protein interaction; ii) ii) electrostatic energy that involves an electrical charge and electrostatic potential; iii) total intermolecular energy; and iv) Van der Waals (vdW) interactions, hydrogen bond (H bond), desolvation energy [44, 45]. Based on these data, in this research, some thermodynamic parameters involved in the interaction of chalcone derivatives with CK2 surface (3fl 5 protein) were evaluated using quinalizarin as a control. Table 3 shows the energy requirements involved in the interaction of compounds 2, 9, 11, and 19 with the 3fl5 protein surface were lower compared to compounds 1, 3-8, 10-18, 20, and quinalizarin. The results indicate that these compounds could interact with the surface of the 3RUK protein, implying differences in energy levels and constant inhibition. This phenomenon may result in changes in the biological activity of the CK2 enzyme, which translates into a decrease in heart failure.

Table 3. Thermodynamic parameters involved the interaction of Bay-K-8644 drug and compounds 4 with 1t0j-

Compound	Est: Free Energy of Binding (kcal/mol)	Est. Inhibition Constant, Ki (mM)	vdW + Hbond + desolv Energy (kcal/mol)	Electrostatic Energy	Total Intermolec. Energy (kcal/mol)	Interact. Surface
Quinalizarin	-5.09	185.45	-3.57	-0.32	-3.89	437.26
C-1	-3.60	2.31	-5.01	-0.11	-5.11	514.86
C-2	-2.98	6.57	-5.25	0.03	-5.28	611.65
C-3	-4.10	993.60	-5.33	0.11	-5.22	535.19
C-4	-5.65	72.29	-6.72	-0.02	-6.74	554.13
C-5	-5.13	173.28	-6.13	-0.28	-6.40	631.31
C-6	-6.34	22.59	-6.54	-0.10	-6.64	626.60
C-7	-4.17	882.31	-5.06	1.05	-5.00	505.48
C-8	-4.24	779.52	-4.61	-0.38	-4.99	545.77
C-9	-3.84	1.52	-5.41	-0.15	-5.96	577.09
C-10	-5.06	195.53	-6.12	-0.14	-6.26	474.70
C-11	-3.26	4.05	-5.13	-0.10	-5.23	674.48
C-12	-4.49	513.08	-5.44	-0.21	-5.66	662.33
C-13	-4.80	301.75	-5.30	-0.03	-5.33	515.46
C-14	-4.77	321.26	-5.19	-0.16	-5.35	479.32
C-15	-4.49	510.79	-5.32	-0.06	-5.38	572.74
C-16	-5.07	190.89	-7.09	-0.11	-7.20	711.60
C-17	-5.54	87.32	-6.39	-0.01	-6.40	552.05
C-18	-5.61	77.57	-5.98	-0.01	-5.99	529.89
C-19	-3.69	1.98	-5.36	-0.08	-5.44	540.00
C-20	-4.41	590.31	-5.78	-0.11	-5.89	482.66

3.7. Pharmacokinetic evaluation.

For several years, different protocols have been used to predict some pharmacokinetic parameters, such as PKQuest [46], PharmPK [47], and SwissADME [48]. In this investigation, some pharmacokinetic factors involved in chalcone derivatives were analyzed using https://biointerfaceresearch.com/

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SwissADME software (Table 3). The results showed differences in gastrointestinal absorption and metabolism (involving different types of cytochrome P450 systems). This phenomenon could depend on each chalcone derivative's chemical structure and the lipophilicity degree (Tables 1, 4, and 5).

Table 4. Pharmacokinetic parameters involved in the chemical structure of compounds 1 to 10.

Parameter	1	2	3	4	5	6	7	8	9	10
GI absorption	High									
BBB										
permeant	Yes	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No
P-gp substrate										
CyP1A2	No	Yes	No							
Inhibitor										
CyP2C19	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes
Inhibitor										
CyP2C9	No	No	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes
Inhibitor										
CyP2D6	Yes	No								
Inhibitor										
CyP3A4	No	No	Yes	Yes	No	Yes	No	No	Yes	No
Inhibitor										
	Yes	Yes	Yes	Yes	No	Yes	No	No	Yes	No

Table 5. Pharmacokinetic parameters involved in the chemical structure of compounds 11 to 20.

Parameter	11	12	13	14	15	16	17	18	19	20
GI absorption	High	Low	High	High						
BBB										
permeant	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
P-gp substrate										
CyP1A2	No	No	No	No	No	Yes	No	No	Yes	No
Inhibitor										
CyP2C19	No	Yes	No	Yes	No	No	Yes	No	Yes	Yes
Inhibitor										
CyP2C9	Yes	Yes	No	No	No	No	Yes	No	Yes	Yes
Inhibitor										
CyP2D6	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	No
Inhibitor										
CyP3A4	No	No	No	No	No	Yes	No	Yes	Yes	Yes
Inhibitor										
	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes

4. Conclusions

Theoretical analyzes on the interaction of chalcone derivatives (compounds 2, 9, 11, and 19) with the 3fl5 protein surface suggest that these chalcone derivatives might have a higher affinity for 3fl5 translated as greater CK2 inhibition compared to quinalizarine drug. These data open the possibility that chalcone derivatives can produce changes in the biological function of CK2, resulting in a decrease in heart failure.

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Conflicts of Interest

We declare that this manuscript has no conflict of financial interests (political, personal, religious, ideological, academic, intellectual, commercial, or otherwise) for publication.

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