

In Silico Studies of Khellin and Related Furochromenes by Modified POM Analysis [†]

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Abstract: POM (Petra/Osiris/Molinspiration) analysis and related in silico tools are well-established methods used to evaluate the potential of molecules to become drug candidates by predicting their biological activity, calculating various physicochemical properties, ADME parameters or toxicity. Khellin **1** is well-known component of *Ammi visnaga* (khella) plant used for centuries in the folk medicine for treatment urinary tract pain associated with kidney stones. Modern medicine has found importance of khellin in the treatment of psoriasis, angina pectoris or vitiligo. However, the oral use of khellin is limited by its potential adverse effects, such as dizziness, constipation, headache, itching, or lack of appetite. Many natural or synthetic furopyrrole derivatives have been extensively studied and reported to possess numerous biological effects, including anticancer, anti-inflammatory or antimicrobial. The present in silico study is aimed at revealing the most promising drug candidates based on favorable pharmacokinetic parameters and toxicological characteristics. A modified POM analysis of sixteen furochromenes was performed using Molinspiration, Osiris and SwissADME softwares. Studied structures were selected due to the modifications of the khellin skeleton. Substitution of the furan or pyran ring, modification of one or both methoxy groups or hydrogenation of one or both heterocyclic rings were included. The results of this preliminary in silico investigations suggest all furopyrroles have good oral bioavailability high level of gastrointestinal absorption. The bioactivity score prediction shows their ability to act predominantly as ion channel modulators or enzyme inhibitors. All compounds exhibit low risk of being irritants, nine of them exhibit low risk of being mutagenic, tumorigenic or to have reproductive effect.

Keywords: furochromene; khellin; biological activity; Molinspiration; Osiris; SwissADME

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1. Introduction

Khellin **1** (Figure 1) is one of furochromenes obtained from fruits and seeds of wild plant *Ammi visnaga* L. (khella), used for many centuries in Egyptian folk medicine to relieve renal colic [1]. Further studies had reported the use of extract of *A. visnaga* for the treatment of psoriasis [2], angina pectoris [3] or vitiligo [4]. However the oral use of khellin is limited by its potential adverse effects, such as dizziness, constipation, headache, itching, insomnia, and lack of appetite [5].

Many in silico tools have been developed to predict physicochemical properties or pharmacokinetic properties (absorption, distribution, metabolism, and excretion—ADME) of molecular structure or to prevent its unwanted effects (toxicity or hazards) on the organism [6]. In silico tools are also important in the druglikeness determination. Druglikeness is estimated from the structure and physico-chemical properties of the chemical structure [7] and represents a term used in drug design to find out the molecule suitable for oral use and therefore promising drug candidate [8]. POM analysis (Petra, Osiris and Molinspiration) represents well-established in silico tool to access the

pharmacokinetic profile of the synthesized molecules [9]. Modified POM analysis [11–13] enables to replace Petra software [10] by swissADME [7] when the prediction of pharmacological parameters is a priority. The aim of this preliminary research is to present in silico evaluation of physicochemical properties, pharmacokinetic parameters and toxicity potential of khellin **1** and related compounds **2–16** (Figure 1) with the intention to find the structure with improved pharmacokinetic properties and low toxicity.

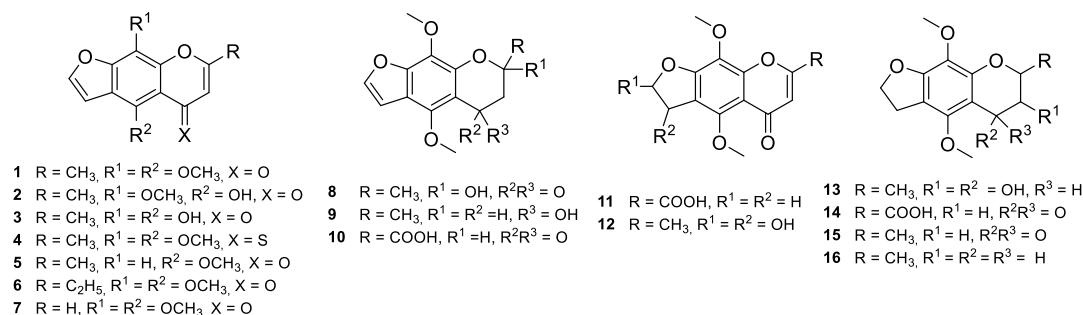


Figure 1. Khellin **1** and related furochromenes **2–16**.

2. Material and Methods

Structures of furochromene derivatives **2–16** (Figure 1) were selected from the SciFinder database [14] due to the modifications of the khellin **1** skeleton. Substitution on the furan or pyran ring, modification of one or both methoxy groups or hydrogenation of one or both heterocyclic rings were included.

Molinspiration [15] was used for the calculation of molecular properties (logP, TPSA, number of H-bond donors and acceptors) and prediction of bioactivity score for the most important drug targets (GPCR ligand, ion channel modulator, kinase inhibitor, nuclear receptor ligand, protease or enzyme inhibitor). SwissADME software [16] was used for the pharmacokinetic parameters calculations such as gastrointestinal absorption, blood-brain barrier permeation, skin permeation, the assessment of whether a compound is a substrate of P-gp, the interactions of the molecule with the cytochrome P450 or the skin permeability (Log Kp). The druglikeness score using five different methods (Lipinski, Ghose, Veber, Egan and Muegge) was calculated. The bioavailability score predicts the probability of the oral bioavailability of the compound. PAINS and Brenk structural alerts are used for the identification of potentially problematic fragments—responsible for positive biological output or putatively toxic, chemically reactive or metabolically unstable. Finally, leadlikeness and synthetic accessibility of structure can be predicted. The toxicity risk based on the mutagenicity, tumorigenicity, irritating effects and reproductive effects of studies compounds is reported using Osiris property Explorer [17]. The results are given as a semaphore light colors.

3. Results and Discussion

3.1. Molinspiration

According to the Lipinski's rule [18], only a molecule with MW ≤ 500, LogP ≤ 5, number of H-donors (OH, NH) ≤ 5 and number of H-acceptors (O, N) ≤ 10 could be a good drug candidate. According to the Verber's rule [19] compounds with TPSA ≤ 140 Å and nROTB ≤ 10 have good oral bioavailability. All furochromenes **1–16** are in the accordance with both Lipinski's and Verber's rules (Table 1).

Table 1. Physicochemical properties of 1–16 calculated using Molinspiration software.

No.	logP	TPSA	n	MW	nON	NHOH	viol	rot	vol
1	2.29	61.82	19	260.25	5	0	0	2	221.80
2	2.01	72.81	18	246.22	5	1	0	1	204.27
3	1.74	83.81	17	232.17	5	2	0	0	186.74
4	2.63	44.75	19	276.61	4	0	0	2	230.68
5	2.30	52.59	17	230.22	4	0	0	1	196.25
6	2.86	61.82	20	274.27	5	0	0	3	238.60
7	2.06	61.82	18	246.22	5	0	0	2	205.24
8	1.64	78.14	20	278.26	6	1	0	2	235.71
9	1.88	61.07	19	264.28	5	1	0	2	233.87
10	1.08	95.21	21	292.24	7	1	0	3	238.45
11	1.60	95.21	21	292.24	7	1	0	3	238.43
12	0.36	98.37	21	294.26	7	2	0	2	244.07
13	0.69	77.39	20	282.29	6	2	0	2	248.10
14	0.81	91.31	21	294.26	7	1	0	3	244.64
15	1.94	54.01	19	264.28	5	0	0	2	234.20
16	2.84	36.94	18	250.29	4	0	0	2	232.02

LogP—Octanol-water partition coefficient; TPSA—topological polar surface area; MW—molecular weight; nON—number of hydrogen bond acceptors; nOHNH—number of hydrogen bond donors; viol—number of Lipinski's rule of five violations; rot—number of rotatable bonds.

A compound with a bioactivity score greater than 0.00 is likely to exhibit considerable bioactivity [20]. Results of Molinspiration bioactivity score prediction suggest that studied furochromenes should exhibit considerable bioactivity as indicated in Table 2. Studied derivatives 1–16 are predicted to be active as ion channel modulators (except 5, 12 and 15). Calculated ICM scores of 2, 7–9 reached high values (0.23–0.30). Hydrogenation of one or both heterocyclic rings led to high values of score as enzyme inhibitors (EI) especially for structures 10–16 (0.22–0.43). Moreover, the calculated scores of carboxylic acid 14 reached high values (0.33) also as the GPCR ligand and nuclear receptor ligand, respectively.

Table 2. Bioactivity scores of 1–16 calculated using Molinspiration software.

No.	GPCR	ICM	KI	NRL	PI	EI
1	-0.36	0.16	-0.51	-0.51	-0.64	-0.07
2	-0.39	0.23	-0.64	-0.49	-0.77	0.01
3	-0.43	0.17	-0.71	-0.53	-0.81	-0.03
4	-0.41	0.03	-0.54	-0.41	-0.54	0.02
5	-0.55	-0.06	-0.79	-0.79	-0.92	-0.28
6	-0.10	0.19	-0.32	-0.29	-0.50	0.08
7	-0.20	0.30	-0.46	-0.60	-0.71	0.10
8	-0.25	0.27	-0.45	-0.18	-0.57	0.10
9	-0.03	0.30	-0.65	-0.15	-0.57	0.18
10	0.08	0.20	-0.59	0.10	-0.33	0.22
11	0.02	0.04	-0.35	-0.12	-0.46	0.31
12	-0.21	-0.14	-0.47	-0.28	-0.39	0.23
13	0.15	0.06	-0.31	-0.07	-0.26	0.34
14	0.33	0.03	-0.41	0.33	-0.13	0.43
15	0.08	-0.06	-0.52	-0.01	-0.45	0.28
16	0.27	0.15	-0.41	0.09	-0.28	0.39

GPCR—GPCR ligand; ICM—ion channel modulator; KI—kinase inhibitor; NRL—nuclear receptor ligand; PI—protease inhibitor; EI—enzyme inhibitor.

3.2. Osiris

Osiris software was used for prediction of toxicity risks—mutagenicity, irritation, tumorigenicity and reproductive effects. Drug score and drug likeness were also calculated (Table 3). Toxicity risk analysis showed all furochromenes 1–16 exhibit low risk of being irritants. A high risk of mutagenicity was calculated for seven compounds (1–3, 6, 7, 11 and 12). Five compounds exhibit high risk to be tumorigenic (1, 6, 7, 11 and 12). Only khellin 1 exhibit high risk to be reproductive toxic and three compounds (2–4) exhibit moderate reproductive effects. It can be concluded, studied derivatives 5, 8–10, 13–16 are low-toxic and safe compounds, while khellin 1 exhibit the high risk in three categories and compounds 2–4, 6, 7, 11 and 12 exhibit high or moderate risk in two categories. Drug score values indicate potential of compound to be a drug. Structures 8, 9, 13 and 15 exhibit good drug score values. Moderate values of drug score were calculated for 4, 5, 10, 14 and 16.

Table 3. OSIRIS toxicity risk, druglikeness and drug score calculations of 1–16.

No	MUT	TUM	IRR	REP	DL	DS
1	●	●	●	●	−6.87	0.09
2	●	●	●	●	−6.79	0.2
3	●	●	●	●	−6.98	0.21
4	●	●	●	●	−3.77	0.34
5	●	●	●	●	−6.84	0.41
6	●	●	●	●	0.47	0.22
7	●	●	●	●	−0.55	0.21
8	●	●	●	●	1.38	0.76
9	●	●	●	●	1.02	0.76
10	●	●	●	●	−1.55	0.51
11	●	●	●	●	−0.21	0.24
12	●	●	●	●	−5.88	0.16
13	●	●	●	●	0.66	0.77
14	●	●	●	●	−1.74	0.52
15	●	●	●	●	0.51	0.72
16	●	●	●	●	−1.28	0.53

MUT—mutagenicity; TUM—tumorigenicity; IRR—irritant; RE—reproductive effect; DL—drug-likeness; DS—drug score.

3.3. SwissADME

SwissADME predictions show that all studied furochromenes 1–16 (Table 4) exhibit high gastrointestinal absorption (GI). The ability to pass through blood-brain barriers (BBB) is predicted for eight structures (1, 2, 5–7, 9, 15, 16), while furochromenes 3, 4, 8, 10–14 were predicted to be unable to permeate the BBB. P-glycoprotein (P-gp) functions as a biological barrier by extruding toxins and xenobiotics out of cells [21]. Most of studied structures were predicted not to be substrates of Pgp, except compounds 8, 9 or 13, 14. For oral drug administration, inhibiting P-gp can increase drug absorption and bioavailability and thus its therapeutic effects [22]. The cytochromes P450 comprise a family of isoenzymes, important in drug elimination through metabolic processes. They catalyze the oxidative metabolism of a variety of xenobiotic chemicals [23]. The examination of the interactions of CYPs with potential drugs is one of the important steps in drug design [24]. Most of studies compounds are supposed to serve as inhibitors of at least one cytochrome P450 isoenzymes (1A2, 2C19, 2C9, 2D6, 3A4), excluding compound 13 which is expected not to inhibit any of five isoenzymes. Thus, compound 13 is unlikely to have adverse effects and the risk of liver toxicity. Compounds which are potential inhibitors of three (1–3, 6) or four (4) P450 isoenzymes are considered less safe with increased toxicity (Table 4).

Table 4. The SwissADME calculations of 1–16.

No	GIA	BBB	P-gpS	CYP	Lipinski	Ghose	Weber	Egan	Muegge	PAINS	Brenk	LL	SA	LogK _p	BA
1	H	Y	N	Y,N,Y,N,Y	Y	Y	Y	Y	Y	0	0	Y	3.16	-6.28	0.55
2	H	Y	N	Y,N,N,Y,Y	Y	Y	Y	Y	Y	0	0	N	2.97	-6.03	0.55
3	H	N	N	Y,N,N,Y,Y	Y	Y	Y	Y	Y	0	1	N	2.91	-6.18	0.55
4	H	N	N	Y,Y,Y,N,Y	Y	Y	Y	Y	Y	0	1	Y	3.19	-5.95	0.55
5	H	Y	N	Y,N,N,N,Y	Y	Y	Y	Y	Y	0	0	N	2.89	-6.08	0.55
6	H	Y	N	Y,Y,Y,N,Y	Y	Y	Y	Y	Y	0	0	Y	3.23	-6.06	0.55
7	H	Y	N	Y,N,N,N,Y	Y	Y	Y	Y	Y	0	0	N	3.17	-6.46	0.55
8	H	N	Y	Y,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.58	-7.01	0.55
9	H	Y	Y	Y,Y,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.83	-6.53	0.55
10	H	N	N	Y,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.55	-7.12	0.56
11	H	N	N	Y,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.21	-7.21	0.56
12	H	N	N	Y,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	4.05	-7.93	0.55
13	H	N	Y	N,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.93	-7.61	0.55
14	H	N	Y	Y,N,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.42	-7.42	0.56
15	H	Y	Y	Y,Y,N,N,N	Y	Y	Y	Y	Y	0	0	Y	3.31	-6.66	0.55
16	H	Y	Y	Y,N,N,Y,N	Y	Y	Y	Y	Y	0	0	Y	3.26	-5.93	0.55

Y—yes, N—no, **GIA**—gastrointestinal absorption, **BBB**—blood brain barrier permeation, **P-gpS**—P-glycoprotein substrate, **CYP**—cytochrome P450 (1A2, 2C19, 2C9, 2D6, 3A4) inhibitors, **PAINS**—pan assay interference structures, **Brenk**—structural alert by Brenk, **LL**—leadlikeness, **SA**—synthetic accessibility, **LogK_p**—skin permeation (cm/s), **BA**—bioavailability score.

Calculation of druglikeness showed all compounds 1–16 obey all five filters (Lipinski, Ghose, Weber, Egan and Muegge). The skin permeation (log K_p) values are in the range of -5.93 to -7.93 cm/s, indicating low skin permeability of studied compounds. The bioavailability score (BA) predicts the probability of a compound having at least 10% oral bioavailability in rats or measurable Caco-2 permeability [13]. The BA values of 1–16 are in 0.55–0.56 range. There is 55 or 56% chance for the compounds to have at least 10% bioavailability in rats. Pan assays interference structure (PAINS) and Brenk structural alerts were calculated. Only two compounds (3, 4) were identified by Brenk alert due to the presence of hydroquinone or thiocarbonyl structural units.

4. Conclusions

The modified POM analysis (SwissADME/Osiris/Molinspiration) of sixteen furo-pyrrole derivatives was accomplished to identify the drug-likeness score, bioactivity, toxicity and ADME parameters. Molinspiration calculations results show all studied structures are predicted to possess good oral bioavailability. Most of the studied structures show significant drug scores as ion channel modulators. Furo-pyrroles with hydrogenated one or both heterocyclic rings express good score as enzyme inhibitors. SwissADME calculations indicated the most promising 4,9-dimethoxy-7-methyl-2,3,6,7-tetrahydro-5H-furo[2,3-g]chromen-5,6-diol **13** is expected to express high intestinal absorption, is unable to permeate the BBB and is a non-inhibitor of CYP450 isoenzymes. However, compound **13** is predicted to be Pgp substrate. Toxicity risk analysis calculated using Osiris software, showed compounds **8**, **9**, **13** and **15** exhibit not only low toxicity risk, but also good drug score and druglikeness values.

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