Selective Inhibition of Carboxylesterases by Isatins, Indole-2,3-diones

Janice L. Hyatt,[†] Teri Moak,[‡] M. Jason Hatfield,[†] Lyudmila Tsurkan,[†] Carol C. Edwards,[†] Monika Wierdl,[†] Mary K. Danks,[†] Randy M. Wadkins,[‡] and Philip M. Potter*,[†]

Department of Molecular Pharmacology, St. Jude Children's Research Hospital, Memphis, Tennessee 38105, Department of Chemistry and Biochemistry, University of Mississippi, University, Mississippi 38677

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Carboxylesterases (CE) are ubiquitous enzymes thought to be responsible for the metabolism and detoxification of xenobiotics. Numerous clinically used drugs including Demerol, lidocaine, capecitabine, and CPT-11 are hydrolyzed by these enzymes. Hence, the identification and application of selective CE inhibitors may prove useful in modulating the metabolism of esterified drugs in vivo. Having recently identified benzil (diphenylethane-1,2-dione) as a potent selective inhibitor of CEs, we sought to evaluate the inhibitory activity of related 1,2-diones toward these enzymes. Biochemical assays and kinetic studies demonstrated that isatins (indole-2,3-diones), containing hydrophobic groups attached at a variety of positions within these molecules, could act as potent, specific CE inhibitors. Interestingly, the inhibitory potency of the isatin compounds was related to their hydrophobicity, such that compounds with clogP values of ≤ 1.25 were ineffective at enzyme inhibition. Conversely, analogs demonstrating clogP values >5 routinely yielded K_i values in the nM range. Furthermore, excellent 3D QSAR correlates were obtained for two human CEs, hCE1 and hiCE. While the isatin analogues were generally less effective at CE inhibition than the benzils, the former may represent valid lead compounds for the development of inhibitors for use in modulating drug metabolism in vivo.

Introduction

Carboxylesterases (CE^a) have been postulated as general detoxification enzymes¹ responsible for the hydrolysis of carboxyl esters to the corresponding alcohol and carboxylic acid. In mammals, they tend to be expressed in tissues likely to be exposed to xenobiotics, including the liver, lung, small intestine, kidney, and so on. CEs also hydrolyze numerous clinically useful drugs such as Demerol and lidocaine, the anticancer agents capecitabine and CPT-11 (irinotecan, 7-ethyl-10-[4-(1piperidino)-1-piperidino]carbonyloxycamptothecin), as well as the narcotics cocaine and heroin.¹⁻⁴ Because these enzymes significantly influence drug biodistribution and half-life, we recently screened for compounds that might inhibit CEs, with the goal of developing these inhibitors for use in vivo. If successful, these inhibitors might be efficacious in prolonging the bioactivity of agents that are inactivated by CEs or, conversely, may reduce the toxicity of compounds that are activated by these enzymes.

Until recently, the identification of stable, potent, selective inhibitors of CEs had remained elusive. This was due, in part, to the considerable homology among CEs and other esterases, including acetylcholinesterase (AChE). While trifluoromethyl

ketones (Figure 1) have been proposed as selective CE inhibitors, these compounds are hygroscopic, hydrolyzed by water to yield inactive components, and inhibit AChE.5,6 While potentially useful in in vitro biochemical studies, it is unlikely that these agents would be employed in preclinical or clinical applications. Several organophosphate-based compounds that have been described as irreversible, selective inhibitors of CEs have been developed (Bomin-1, -2, and -3; Figure 1); however, these agents also inhibit butyrylcholinesterase (BChE), and there are no published reports of these inhibitors being used in biological systems.

Our previous studies to identify selective CE inhibitors, based upon Telik's target-related affinity profiling technology,7-9 identified benzil (diphenylethane-1,2-dione; Figure 1) as a prototypic member of a class of diones that could inhibit these enzymes.¹⁰ In addition, heterocyclic analogues of benzil have also been demonstrated to be effective inhibitors of these proteins.¹¹ None of these dione-based inhibitors demonstrated any effect on human AChE or BChE. Furthermore, benzil and its analogues are stable under normal physiological conditions and are nontoxic.

Both biochemical and QSAR (quantitative structure-activity relationship) analyses of the benzil-based compounds indicated that the presence of aromatic moieties adjacent to the dione structure improved the potency of CE inhibition. In addition, we determined that both substrate hydrolysis and CE inhibition by different agents was dependent upon the size of the target molecule.^{10,12} Therefore, we attempted to identify small dionecontaining compounds that might inhibit a wide spectrum of CEs. We reasoned that incorporating the dione chemotype within fused aromatic rings may reduce the size of the inhibitor and would likely retain the aromatic character of the molecule necessary for CE inhibition. Therefore, we hypothesized that their inhibitory activity toward a panel of CEs would be improved. Consequently, we searched databases of commercially available compounds for molecules that contained the dione

^{*} To whom correspondence should be addressed. Dr. Philip M. Potter, Department of Molecular Pharmacology, St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38105-2794. Tel.: 901-495-3440. Fax: 901-521-1668. E-mail: phil.potter@stjude.org.

St. Jude Children's Research Hospital.

[‡] University of Mississippi.

^a Abbreviations: AChE, acetylcholinesterase; BChE, butyrylcholinesterase; benzil, diphenylethane-1,2-dione; BNPP, bis(4-nitrophenyl) phosphate; CE, carboxylesterase; clogP, calculated logP value; CPT-11, irinotecan, 7-ethyl-10-[4-(1-piperidino)-1-piperidino]carbonyloxycamptothecin; DMSO, dimethyl sulfoxide; hCE1, human carboxylesterase 1; hiCE, human intestinal carboxylesterase; i, fractional inhibition; isatin, 1H-indole-2,3-dione; Ki, inhibition constant; MAO, monoamine oxidase; o-NPA, o-nitrophenyl acetate; q², cross correlation coefficients; QSAR, quantitative structureactivity relationship; rCE, rabbit liver carboxylesterase; Spearman r, Spearman rank correlation coefficient.



Figure 1. Chemical structures of CE inhibitors.

moiety present within their aromatic rings. This identified isatin (1*H*-indole-2,3-dione) as a potential target molecule. Our studies indicate that while isatin is a relatively poor inhibitor of CEs, substitutions that increased the hydrophobicity of the molecule (e.g., 1-phenylisatin, 5-bromoisatin, and 1-dodecylisatin) resulted in potent, selective CE inhibitors.

Materials and Methods

Chemicals and Enzymes. The structures of the compounds used in this study are indicated in Table 1. All reagents were of the highest available grade and were purchased from one of the following suppliers: Alfa Aesar (Ward Hill, MA); Fisher Scientific (Pittsburgh, PA); Florida Center for Heterocyclic Compounds (Gainesville, Fl); Oakwood (West Columbia, SC); Pfaltz and Bauer (Waterbury, CT); SciChem (Bilston, England); Sigma Aldrich (St. Louis, MO); and TOCRIS (Ellisville, MO).

The mammalian CEs were purified from media harvested from baculovirus-infected *Spodoptera frugiperda* sf21 cells. The human liver CE,¹³ hCE1, and a rabbit liver CE, rCE,¹⁴ were purified as previously described¹⁵ and were essentially homogeneous. A human intestinal CE (hiCE^{3,16}) was prepared in a similar manner, and although not homogeneous, it represented greater than 50% of the total protein present within the sample. No other CEs were present within these preparations.

Enzyme Inhibition Assays. Carboxylesterases. CE inhibition was determined using a spectrophotometric multiwell plate assay with 3 mM o-nitrophenyl acetate (o-NPA) as a substrate.^{14,17} Briefly, test compound (100 μ M) and substrate were aliquoted into wells and enzyme was added using a multiwell pipettor. The rate of change in absorbance at 420 nm was measured at 15 s intervals for 5 min and compared to wells containing no inhibitor. Compounds that demonstrated 50% reduction in CE activity were subsequently evaluated in detail. Typically, inhibitor concentrations ranged from 1 pM to 100 μ M, and at least eight concentrations within this ranged were assayed. Routinely, assays were performed in duplicate and included both positive (50 μ M bis(4-nitrophenyl) phosphate (BNPP)) and negative controls (DMSO, no enzyme).

Acetylcholinesterase. Inhibition of AChE was determined using acetylthiocholine as a substrate in a modified 96-well plate assay.^{18,19} Compounds were assayed at 100 μ M, and the DMSO concentration did not exceed 2%.

Butyrylcholinesterase. Inhibition of BChE was determined using butyrylthiocholine as a substrate in a similar manner to that described for AChE.

Determination of K_i **Values.** K_i (inhibition constant) values were determined using a range of concentrations of inhibitors using the conditions described above. Inhibitor concentrations varied between 1 pM to 100 μ M, and data were fitted to the following equation to determine the mode of enzyme inhibition²⁰

$$i = \frac{[I]\{[s](1-\beta) + K_{s}(\alpha-\beta)\}}{[I]\{[s] + \alpha K_{s}\} + K_{i}\{\alpha[s] + \alpha K_{s}\}}$$

where *i* = fractional inhibition, [*I*] = inhibitor concentration, [*s*] = substrate concentration, α = change in affinity of substrate for enzyme, β = change in the rate of enzyme substrate complex decomposition, K_s is the dissociation constant for the enzyme substrate complex, and K_i is the inhibitor constant. Examination of the curve fits, where α ranged from 0 to ∞ and β from 0 to 1, were

performed using GraphPad Prism software and Perl Data Language. The curves generating the highest r^2 values were analyzed using Akaike's information criteria^{21,22} to identify the best model for enzyme inhibition. K_i values were then calculated from the equation predicted by Prism to be the best fit for the experimental data.

Irreversible Enzyme Inhibition Assays. Irreversible inhibition of CEs was determined by preincubating the enzyme on ice with 1 μ M inhibitor in 50 mM Hepes pH 7.4 for 1 h. Because this concentration of inhibitor resulted in marked inhibition of the proteins after incubation, the sample was diluted extensively with buffer such that the final concentration of the isatin was 2 nM. The CE activity remaining in these diluted samples were then assessed using the spectrophotometric assay and 3 mM o-NPA as a substrate, as described above. All assays included both positive (50 μ M BNPP for hiCE and rCE, 1 mM BNPP for hCE1) and negative (DMSO) controls. The former compound irreversibly inhibits CEs by reaction with the serine O γ atom to yield a stable organophosphate ester. Data were expressed as the percent of enzyme activity remaining as compared to DMSO-treated enzyme.

LogP Calculation. LogP values were calculated using Chem-Silico Predict v2.0 software (ChemSilico LLC, Tewksbury, MA).

Graphical and Statistical Analysis. Data were plotted and analyzed using GraphPad Prism software (San Diego, CA). Statistical analyses were performed with the same software to determine the Spearman rank correlation coefficient (Spearman r) for the different datasets.

3D-QSAR Modeling of Inhibitors of Carboxylesterase. Assessment of 3D (three-dimensional)-QSAR was performed using Quasar 5.0 software.^{23–26} Briefly, the structure for each analogue was constructed using Chem3D and partial atomic charges were assigned using the bond charge correction method.²⁷ AMBER atom types were then assigned using the *antechamber* module of AMBER7 (University of California, San Francisco, CA). Quasar 5.0 generates a 3D-receptor-surface model that contains information regarding the molecular properties of both the ligand and the receptor site. Routinely, 200 independent models are generated for each data set and these are then further evaluated to yield 7000 pseudoreceptor site models. Analysis of these models was then undertaken until the cross correlation coefficients (q^2) exceeded 0.7 for the observed versus the predicted K_i values. Typically this produced correlation coefficients (r^2) of >0.8.

Molecular Modeling of Inhibitors in the Carboxylesterase Crystal Structure. Isatin analogues were docked into the active site of the hCE1 crystal structure (1MX1)²⁸ using ICM-Pro software (Molsoft, San Diego CA). ICM-Pro scores the binding of a ligand to a receptor based upon the comparison of a series of small molecule/protein interactions that have been reported in the PDB database. A rigid receptor/flexible ligand approach is adopted that uses five potential energy maps combining hydrophobicity, electrostatics, hydrogen bond formation, and two van der Waals parameters. Recent studies indicate that docking experiments using ICM-Pro compare favorably with FlexX, GOLD, and GLIDE.²⁹

For these analyses, inhibitor structures were constructed in ChemDraw and subjected to energy minimization using ICM-Pro. The receptor site, consisting of the residues that encompassed the enzyme active site gorge, was then selected as a pocket into which the minimized ligand could be docked. In all cases, the program's default parameters were used.^{30,31} All modeling was performed on a Dell Precision 470 dual 2 GHz processor computer.

Results

Identification of Isatins as CE Inhibitors. We recently identified benzil (Figure 1) as a selective inhibitor of CEs, and this compound demonstrated no inhibition of AChE or BChE up to 100 μ M.¹⁰ Further analysis indicated that the ethane-1,2-dione chemotype was a requirement for efficient enzyme inhibition, and that the potency of analogues of benzil was dependent upon the presence of hydrophobic domains adjacent to this moiety. Additionally, the presence of aromatic ring structures within the benzil-based compounds significantly

Table 1. Structure of the Isatins Used in This Article



R = H unless otherwise indicated

		_	-	-	_	_
<u>ID</u>	Name	R ₁	R ₂	R ₃	R ₄	R₅
1	1H-Indole-2,3-dione					
2	dione	CH ₃				
2	1-Hydroxymethyl-1H-	CH-OH				
3	indole-2,3-dione					
4	dione	CI				
5	1-(2-Bromoethyl)-1H-	C _o H ₋ Br	1			
-	indole-2,3-dione	021 1401				
6	2,3-dione	C ₂ H ₄ I				
7	1-Acetyl-1H-indole-2,3-	COCH				
⊢.	dione	000113				
8	indole-2,3-dione	COCH ₂ CI				
9	1-Propionyl-1H-indole-2,3-	COC ₂ H ₅				
+	dione 1-Butyryl-1 <i>H</i> -indole-2 3-					
10	dione	COC ₃ H ₇				
11	(2,3-Dioxo-2,3-dihydro- 1 <i>H</i> -indol-1-vl) acetic acid	CH₂COOH				
-						
12	2-(2,3-Dioxo-2,3-dihydro-	CH ₂ CONH ₂				
13	1-Phenyl-1 <i>H</i> -indole-2,3- dione					
-	diono					
14	1-Benzyl-1 <i>H</i> -indole-2,3-	CH2				
	4016					
		CH2				
15	1-(4-Chlorobenzyl)-1H-					
	indole-2,3-dione	>=/				
<u> </u>		CÍ CHA				
	1-(3.4-Dicblorobonzel) 1-					
16	indole-2,3-dione	ci—《》				
	1_///	NH-CH ₂				
47	Methylphenyl)amino]					
17	methyl}-1H-indole-2,3-					
	dione	H ₃ C				
	1_/[(2 / 5	H ₃ C NH-CH ₂				
40	-۲۱(۲,4,۵- Trimethylphenyl)aminol					
18	methyl}-1H-indole-2,3-					
	aione	H₃C СН₃				
		NH-CH ₂				
10	1-{[(4-Ethylphenyl)amino] methyl}-1H-indole-2.3					
19	dione					
		H ₅ C ₂				
	1-{[(4-tert-	NH-CH ₂				
	Butylphenyl)amino]					
20	methyl}-1H-indole-2,3-	>=/				
	0.016	(H ₃ C) ₃ C				
-		NH-CH ₂				
	1-{[(3 4 5-		1			
21	Trimethoxyphenyl)amino]	H₃CO──<				
_	methyl}-1H-indole-2,3-					
	uone	□300 OCH3				
		NH-CH ₂				
	1-[(2-					
22	Naphthyl)amino]methyl}-					
	1H-indole-2,3-dione					
		NULCU.				
	1-{[(4-					
23	Chlorophenyl)amino] methyl}-1H-indole-2 3-	《 》				
	dione					
<u> </u>	1-{[(2-	CI Br NH-CH ₂				
24	Bromophenyl)amino]					
.	methyl}-1H-indole-2,3- dione	<_>				
	1_////_	NH-CH ₂				
	I-{[(4- Bromophenyl)aminol					
25	methyl}-1H-indole-2,3-	<u>`</u> _`				
	dione	Br				
		O CH2				
	2-(2,3-Dioxo-2,3-dihydro-	мн				
26	1H-indol-1-yl)-N-(4-	\sim				
	nyuroxypnenyi) acetamide					
				1		

ID	Name	R ₁	R ₂	R ₃	R4	R ₅
	2-(2,3-Dioxo-2,3-dihydro-	O CH ₂	-			
27	1 <i>H</i> -Indol-1-yi)- <i>N</i> -(3- methylphenyl) acetamide	H ₃ C				
28	4-Ethyl-1 <i>H</i> -indole-2,3-		C₂H₅			
29	4-Chloro-1 <i>H</i> -indole-2,3- dione		CI			
30	5-Methyl-1 <i>H</i> -indole-2,3-			CH₃		
31	5-Methoxy-1 <i>H</i> -indole-2,3-			CH ₃ O		
32	5-Fluoro-1 <i>H</i> -indole-2,3-			F		
33	5-Chloro-1 <i>H</i> -indole-2,3-			CI		
34	5-Bromo-1 <i>H</i> -indole-2,3-			Br		
35	5-lodo-1 <i>H</i> -indole-2,3- dione			T		
36	5-(Trifluoromethoxy)-1H- indole-2.3-dione			CF₃O		
37	5-Nitro-1 <i>H</i> -indole-2,3- dione			NO ₂		
38	5-Bromo-1-(2-methylprop- 2-en-1-yl)-1H-indole-2.3-	CH ₂ (C=CH ₂)CH ₂		Br		
39	6-Ethyl-1 <i>H</i> -indole-2,3- dione	0.12(0 0.12)01.13			C ₂ H ₅	
40	6-Chloro-1 <i>H</i> -indole-2,3- dione				CI	
41	7-Methyl-1 <i>H</i> -indole-2,3- dione					CH₃
42	7-Fluoro-1 <i>H</i> -indole-2,3- dione					F
43	7-Chloro-1 <i>H</i> -indole-2,3- dione					CI
44	7-Methoxy-1 <i>H</i> -indole-2,3- dione					СН₃О
45	7-(Trifluoromethyl)-1 <i>H-</i> indole-2,3-dione					CF₃
46	1 <i>H</i> -Indole-2,3-dione -7- carboxylic acid					соон
47	4,7-Methyl-1 <i>H</i> -indole-2,3- dione		CH₃			CH₃
48	5,7-Methyl-1 <i>H</i> -indole-2,3- dione			CH₃		CH ₃
49	4,5-Dichloro-1 <i>H</i> -indole- 2,3-dione		CI	CI		
50	4,6-Dichloro-1 <i>H</i> -indole- 2,3-dione		CI		CI	
51	4,7-Dichloro-1 <i>H</i> -indole- 2,3-dione		CI			CI
52	5,6-Dichloro-1 <i>H</i> -indole- 2,3-dione			CI	CI	
53	5,7-Dichloro-1 <i>H</i> -indole- 2,3-dione			СІ		СІ
54	6,7-Dichloro-1 <i>H</i> -indole- 2,3-dione				CI	CI
55	4-Chloro-7-methyl-1H- indole-2,3-dione		CI			CH ₃
56	5-Chloro-7-methyl-1H- indole-2,3-dione			CI		СН₃
57	6-Chloro-7-methyl-1H- indole-2,3-dione				CI	CH3
58	o-Bromo-5-methyl-1H- indole-2,3-dione	011		CH₃	Br	
59	1-(1 hiomorpholin-4- ylmethyl)-1 <i>H</i> -indole-2,3- dione	S S S				
60	1-(Piperidin-1-ylmethyl)- 1 <i>H</i> -indole-2,3-dione	CH2				
61	1-(Morpholin-4-ylmethyl)- 1 <i>H</i> -indole-2,3-dione	CH ₂				
62	1-Dodecyl-1 <i>H</i> -indole-2,3- dione	C ₁₂ H ₂₅				
63	1-Hexadecyl-1 <i>H</i> -indole- 2,3-dione	C ₁₆ H ₃₃				
64	1,1'-Ethane-1,2-diylbis(1 <i>H</i> - indole-2,3-dione)	O C2H4				
65	1-(4-{4[(2,3-Dioxo-2,3- dihydro-1 <i>H</i> -indol-1-yl) methyl]benzyl}benzyl)-1 <i>H</i> - indole-2,3-dione					

Table 2.	$K_{\rm i}$	Values	for	the	Isatins	with	Mammalian	Esterases
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$K_{\rm i} \pm {\rm SE} \ (\mu {\rm M})$ for indicated enzyme							
ID	hiCE	hCE1	rCE	AChE	BChE	clogP	
1	>100	>100	>100	>100	>100	0.87	
2	38.2 ± 4.0	5.38 ± 0.41	>100	>100	>100	0.65	
3	34.5 ± 1.0	>100	>100	>100	>100	0.53	
4	29.2 ± 10.3	22.8 ± 4.1	4.83 ± 0.5	>100	>100	1.30	
5	1.58 ± 0.05 0.74 ± 0.10	0.29 ± 0.03 0.12 \pm 0.01	5.15 ± 0.35 2.15 ± 0.22	>100	28.1 ± 0.4	1.04	
0	0.74 ± 0.10	0.13 ± 0.01 36.0 + 5.3	2.13 ± 0.33 >100	>100	>100	0.41	
8	>100	>100	>100	>100	>100	0.41	
9	>100	17.5 ± 1.5	>100	>100	>100	1.04	
10	68.2 ± 16.6	7.69 ± 0.93	27.4 ± 13.8	>100	>100	1.69	
11	>100	>100	>100	>100	>100	-0.02	
12	>100	>100	>100	>100	>100	-1.39	
13	0.95 ± 0.12	0.023 ± 0.002	0.61 ± 0.10	>100	68.8 ± 14.4	1.66	
14	0.87 ± 0.05	1.70 ± 0.36	19.0 ± 5.7	>100	>100	1.89	
15	0.032 ± 0.003	0.025 ± 0.003	0.75 ± 0.13	>100	21.9 ± 6.9	2.68	
10	0.067 ± 0.005 1.08 \pm 0.00	0.031 ± 0.001 2.65 ± 0.27	0.005 ± 0.003 7 40 \pm 2 45	48.2 ± 17.8	12.0 ± 1.8 18.1 \pm 0.5	3.23	
18	1.03 ± 0.09 2.88 ± 0.04	2.03 ± 0.27 1.62 ± 0.10	7.40 ± 2.43 8 29 + 0 22	> 100	13.1 ± 0.3 2 39 + 0 27	3.98	
19	0.41 ± 0.04	1.82 ± 0.10 1.88 ± 0.17	4.04 ± 0.32	>100	12.3 ± 0.3	4.06	
20	0.61 ± 0.07	1.42 ± 0.24	16.7 ± 3.4	>100	12.0 ± 0.0 18.9 ± 8.2	4.56	
21	2.69 ± 0.15	19.5 ± 5.0	>100	>100	>100	3.01	
22	0.11 ± 0.03	>100	>100	>100	>100	2.59	
23	0.20 ± 0.01	0.61 ± 0.08	1.12 ± 0.42	>100	>100	3.62	
24	0.047 ± 0.002	36.0 ± 5.3	1.15 ± 0.23	>100	7.40 ± 2.1	2.99	
25	0.17 ± 0.01	0.58 ± 0.13	1.25 ± 0.14	>100	>100	2.95	
26	>100	>100	>100	>100	>100	0.98	
27	3.31 ± 0.37 37.9 ± 9.7	4.33 ± 0.32 >100	4.90 ± 0.83 34.9 ± 3.9	> 100	21.0 ± 3.2 >100	1.93	
20	7.7 ± 0.7	825 ± 0.88	329 ± 0.15	>100	>100	1.25	
30	>100	>100	26.2 ± 3.5	>100	>100	1.23	
31	>100	>100	26.7 ± 3.5	>100	>100	1.17	
32	>100	>100	>100	>100	>100	0.83	
33	14.9 ± 4.0	1.22 ± 0.62	4.37 ± 2.64	>100	>100	1.57	
34	13.3 ± 2.3	31.7 ± 6.6	1.32 ± 0.45	>100	>100	1.60	
35	22.8 ± 3.6	26.9 ± 8.4	1.16 ± 0.09	>100	>100	1.95	
30 37	7.94 ± 1.54	16.5 ± 10.0	0.36 ± 0.12 6.42 ± 0.15	>100	>100	1.56	
38	2000 - 28 + 0.02	$^{>}100$ 0.066 \pm 0.003	0.43 ± 0.13 0.13 + 0.01	> 100	>100	1.89	
39	>100	>100	29.5 ± 6.01	>100	>100	1.84	
40	29.7 ± 12.1	53.9 ± 7.7	14.6 ± 0.9	>100	>100	1.57	
41	>100	>100	>100	>100	>100	0.74	
42	>100	>100	>100	>100	>100	0.78	
43	9.55 ± 4.71	11.4 ± 0.6	4.51 ± 0.19	>100	30.6 ± 12.2	1.38	
44	>100	>100	16.1 ± 9.4	>100	>100	0.84	
45	33.4 ± 6.0	13.1 ± 1.2	2.15 ± 0.33	>100	>100	1.30	
40	$^{2}100$	>100	>100	>100	>100	1.07	
48	30.8 ± 0.2 84 6 + 19 8	> 100	305 ± 18	> 100	> 100	1.12	
49	2.56 ± 0.18	3.02 ± 0.25	0.41 ± 0.02	>100	>100	1.90	
50	0.62 ± 0.03	0.89 ± 0.06	0.53 ± 0.01	>100	>100	2.02	
51	0.65 ± 0.05	0.59 ± 0.05	0.41 ± 0.04	>100	>100	1.85	
52	16.6 ± 2.8	21.0 ± 2.0	0.49 ± 0.03	>100	>100	2.18	
53	4.08 ± 0.37	3.52 ± 0.33	0.76 ± 0.03	>100	>100	2.06	
54	21.8 ± 2.6	9.40 ± 0.7	1.42 ± 0.11	>100	>100	1.94	
55 56	17.2 ± 1.6	5.53 ± 0.23	16.7 ± 4.1	>100	>100	1.33	
50 57	21.0 ± 2.0 53.5 + 20.6	54.1 ± 10.7 55 3 + 10 1	14.1 ± 2.1 12.1 ± 3.3	>100	>100	1.07	
58	7.41 ± 0.88	16.5 ± 2.0	0.42 ± 0.07	>100	56.5 ± 17.8	1.83	
59	22.2 ± 8.1	>100	>100	>100	98.9 ± 3.8	0.75	
60	27.4 ± 11.3	>100	>100	>100	>100	1.24	
61	22.5 ± 4.3	>100	>100	>100	>100	0.25	
62	0.008 ± 0.001	0.010 ± 0.002	0.088 ± 0.006	>100	>100	6.27	
63	0.011 ± 0.001	0.016 ± 0.001	>100	>100	>100	6.58	
64	1.54 ± 0.08	1.56 ± 0.31	10.5 ± 1.2	>100	6.71 ± 1.78	1.40	
05	0.010 ± 0.002	0.008 ± 0.002	0.006 ± 0.002	5.28 ± 0.73	>100	5.11	

increase the potency of CE inhibition.^{10,11} Based upon this information, we searched for molecules that contained a dione group located proximal to an aromatic ring. These criteria identified isatin (Figure 1) as a potential target molecule. Because numerous analogues of isatin were available, we assessed the ability of these compounds to inhibit metabolism of the general esterase substrate o-NPA by CEs.

 K_i Values for Isatin Analogues with Mammalian CEs. We identified 65 commercially available isatin analogues, which included 33 with *N*-substitutions, 2 with substituents at the 4-position, 8 at the 5-position, 2 at the 6-position, and 6 at the 7-position. Thirteen analogues contained different chemical groups at multiple positions within the benzene ring. The structures of these compounds are indicated in Table 1. We then





^{*a*} None of these isatin analogues demonstrated any enzyme inhibition at concentrations up to 100 μ M.

determined the K_i values for these compounds with two human CEs, hiCE and hCE1, and rCE, using o-NPA as a substrate. The K_i values for the inhibition of the mammalian CEs are displayed in Table 2.

A wide variation in the K_i values were observed with the isatin analogues ranging from > 100 μ M (no enzyme inhibition) to as low as 6 nM (compound **65** with rCE). Generally, compounds that inhibited one CE also inhibited the other two enzymes, however, there were exceptions. For example, the *N*-naphthylamino derivative (**22**) was a potent inhibitor of hiCE ($K_i = 110$ nM), but demonstrated no activity against hCE1 or rCE. Similarly, compound **37** was a relatively good inhibitor of rCE ($K_i = 6.43 \ \mu$ M), but demonstrated no activity toward the two human proteins. However, it should be noted that for the vast majority of the isatin analogues, inhibition demonstrated by most of the compounds was common among the three mammalian CEs.

Analysis of CE inhibition was also undertaken using a series of analogues demonstrating structural homology to isatin (Table 3). None of these compounds inhibited the mammalian CEs at concentrations up to 100 μ M (data not shown). Because these analogues lack the 1,2-dione moiety, these studies suggest that this function is essential for CE inhibition.

Inhibition of Human Acetyl- and Butyrylcholinesterase. To assess the specificity of CE enzyme inhibition, we assayed the ability of these compounds to inhibit human AChE or BChE. As indicated in Table 2, inhibition of AChE was only observed with two compounds, **16** and **65**, with K_i values of 48.2 μ M and 3.28 μ M, respectively. More commonly, however, BChE

Table 4. Correlation Parameters for the ClogP Values of the Inhibitors with the Observed K_i Values for the Mammalian CEs

		enzyme			
parameter	hiCE	hCE1	rCE		
r^2 (linear regression) Spearman r <i>P</i> value for Spearman	0.635 -0.809 <0.0001	$0.388 \\ -0.518 \\ 0.0004$	$0.211 \\ -0.465 \\ 0.0011$		

was inhibited by these isatin analogues (Table 2). Fourteen compounds demonstrated inhibition of human BChE; however, the majority of these were relatively weak inhibitors, with K_i values typically in the 20–60 μ M range. In contrast, several molecules were relatively potent at inhibiting this enzyme. For example, **24** and **64** had K_i values of less than 10 μ M (7.40 μ M and 6.71 μ M, respectively). However, because the exact function and endogenous substrate of BChE is unclear and individuals who demonstrate reduced levels or complete loss of this protein are apparently healthy,^{32–34} it is unlikely that the clinical use of these inhibitors would yield effects related to inhibition of this protein.

Correlation between K_i **Values and logP.** In general, for the isatin analogues, there was a correlation between the calculated logP and the K_i values for the inhibition of CEs. For example, compounds with predicted logP values of less than 1.25 (compounds 1, 3, 7–9, 11, 12, 25, 29–31, 36, 40, 41, 43, 45–47, and 58–60) were poor inhibitors of o-NPA hydrolysis. Interestingly, regression analysis of the clogP versus the K_i constants for the different enzymes did yield moderate linear correlation coefficients, (r^2 ranging from 0.211 to 0.635; Table 4; Figure 2).

However, because any correlation between the K_i and the logP values was unlikely to be linear, we performed nonparametric statistical analysis. The Spearman r values, comparing the observed K_i values with the calculated logP of the inhibitors, were therefore calculated. These analyses yielded Spearman r values of -0.809, -0.518, and -0.465, for hiCE, hCE1, and rCE, respectively (Table 4). Because a Spearman r value of -1 indicates a perfect negative correlation and 0 indicates no correlation, these analyses suggest that there is a strong associated with the statistical analyses of these data sets ranged from <0.0001 to 0.0011 (Table 4), indicating that the K_i values were highly correlated with the clogP of the inhibitor.

Assessment of the Mode of Carboxylesterase Inhibition by the Isatin Analogues. To determine whether the inhibition of CEs was reversible, we preincubated selected inhibitors (compounds 13, 16, 23, and 38) with the enzymes on ice for 1 h and then assessed enzyme activity. As indicated in Figure 3, after dilution of the inhibitor from the reactions, all of the enzymes retained hydrolytic activity. Irreversible inhibition of all of the CEs was only seen with the control organophosphate BNPP. Because none of the isatin analogues analyzed irreversibly inhibit the enzymes, it is likely that the compounds interact with the catalytic amino acids in a fashion similar to benzil.¹⁰

3D-QSAR Pseudoreceptor Models of Isatin-Mediated Inhibition of CEs. Using Quasar software, 3D pseudoreceptor models were generated from the inhibition datasets for the isatin analogues and enzyme-ligand binding sites. These models for the human CEs good q^2 values with values of 0.767 and 0.729 for hiCE and hCE1, respectively (Table 5). In addition, r^2 correlates for the observed versus predicted K_i values were >0.79, demonstrating the validity of the 3D-QSAR analyses (Figure 4). We derived pseudoreceptor site models for hiCE and hCE1 from these analyses, and these are depicted in Figure 5.



Figure 2. Graphs demonstrating the correlation between the K_i values for enzyme inhibition and the calculated logP constants for the isatin analogues for three mammalian CEs. The r^2 values for the line fits were 0.64, 0.39, and 0.21 for hiCE, hCE1, and rCE, respectively.

As can be seen, a distribution of anionic (red) and cationic (blue) regions within the pseudoreceptor site were required for the accurate fitting of the data set to the 3D models. This is consistent with previous models that we have generated by this method for benzene sulfonamide,35 benzil,10 and trifluoroketone³⁶ inhibitors of CEs. The isatin analogue **14** is positioned within the model in an orientation similar to that of benzil in previous studies. While it is impossible to assign an orientation to a QSAR model, mapping of the charge distribution of the model to the corresponding amino acid types in the CE crystal structure¹⁰ suggests that the orientation shown in Figure 5 is such that the bottom of the figure represents the region of active site containing the catalytic amino residues. The relatively uncharged region toward the top likely represents the active site gorge, which is lined with hydrophobic residues in these enzymes. This model indicates that the indole ring system of 14 interacts with a highly polarized environment in the gorge, whereas the upper ring (the benzyl moiety in 14) is located in a more hydrophobic region of the protein, as indicated by the absence of charged spheres in Figure 5. This is particularly apparent for the 3D-pseudoreceptor site model of hiCE.

However, for rCE, both the r^2 value for the observed versus predicted K_i values and the q^2 were poor (0.297 and 0.309, respectively). Because the latter value is below that required for acceptable inhibitor design (0.4),³⁷ it is unlikely that the rCE QSAR model would be suitable for further improvement in the potency of the isatin analogues. We believe that the poor correlations observed with rCE are due to the relatively small range of K_i values over the $10^{-5}-10^{-7}$ M inhibitor concentrations. We did not generate a 3D-QSAR pseudoreceptor site model for rCE, because the validity of such a model, in light of the r^2 and q^2 values, was unclear.

Molecular Modeling of Isatin Inhibitors. The pseudoreceptor site models are generated in the absence of information from the protein and represent the field in which the inhibitor interacts with the amino acid residues. In an attempt to directly determine how the isatins associate with the catalytic amino acids in the CEs, we performed molecular modeling using ICM-Pro software. Four analogues were chosen for analysis, compounds 1, 14, 32, and 38, because they represent analogs that demonstrate no inhibition (1 and 32) and good inhibition (14 and 38) with the different CEs. After docking into the active site of hCE1 (using the coordinates of the X-ray crystal structure of this protein), the distances between catalytic serine and the inhibitor atoms were measured. While we observed no significant differences between compounds that could and could not inhibit the enzymes, all of the isatins localized such that at least one of the carbonyl carbon atoms was within 3.6 Å of the serine $O\gamma$ atom (Figure 6). This was comparable to the distance (3.4)

Å) observed between the corresponding atoms following docking of the CE substrate o-NPA into the hCE1 active site. Because nucleophilic attack by the serine $O\gamma$ atom toward the carbonyl carbon in the ester group is the initial step in substrate hydrolysis,³⁸ it is likely that a similar mechanism may occur with isatin-mediated inhibition of CEs (Figure 7).

However, it should be noted that compounds 1 and 32 adopted a similar conformation within the active site gorge of hCE1. As can be seen in Figure 6 (panels A and C), isatin (1) and 5-fluoroisatin (32) could be overlaid in an almost identical position (Figure 6E), with both indole carbonyl carbon atoms approximately 3.6 Å from the serine $O\gamma$ atom. In contrast, the compounds that effectively inhibited hCE1 (14 and 38) localized in a different conformation to 1 and 32, with at least one of the carbonyl carbon atoms within 3.5 Å of the oxygen nucleophile. Whether these differences account for enzyme inhibition is unclear, but these studies clearly demonstrate that the isatin analogues can juxtapose to the catalytic amino acids in hCE1, at distances where interactions with active site serine are likely to occur.

Discussion

Until recently, the identification of selective CE inhibitors has proven problematic. This is, in part, due to the fact that these enzymes demonstrate considerable amino acid and structural homology to AChE. Hence, compounds that are marketed as general esterase inhibitors (e.g., BNPP) inhibit many different enzymes, including CEs, AChE, and BChE. Recently, we identified benzil as a selective CE inhibitor¹⁰ and demonstrated that the 1,2-dione domain was crucial for enzyme inhibition. Subsequently, we observed that the aromaticity of the ring domains was an important factor in the biological activity of these compounds.¹¹ Therefore, using this information, we searched the chemical databases for molecules that contained a 1,2-dione moiety within an aromatic ring structure. This identified isatin as a potential CE inhibitor. However, biochemical studies using this compound demonstrated no inhibition of the mammalian CEs when using o-NPA as a substrate (Table 2). In contrast, analogues containing hydrophobic substitutions, essentially at any position within the molecule (e.g., Nphenylisatin (13), 5-iodoisatin (35), 4,7-dichloroisatin (51)), were all potent inhibitors of CEs.

As indicated by the control compounds that we assayed (66– 74), for a molecule to be an effective CE inhibitor it was necessary to contain the dione moiety in the 1,2-configuration. Additionally, we observed that compounds that were more lipophilic were better inhibitors (Table 2), with good correlations between inhibitor potency and the clogP of the molecule (Figure 2 and Table 3). As the catalytic amino acid residues of CEs are



Figure 3. Graphs demonstrating the reversible inhibition of CEs by selected isatin analogues. Enzyme activity was determined after preincubation with the isatin analogues or BNPP for 1 h. The open bars represent results obtained from samples that have not been diluted, whereas the solid bars are data generated following a 500-fold dilution of the inhibitor (2 nM final concentration for the isatins).

buried at the bottom of deep hydrophobic gorges in these proteins,^{12,28,39,40} it is likely that this environment would be favorable for the localization of more lipophilic compounds. Hence, the binding affinity for more hydrophobic molecules (i.e., those with higher logP values) would be expected to be greater. The results that we have observed with the isatin analogues are consistent with this hypothesis.

The studies presented here, therefore, demonstrate the properties necessary for CE inhibition by these types of compounds.

Table 5. Correlation Coefficients for the Isatin CE QSAR Models

enzyme	observed versus predicted K_i values (r^2)	q^2	$q^{2/r^{2}}$
hiCE	0.810	0.767	1.05
hCE1	0.794	0.729	1.09
rCE	0.297	0.309	0.96

First, a 1,2-dione chemotype is required preferably within, or adjacent to, an aromatic moiety. Second, the logP of the inhibitor must be greater than 1.25. By comparison, benzil has a clogP of 3.02. Third, any substitution within the fused benzene ring of the isatin must be small enough such that it does not impede access of the inhibitor to the enzyme active site. For example, the K_i values for the inhibition of hCE1 by 34, 35, or 36 are considerably lower than those seen for rCE with the same compounds (Table 2). As we have previously demonstrated that the entrance to the active site gorge in hCE1 is considerably smaller that that seen in rCE,¹² it is likely that bulky Br, I, or CF₃O groups present within these inhibitors reduce the ability of these compounds to access the catalytic amino acids that are located at the base of the active site gorge. For smaller substitutions, the effect on the K_i was negligible, as exemplified by inhibitors 29 and 43 (4-chloro- and 7-chloroisatin, respectively), which had very similar K_i values for all of the CEs tested.

The 3D-QSAR models generated for hiCE and hCE1 (Figure 5) provided some insights as to why the hydrophobicity of the isatin analogues is an important factor in enzyme inhibition. The models demonstrate hydrophobic zones in the center of an otherwise highly polar region. Addition of a second aromatic group, such as a phenyl or benzyl ring within the isatin molecule, allows the inhibitor to interact with this hydrophobic area (note the absence of spheres around the benzyl ring in Figure 5). Such a zone would likely be formed by the side chains from one or more hydrophobic amino acids in the catalytic regions of the protein. Because the active site gorges of CEs are known to be lined with many residues containing aromatic rings (e.g., Phe, Tyr, His, Trp³⁸), it is likely that this hydrophobic domain represents an important factor in the interaction of the isatin analogues with the catalytic amino acids.

Molecular modeling studies using selected isatin analogues (1, 14, 32, and 38) and the crystal structure of hCE1 did not identify any obvious reason for the lack of enzyme inhibition by compounds 1 and 32. However, in these studies, the inhibitor was modeled within the active site gorge, and this approach would, therefore, eliminate any interactions that would occur with other domains of the protein. We have previously reported that the loops that form the entrance to the active site of hCE1 are highly ordered as compared to rCE^{28,40} and that these domains impact substrate metabolism.¹² Hence, while the modeling studies indicate that the inhibitors localize adjacent to the active site serine and likely interact with this amino acid, these models cannot explain the inhibitory action of the isatins.

The preincubation assays indicated that the inhibition of CEs by the isatin analogues was reversible. In addition, because the molecular modeling studies demonstrated that the carbonyl carbon atoms within the indole ring could localize within 3.5 Å of the catalytic nucleophile (the serine $O\gamma$ atom; Figure 6), our results suggest that enzyme inhibition could be mediated by attack of either of these carbon atoms by the serine residue. Such a mechanism is depicted in Figure 7. Hence, following formation of the nucleophile by proton transfer through the histidine to the glutamic acid, the serine $O\gamma$ atom would then attack the indole carbonyl group to generate the transient intermediate. However, for the reaction to continue, either the



Figure 4. Graphs comparing the observed versus the predicted K_i values for the isatin analogues for hiCE and hCE1. Predicted data was obtained from the 3D-QSAR models obtained using Quasar software. In each case, the model was built using the training set (black diamonds) and then validated using the test set (red diamonds).



Figure 5. 3D-QSAR pseudoreceptor models obtained from the enzyme inhibition data for hiCE (panel A) and hCE1 (panel B) with the isatin analogues. The models are depicted as colored spheres on a hydrophobic gray grid. Hydrophobic areas are shown in gray, with dark blue spheres representing areas of positive charge (+0.1*e*) and light blue spheres corresponding to hydrogen bond donors. Orange spheres represent hydrogen bond acceptors and areas that are negatively charged (-0.1*e*) are displayed as orange-red spheres. In all cases, *e* corresponds to the charge of a proton. A representative isatin analogue (compound **14**) is drawn in black. The figure was constructed using Raster3D⁴⁵ and Molscript.⁴⁶

C-C or the C-N bond in the five-membered ring must be broken (Figure 7). This would then result in a covalent product bound to the serine residue that would likely irreversibly inhibit enzyme activity. A much more plausible scenario, based upon both the biochemical data and the molecular modeling studies, suggests that the formation of the initial intermediate is rapidly reversible, readily liberating free enzyme and inhibitor (Figure 7, lower panel). This mechanism is comparable to that observed for the inhibition of CEs by benzil.¹⁰

Because the indole moiety is present within a whole host of clinically used drugs (e.g., indomethacin, indoramin), it is likely that the isatin inhibitors will be better tolerated in vivo than the benzil derivatives. However, isatin and its analogues have also been demonstrated to be monoamine oxidase (MAO) inhibitors, with the most potent compounds containing substitutions at the 5-position within the indole ring.⁴¹ Additionally, the moieties appended at this position were small and demonstrated low hydrophobicity (e.g., OH, C₂H₅, C₄H₉). This is in contrast to the majority of the potent CE inhibitors described here that



Figure 6. Molecular modeling of compounds 1 (panel A), 14 (panel B), 32 (panel C), and 38 (panel D) into the active site of hCE1. The three residues necessary for catalysis (S221, E354, and H468) are displayed, and the distances between the carbonyl carbon atoms and the serine $O\gamma$ are indicated in Angstroms. By comparison, the corresponding distance for the docking of the CE substrate o-NPA into the hCE1 active site is 3.4 Å. Panel E represents an overlay of all four of the isatin molecules using the coloring scheme in the previous panels. In all molecules, oxygen atoms are displayed in yellow, and bromine atoms are shown in orange.

contain large bulky hydrophobic substituents, mainly at the 1-position of the molecule (Tables 1 and 2). Furthermore, the IC₅₀ values for the inhibition of either MAO A or MAO B by the isatin analogues were considerably higher (typically 1–20 μ M) than that seen for CE-mediated enzyme inhibition. By comparison, the most potent inhibitor that we have identified is compound **62** (1-dodecyl-1*H*-indole-2,3-dione), which demonstrates a K_i value of 8 nM for hiCE. Due to the increase in potency and the difference in the position of substitution within the molecule, we believe it is unlikely that inhibition of MAO would preclude the use of the isatins for CE inhibition in vivo.



Figure 7. Proposed mechanism of interaction of isatin inhibitors with the catalytic amino acids in CEs. The upper panel depicts the mechanism of the initial stages of ester (RCOOR₁) hydrolysis by CEs with the serine (Ser), histidine (His), and glutamic acid (Glu). Nucleophilic attack by the serine O_Y on the carbonyl carbon results in a tetrahedral intermediate that decomposes to release the alcohol (R₁OH) and form a serine ester. In the lower panel, attack by the O_Y on one of the carbonyl carbons in an isatin analogue is displayed. However, for the reaction to continue, cleavage of the C–C bond in the pyrrole ring must occur. This is unlikely to happen in comparison to the cleavage of the ester C–O bond due to the enhanced strength of the former bond.

Recently, several isatin derivatives containing substitutions at the 5-position of the molecule have been demonstrated to be caspase 3/7 inhibitors.^{42–44} The most potent of these analogues contained a sulfonyl group attached to the nitrogen-containing ring as the substituent. In addition, 5-nitroisatin (**37**) was shown to be a good inhibitor of these caspases, with an IC₅₀ value of 3 μ M.⁴⁴ We have not assayed the ability of the sufonyl derivatives to inhibit CEs, however, compound **37** is not an inhibitor of the human CEs (Table 2). Clearly though, before development of any compounds for the in vivo inhibition of CEs (or capsases), the specificity of the isatins toward these classes of enzymes will need to be assessed.

Overall, the studies presented here demonstrate that isatin analogues, primarily those containing hydrophobic substituents, are potent, selective inhibitors of mammalian CEs. Their potency correlates with the clogP of the molecule, and 3D-QSAR models should allow for the design of more bioavailable, less toxic analogues. Such studies are currently underway.

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