

A Series of Quinoline Analogues as Potent Inhibitors of C. albicans Prolyl tRNA Synthetase

Xiang Y. Yu,^{a,*} Jason M. Hill,^a Guixue Yu,^a Yifeng Yang,^a Arthur F. Kluge,^a Dennis Keith,^a John Finn,^a Paul Gallant,^b Jared Silverman^b and Audrey Lim^b

^aDepartment of Medicinal Chemistry, Cubist Pharmaceuticals, Inc., 24 Emily Street, Cambridge, MA 02139, USA

^bDepartment of Biology, Cubist Pharmaceuticals, Inc., 24 Emily Street, Cambridge, MA 02139, USA

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Abstract—A series of quinoline inhibitors of *C. albicans* prolyl tRNA synthetase was identified. The most potent analogue, 2-(4-bromo-phenyl)-6-chloro-8-methyl-4-quinolinecarboxylic acid, showed $IC_{50} = 5 \, \text{nM}$ (Ca. ProRS) with high selectivity over the human enzyme. © 2001 Elsevier Science Ltd. All rights reserved.

The incidence of serious fungal infection continues to grow and there is an urgent need for novel antifungal therapies. 1,2 Aminoacyl-tRNA synthetases (aaRSs) are essential enzymes for biological cell growth.^{3–7} Because there are significant structural difference between fungal and human enzymes, selective inhibition of aaRSs offers a potential pathway for discovery of novel antifungal agents. Previously, we have described novel antibacterials targeting aminoacyl-tRNA synthetases.^{8,9} Herein, we report novel quinoline inhibitors of C. albicans prolyl tRNA synthetase. The quinoline lead, 2-(4-bromo-phenyl)-4-quinolinecarboxylic acid 1a, was identified from high-throughput screening of library compounds. Compound 1a inhibits C. albicans prolyl-tRNA synthetase (IC₅₀ = $0.5 \mu M$) with high selectivity over the human enzyme (IC₅₀ >100 μ M). To examine the structure–activity relationships, we have prepared and evaluated a series of quinoline analogues.

Our synthetic approach for the preparation of quinoline analogues is shown in Scheme 1. Reaction of a substituted isatin with a ketone gave 4-quinoline carboxylic acid derivative 1.¹⁰ The 6-alkenyl group (2a) was introduced from coupling of iodoquinoline 1b with alkene under a typical Heck condition.¹¹ The 6-aryl group (2b) was introduced from a palladium-catalyzed (Suzuki) coupling of arylboronic acid and iodoquinoline 1b.¹²

Quinoline analogues with modification at the 8-methyl position were prepared as shown in Scheme 2. The

$$\begin{array}{c} \text{R-CH}_2 = \text{CH}_2 \\ \text{Pd(cat)} \end{array} \begin{array}{c} \text{R-CH}_2 = \text{CH}_2 \\ \text{Pd(cat)} \end{array} \begin{array}{c} \text{Pd(PPh}_3)_4 \\ \text{K}_2\text{CO}_3/\text{DMF/H}_2\text{O} \end{array} \begin{array}{c} \text{2a R'} = \text{R''-CH=CH} \\ \text{B(OH)}_2 \end{array} \begin{array}{c} \text{2b R'} = \text{Ar-X} \end{array}$$

Scheme 1.

quinoline 1c was esterified and converted to the bromide quinoline 3.¹³ Treatment of 3 with aqueous silver nitrate followed by hydrolysis gave the corresponding alcohol 4.¹⁴ Dibromination of 1c followed by a similar treatment with aqueous silver nitrate, depending upon the conditions, yielded benzaldehyde quinoline 6 or benzoic acid quinoline 7.

Derivatives of the 4-quinolinecarboxylic acid were prepared as shown in Scheme 3. Reduction of 1c gave the hydroxyl derivative 8, which was converted to the sulfamoyl derivative 9.8 Treatment of the primary amide with thionyl chloride yielded the nitrile derivative 12,15 which

^{*}Corresponding author. Tel.: +1-617-576-4171; fax: +1-617-576-0232; e-mail: xiang@cubist.com

was reacted with trimethylsilyl azide in the presence of dibutyltin oxide to afford the tetrazole derivative 13. 16

2-Aryl analogues were evaluated in assays of the amino-acylation activity of C. albicans prolyl-tRNA synthetase and the results are shown in Table 1. The bromophenyl compound $\mathbf{1a}$ was significantly more potent than the simple phenyl analogue $\mathbf{1d}$. Analogue $\mathbf{1e}$ with an electron-donating -OMe group and analogue $\mathbf{1f}$ with an electron-withdrawing -CF₃ group showed a significant loss in potency. Replacement of the bromophenyl group by a heterocyclic group such as the 2-Cl-thiophene group ($\mathbf{1i}$) decreased the activity. The furyl analogue $\mathbf{1j}$ and the pyridyl analogue $\mathbf{1k}$ were inactive.

Substitution in the benzene portion of quinoline can dramatically improve the activity (Table 2). 6-Halogen substituted analogues (**1b**, **1l** and **1m**) were all very active. However, incorporation of hydrophilic moieties at the 6-position (**1o** and **1p**) decreased the potency. The 6-chloro-8-methyl analogue **1c** was the most potent compound ($IC_{50} = 5 \text{ nM}$). The 6-chloro-8-hydroxylmethlene analogue **4** ($IC_{50} = 1500 \text{ nM}$), however, was considerably less potent. This observation implied the importance of lipophilicity of the substitution in the 8-position for good inhibition. A comparison of analogue **1c** and analogue **1r** reveals that changing the relative position of the chloro group and the methyl group resulted in a 5-fold weaker inhibition. The 6,8-dimethyl analogue **1q** was 5000 times less potent than the 6-chloro-

8-methyl analogue 1c. Substitution with a halogen at the 7-position and a methyl at the 8-position (1v) and (1w) decreased the potency. All of these compounds have high selectivity over the human enzyme.

To explore other functional groups at the 4-position, we replaced the carboxylic acid with sulfamoyl amide, amide, ester, and tetrazole (Table 3). The replacement of the carboxylic acid with the methylene sulfomyl amide (9), the amide (10a) and the phenylbenzyl ester (11a) decreased the potency. The 3,4-dichlorobenzyl ester (11b), the furfuryl ester (11c), and the tetrazole derivative 13 had a moderate inhibition. The results suggest that a carboxylic acid functionality at this position is critical for good enzyme inhibition.

In summary, we have developed a series of potent and selective C. albicans prolyl-tRNA synthetase inhibitors. The enzymatic potency observed with several of these analogues is significantly superior to that of lead compound $\mathbf{1a}$ (IC₅₀=500 nM, C. albicans ProRS). SAR studies suggest that the potency is greatly influenced by the substitution pattern on the quinoline. Analogue $\mathbf{1c}$ possesses excellent activity against C. albicans ProRS (IC₅₀=5 nM) with high selectivity over the human enzyme (IC₅₀ >100 μ M). Enzymology studies indicate that compound $\mathbf{1c}$ is a non-competitive inhibitor of the C. albicans ProRS with respect to proline and a competitive inhibitor with respect to ATP. The K_i 's were 15 and 5.1 nM versus proline and ATP, respectively. However, the

$$\begin{array}{c} \text{1. POCl}_3; \text{ MeOH} \\ \text{2. NBS, (PhCOO)}_2\text{O} \\ \text{CCl}_4, \text{ reflux} \\ \text{1c} \\ \\ \text{1c$$

Scheme 2.

$$CI \longrightarrow CI \longrightarrow BH_3, THF \longrightarrow BH_3, THF \longrightarrow BI$$

$$CI \longrightarrow BH_3, THF \longrightarrow BI$$

$$SOCl_2, reflux; NH_2R \longrightarrow CI \longrightarrow BI$$

$$SOCl_2, reflux; NH_2R \longrightarrow BI$$

Table 1. Inhibition of *C. albicans* prolyl-tRNA synthetase

Y Compd	∕\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	\\O	∕′C) _{OMe}	, CF₃	, CCI	· \	, SCI	\\\^_\)	, C
	1a	1d	1e	1f	1g	1h	1i	1j	1k
IC ₅₀ (μM) (Ca. ProRS) IC ₅₀ (μM) (human ProRS)	0.5 >100	>100 >100	>100 >100	>100 >100	19 >100	3.6 >100	32 >100	>100 >100	>100 >100

Table 2. Inhibition of *C. albicans* prolyl-tRNA synthetase

Compd	\mathbb{R}^5	R^6	\mathbb{R}^7	\mathbb{R}^8	IC_{50} (µM) (Ca. ProRS)	IC_{50} (μM) (human ProRS)
1a	Н	Н	Н	Н	0.500	>100
1b	H	I	Н	Н	0.019	>100
11	H	Cl	Н	Н	0.026	>20
1m	H	Br	Н	Н	0.025	>20
1n	H	CF ₃ O	Н	Н	0.053	>100
10	H	HOS_2O	Н	Н	15	>100
1p	H	NH_2	Н	Н	3.3	95
2a	H	HO ₂ CCH=CH ₂	Н	Н	1.3	80
2b	H	4'-OH-PH	Н	Н	0.350	35
1c	H	Cl	Н	Me	0.005	>20
1q	H	Me	Н	Me	25	>100
1r	H	Me	Н	Cl	0.025	>20
4	H	Cl	Н	CH ₂ OH	1.5	>100
1s	Me	Н	Cl	Ĥ	1.5	>100
1t	C1	Н	Cl	Н	0.140	>100
1u	H	Br	Н	CF_3	0.220	56
1v	H	Н	Br	Me	0.150	70
1w	Н	Н	F	Me	0.120	60

Table 3. Inhibition of *C. albicans* prolyl-tRNA synthetase

X Compd	CO ₂ H	CH ₂ OSO ₂ NH ₂	CH ₂ Ph CONH OMe	CO ₂ CH ₂ PhPh	, , , , , Cl	· Long	NH NH
	1c	9	10a	11a	11b	11c	13
IC ₅₀ (Ca. ProRS, μM) IC ₅₀ (human ProRS, μM)	0.005 >100	2.4	5.7 >100	8.8 >100	0.02 >100	0.07 >100	0.03 >100

most active analogue **1c** has no whole cell activity (MIC > $100 \,\mu\text{g/mL}$, *C. albicans*). Analogue **1v** has cellular activity (MIC = $25 \,\mu\text{g/mL}$, *C. albicans*). Further studies indicate that the activity is due to a lytic mechanism.

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