

Selective Urokinase-Type Plasminogen Activator (uPA) Inhibitors. Part 1: 2-Pyridinylguanidines

Christopher G. Barber,* Roger P. Dickinson and Valerie A. Horne

Department of Discovery Chemistry, Pfizer Global Research and Development, Sandwich, Kent CT13 9NJ, UK

Received 9 July 2001; revised 10 October 2001; accepted 19 October 2001

Abstract—The identification of 2-pyridinylguanidines (e.g., 27 and 28) as selective inhibitors of urokinase-type plasminogen activator (uPA) is described. The X-ray crystal structure of 27 has been determined, and modelling has been used to predict binding in the enzyme active site. © 2002 Elsevier Science Ltd. All rights reserved.

Introduction

Urokinase-type plasminogen activator (uPA) is a trypsin-like serine protease which converts the zymogen plasminogen into its active form plasmin. Studies have indicated that because of its ability to degrade extracellular matrix, either directly or via plasmin formation, uPA is a key mediator of cellular invasion in a range of processes including tumour growth and metastasis, angiogenesis and tissue remodelling. Levidence has also been obtained to suggest that uPA, or plasmin produced by its action, may play a role in preventing healing of chronic wounds. Consequently, a selective inhibitor for uPA could have therapeutic value in cancer and wound healing.

Several related enzymes such as tissue plasminogen activator (tPA) also act via activation of plasminogen to plasmin, and play a key role in the fibrinolytic cascade. Therefore, it is desirable that a uPA inhibitor has adequate potency and selectivity for uPA relative to both tPA and plasmin to avoid the possiblity of antifibrinolytic side effects.

Several small molecule inhibitors of uPA are known. For example, aromatic and heteroaromatic amidine derivatives have been reported with moderate potency, but low selectivity over related enzymes. 9–11 Greater selectivity relative to tPA and plasmin has been reported for a series of benzo[b]thiophene-2-carboxamidines such

as **1**, and the more potent analogue **2**. ^{12,13} Guanidine derivatives are also reported to have some degree of selectivity including amiloride (**3**) ¹⁴ and a series of phenylguanidine derivatives as exemplified by **4**. ¹⁵ Since the current work was carried out, a number of templates based upon amidines and guanidines have been reported. ^{16–24}

In attempting to develop a novel class of uPA inhibitor, we focused upon systems which would bind strongly at the key S₁ binding site and demonstrate intrinsic selectivity over related enzymes. The X-ray crystal structures of 1, 3 and phenylguanidine bound to re-engineered human uPA have been reported recently, and the results confirm that all three inhibitors bind in the S₁ site of the enzyme.²⁵ Knowledge of the preference for Arg at S₁ enabled us to limit our attentions to amidines and guanidines, especially the latter where a greater number of the key H-bonding interactions that bind Arg560 of plasminogen would be available. After screening a number of simple guanidine and amidine derivatives, it

^{*}Corresponding author. Fax: +44-1304-651987; e-mail: christopher_barber@sandwich.pfizer.com

became apparent that aromatic guanidines were favoured, encouraging us to prepare a series of simple guanidino-heterocycles. This paper describes the discovery of 2-pyridinylguanidines as selective inhibitors of uPA, and fundamental SAR in the series. Future papers in the series will describe our efforts to increase potency by introducing substituents capable of achieving binding interactions outside the S_1 binding site.

Chemistry

Most of the guanidines described were prepared from the corresponding heterocyclic amines $\mathbf{5}$ by reaction with N,N'-bis(t-butoxycarbonyl)-S-methylisothiourea ($\mathbf{6}$) in the presence of mercury(II) chloride, followed by deprotection of the product $\mathbf{7}$ with either saturated HCl in dichloromethane or with neat trifluoroacetic acid (Scheme 1). In all cases, the starting amines were available commercially or were prepared by literature methods.

The 2-pyrimidinyl analogue 11 was prepared by the direct reaction of the free base of guanidine with 2-chloropyrimidine. The 3-pyridazinyl analogue 15 was prepared by reaction of guanidine with 3,6-dichloropyridazine followed by dechlorination of the intermediate product 14 by hydrogenolysis (Scheme 2).

Results and Discussion

Compounds were tested for their ability to inhibit uPA, tPA and plasmin as described by Yang et al.¹⁵ The uPA assay was carried out using HWMT human uPA (Calbiochem) and S-2444 (Quadratech) as substrate. The tPA assay was carried out using human tPA (Quadratech), S-2444 as substrate and tPA stimulator (Quadratech). The plasmin assay was carried out using human

Het
$$NH_2 + CH_3S$$
 NCO_2Bu^t a
 $NHCO_2Bu^t$
 $NHCO_2Bu^t$

Scheme 1. Reagents and conditions: (a) HgCl₂, Et₃N (3 equiv), CH₂Cl₂; (b) satd HCl/CH₂Cl₂ or TFA.

Scheme 2. Reagents and conditions: (a) 2-chloropyrimidine, *t*-BuOH; (b) 3,6-dichloropyridazine, DMSO; (c) H₂, Pd/C, EtOH.

plasmin (Quadratech) and Chromozym-PL (Boehringer) as substrate.

Calculated K_i values for simple heterocyclic guanidine derivatives are listed in Table 1, together with comparative figures for compound 4.

2-Pyridinylguanidine (8) showed encouraging potency against uPA, and excellent selectivity over both tPA and plasmin. However, the 3- and 4-isomers 9 and 10 showed negligible inhibition up to millimolar concentrations, although the latter showed significant activity against plasmin. Introduction of an additional ring nitrogen atom (11–15) was also detrimental. In view of its potency and selectivity, the 2-pyridinyl analogue 8 was considered a suitable starting point for the design of more potent novel uPA inhibitors, and the effect of simple ring substitution was then explored (Table 2).

Examination of methyl substitution demonstrated that substituents are tolerated at the 3- and 5-positions of the pyridine ring (16 and 18), but substitution is highly detrimental at the 6-position (19). The 4-methyl isomer 17 was less potent than the parent, but substitution by a phenyl group (20) led to a 4-fold increase. Introduction of 5-halo or 3,5-dihalo substituents gave a marked increase in potency, generally without loss of selectivity over tPA and plasmin (24–28, 30). Introduction of a 5-CF₃ substituent was unfavourable (cf. 29 with 26 and 28).

Modelling studies were carried out on the active pyridinylguanidines with the aim of identifying the most suitable position for appending further substitution to increase binding interactions with the enzyme. The X-ray crystal structure of 27 was determined (Fig. 1)²⁶ and compared with the reported crystal structure of the phenylguanidine derivative 31.²⁷ Compared with 31, compound 27 was found to be more planar (Ar–guanidine torsion angle 5.2° compared with 49°) which we believe to be a result of both the loss of a steric clash on replacing a CH with a N, and formation of an intra-

Table 1. Enzyme inhibition data for guanidine-substituted heterocycles

Compd	Het	K_{i} (μ M) or % inhibition		
		uPA	tPA	Plasmin
4		6.70	a	b
8	2-Pyridinyl	29.5	b	b
9	3-Pyridinyl	b	b	b
10	4-Pyridinyl	b	b	16.9
11	2-Pyrimidinyl	292.0	b	b
12	4-Pyrimidinyl	b	b	b
13	2-Pyrazinyl	b	b	b
15	3-Pyridazinyl	c	с	a

 $^{^{}a}$ < 50% inhibition at 30 μ M.

 $^{^{\}rm b}$ < 50% inhibition at 1 μ M.

 $^{^{}c}$ < 50% inhibition at $100 \, \mu M$.

molecular H-bond between the pyridine N atom and a guanidine proton.

Compound 27 was docked and minimised²⁸ into the human uPA X-ray structure²⁹ over the GluGlyArgchloromethyl-ketone, which is covalently bound in this uPA structure (Fig. 2). The available SAR could be rationalised using this model. The pyridinylguanidine system fills the S₁ pocket with the guanidine forming a strong interaction with Asp189 at the bottom of the pocket (Fig. 2a). The 5-substituent must be small to be accommodated as it is directed towards Ser195. Based on the structure of phenylguanidine bound to human uPA, it has recently been proposed that additional binding energy may be obtained by interaction of a small substituent such as the 4-Cl in compound 4 with Ser195.²² The 4-position in **27** is adjacent to Glu192, but any substituent would lie substantially in solvent and therefore, although a range of substituents would be accommodated, they would not be expected to form extensive interactions with the protein. Substituents at the 3-position are directed along the binding groove towards Arg217, suggesting this as being the best position from which to capitalise upon the available sites of interaction in order to optimise uPA potency. Figure 2b shows more clearly the spatial fit of the molecule into the S_1 pocket, and the 3-substituent pointing along the binding groove.

In summary, we have demonstrated that simple 2-pyridinyl guanidines, especially those with halogen sub-

Table 2. Enzyme inhibition data for 2-pyridinylguanidine derivatives

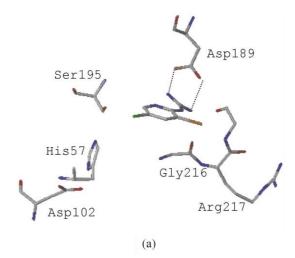
Compd	Het	$K_{\rm i} (\mu { m M})$ or % inhibition		
		uPA	tPA	Plasmin
8	Н	29.5	a	a
16	3-CH ₃	37.7	a	a
17	4-CH ₃	83.8	a	a
18	5-CH ₃	32.3	a	245.0
19	6-CH ₃	173.0	a	a
20	$4-C_6H_5$	7.10	54% @ 1 mM	a
22	4-OCH ₃	53.3	a	a
21	3-OH	147.0	a	a
23	3-OCH ₃	62.0	a	232.5
24	5-C1	10.0	a	a
25	5-Br	3.13	a	a
26	3,5-diCl	5.47	a	a
27	3-Br, 5-Cl	4.83	272.0	a
28	3-Cl, 5-Br	2.90	a	a
29	3-Cl, 5-CF ₃	40.7	a	a
30	3,5-diCl-4-Me	8.70	a	176.5

 $^{^{}a}$ < 50% inhibition at 1 mM.

stitution at the 3- and/or 5-positions, are selective inhibitors of uPA. Modeling, using the published X-ray crystal structure of the human enzyme, has been used to predict the likely binding interactions of this class of inhibitor in the S_1 pocket of the enzyme. The results of the modelling suggest that it should be possible to increase potency by introduction of suitable substitution at the 3-position of the pyridine ring to interact in the



Figure 1. X-ray structure of 27.



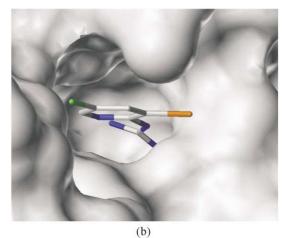


Figure 2. Compound 27 docked into active site of uPA.

binding groove of the enzyme. The synthesis and properties of such compounds are described in the following paper.

Acknowledgements

We thank N. Smith for his assistance in preparing the compounds, M. F. Burslem, G. Easter and B. Williams-Jones for the biological data, the staff of the Physical Sciences Department, Sandwich, for analytical data and J. Bordner, Pfizer, Groton for determining the X-ray crystal structure of 27.

References and Notes

- 1. Fazioli, F.; Blasi, F. Trends Pharmacol. Sci. 1994, 15, 25.
- 2. Evans, D. M.; Sloan-Stakleff, K. D. Drug News Perspect. 1997, 10, 85
- 3. Stacey, M. C.; Burnand, K. G.; Mahmoud-Alexandroni, M.; Gaffney, P. J.; Bhogal, B. S. Br. J. Surg. 1993, 80, 596.
- 4. Palolahti, K.; Lauharanta, J.; Stephens, R. W.; Kuusela, P.; Vaheri, A. Exp. Dermatol. 1993, 2, 29.
- 5. Rogers, A. A.; Burnett, S.; Moore, J. C.; Shakespeare, P. G.; Chen, W. Y. J. *Wound Rep. Reg.* **1995**, *3*, 273.
- 6. Wysocki, A. B.; Kusakabe, A. O.; Chang, S.; Tuan, T.-L. Wound Rep. Reg. 1999, 7, 154.
- 7. Madison, E. L. Fibrinolysis **1994**, 8 (Suppl. 1), 221.
- 8. Collen, D.; Lijnen, H. R. Thromb. Haemostasis 1995, 74, 161.
- 9. Geratz, J. D.; Cheng, M. C.-F. Thrombos. Diathes. Haemorrh. (Stuttg.) 1975, 33, 220.
- 10. Geratz, J. D.; Stevens, F. M.; Polakoski, K. L.; Parrish, R. F.; Tidwell, R. R. *Arch. Biochem. Biophys.* **1979**, *197*, 551. 11. Geratz, J. D.; Shaver, S. R.; Tidwell, R. R. *Thromb. Res.* **1981**, *24*, 73.
- 12. Bridges, A. J.; Lee, A.; Schwartz, C. E.; Towle, M. J.; Littlefield, B. A. *Bioorg. Med. Chem.* **1993**, *1*, 403.
- 13. Towle, M. J.; Lee, A.; Maduakor, E. C.; Scwartz, C. E.; Bridges, A. J.; Littlefield, B. A. *Cancer Res.* **1993**, *53*, 2553.
- 14. Vassalli, J.-D.; Belin, D. FEBS Lett. 1987, 214, 187.
- 15. Yang, H.; Henkin, J.; Kim, K. H.; Greer, J. J. Med. Chem. 1990, 33, 2956.
- 16. Weinhouse, M. I.; Roberts, C.; Cohen, C. R.; Bradbury, A. E.; Ma, M. G.; Dixon, S. A.; Nolan, T. G.; Tamura, S. Y.; Brunck, T. K. *Abstracts of Papers*, 217th ACS National Meeting 1999; MEDI 093. Tamura, S. Y.; Weinhouse, M. I.; Roberts, C. A.; Goldman, E. A.; Masukawa, K.; Anderson, S. M.; Cohen, C. R.; Bradbury, A. E.; Bernardino, V. T.; Dixon, S. A.; Ma, M. G.; Nolan, T. G.; Brunck, T. K. *Bioorg. Med. Chem. Lett.* 2000, 10, 983.

- 17. Nienaber, V. L.; Davidson, D.; Edalji, R.; Giranda, V. L.; Klinghofer, V.; Henkin, J.; Magdalinos, P.; Mantei, R.; Merrick, S.; Severin, J. M.; Smith, R. A.; Stewart, K.; Walter, K.; Wang, J.; Wendt, M.; Weitzberg, M.; Zhao, X.; Rockway, T. *Structure* **2000**, *8*, 553.
- 18. Rockway, T. W.; McClellan, W. J.; Dellaria, J. F.; Gong, J.; Mantei, R. A.; Geyer, A.; Wendt, M.; Zhao, X.; Weitzberg, M.; Sauer, D.; Bruncko, M.; Dalton, C.; Kaminski, M.; Giranda, V.; Butler, C.; Klinghofer, V.; Joseph, M.; Nienaber, V.; Stewart, K. *Abstracts of Papers*, 219th ACS National Meeting, 2000; MEDI 30.
- 19. Allen, D.; Hataye, J. M.; Hruzewicz, W. N.; Kolesnikov, A.; Mackman, R. L.; Rai, R.; Spencer, J. R.; Verner, E. J.; Young, W. B. Patent WO00/35886.
- 20. Stürzebecher, J.; Vieweg, H.; Steinmetzer, T.; Schweinitz, A.; Stubbs, M. T.; Renatus, M.; Wikström, P. *Bioorg. Med. Chem. Lett.* **1999**, *9*, 3147.
- 21. Sperl, S.; Jacob, U.; Arroyo de Prada, N.; Stürzebecher, J.; Wilhelm, O. G.; Bode, W.; Magdolen, V.; Huber, R.; Moroder, L. *PNAS* **2000**, *97*, 5113.
- 22. Illig, C. R.; Subasinghe, N.; Hoffman, J.; Rudolph, J.; Wilson, K.; Green, D.; Randle, T.; Molloy, C.; Soll, R.; Lewandowski, F.; Zhang, M.; Spurlino, J.; Bone, R.; Deckman, I.; Manthey, C.; Zhou, Z.; Sharp, C.; Kratz, D.; Grasberger, B.; DesJarlais, R. *Abstracts of Papers*, 218th ACS National Meeting, 2000; MEDI 78.
- 23. Rudolph, M. J.; Subasinghe, N. L.; Illig, C. R.; Wilson, K. J.; Hoffman, J. B.; Randle, T.; Green, D.; Molloy, C. J.; Soll, R. M.; Lewandowski, F.; Zhang, M.; Bone, R.; Spurlino, J.; Deckman, I.; Manthey, C.; Zhou, Z.; Sharp, C.; Kratz, D.; Grasberger, B.; DesJarlais, R.; Abstracts of Papers, 218th ACS National Meeting, 2000; MEDI 233.
- 24. Wilson, K. J.; Illig, C. R.; Subasinghe, N.; Hoffman, J. B.; Rudolph, M. J.; Soll, R.; Randle, T.; Green, D.; Bone, R.; Molloy, C. J.; Manthey, C.; Zhou, Z.; Sharp, C.; Deckman, I.; Kratz, D.; Grasberger, B.; Zhang, M.; Spurlino, J.; Lewandowski, F.; DesJarlais, R. *Abstracts of Papers*, 218th ACS National Meeting, 2000; MEDI 234.
- 25. Nienaber, V.; Wang, J.; Davidson, D.; Henkin, J. J. Biol. Chem. **2000**, 275, 7239.
- 26. Detailed crystallographic data for **27** have been deposited at the Cambridge Crystallographic Data Centre.
- 27. Matsomoto, O.; Taga, T.; Machida, K. Acta Crystallog., C (Cryst. Struct. Commun.) 1989, 45, 913.
- 28. Compound **27** was docked using QUANTA. It was then minimised within S₁, followed by minimisation of the protein and the ligand together using the programme CHARMm[®]. QUANTA and CHARMm[®] are distributed by Molecular Simulations Inc.
- 29. Spraggon, G.; Phillips, C.; Nowak, U. K.; Ponting, C. P.; Saunders, D.; Dobson, C. M.; Stuart, D. I.; Jones, E. Y. *Structure* **1995**, *3*, 681.