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Plasmepsin Inhibitory Activity and Structure-Guided Optimization of a Potent Hydroxyethylamine-Based Antimalarial Hit

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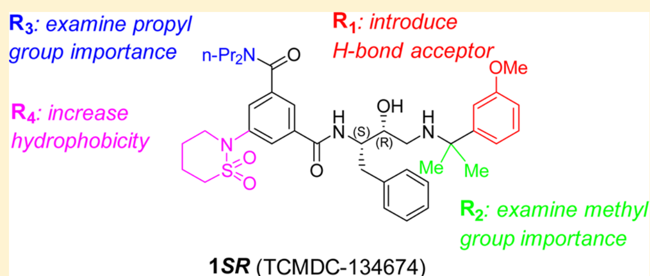
Supporting Information

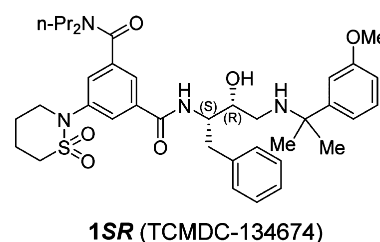
ABSTRACT: Antimalarial hit **1*SR*** (TCMDC-134674) identified in a GlaxoSmithKline cell based screening campaign was evaluated for inhibitory activity against the digestive vacuole plasmepsins (Plm I, II, and IV). It was found to be a potent Plm IV inhibitor with no selectivity over Cathepsin D. A cocrystal structure of **1*SR*** bound to Plm II was solved, providing structural insight for the design of more potent and selective analogues. Structure-guided optimization led to the identification of structurally simplified analogues **17** and **18** as low nanomolar inhibitors of both, plasmepsin Plm IV activity and *P. falciparum* growth in erythrocytes.



KEYWORDS: *Malaria, Plasmodium falciparum, plasmepsins, Cathepsin D, inhibition, structure-guided optimization, hydroxyethylamine*

Despite extensive eradication campaigns, malaria caused by *Plasmodium* parasites remains a devastating disease with an estimated 219 million cases and 660 thousand lethal outcomes in 2010.[1] Widespread resistance to practically all currently used drugs has activated the search for antimalarials with novel mechanisms of action.[2−4] Low profit potential of antimalarial drugs has promoted collaboration between academic, private, and charitable organizations to establish novel drug discovery programs. As a part of an antimalarial initiative, pharmaceutical companies contribute with their unique resources to the development of antimalarials, making their data publicly available.[5] Recently, researchers at GlaxoSmithKline (GSK) published the structures of 13 533 hits from the screening of nearly 2 million compounds that inhibited malaria parasite growth by at least 80% at 2 μM concentration.[6] These hits were further analyzed using cheminformatics to identify 47 series of high-quality starting points for lead optimization.[7] The series 3 included 74 compounds based on a hydroxyethylamine scaffold that is characteristic for plasmepsin inhibitors.[8−11] Given the interest in the digestive vacuole plasmepsins (Plm I, II, and IV) as targets for antimalarial drug discovery, we selected the most active compound from this series, **1*SR*** (TCMDC-134674), for investigation of its Plm I, II, and IV inhibitory activity (Chart 1).[12]

Chart 1. Structure of GSK Cell Based HTS Antimalarial Hit



Compound **1*SR*** was resynthesized (see Supporting Information) and tested in enzymatic assays, which showed that it is a potent Plm IV inhibitor (IC_{50} = 29 nM) while being a less effective inhibitor of Plm II (IC_{50} = 0.15 μM) and Plm I (IC_{50} = 0.70 μM) (Table 1). Selectivity studies of compound **1*SR*** showed that it was not a selective inhibitor of plasmesins over the human aspartic protease Cathepsin D (CatD, IC_{50} of 43 nM, Table 1).

While a number of digestive vacuole plasmepsin inhibitors have been previously identified, to the best of our knowledge none of them displayed low nanomolar activity in cell based models. Therefore, it was an exciting finding that compound **1*SR***, which was reported as highly active against intra-erythrocytic *P. falciparum* cell growth (IC_{50} of 30 nM),[6] is a

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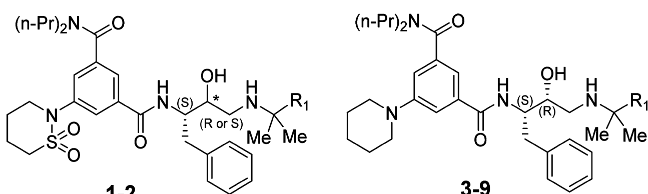
Table 1. SAR of R_1 Group

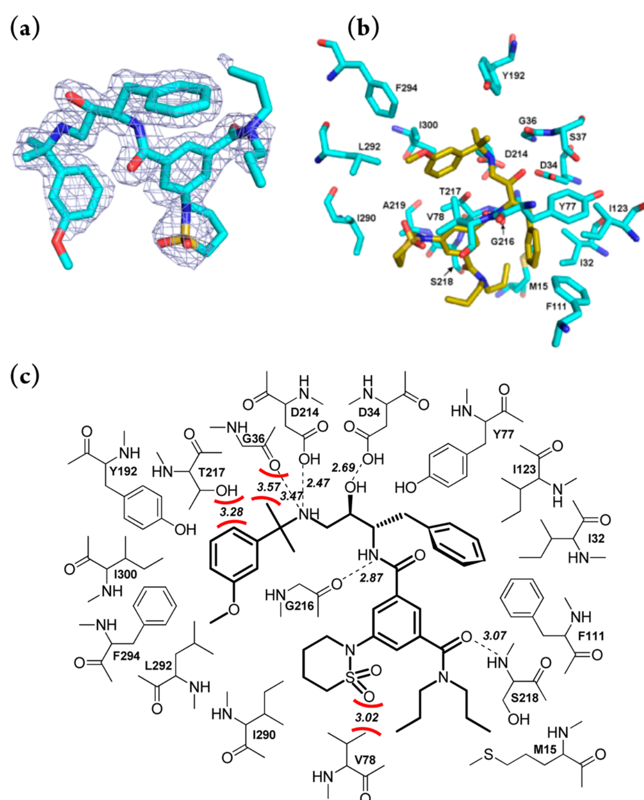


Comp.	R_1	IC_{50} (μM)			
		Plm I	Plm II	Plm IV	Cat D
1*SR*	3-MeO-C_6H_4	0.70	0.15	0.029	0.043
1*SS*	3-MeO-C_6H_4	18	14	0.47	4.4
2*SR*	Ph	2.3	0.32	0.048	0.12
2*SS*	Ph	45	24	0.72	5.8
3	3-MeO-C_6H_4	0.30	0.070	0.024	0.042
4	3-HO-C_6H_4	0.36	0.10	0.019	0.040
5	Ph	0.38	0.11	0.023	0.051
6		4.1	0.80	0.25	0.35
7		0.35	0.19	0.064	0.14
8		0.47	0.27	0.09	0.17
9		0.60	0.19	0.023	0.068

potent Plm IV inhibitor. The critical role of Plm IV is still unclear, ; however, gene knockout studies have revealed that out of all individual digestive vacuole plasmepsin knockouts only Δ*pfpm*4 produced a statistically significant reduction in hemozoin accumulation indicating impaired hemoglobin digestion.[13] In addition, the quadruple-plasmepsin knockout mutant (Δpfpm1−4) showed a significantly slower rate of growth in contrast to a triple plasmepsin knockout mutant (Δpfpm1−3).[14] On the basis of the available data, it was intriguing to speculate that inhibition of Plm IV could be responsible for the activity of compound **1*SR*** in the cell based assay. Nevertheless, it cannot be excluded that any other of the nondigestive plasmepsins structurally similar to PlmIV could be the target (or an additional target) for compound **1*SR***.[15,16]

To provide a structural basis for the design of structurally simplified, potent and selective analogues of compound **1*SR***, the X-ray crystal structure of Plm II in complex with compound **1*SR*** was solved (Chart 2). Plm II was chosen for the crystallization studies because it was easily obtainable in milligram quantities, and its crystallization conditions have been described previously.[17] Plm II mutant M205S was used, which displays enhanced resistance to self-cleavage compared to the wild type enzyme.[18] The obtained crystals diffracted to 1.85 Å resolution and belonged to space group C_2 with six molecules in the asymmetric unit. The electronic density of the inhibitor was very similar in all six subunits and did not improve significantly upon averaging. As shown in Chart 2a, electron

Chart 2. Binding of 1 (TCMDC-134674)[6] within the Active Site of Plm II[a]



[a](a) X-ray crystal structure showing the ligand and residues located within 4 Å from it as stick models (colored in yellow and cyan, respectively). (b) $2F_o - F_c$ electron density of the bound ligand contoured at 1σ. The figure was generated using PyMOL.[22] (c) Ligand interaction diagram. Hydrogen bonds are shown as dashed lines, and distances between heavy atoms are indicated. Potentially repulsive interactions between the ligand and protein atoms are shown as red curves, and distances between the closest heavy atoms are indicated in Å.

density was good for the central part of the inhibitor but was weak or lacking for aliphatic propyl groups, the methoxy moiety and part of the 1,2-thiazinane-1,1-dioxide ring. As expected, the structure shows an interaction between the hydroxyethylamine core of **1*SR*** and the Plm II catalytic dyad Asp34−Asp214 (Chart 2b). However, in contrast to other structures of transition state analogue−Plm II complexes,[17,19,20] the hydroxyl group is not within the characteristic hydrogen-bond distances to both carboxylic acids, but only Asp34 (O−O distance of 2.69 Å) and Asp214 is hydrogen-bonded with the secondary amino group (N−O distance of 2.47 Å, Chart 2c). The secondary amine is linked to the isopropyl-2-(3-methoxyphenyl) moiety that occupies the S1′ and part of the S2 pockets. The other side of the hydroxyethylamine core is linked via a methine bridge to the benzyl group positioned in the S1 pocket and the 3,5-disubstituted benzamide moiety, whose *N*,*N*-dipropylamide and 2-(1,2-thiazinane-1,1-dioxide)-substituents bind in the S3 and S4 pockets, respectively. The interactions in the S1−S4 and S1′ pockets are predominantly hydrophobic, while a few H-bond interactions are formed with the more central groups of the inhibitor, i.e., between the benzamide and Gly216 and the *N*,*N*-dipropylamide and Ser218 (Chart 2c). Additionally, the secondary amino group seems to interact simultaneously with

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the carboxylate of Asp214 and the carbonyl of Gly36. Detailed inspection of the structure highlighted three sites of potentially repulsive interactions between the inhibitor and Plm II active-site residues (Chart 2c). First, the sulfonyl group of the 2-(1,2-thiazinane-1,1-dioxide) moiety is only 3.0 Å from the hydrophobic Val78 side chain. This repulsion seems to interfere with flap closing, making the binding cavity more open than in other Plm II−inhibitor complexes.[21] Second, the 6-C atom of the 3-methoxyphenyl group lies 3.3 Å from the hydrophilic side chains of Thr217 and Asp214, and third, one methyl group of the isopropyl-2-(3-methoxyphenyl) moiety is 3.6 Å from the carbonyl of Gly36. Importantly, these interactions may also be present in complexes with Plm I and IV as the interacting residues are conserved among the food vacuole plasmepsins, except Val78, which is replaced by a Gly in Plm IV. It was also apparent that the aliphatic chains of the *N,N*-dipropylamide moiety make only weak contacts with the protein as their electron density was indiscernible (Chart 1a).

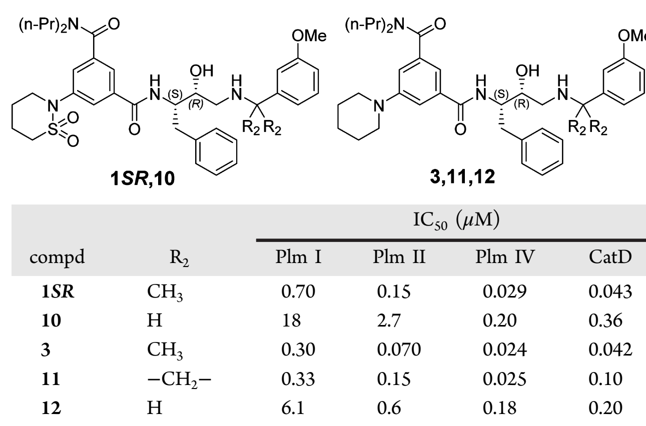
Guided by these insights from the crystal structure, we started our SAR study of **1*SR*** and defined four positions, where appropriate chemical modifications were likely to improve intermolecular interactions (Tables 1−4, R_1 to R_4). Modifications of R_1, R_2, and R_4 were also expected to contribute to the selectivity versus CatD as these moieties are located in the S1′ and S2 and S4 pockets that are most different between the two enzymes.[21] Keeping R_4 substituent (2-(1,2-thiazinane-1,1-dioxide)) constant while optimizing substituents R_1−R_3 proved to be impractical due to the very lengthy synthesis. Therefore, we preferred to use the more accessible piperidinyl group as the R_4 substituent for optimization around R_1−R_3. To confirm that this modification does not significantly alter the bound conformation observed in the crystal structure, a few analogues were synthesized with both piperidinyl and 1,2-thiazinane-1,1-dioxide groups. Comparison of their activities (compound pairs **2*SR*** and **5**, **10**, and **12**) led to similar conclusions about changes in inhibition activity suggesting that the piperidinyl analogue binds similarly to compound **1*SR***.

Previous SAR studies of statine- and hydroxyethylamine-based Plm II inhibitors have indicated a preference for the S-configuration at the central hydroxyl group;[21,23] therefore, we were surprised that compound **1** has the R-configuration at this stereogenic center. We prepared both diastereoisomers of two of the studied compounds (**1** and **2**) and tested their inhibitory activity against Plm I, II, and IV. The stereoisomers **1*SS*** and **2*SS*** showed 15−90 -fold lower activity than the isomers **1*SR*** and **2*SR*** indicating that the R-configuration of the central hydroxyl-bearing stereo center is critical for plasmepsin inhibition (see Table 1) opposed to statine based inhibitors.[21] This may be explained by the different binding mode of the hydroxyethylamine core of **1*SR*** in the Plm II catalytic center as was observed in the crystal structure of the complex and discussed above.

SAR studies on R_1 (Table 1) were performed to evaluate the importance of the 3-methoxy group as well as to explore the possibility of introducing an H-bond acceptor for the adjacent hydroxyl group of Thr217. After preparing compound **2**, the unsubstituted phenyl analogue of **1**, we decided to perform further studies with piperidinyl group as the R_4 substituent for the reasons described above and synthesized compounds **3**−**5**. It should be noted that this R_4 substitution yielded 2-fold higher activity against Plm I and II, while the activity increase against Plm IV was negligible. Replacing the methoxy group with a hydroxyl functionality (compound **4**) did not change its activity. The phenyl-substituted analogue (compound **2**) of **1** was 2- to 3-fold less active, while the corresponding analogue (compound **5**) of **3** was of similar potency, indicating some cooperativity between the R_1 and R_4 substituents in the case of **5**. In order to explore possible H-bonding interactions with the hydroxyl group of Thr217, we prepared compounds **6**−**8** by replacing the 3-methoxyphenyl group with 2-, 3-, and 4-pyridyl, respectively, hoping that the nitrogen atom might act as the H-bond acceptor. However, this did not result in improved activity, possibly, due to protonation of the pyridine nitrogen atom at the pH of the assay (pH 4.6). The 3-pyridyl-substitution (compound **7**) was tolerated best from this series and in combination with the 5-methoxy group yielded compound **9** with similar activity (IC_{50} of 23 nM) against Plm IV as **3** (IC_{50} of 24 nM).

Next, we investigated SARs associated with R_2 (Table 2). Although the crystal structure showed that one methyl group is located in a polar environment while the other one lies in a hydrophobic environment, we synthesized symmetrically substituted analogues to avoid the complication associated with an additional stereogenic center. Removal of both methyl groups (compounds **10** and **12**) resulted in a significant decrease in activity, whereas a cyclopropyl functionality (compound **11**) was well tolerated at this position and at the same time slightly enhanced selectivity for Plm IV over Cat D.

Table 2. SAR of R_2 Group

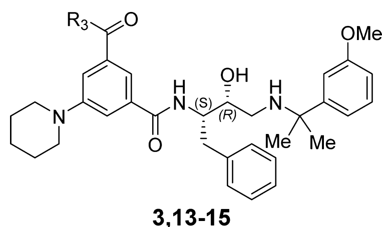


compd	R_2	IC_{50} (μM) Plm I	Plm II	Plm IV	CatD
1*SR*	CH_3	0.70	0.15	0.029	0.043
10	H	18	2.7	0.20	0.36
3	CH_3	0.30	0.070	0.024	0.042
11	$-CH_2-$	0.33	0.15	0.025	0.10
12	H	6.1	0.6	0.18	0.20

Further we examined the importance of the propyl groups in the *N,N*-dipropylamide moiety (R_3) that showed poor electron density in the crystal structure. Removal of one propyl group (compound **13**) resulted in 2- to 7-fold decreased activity. A decrease in activity was also observed upon changing the *N,N*-dipropyl for a pyrrolidinyl group (compound **14**) (Table 3). Removal of both propyl groups (compound **15**) resulted in substantial activity loss suggesting that the propyl chains may make transient contacts with the protein that are important for binding affinity.

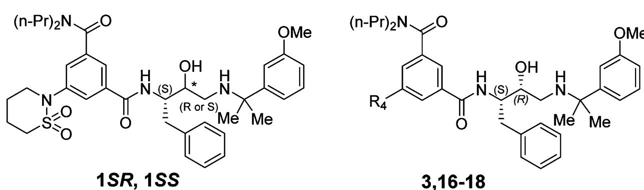
Initial optimization of R_4 was achieved by replacing the 2-(1,2-thiazinane-1,1-dioxide) moiety with the piperidinyl group to ease the synthesis of new analogues. This resulted in a 2-fold higher activity against Plm I and II, but only a small improvement against Plm IV (Table 4). A similar, but more pronounced trend was observed also by changing R_4 to a cyclohexyl moiety (compound **16**). In contrast, changing R_4 to pyrrolidinyl (compound **17**) and phenyl (compound **18**) resulted in more than 4-fold higher activity against Plm IV, while the improvement against Plm I and II was up to 2-fold. It

Table 3. SAR of R_3 Group



compd	R_3	Plm I	Plm II	Plm IV	CatD
		IC50 (μM)			
3	$N(Pr)_2$	0.30	0.070	0.024	0.042
13	NHPr	0.75	0.50	0.038	0.11
14	$N(CH_2)_4$	1.6	0.50	0.11	0.038
15	NH_2	7.6	4.4	0.17	0.50

Table 4. SAR of R_4 Group



Comp.	R_4	Plm I	Plm II	Plm IV	Cat D	Parasite growth[a]
		IC50 (μM)				
1SR		0.70	0.15	0.029	0.043	0.002
1SS		18	14	0.47	4.4	0.20
3	$(CH_2)_5N$	0.30	0.07	0.024	0.042	0.006
16	$(CH_2)_5CH$	0.20	0.036	0.025	0.019	n.d.
17	$(CH_2)_4N$	0.43	0.12	0.007	0.032	0.004
18	Ph	0.25	0.072	0.006	0.054	0.002

[a] 3D7 strain of *P. falciparum*

implies that nonplanar hydrophobic groups such as piperidinyl and cyclohexyl at this position are better accommodated by Plm I and II because of the favorable interaction with Val78, while planar and more compact groups are preferred by Plm IV, possibly, due to favorable flap-closing interactions. Importantly, inhibitory activity of CatD for compounds **17** and **18** remained at the level of starting hit **1**, which improved selectivity for Plm IV versus CatD inhibition (ratios of 4.6 and 9, respectively) as compared to all other analogues. This indicates that interactions with flap residues are important for Plm IV selectivity.

Selected compounds exhibiting high Plm IV inhibitory activity were tested for inhibition of *P. falciparum* parasite growth in erythrocytes using a SYBR green assay (Table 4). Compound **1*SR*** showed somewhat higher activity to inhibit the growth 3D7 parasite strain in erythrocytes compared to GSK LDH assay.[6] This deviation can be due to the different assays used to monitor parasite growth. The results of parasite growth inhibition of compounds **1*SS***, **1*SS***, **3**, and **16**−**18** again showed a clear correlation between parasite growth suppression and Plm IV inhibition, and not with Plm I or Plm II inhibition. Compounds **17** and **18**, which were high nanomolar inhibitors of Plm I and Plm II, were still very active in the cell based assay. In addition, diastereomer **1*SS***, which was a micromolar inhibitor of PlmI and II but a high nanomolar inhibitor of Plm IV, exhibited considerable activity in the cell based assay (Table 4).

In conclusion, we have identified Plm IV as the putative target of **1*SR*** (TCMDC-134674) in the malaria parasite *P. falciparum*. A cocrystal structure of **1*SR*** bound to Plm II was solved and provided structural insight for the design of more potent and selective analogues. Structure-guided optimization then led to the identification of simplified analogues **17** and **18** as a low nanomoalr inhibitors of Plm IV activity and *P. falciparum* growth in erythrocytes. Selectivity of PlmIV versus CatD inhibition for these compounds was improved by increasing their PlmIV inhibitory activity. Structure guided optimization studies provide a base to further optimize drug-like properties of this series of compounds.

■ ASSOCIATED CONTENT

Supporting Information

Description of the synthesis of compounds **1**−**18**, description of crystallographic studies, description of PlmI, II, IV, and CatD enzymatic assays, and parasite growth inhibition assays. This material is available free of charge via the Internet at http://pubs.acs.org.

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

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Notes

The authors declare no competing financial interest.

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■ ABBREVIATIONS

GSK, GlaxoSmithKline; Plm I, plasmepsin I; Plm II, plasmepsin I; Plm IV, plasmepsin IV; Cat D, cathepsin D

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