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Pseudo Cyclization through Intramolecular Hydrogen Bond Enables Discovery of Pyridine Substituted Pyrimidines as New Mer Kinase Inhibitors

Weihe Zhang^{†,‡,¶,||}, Dehui Zhang^{†,‡,¶,||}, Michael A Stashko^{†,‡,¶}, Deborah DeRyckere^{||}, Debra Hunter[‡], Dmitri Kireev^{†,‡,¶}, Michael J Miley[§], Christopher Cummings^{||}, Minjung Lee^{||}, Jacqueline Norris-Drouin^{†,‡,¶}, Wendy M. Stewart^{†,‡,¶}, Susan Sather^{||}, Yingqiu Zhou[¶], Gregory Kirkpatrick^{||}, Mischa Machius[§], William P. Janzen^{†,‡,¶}, H Shelton Earp^{‡,§}, Douglas K. Graham^{||}, Stephen V. Frye^{†,‡,¶,‡}, and Xiaodong Wang^{†,‡,*}

[†]Center for Integrative Chemical Biology and Drug Discovery, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

[‡]Division of Chemical Biology and Medicinal Chemistry, Eshelman School of Pharmacy, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

[§]Department of Pharmacology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

[‡]Lineberger Comprehensive Cancer Center, Department of Medicine, School of Medicine, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

^{||}Department of Pediatrics, School of Medicine, University of Colorado Denver, Aurora, CO 80045, USA

Abstract

Abnormal activation or overexpression of Mer receptor tyrosine kinase has been implicated in survival signaling and chemoresistance in many human cancers. Consequently, Mer is a promising novel cancer therapeutic target. A structure-based drug design approach using a pseudo-ring replacement strategy was developed and validated to discover a new family of pyridinepyrimidine analogs as potent Mer inhibitors. Through SAR studies, **10** (UNC2250) was identified as the lead compound for further investigation based on high selectivity against other kinases and good pharmacokinetic properties. When applied to live cells, **10** inhibited steady-state phosphorylation of endogenous Mer with an IC₅₀ of 9.8 nM and blocked ligand-stimulated activation of a chimeric EGFR-Mer protein. Treatment with **10** also resulted in decreased colony-forming potential in rhabdoid and NSCLC tumor cells, thereby demonstrating functional anti-tumor activity. The results provide a rationale for further investigation of this compound for therapeutic application in patients with cancer.

Keywords

Mer inhibitors; leukemia; solid tumor; NSCLC; pyridinepyrimidine; pseudo-ring replacement

Corresponding Author Information: Tel: 919-843-8456. xiaodonw@unc.edu.

[¶]These authors contributed equally

SUPPORTING INFORMATION Experimental details, and characterization of all compounds, and selectivity profiling. This material is available free of charge via the internet at <http://pubs.acs.org>.

PDB ID Codes: The atomic coordinates for the X-ray crystal structure of **3** have been deposited with the RCSB Protein Data Bank under the accession code 4M3Q.

INTRODUCTION

Mer belongs to the TAM (Tyro3, Axl, Mer) family of receptor tyrosine kinases (RTK) which share at least one common biological ligand—growth arrest-specific-6 (Gas6). Other ligands, including Protein S¹, Tubby², TULP-1², and Galectin-3³ can also stimulate Mer. Under normal physiologic conditions, Mer mediates the second phase of platelet aggregation, macrophage and epithelial cell clearance of apoptotic cells, modulation of macrophage cytokine synthesis, cell motility, and cell survival.⁴ Abnormal activation or overexpression of Mer RTK has been implicated in neoplastic progression of many human cancers and has been correlated with poorer prognosis. For example, Mer is ectopically expressed in both B-cell and T-cell acute lymphoblastic leukemia (ALL), the most common pediatric malignancy, but is not expressed in normal mouse and human T- and B-lymphocytes at any stage of development.⁵ Inhibition of Mer by si/sh-RNA knockdown sensitizes cells to chemotherapy-induced apoptosis and doubles survival in a xenograft model of acute leukemia.^{5c} Similar effects are observed when Mer expression is abrogated with shRNA in non-small cell lung cancer (NSCLC) cells.⁶ In addition, treatment of melanoma cells with a small molecule Mer inhibitor **UNC1062**⁷ results in effects comparable to shRNA-mediated Mer inhibition, including reduced colony formation in soft agar and decreased invasion into collagen matrix.⁸ Taken together these data indicate that Mer is a novel therapeutic target for the treatment of ALL and other cancers that ectopically or overexpress Mer. Therefore, Mer inhibition with small molecule inhibitors may have clinical benefit either alone or in combination with chemotherapeutic agents.

We have previously developed several potent small molecule Mer inhibitors within the pyrazolopyrimidine scaffold.^{7,9} However, we were motivated to explore other scaffolds to potentially increase selectivity within the TAM family of kinases^{9a} and address solubility and pharmacokinetic properties required for further in vivo studies⁷. In order to design new Mer inhibitors, we revisited the co-crystal structure of Mer in complex with **1** (**UNC569**) (Figure 1a).^{9a} Wherein the inhibitor **1** is fully confined to the relatively small adenine pocket, including its flexible lipophilic butyl side chain, the pyrazole ring of **1** does not interact with any amino acid residue directly, suggesting that its main role might be to maintain the molecule's overall conformation. Replacing the pyrazole ring with a pseudo-ring¹⁰ constrained by an intramolecular hydrogen bond as shown in compound **2** (Figure 1b) could potentially generate potent Mer inhibitors displaying different physicochemical properties when compared to pyrazolopyrimidines. Additionally, because the pseudo ring in **2** is formed through a hydrogen bond between the pyridine nitrogen and the 4-amino group, it is less rigid than pyrazolopyrimidine and therefore is more likely to undergo “induced-fit” to optimize its interaction with the binding pocket. This scaffold would also simplify analog synthesis and facilitate exploration of structure-activity relationships (SAR).

CHEMISTRY

The proposed pyridinepyrimidines were synthesized using the route shown in Scheme 1.

Starting with the commercially available compound 5-bromo-2,4-dichloropyrimidine, a S_NAr displacement of the chloride at the C4 position of the pyrimidine ring with an amine (R^2NH_2) introduces substituents at the R^2 position in **I**. The second S_NAr reaction at a higher temperature installs the R^3 group at the C2 of the pyrimidine ring to yield the intermediate **II**. Finally, cross-coupling between **II** and a lithium trihydroxy borate salt of 2-pyridine or its derivatives provides the desired analogs **III**. We used 2-pyridyl trihydroxy borate salts for the coupling as they are easily prepared.¹¹ In contrast, the corresponding boronic acid/ester of 2-pyridine and its derivatives are either very expensive or not readily

available. Alternatively, **I** can also be converted to the corresponding boronic ester **IV** and subsequently be coupled with 2-chloro-pyridine or its derivatives to introduce the R¹ group at the C5 of the pyrimidine ring.¹² Overall, this route is optimal to explore the structure-activity relationship (SAR) at the R¹ site; it can also be used for SAR exploration at the R² and R³ sites.

In addition, we developed an alternative route to synthesize analogs with different R³ groups as shown in Scheme 2 because the most efficient way to prepare analogs was to place the exploration step at the last step of the synthesis. The S_NAr replacement of the chloride of commercially available 5-bromo-4-chloro-2-(methylthio)pyrimidine provides the intermediate **V** which can be transformed to **VI** via a Suzuki-Miyaura cross-coupling reaction with a lithium trihydroxy borate salt of 2-pyridinyl compounds. *m*-CPBA oxidation of **VI** followed by the second S_NAr replacement by various amines (R³NH₂) yields the final products **III**.

RESULTS AND DISCUSSION

To validate the pseudo-ring strategy, we first synthesized compound **2** and its structurally close analogs (Figure 2) using the route shown in Scheme 1. Their activities against Mer kinase were then determined in a microfluidic capillary electrophoresis (MCE) assay^{7, 9a, 13}. The IC₅₀ value of **2** was 18 nM which was in the same range as that of the parent pyrazolopyrimidine compound **1**. Replacing the *trans*-4-aminocyclohexylmethylamino substitution in **2** with a *trans*-4-hydroxycyclohexylamino group also resulted in a potent Mer inhibitor **3**. This will likely diminish the undesired hERG activity present in **1** as previously demonstrated with **UNC1062**.⁷ In contrast, the Mer activity decreased dramatically when the intramolecular hydrogen bond was disrupted either by moving the nitrogen of 2-pyridinyl to the C6 position of the pyridine ring (**4**, 34-fold) or by replacing it with a CH group (**5**, 56-fold). The complete removal of the 2-pyridinyl substitution also rendered the corresponding **6** much less active (900-fold). Collectively, these results validate that the pseudo-ring design through an intra-molecular hydrogen bond maintains a conformation similar to the pyrazolopyrimidine. Compared to **1**, compounds **2** and **3** are also more selective for Mer relative to Axl (38-fold and 67-fold respectively) and Tyro3 (10-fold and 37-fold respectively). This enhanced selectivity was fortuitous, but subsequent co-crystal structures (see below) may provide an explanation.

To develop potent Mer inhibitors with improved properties, we investigated the SAR with this newly discovered pyridinepyrimidine scaffold at the R¹, R² and R³ positions. First, different substituents at the R¹ position were explored while fixing the R² site as a *trans*-4-hydroxycyclohexyl group and the R³ site as a butyl group. As shown in Table 1, a fluorine at the 5-position of the pyridine ring did not affect the Mer activity of analog **7** significantly while a larger group such as *N*-methylpiperazine at the same position led to a 6-fold more active analog **8**. An extra methylene group between pyridine and *N*-methylpiperazine (**9**) was also tolerated. The *N*-methylpiperazine ring could be replaced by a morpholine ring to yield an equipotent analog **10** (**UNC2250**). Interestingly, the substitution pattern on the pyridine ring played an important role in the activity of these compounds. The most active analog **10** was generated from substitution at the 5-position of the pyridine ring while a substituent at the 3-position (**11**) totally abolished the Mer activity, possibly due to steric clash of the substituents with the Mer protein backbone. The substitutions at the 4-position (**12**) and the 6-position of the pyridine ring (**13**) were tolerated but were not as active as when substituted at the 5-position (**10**). In addition, *N*-methylpiperazine at the 5-position of the pyridine in **9** could also be replaced with other groups such as 4,4-difluoropiperidine (**14**) and dimethylamine (**15**) without disrupting activity. Furthermore, other functionalities such as the sulfonamide (**16**), amide (**17**) or reversed amide (**18**) could be used to link the

pyridine with another group such as morpholine (**16**) or *N*-methylpiperazine (**17** & **18**) resulting in similarly active analogs. However, the amide bond in **17** was not as stable to hydrolysis as the reversed amide bond in **18**. 4-Amino-*N*-methyl piperidine was partially replaced by the solvent—*isopropanol*, during the workup of the amide bond coupling reaction (the reaction was quenched with a 1.0 N aqueous solution of NaOH or a saturated aqueous solution of NaHCO₃ and extracted with a mixture of *isopropyl alcohol* and CH₂Cl₂ (1:10)). In addition, the secondary amines cyclohexylamino (**19**), cyclopropylamino (**20**), and even 2-hydroxyethylamino group (**21**) could serve as substituents on the methylene group at the 5-position of the pyridine ring. This is consistent with our docking model in which the R¹ group is exposed mostly to solvent and there is space to accommodate a variety of groups. This feature makes this position ideal for substitutions that modify the physical and pharmacokinetic (PK) properties of these analogs. In general, this series is more potent for Mer than the other TAM kinases and some are quite Mer-specific. For example, **10** is 160-fold more active for Mer versus Axl and 60-fold versus Tyro3.

Next, the SAR at the R² site was explored (Table 2). As predicted from the docking model, the polar group on the R² site is critical and can form a hydrogen bond with the carbonyl of Glu595. For example, removing the hydroxyl group from the cyclohexyl substituent in compound **3** to produce analog **22** dramatically decreased Mer activity (74-fold), while introducing an amino group at the same position of the cyclohexyl ring increased the activity of analog **23**. Even an aminomethyl group at this position yielded a similarly active analog **24**. However, introducing of an aniline group at the R² position resulted in a 10-fold less inhibitory analog (**25** versus **23**). A secondary amino group was less tolerated in analogs **26** and **27**. In addition, the cyclohexyl ring itself may have favorable hydrophobic interactions with the protein. When reducing the ring size to a 5- or 4-membered ring, the activities of the corresponding analogs decreased (**28** & **29**) and the open-chained analogs **30** & **31** were further reduced in activity. In addition, the proton on the amino group which connects the substituents at the R² site to the pyrimidine ring played a key role in our design as it forms an intramolecular hydrogen bond with the 2-pyridinyl maintaining the overall conformation of the molecule. Without this proton (**32**), the Mer activity was completely lost. Again, several of the analogs in Table 2 are quite Mer-selective (e.g. **23** has 300- fold selectivity for Mer over Axl and 50-fold over Tyro3).

Analogues were also synthesized to investigate the SAR at the R³ position using the synthetic route shown in Scheme 2 (Table 3). Based on the X-ray crystal structure of **1** in complex with the Mer protein (Figure 1a), the NH from the butyl amino side chain forms a hydrogen bond with the hinge region of the Mer protein. When a sulfur atom was placed at this position, the corresponding analog **33** was much less active than analog **34**; this was due to absence of this key hydrogen bond. Analog **34** was a less potent Mer inhibitor compare to **3** due to the diminished hydrophobic interaction at the R³ site. When the alkyl side chain at the R³ position was made longer, the resulting analogs **35** & **36** gained activity until the side chain reached 5 carbons in length (**37**). Analog **37** was equally potent to **3**. A branched methyl group at the α -position of the NH (**38**) decreased the activity slightly. However, the activity dropped dramatically (22-fold) when the hydrogen on the NH was replaced with a methyl group (**39**), which further confirmed the importance of the hydrogen bond formed between the NH and the hinge region of the Mer kinase domain. This effect was more evident when a larger piperidine group was placed at the R³ position; the corresponding analog **40** lost almost all activity against Mer. A cycloalkyl group at this position had a similar effect as a branched alkyl side chain; analog **41** had similar potency to **38**. A phenyl ring was also tolerated at the side chain; comparing analogs **42** to **35** and **43** to **36**. In addition, a polar hydroxyl group at the end of the alkyl side chain decreased the activity of the resulting analogs due to a weaker binding caused by a less favorable hydrophobic

contribution (**44** vs **36**, **45** vs **3**). When the length of the side alkyl chain reached 4 carbons, the corresponding analog **46** regained its activity comparable to **37**, probably due to the vicinity of the polar hydroxyl group to the solvent front. Again, these analogs were quite Mer-selective as compared to the pyrazolopyrimidines.

To provide a deeper insight into the binding interactions of the pyridine-pyrimidine inhibitors and afford structural guidance for further chemical optimization, a co-crystal structure of Mer in complex with compound **3** was obtained (Figure 3). In this structure, the inhibitor **3** demonstrates a binding mode in which the pyrimidine-2-amine group mimics the interactions of the cofactor's adenine with the backbone atoms of the hinge (residues Pro672 and Met674). Similar to the previously published structure of the Mer:**1** complex, the aminobutyl R³ substituent is bent within the adenine sub-pocket. Unlike the former structure, the hydroxyl group of the R² substituent forms a hydrogen bond with the backbone carbonyl of Glu595 (the analogous R² amino group of **1** interacts with Arg727). This difference is most likely because the cyclohexyl group reoriented due to the intramolecular H-bond between the pyridine and 4-amino groups. It is noteworthy that one of the gate-forming residues, Ile650, is not conserved in the other two TAM family members. Axl and Tyro3 feature methionine and alanine, respectively, at this position. This variability is one likely reason for significant intra-family selectivity. Consistent with the SAR outlined above, the R¹ substituent interacts mostly with the solvent and does not significantly impact the activity. Consequently, it can be utilized for tuning solubility and PK properties. Nevertheless, the freedom to modify R¹ has its limits, as demonstrated by compound **11**, whose bulky pyridine-morpholine R¹ substituent precludes an efficient interaction with the hinge.

Four potent analogs (**10**, **14**, **16**, & **20**) with distinctively different R¹ groups were chosen for PK studies (Table 4). The *in vivo* PK properties of these compounds were assessed in mice following intravenous (IV) or oral (PO) administration (Table 4). All four compounds had high systemic clearance (69—149% of normal liver blood flow in mice). Among them **20** had the longest half-life (4.71 h) but also had an extremely high volume of distribution (56-fold higher than the normal volume of total body water in mice) and low plasma concentrations. Compound **14** had the best oral bioavailability (55%) but a high volume of distribution (20-fold); while **16** had a short half life and low oral exposure. Compound **10** had a moderate half-life, clearance and volume of distribution as well as reasonable oral bioavailability and good solubility and was thus chosen for characterization of kinase selectivity and further evaluation in cell-based studies of Mer activity.

The inhibitory activity of **10** against 30 Kinases (detailed in supplemental materials) was determined at a concentration 100 fold above its Mer IC₅₀ (Figure 4). The kinase panel selected emphasized tyrosine kinases along with a selection of serine/threonine kinases, providing a broad survey of kinase families. Five out of thirty kinases were inhibited greater than 50% in the presence of 180 nM **10** and none of the serine/threonine kinases were appreciably inhibited.

In cell-based assays, **10** mediated inhibition of Mer phosphorylation in 697 B-ALL cells with an IC₅₀ value of 9.8 nM (Figure 5). Mer phosphorylation was also inhibited in Colo699 NSCLC cells (Figure 6A). In addition to these effects on steady-state levels of Mer tyrosine phosphorylation, **10** efficiently inhibited ligand-dependent phosphorylation of a chimeric protein consisting of the extracellular and transmembrane domains of the epidermal growth factor (EGF) receptor and the intracellular tyrosine kinase domain of Mer (Figure 6B). Moreover, **10** incubation inhibited colony formation in soft agar cultures of the BT-12 rhabdoid tumor and the Colo699 NSCLC cell lines (Figure 7). In the Colo699 NSCLC cell line, the concentrations of **10** required to inhibit colony formation and Mer phosphorylation

were similar. These data suggest that the functional anti-proliferative activity mediated by **10** resulted from Mer inhibition, rather than a consequence of off-target inhibition of other kinases.

CONCLUSIONS

A new pyridinepyrimidine scaffold has been discovered and developed to create potent Mer kinase inhibitors by applying a structure-based drug design approach using a pseudo-ring replacement strategy. A co-crystal structure of Mer with one inhibitor (**3**) has been obtained and supports the predicted binding mode where an intramolecular hydrogen bond is used to induce conformational rigidity. The selectivity and PK properties of the lead compound **10** (**UNC2250**) are promising and further optimization of this series is ongoing. When applied to live cells, **10** efficiently inhibited both steady state and ligand-stimulated phosphorylation of Mer. Furthermore, treatment with **10** was sufficient to reduce colony-forming potential in both rhabdoid tumor cells and NSCLC cells, confirming functional anti-tumor activity mediated by **10** and suggesting the tractability of this new series to deliver clinically useful agents.

EXPERIMENTAL SECTION

Details on the synthesis of all compounds are given in the Supporting Information. The purity of all tested compounds was determined by LC/MS to be >95%.

Microfluidic Capillary Electrophoresis (MCE) Assay^{9a}

Activity assays were performed in a 384 well, polypropylene microplate in a final volume of 50 μ L of 50 mM Hepes, Ph 7.4 containing 10 mM $MgCl_2$, 1.0 mM DTT, 0.01% Triton X-100, 0.1% Bovine Serum Albumin (BSA), containing 1.0 μ M fluorescent substrate (Table 5) and ATP at the K_m for each enzyme (Table 5). All reactions were terminated by addition of 20 μ L of 70 mM EDTA. After a 180 min incubation, phosphorylated and unphosphorylated substrate peptides (Table 5) were separated in buffer supplemented with 1 \times CR-8 on a LabChip EZ Reader equipped with a 12-sipper chip. Data were analyzed using EZ Reader software.

Cell Based Assays for Mer Kinase Inhibition

697 B-ALL, 32D cells expressing a chimeric EGFR-MerTK receptor, BT-12 rhabdoid tumor, or Colo699 NSCLC cells were cultured in the presence of **10** or vehicle only for 1.0 h (697 B-ALL, 32D, BT-12 rhabdoid tumor) or 72 h (Colo699 NSCLC). Pervanadate solution was prepared fresh by combining 20 mM sodium orthovanadate in 0.9 \times PBS in a 1:1 ratio with 0.3% (w/w) hydrogen peroxide in PBS for 15-20 min at room temperature. Cultures were treated with 120 μ M pervanadate prior to collection for preparation of whole cell lysates, immunoprecipitation of Mer, and analysis by western blot.

697 B-ALL and Colo699 NSCLC cells were treated with pervanadate for 3.0 and 1.0 min respectively. Cell lysates were prepared in 50 mM HEPES pH 7.5, 150 mM NaCl, 10 mM EDTA, 10% glycerol, and 1% Triton X-100, supplemented with protease inhibitors (Roche Molecular Biochemicals, #11836153001). Mer protein was immunoprecipitated with a monoclonal anti-Mer antibody (R&D Systems, #MAB8912) and Protein G agarose beads (Invitrogen). Phospho-Mer was detected by western blot using a polyclonal anti-phospho-Mer antibody raised against a peptide derived from the triphosphorylated activation loop of Mer. Nitrocellulose membranes were stripped and total Mer protein was detected using a second anti-Mer antibody (Epitomics Inc., #1633-1). For 697 B-ALL cells, relatively

phosphorylated and total Mer protein levels were determined by densitometry using Image J software and IC₅₀ values were calculated by non-linear regression.

Confluent BT-12 rhabdoid tumor cultures were treated with pervanadate for 15 min. Confluent 32D cells expressing EGFR-MerTK chimeric protein were treated with 100 ng/mL EGF ligand for 15 min and were collected without pervanadate treatment. Cell lysates were prepared in 20 mM HEPES pH 7.5, 50 mM sodium fluoride, 500 mM NaCl, 5.0 mM EDTA, 10% glycerol, and 1% Triton X-100, supplemented with protease inhibitors (10 µg/mL leupeptin, 10 µg/mL phenylmethylsulfonyl fluoride, and 20 µg/mL aprotinin) and phosphatase inhibitors (50 mM sodium fluoride and 1.0 mM sodium orthovanadate) and Mer protein was immunoprecipitated using a polyclonal rabbit anti-Mer antisera raised against a peptide derived from the C-terminal 100 amino acids of human Mer expressed as AST protein and Protein A agarose beads (Santa Cruz Biotechnology). Phosphotyrosine-containing proteins were detected by western blot with a monoclonal HRP-conjugated anti-phosphotyrosine antibody (Santa Cruz Biotechnology, #sc-508). Antibodies were stripped from membranes and total Mer levels were determined using a custom polyclonal rabbit anti-Mer antibody raised against a peptide derived from the catalytic domain of Mer.

32D-EMC suspension cultures were treated with the indicated of **10** or vehicle before stimulation with 100 ng/mL EGF (BD Biosciences #354010) for 15 min. Cells were centrifuged at 1000g for 5 min and washed with 1× PBS. Cell lysates were prepared in 20 mM HEPES (pH 7.5), 50 mM NaF, 500 mM NaCl, 5.0 mM EDTA, 10% glycerol, and 1% Triton X-100, supplemented with protease inhibitors (10 µg/mL leupeptin, 10 µg/mL phenylmethylsulfonyl fluoride, and 20 µg/mL aprotinin) and phosphatase inhibitors (50 mM NaF and 1.0 mM sodium orthovanadate) and Mer protein was immunoprecipitated using the polyclonal rabbit anti-Mer C-terminus antisera and Protein A agarose beads (Santa Cruz Biotechnology). Phosphotyrosine-containing proteins were detected by western blot with a monoclonal HRP-conjugated anti-phosphotyrosine antibody (Santa Cruz Biotechnology, #sc-508). Antibodies were stripped from membranes and total Mer levels were determined using the custom polyclonal rabbit anti-Mer antibody raised against a peptide derived from the catalytic domain of Mer.

Soft Agar Colony Formation Assays

BT-12 rhabdoid tumor cells (10,000 cells) were cultured in 2.0 mL of 0.35% soft agar containing 0.5× RPMI medium, 7.5% FBS, and the indicated concentrations of **10** or DMSO vehicle only and overlaid with 0.5 mL of 1× RPMI medium containing 15% FBS and **10** or DMSO vehicle only. Medium and **10** or vehicle were refreshed 2 times per week. Colonies were stained with thiazolyl blue tetrazolium bromide (Sigma Aldrich, #M5655) and counted after 3 weeks.

Colo699 NSCLC cells (15,000 cells) were cultured in 1.5 mL of 0.35% soft agar containing 1× RPMI medium and 10% FBS and overlaid with 2.0 mL of 1× RPMI medium containing 10% FBS and the indicated concentrations of **10** or DMSO vehicle only. Medium and **10** or vehicle were refreshed 3 times per week. Colonies were stained with nitrotetrazolium blue chloride (Sigma Aldrich, #N6876) and counted after 2 weeks.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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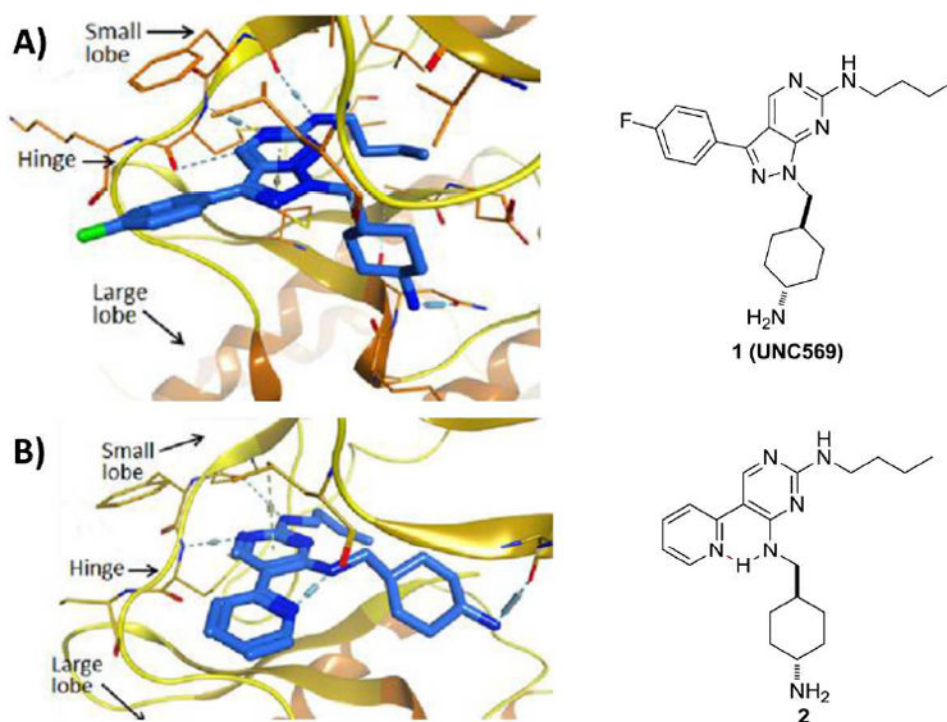


Figure 1. Structure-based design of a scaffold that relies on pseudo-ring formation through an intramolecular hydrogen bond. A). X-ray structure of **1** in complex with Mer protein (kinase domain) (PDB ID code 3TCP); B). Docking model (based on X-ray structure PDB ID code 3TCP) of the designed molecule **2**.

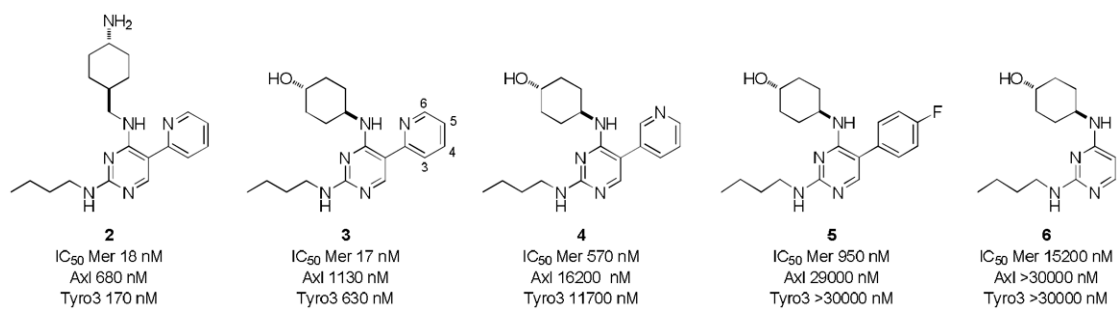


Figure 2.
Structure and enzymatic activity of compound **2** and its close analogs.

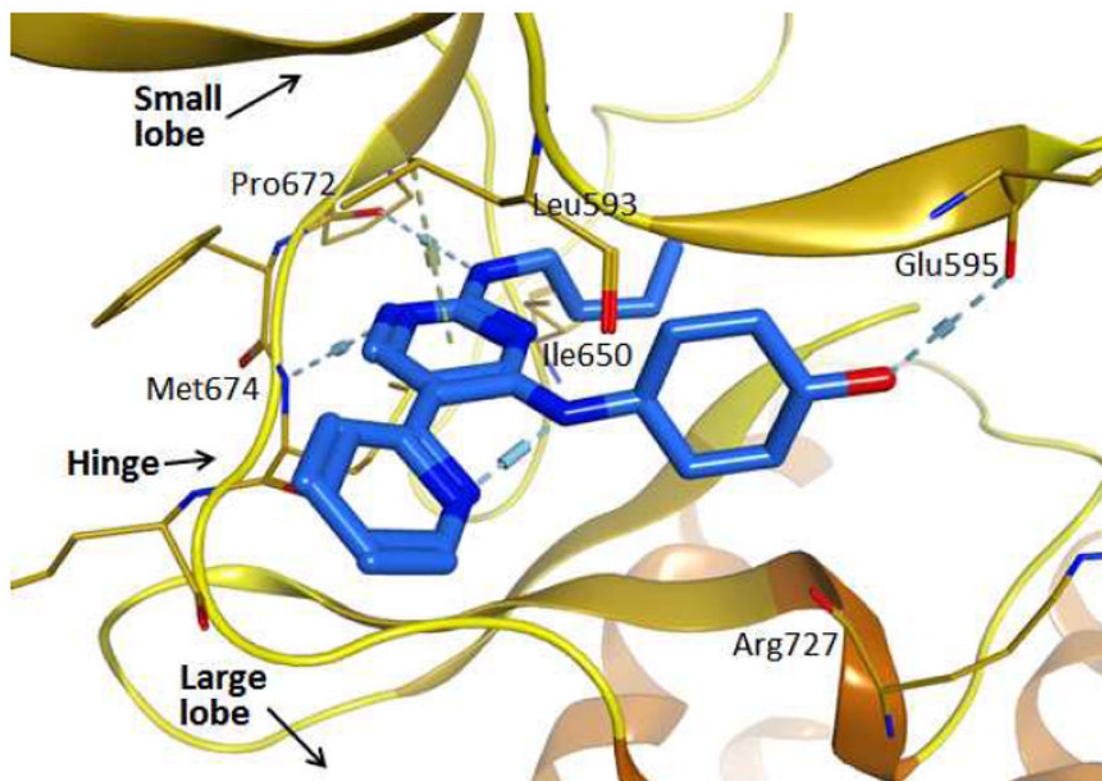


Figure 3.
X-ray structure of **3** in complex with Mer kinase domain (PDB ID Code: 4M3Q).

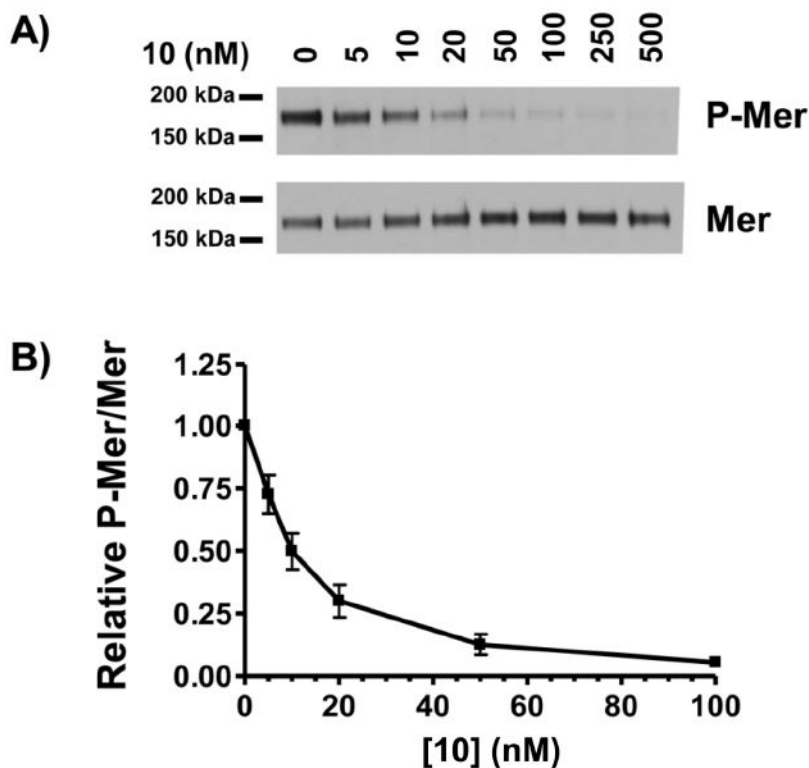


Figure 5. 10 inhibits Mer tyrosine kinase activation in acute leukemia cells
697 B-ALL cells were treated with the indicated concentrations of **10** for 1 h. Pervanadate was added to cultures for 3 min to stabilize the phosphorylated form of Mer. Mer was immunoprecipitated from cell lysates and total Mer protein and Mer phosphoprotein were detected by immunoblot. A) Representative western blots. B) Relative levels of phospho-Mer and Mer proteins were determined. Mean values \pm standard error derived from 3 independent experiments are shown. $IC_{50} = 9.8$ nM with a 95% confidence interval of 7.9 nM to 12.3 nM.

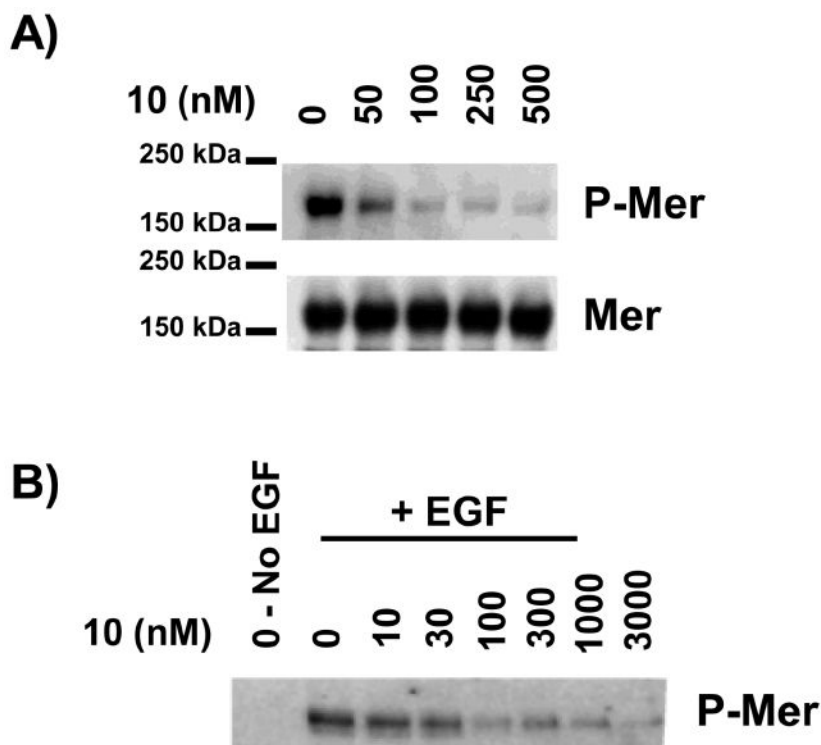


Figure 6. 10 inhibits Mer activation in adherent tumor cell lines

A) Colo699 NSCLC cells were treated with **10** or vehicle for 72 h followed by treatment with pervanadate for 3 min. Whole cell lysates were prepared, Mer protein was immunoprecipitated, and phosphorylated and total Mer proteins were detected by western blot. B) 32D cells stably expressing a chimeric receptor consisting of the extracellular ligand-binding and transmembrane domains of the EGF receptor and the intracellular kinase domain of Mer were treated with **10** or vehicle for 1 h prior to stimulation for 15 min with 100 ng/ml EGF. Mer was immunoprecipitated from whole cell lysates and phospho-tyrosine containing and total Mer proteins were detected by western blot. Results shown are representative of 4 (A) or 3 (B) independent experiments.

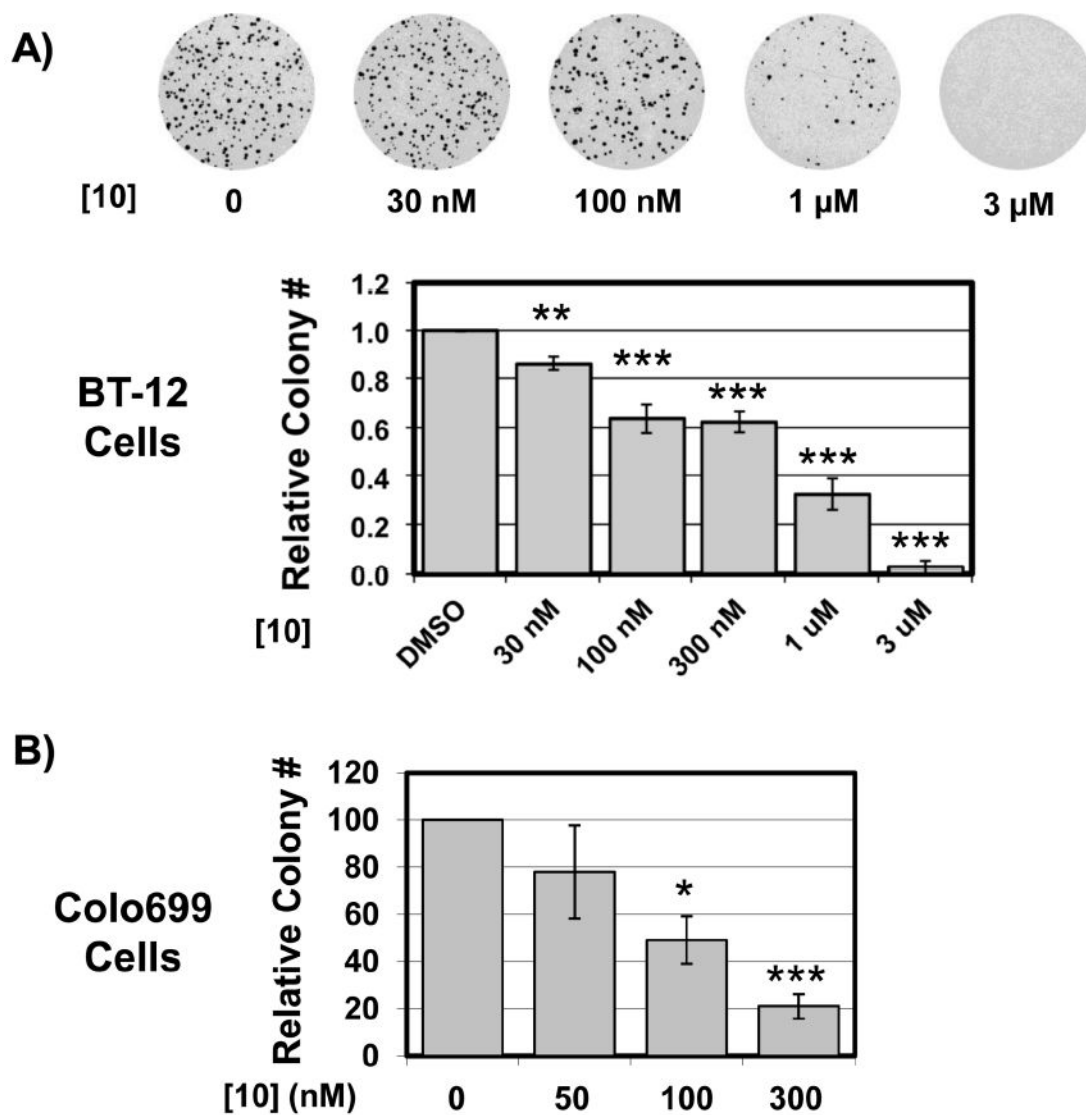
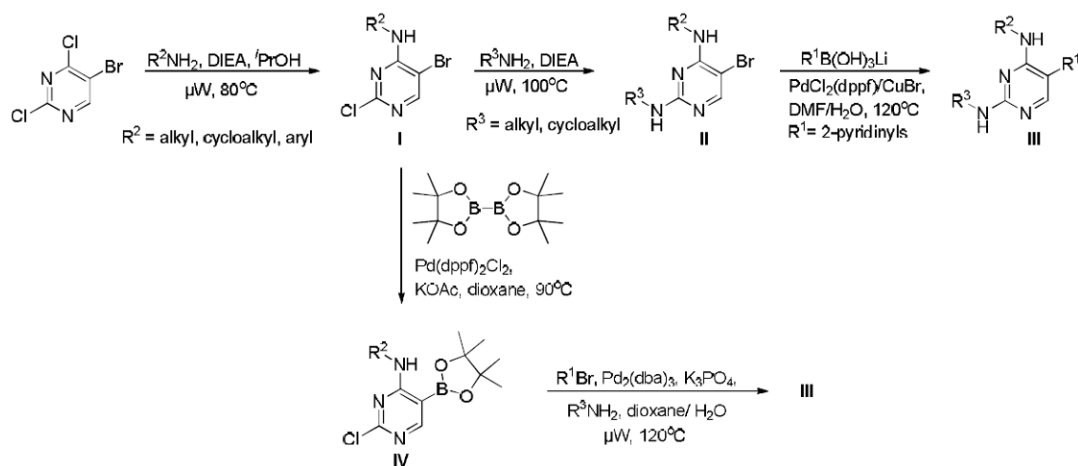
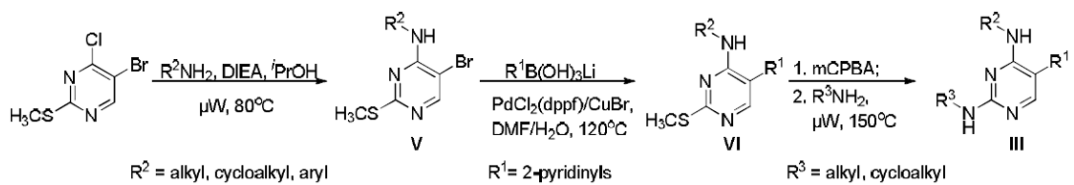


Figure 7. 10 inhibits colony formation in solid tumor cell lines

A) BT-12 rhabdoid tumor cells were cultured in soft agar containing 10 nM to 3 μ M **10** or vehicle only and overlaid with medium containing **10** or vehicle only. Medium and **10** were refreshed twice weekly. Colonies were stained and counted. Representative plates are shown. B) Colo699 NSCLC cells were cultured in 0.35% soft agar overlaid with medium containing **10** or vehicle. Medium and **10** were refreshed 3 times per week. Colonies were stained and counted. Mean values \pm SEM derived from 4 independent experiments are shown. *Statistically significant differences were determined using the student's paired t test (* $p < 0.02$, ** $p < 0.01$, *** $P < 0.001$ relative to vehicle only).

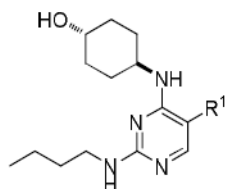
**Scheme 1.**

The general synthetic routes for pyridinepyrimidine analogs **II**

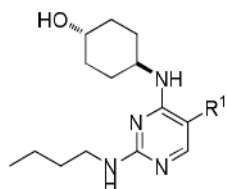
**Scheme 2.**

General synthetic route to explore SAR at the R^3 position.

Table 1

Preliminary SAR at the R¹ position

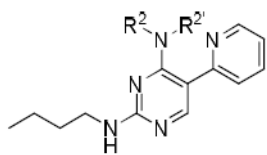
Compound	R ¹	IC ₅₀ (nM) ^a		
		Mer	Axl	Tyro3
7		6.3	460	270
8		2.8	180	88
9		3.9	260	110
10		1.7	270	100
11		>30000	>30000	>30000
12		12	930	810
13		18		390
14		1.1	130	36
15		1.7	63	21
16		0.70	72	28



Compound	R ¹	IC ₅₀ (nM) ^a		
		Mer	Axl	Tyro3
17		0.69	61	24
18		3.4	170	94
19		0.69	38	24
20		1.3	84	33
21		0.81	70	21

^aValues are the mean of two or more independent assays.

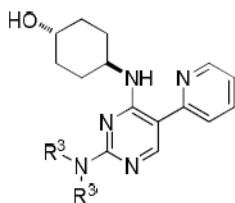
Table 2

SAR study of R² site

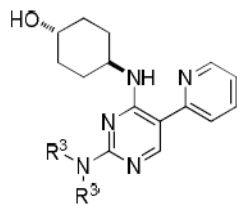
Compound	R ² R ^{2'} N	IC ₅₀ (nM) ^a		
		Mer	Axl	Tyro3
22		1250	>30000	>30000
23		1.8	550	84
24		4.5	180	58
25		18	830	280
26		34	1580	430
27		72	1280	390
28		160	3700	1370
29		200	2790	1340
30		1130	9890	4910
31		600	20800	4060
32		>30000	>30000	>30000

^aValues are the mean of two or more independent assays.

Table 3

Further SAR study of R³

Compound	R ³ R ³ N	IC ₅₀ (nM) ^a		
		Mer	Axl	Tyro3
33		2700	>30000	>30000
34		540	3920	6850
35		170	3530	2580
36		50	6180	1590
37		19	650	440
38 ^b		44	8040	370
39		380	>30000	>30000
40		16500	>30000	>30000
41		83	20300	1160
42		110	>30000	300
43		14	430	80
44		320	18500	8940
45		220	15000	6140



Compound	R ³ R ³ N	IC ₅₀ (nM) ^a		
		Mer	Axl	Tyro3
46		44	3460	2930

^aValues are the mean of two or more independent assays.

^bRacemate.

Table 4

PK profile of 10, 14, 16 & 20

Compound	Structure	Route ^a	T _{1/2} (h)	T _{max} (h)	C _{max} (ng/mL)	AUC _{last} (h ³ ·ng/mL)	CL _{obs} (mL/min/kg)	V _{ss} (L/kg)	%F
10		IV	1.59	-	1975	794	62.2	3.90	-
		PO	-	0.25	162	180	-	-	23
14		IV	2.97	-	737	381	123	13.72	-
		PO	-	0.25	71	210	-	-	55
16		IV	0.91	-	1980	355	134	2.90	-
		PO	-	0.25	13.9	4.68	-	-	1.3
20		IV	4.71	-	277	376	130	39.02	-
		PO	-	0.50	33	103	-	-	27

^a a dose of 3 mg/kg for both routes.

Table 5

Assay conditions for MCE assays

Kinase	Peptide Substrate	Kinase (nM)	ATP (uM)
Mer	5-FAM-EFPIYDFLPAKKK-CONH ₂	2.0	5.0
Axl	5-FAM-KKKKEEIYFFF-CONH ₂	120	65
Tyro	5-FAM-EFPIYDFLPAKKK-CONH ₂	10	21