"Sleeping beauty" phenomenon: SuFEx-enabled discovery of selective covalent inhibitors of human neutrophil elastase

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Abstract:

Sulfur-Fluoride Exchange (SuFEx) has emerged as the new generation of click chemistry. We report here a SuFEx-enabled approach exploiting the "sleeping beauty" phenomenon of sulfur fluoride compounds in the context of the serendipitous discovery of selective covalent human neutrophil elastase (hNE) inhibitors. Evaluation of an ever-growing collection of SuFExable compounds toward various biological assays unexpectedly yielded a selective and covalent hNE inhibitor, benzene-1,2-disulfonyl fluoride. Derivatization of the initial hit led to a better agent, 2-triflyl benzenesulfonyl fluoride, itself made through a SuFEx trifluoromethylation process, with $IC_{50} = 1.1 \mu M$ and ~200-fold selectivity over the homologous neutrophil serine protease, cathepsin G. The optimized probe only modified active hNE and not its denatured form, setting another example of the "sleeping beauty" phenomenon of sulfur fluoride capturing agents for the discovery of covalent medicines.

Sulfur fluoride exchange (SuFEx)—the new generation click chemistry, since first introduced in 2014 (1), has quickly found diverse applications across an array of fields including chemical synthesis (2-12), material science (13-19), chemical biology (20-31), and drug discovery (32, 33). SuFEx creates robust intermolecular links between modules. The extreme fidelity stems from the ability of otherwise, very stable higher oxidation state sulfur fluorides (34-38) to exchange S–F with incoming nucleophiles under SuFEx catalysis conditions, forming stable and irreversible linkages united through a sulfur center. These SuFEx reactions are made possible by the unique requirements set to stabilize a departing fluoride ion in its transit away from a strong covalent bond, with "H⁺" or "R₃Si⁺" mediators, and especially favored by DBU-type amine catalysts (13, 39, 40), and also thought to involve bifluoride counter ion species (16, 17, 41).

In the context of selective *in vitro* or *in vivo* covalent capture of proteins by SuFExable^{*} compounds, examples are accumulating rapidly (20-31), but we are still reluctant to make strong *a priori* inferences about the factors which determine a given capture's occurrence. This said, there is one remarkable fact shared by all SuFEx-based protein captures that the probes' special S–F links are among the most demure electrophiles known[†] (1, 34-38). Only a correctly folded and functionally active protein can serve as a catalyst[‡] for a SuFEx capture event upon one of its own nucleophilic amino acid sidechains (**Fig. 1A**). These bio-compatible SuFEx reactions are presumably mediated by environmental factors unique to the "live" system, thereby facilitating displacement of the otherwise stable sulfur-fluoride by the partner protein. In contrast, the denatured proteins are completely inert to the same S–F probes (24, 32). We name this special relationship between functional living proteins and SuFExable probes the "sleeping beauty" phenomenon[§], which mirrors very closely our earlier protein enabled Huisgen azide-alkyne cycloaddition (i.e. *in situ* click chemistry) (42, 43), in terms of the "live" enzyme requirement.

Taking inspiration from the original click chemistry manifesto (44); that molecular diversity can be achieved with ease through the connection of small modules, using just a few good reactions, in sequences of usually no more than three steps, we demonstrate here two distinct but logically connected, sequential SuFEx-enabled entities: (1) efficient construction of a pool of SuFExable compounds *via* click chemistry principles, and (2) bioprospecting this library for covalent capture agents for important protein targets *via* "sleeping beauty" reactivity. The expectation, based on previous experience, is that evaluation of a SuFEx library will often result in multiple lead compounds. The latter can usually be followed up by easily deployed SAR-based (structure-activity-relationship-based) lead studies. This "compound-bank" mode of the SuFEx-enabled platform, itself contributes to the ever-growing library of SuFExable modules and candidates, and like "compounding-interest", rewards the principle library with expanding opportunities for discovering new kinds of phenotypic modulators; including useful new functions for medicines in the long term (**Fig. 1B**).

Over the past five years, we (1, 5, 8, 45) and others (12, 46-49) have developed a valuable collection of efficient methods to synthesize SuFExable compounds from either simple or complex organic molecules using highly connective SuFEx core electrophiles (e.g. SO_2F_2 , $O=SF_4$, $CH_2=CHSO_2F$). Collective work within the Sharpless laboratory continues to build a library of SuFExable small modules. There are >1000 compounds in this collection[¶]. Thanks to the great stability of the SuFExable S–F links toward water and oxygen, the oldest library deposits (as DMSO solutions) are still pure. The individual compounds are dissolved as 10 mM DMSO stock solutions and stored in –20 °C freezer, with most being stable at –20 °C as evidenced by periodic inspection by LC-MS of randomly sampled compound over 2 years. To date, the library and/or its sub-libraries have been screened with collaborators at Scripps Research and other institutes against multiple targets. Here we report a case study using the SuFEx-enabled approach to the discovery of selective, covalent inhibitors of human neutrophil elastase (hNE).

Human neutrophil elastase; a member of the serine protease superfamily, is aberrantly active in cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD), and inflammatory bowel diseases (IBD) (50-66). This protease is therefore a key target for the development of antiinflammatory agents to combat these diseases. Alkyl and aryl sulfonyl fluorides have a long history as rather promiscuous covalent inhibitors of serine proteases (67-76). In the late 1970's, the Powers group demonstrated the intrinsic reactivity differences across several serine proteases, including elastase, with 2-amido(peptido) benzenesulfonyl fluoride inhibitors (77, 78). Their results encouraged us to investigate our library of SuFExable compounds as potential covalent inhibitors of hNE.

Results and Discussion

A set of 105 compounds (**SI Appendix, Table S1**), many of which appear to be new compounds, were selected without bias, to form a primary library for the screen against hNE. The selected compounds can be categorized into four subsets by the nature of S–F functional groups (**Fig. 1C**). Each group tends to have its own intrinsic zone of reactivity in acid-base environments. To give a general impression, the relative rate measured on a representative molecule of each subset under SuFEx catalysis are 28.5 (I), 1.0 (II, reference), 14.1 (III), and 4.1 (IV), respectively (**SI Appendix, Figure S6**). Aryl sulfonyl fluorides (I), despite their own extreme resistance toward nucleophiles^{*}, top the SuFEx reactivity hierarchy among the four subsets, while aryl fluorosulfates (II) lie at the bottom.

Elastase (5 nM) was incubated with each entry of the primary SuFEx library (final compound concentration 200 μ M) for 10 min at room temperature prior to the addition of peptide substrate MeOSuc-AAPV-AMC (50 μ M). Increase in fluorescence was measured for 30 min at 30 sec intervals. The assay was well behaved, as evidenced by a Z' of 0.86, signal-to-background of ~3000:1, and a hit cutoff of >95% inhibition. Reasoning that a covalent inhibitor, which presumably targets a catalytic residue, should completely inactivate the enzyme at high compound concentration (200 μ M), a high threshold (95%) was chosen for hit identification. Under this criterion, the screen yielded 7 hits as probable covalent inhibitors (**Fig. 2A**, 6.7% overall hit rate and 23% hit rate within subset I). All 7 compounds belong to subset I, which suggests a rough cut off based on the S-link's inherent reactivity. After validation by NMR, LC-MS, and dose-dependent

response, benzene-1,2-disulfonyl fluoride (1) proved to be the leading candidate, inhibiting hNE with $IC_{50} = 3.3 \pm 1.0 \ \mu M$ (Fig. 2B,C).

The covalent inhibition of hNE by **1** was examined by high-resolution MALDI-TOF mass spectrometry (**Fig. 3A**). Incubation of **1** (exact mass 242) with hNE yielded a peak shift from the protein mass by ~223 Da. Increased mass corresponds to: (1) a single molecule of **1** covalently captured by hNE; (2) the loss of one hydrogen from the protease (possibly from the catalytic serine); (3) the loss of one fluorine from **1**.

We also subjected hNE to co-crystallization with **1** in order to corroborate the covalent binding. The structure was determined using molecular replacement with PDB ID 5adw and the cocomplex was refined to 2.33 Å resolution (**SI Appendix, Table S2**). Importantly the naïve Fo-Fc electron density maps contoured to 4 σ clearly position **1**, as a result of the strong diffraction of sulfurs (**Fig. 3B**). The aryl group of **1** is nestled into a hydrophobic pocket consisting of residues Phe192 and Val216 and the compound is covalently bound to the catalytic Ser195, as highlighted by continuous electron density and a bond distance of ~1.6 Å (**Fig. 3C,D**). The covalent inhibition of hNE *via* sulfonylation by **1** appeared to be permanent—dialyzing away small molecules after incubation did not recover enzyme function (**SI Appendix, Figure S2**).

Considering the mono-covalent attachment mode of **1**, with the second $-SO_2F$ intact, it was envisaged that one of the two sulfonyl fluoride groups could be substituted so as to perhaps improve the capture rate, and/or selective binding. A set of benzenesulfonyl fluoride cores carrying *ortho*-substituents (**8–23**) was therefore examined. Compounds **8–18** were synthesized by the efficient aqueous potassium bifluoride exchange procedure from commercially available sulfonyl chlorides but showed poorer reactivity/binding with hNE[#]. Of the two improved compounds found in **Table 1**, **19**, the mono-vinylogous derivative of **1**, was a more active inhibitor with $IC_{50} = 2.2 \pm 0.7 \mu M$. The *ortho*-sulfamoyl benzenesulfonyl fluorides (**20**, **21**) led to considerably lower activity. A recently developed potassium bifluoride catalyzed SuFEx trifluoromethylation of aryl sulfonyl fluorides (**7**9) enabled us to quickly convert **1** to the perfluoroalkyl sulfones (22, 23). Compound 22 with the *ortho*-triflyl group emerged as the best lead molecule to date with $IC_{50} = 1.1 \pm 0.1 \mu M$.

	₩ [°] R		
Compound	R	IC ₅₀ (µM)	-
1	SO ₂ F	3.3 ± 1.0	-
8	F	~120	
9	CI	82 ± 16	
10	Br	20 ± 10	
11	Ι	9.7 ± 1.2	
12	Ме	>200	
13	OMe	73 ± 4	
14	CN	13.3 ± 0.5	
15	CF ₃	60 ± 8	
16	NO ₂	20 ± 1	
17	CO ₂ Me	37 ± 2	
18	Ph	27 ± 1	
19	rrun SO ₂ F	2.2 ± 0.7	
20	ξ−s−n 0 0	84.4 ± 0.6	
21	₹-S-N N-S-F	>200	
22	SO_2CF_3	1.1 ± 0.1	
23	SO ₂ (CF ₂) ₂ CF ₃	48 ± 2	

SO₂F

Table 1. Efforts of optimization of lead compound 1 with alternative ortho-substitutions.

High resolution MALDI-TOF mass spectrometry study supports the covalent inhibition mechanism of **22** to be sulfonylation of hNE (+ ~273 Da) possibly at its active site serine (**Fig. 4A,B**). In contrast, the incubation of compound **22** with inactive denatured hNE led to no detectable covalent modification of the enzyme (**Fig. 4C**). The requirement for the naturally folded enzyme represents another example of the unusual "sleeping beauty" phenomenon of SuFEx, wherein the sulfur fluoride probes are inert in biological fluids/buffer if the capture protein or proteins presented are denatured (24, 32).

Intriguingly, testing the lead compounds (**1**, **19**, **22**) against a panel of serine proteases, we found that two (**1**, **22**) among the three effective hNE inhibitors did not inactivate the homologous serine protease, human cathepsin G (hCG), which has 37% sequence identical to hNE and highly similar crystal structure (root-mean-square deviation (rmsd) = 0.82 Å, max rmsd = 5.89 Å for 180 out of 218 C α residues of hNE). Unlike PMSF (PhCH₂SO₂F) long known for ablating the hydrolytic activity of almost all serine proteases, the compounds **1** and **22** identified in this study showed 58 and 182-fold specificity for hNE over hCG, respectively (**Table 2**). The selective inhibition of hNE could be partly attributed to a proximity factor as suggested by molecular modeling using a reactive docking protocol (**SI Appendix, Figure S5**).

Compound	Structure	hNE IC₅₀ (µM) [∥]	hCG IC₅₀ (µM) [∥]	S**
1	SO ₂ F SO ₂ F	3.3 ± 1.0	190 ± 40	58
19	SO ₂ F SO ₂ F	2.2 ± 0.7	6.0 ± 0.7	2.7
22	SO ₂ F SO ₂ CF ₃	1.1 ± 0.1	>200	>182



 Table 2. Selectivity of the most potent compounds 1, 19, 22 against hNE and hCG.

To conclude, we have demonstrated a SuFEx library-enabled approach to discover covalent deactivators of an enzyme's function, the protein at hand being human neutrophil elastase. Its structure is known, including complexed with reversible inhibitors in the active site, but the library of sulfonyl fluorides used in the screen was chosen without regard to any enzyme•potential ligand relationships. In other words, agnostic of structural considerations, the library yielded two more examples of the "sleeping beauty" phenomenon, and in this instance its successful outcome is distinguished by lack of known design elements around the pendant S–F electrophiles on the candidate "ligand" scaffolds. This successful sulfur fluoride library is being used and augmented regularly at Scripps Research, and it will hopefully contribute to future SuFEx-driven covalent drug discovery endeavors.



Fig. 1. Overview of SuFEx-enabled covalent drug discovery. (A) The "sleeping beauty" phenomenon: sulfur fluoride probes only capture a naturally folded protein where a nucleophilic sidechain (Nu) and activating sidechains (Act) are correctly positioned. (B) Cartoon schematic of the SuFEx-enabled covalent drug discovery process. (C) Efficient SuFEx derivatization of abundant building blocks yields a SuFExable library with four subset groups, categorized according to their sulfur-fluoride based functionalities.



Fig. 2. Screen of the primary SuFEx library toward elastase inhibitory activity. (A) Initial screen with 105 SuFExable compounds yielded 7 hits with >95% inhibition at 200 μ M. (B) Dose-response curves of hit compounds against hNE (AAPV-AMC fluorescence assay). Each compound was assessed over a two-fold logarithmic dilution series. (C) Structures and IC₅₀ values of compounds **1–7** and PMSF (phenylmethane sulfonyl fluoride). IC₅₀ values were measured based on 10 min incubation and are shown in mean ± SD (n ≥ 3).



Fig. 3. Compound **1** is a covalent inhibitor of hNE. (A) MALDI-TOF mass spectrometry evidence of covalent complex **1**:hNE formation. (B) Naïve Fo-Fc map contoured at 1.5σ (green) and 4σ (magenta) clearly delineate the binding orientation of **1** to Ser195 and the specific location of the sulfur groups, respectively. Residue of **1** is shown as a stick model with yellow carbon, red oxygen, light blue fluorine, mustard sulfur. (C) Active site residues that provide potential hydrogen bonds (black dashes), repulsive interactions (brown dash), and hydrophobic residues that bind **1** (grey elastase carbon, nitrogen blue). (D) Schematic of bond distances between **1** and elastase with potential hydrogen bonds (black dashes) and negative repulsive interactions (brown dash) with bond distances in Å. The covalent bond (red) between Ser195 and the sulfur of **1** were set at 1.57 Å during structure refinement.



Fig. 4. The "sleeping beauty" phenomenon of sulfonyl fluoride **22** demonstrated by the MALDI-TOF mass spectra of (A) naturally folded hNE; (B) naturally folded hNE incubated with **22**; (C) denatured hNE (boiled) incubated with **22**.

Footnotes:

*SuFExable are defined to describe those compounds containing a sulfur fluoride link that can undergo SuFEx reaction.

[†]For example, no reaction occurred in the neat mixture of refluxing benzenesulfonyl fluoride (4 mL, ~33 mmol) and aniline (45 mL, ~500 mmol) at 184 °C for 3 h. Under the same conditions, electrophiles commonly studied as covalent "warheads" in medicinal chemistry including epoxide, acrylamide, vinyl sulfone, chloroacetamide, chloromethyl ketone, β-lactam, maleimide, and fluorophosphate are not stable. (**SI Appendix, Table S3**).

[‡]As long as the accelerating AA sidechains (including but not limited to His57) and reactive moiety (Ser195) are separately considered, and the former remain overall unchanged, the intramolecular activation mode can be seen as "catalytic", even if the TON equals 1. For a similar case, see: Kassem S, *et al.* (2017) Stereodivergent synthesis with a programmable molecular machine. *Nature* 549(7672):374-378.

[§]"Sleeping beauty" here defines the phenomenon of the remarkable acceleration of a SuFEx reaction for otherwise very stable higher valent sulfur fluoride compounds, by the right, naturally folded protein catalyst for its own covalent capture. The term has been used by Izsvák and coworkers in molecular biology to describe the use of a specifically designed transposon system (i.e. Tc1/mariner-type transposase and transposon) that can selectively insert genes into the genomes of vertebrates. The genome of humans as well as of other mammals encodes for non-functional transposases and the introduction of an active transposase from lower vertebrate fish and amphibian species "awakens the system from an evolutionary sleep". For the original paper on sleeping beauty transposon, see: Ivics Z, Hackett PB, Plasterk RH, & Izsvak Z (1997) Molecular reconstruction of Sleeping beauty, a Tc1-like transposon from fish, and its transposition in human cells. *Cell* 91(4):501-510.

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[#]At the time of manuscript preparation, Murthy and co-workers reported a study on 2nitrobenzenesulfonyl fluoride (**19**) and derivatives as covalent capture agents for new antibiotics development. Compound **17** showed only moderate inhibitory potency in our elastase activity assay. For Murthy's paper, see: Sadlowski C, *et al.* (2018) Nitro sulfonyl fluorides are a new pharmacophore for the development of antibiotics. *Mol Syst Des Eng* 3(4):599-603.

||IC₅₀ values were measured based on 10 min incubation and are shown in mean ± SD (n ≥ 3).

**S value denotes the selectivity, defined by the ratio of IC₅₀ (hCG) over IC₅₀ (hNE).

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