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Targeting Host Cell Furin Proprotein Convertases as a Therapeutic Strategy against Bacterial Toxins and Viral Pathogens*[S]

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Sergey A. Shiryaev[‡1], Albert G. Remacle[‡1], Boris I. Ratnikov[‡1], Nicholas A. Nelson[§], Alexei Y. Savinov[‡], Ge Wei[‡], Massimo Bottini[‡], Michele F. Rega[‡], Amelie Parent[¶], Roxane Desjardins[¶], Martin Fugere[¶], Robert Day[¶], Mojgan Sabet[‖], Maurizio Pellecchia[‡], Robert C. Liddington[‡], Jeffrey W. Smith[‡], Tomas Mustelin[‡], Donald G. Guiney[‖], Michal Lebl[§], and Alex Y. Strongin[‡2]

From the [‡]Burnham Institute for Medical Research, La Jolla, California 92037, [§]Illumina, Inc., San Diego, California 92121, the Department of Pharmacology, [¶]University of Sherbrooke, Sherbrooke, Quebec, Canada J1H SN4, and the [‖]Department of Medicine, School of Medicine, University of California-San Diego, La Jolla, California 92093

Pathogens or their toxins, including influenza virus, *Pseudomonas*, and anthrax toxins, require processing by host proprotein convertases (PCs) to enter host cells and to cause disease. Conversely, inhibiting PCs is likely to protect host cells from multiple furin-dependent, but otherwise unrelated, pathogens. To determine if this concept is correct, we designed specific nanomolar inhibitors of PCs modeled from the extended cleavage motif TPQRERRRKKR ↓ GL of the avian influenza H5N1 hemagglutinin. We then confirmed the efficacy of the inhibitory peptides *in vitro* against the fluorescent peptide, anthrax protective antigen (PA83), and influenza hemagglutinin substrates and also in mice *in vivo* against two unrelated toxins, anthrax and *Pseudomonas* exotoxin. Peptides with Phe/Tyr at P1′ were more selective for furin. Peptides with P1′ Thr were potent against multiple PCs. Our strategy of basing the peptide sequence on a furin cleavage motif known for an avian flu virus shows the power of starting inhibitor design with a known substrate. Our results confirm that inhibiting furin-like PCs protects the host from the distinct furin-dependent infections and lay a foundation for novel, host cell-focused therapies against acute diseases.

Furin and related PCs are specialized serine endoproteases that cleave the multibasic motifs R*X*(R/K/*X*)R and transform proproteins into biologically active proteins and peptides (1). Structurally and functionally, furin resembles its evolutionary precursor: the prohormone-processing kexin of yeast *Saccharomyces cerevisiae*. Furin is currently the most studied enzyme of the PC family. Seven PCs (furin, PC2, PC1/3, PC4, PACE4, PC5/6, and PC7) have been identified in humans (2). Furin is expressed in all examined tissues and cell lines and is mainly localized in the trans-Golgi network. Some proportion of the furin molecules cycles between the trans-Golgi and the cell surface. Because of the overlapping substrate preferences and cell/tissue expression, there is redundancy in the PC functionality, albeit certain distinct functions of the individual PCs have also been demonstrated. Furin knockout, however, is lethal in mice (3).

In addition to normal cell functions, PCs,[3] including furin, are implicated in many pathogenic states, because they process to maturity membrane fusion proteins and pro-toxins of a variety of both bacteria and viruses, including anthrax and botulinum toxins and influenza A H5N1 (bird flu), flaviviruses, and Marburg and Ebola viruses (1). After processing by furin and the subsequent endocytic internalization in the complex with the respective cell surface receptor followed by acidification of the endosomal compartment, the processed, partially denatured, infectious proteins expose their membrane-penetrating peptide region and escape into the cytoplasm (4). The intact toxins and viral proteins are incapable of accomplishing these processes. Evidence suggests that the inhibition of cellular furin prevents aggressive disease (2, 5). These results lead to the logical suggestion that furin is a promising drug target in infectious diseases; an experimental confirmation, however, has been limited because research efforts have been focused primarily on anthrax (5–7). Because no natural protein inhibitors of furin are known, D-Arg-based peptides, α1-antitrypsin Portland, and the synthetic inhibitor decanoyl-Arg-Val-Lys-Arg-chloromethylketone (DEC-RVKR-CMK) are used *in vitro* and in cell-based tests (1, 2). Arg-based peptides such as hexa- and nona-D-Arg (8) have either low or no therapeutic potential because of their intrinsic ability to cross-react with multiple, pathogen and host, proteinase and non-proteinase targets, which are unrelated to furin (6, 9–11).

Here, we designed nanomolar peptide inhibitors modeled from the extended furin cleavage sequence of avian influenza A

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[S] The on-line version of this article (available at http://www.jbc.org) contains supplemental Tables S1 and S2.

[1] These authors contributed equally to this work.

[2] To whom correspondence should be addressed: Burnham Institute for Medical Research, 10901 North Torrey Pines Rd., La Jolla, CA 92037. Tel.: 858-713-6271; Fax: 858-646-3192; E-mail: strongin@burnham.org.

[3] The abbreviations used are: PC, proprotein convertase; Cipro, ciprofloxacin; DEC-RVKR-CMK, decanoyl-Arg-Val-Lys-Arg-chloromethylketone; HA, hemagglutinin; LF, lethal factor; PA, protective antigen; PEx, *Pseudomonas* exotoxin A; Pyr-RTKR-AMC, pyroglutamic acid-Arg-Thr-Lys-Arg-methylcoumaryl-7-amide; SiNPs, silica nanoparticles; MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide.

H5N1 (12–14). We then proceeded to demonstrate the efficacy of the inhibitory peptides in assays *in vitro* and in cell-based and animal tests. Our results suggest that furin antagonists can provide host protection against multiple furin-dependent, but otherwise unrelated pathogens.

MATERIALS AND METHODS

Reagents—Reagents were purchased from Sigma unless indicated otherwise. A TMB/M substrate and GM6001 were from Chemicon. The inhibitor DEC-RVKR-CMK was obtained from Bachem. The protease inhibitor mixture set III and the fluorescence peptide substrate pyroglutamic acid-Arg-Thr-Lys-Arg-methyl-coumaryl-7-amide (Pyr-RTKR-AMC) were obtained from Calbiochem. Sulfosuccinimidyl-6-(biotinamido)hexanoate (EZ-Link sulfo-NHS-Long Chain(LC)-biotin) was from Pierce. Anthrax PA83 and *Pseudomonas* exotoxin A were purchased from List Biological Laboratories. Recombinant human furin, PC5/6, PC4, and PC7, and rat PACE4 were prepared in the S2 *Drosophila* expression system (Invitrogen) and purified to homogeneity as described previously (15).

Expression and Purification of Avian Influenza A H5N1 HA—The ectodomain of HA was cloned into the baculovirus pAcGP67A transfer vector (BD Biosciences) to allow for secretion of the recombinant protein. To facilitate the yield of the HA precursor, the C-terminal region of the contract contained the bacteriophage T4 fibritin "foldon" trimerizing sequence, a thrombin cleavage site, and a His_6 tag (R*SLVPRGS*PGSGYIPE-APRDGQAYVRKDGEWVLLSTFLG**HHHHHH**; the thrombin site, the T4 foldon, and His tag sequences are italicized, underlined, and shown in bold, respectively). Infection of Sf9 insect cells and virus amplification were performed according to the manufacturer's instructions (BD Pharmingen). Infected cells (3×10^6 cells/ml infected at a multiplicity of infection equal to 1–3) were cultured in suspension for 3 days in 4 liters of sf900-II SFM serum-free medium (Invitrogen). Cells were then removed by centrifugation. The soluble HA was purified from the supernatant by metal affinity chromatography on an nickel-nitrilotriacetic acid column followed by the Mono Q fast-protein liquid chromatography and size-exclusion chromatography on a Superdex-200 10/30 column equilibrated with 10 mM Tris-HCl buffer, pH 7.5, containing 80 mM NaCl. The yield of the purified HA trimer was 1.5 mg/liter of cell culture.

In Vitro Cleavage of PA83, HA, and PEx—PA83, HA, and *Pseudomonas* exotoxin A (PEx) were each labeled with EZ-Link sulfo-NHS-LC-biotin (at a 1:20 protein-biotin molar ratio) for 30 min on ice. Biotin-labeled PA83, PEx, and HA (500 ng each) were co-incubated for 3 h at 37 °C with furin, PC7, PACE4, PC4, and PC5/6 (one unit of activity each). One unit of activity is equal to the amount of the enzyme that is required to cleave 1 pmol/min of the Pyr-RTKR-AMC substrate at 37 °C. The 100 mM HEPES (pH 7.5), 20 mM Tris-HCl (pH 6.5), and 100 mM sodium acetate (pH 5.5) buffers were supplemented with 1 mM $CaCl_2$ and 0.5 mg/ml bovine serum albumin. The cleavage was stopped by adding a 5× SDS sample buffer. The digested samples were analyzed by Western blotting with ExtrAvidin conjugated with horseradish peroxidase and a 3,3′,5,5′-tetramethyl benzidine (TMB/M) substrate.

Binding and Processing of PA83 by Cultured Cells—Glioma U251 cells (3×10^5) were incubated for 3 h at 37 °C in serum-free Dulbecco's modified Eagle's medium supplemented with biotin-labeled PA83 (1 μg/ml). Where indicated, DEC-RVKR-CMK (20 μM) and the inhibitory peptides (2–20 μM) were added to the cells. After incubation, cells were washed and lysed in an radioimmune precipitation assay buffer (20 mM Tris-HCl, 150 mM NaCl, 0.1% SDS, 1% Triton X-100, 1% deoxycholate, 1% IGEPAL, pH 7.4) containing a protease inhibitor mixture set III, 1 mM phenylmethylsulfonyl fluoride, and 10 mM EDTA. To measure cell-associated PA83 and PA63, the samples were analyzed by Western blotting with ExtrAvidin conjugated with horseradish peroxidase and a TMB/M substrate.

Cytotoxicity Assay—Murine macrophage-like cells RAW 264.7 were grown to confluence in wells of a 48-well plate in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum (16). The cells were replenished with fresh medium (0.1 ml/well) and then incubated with inhibitors for 4 h. To protect the peptide from proteolysis *in vivo*, the TPRARRRKKRT peptide sequence was amidated at the C terminus and had β-Ala at the N terminus. Anthrax protective antigen-83 (PA83) and lethal factor (LF) were then added to the final concentrations of 500 ng/ml and 25 ng/ml, respectively. After incubation for an additional 1 h, cell viability was assessed by using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) staining. Cells were incubated with 0.5 mg/ml MTT in Dulbecco's modified Eagle's medium for 45 min at 37 °C; the medium was aspirated, and the blue pigment produced by the viable cells was solubilized with 0.5% SDS/25 mM NaCl in 90% isopropyl alcohol. The concentration of oxidized MTT in the samples was measured at 570 nm. Each datum point represents the results of at least three independent experiments performed in duplicate. The percentage of viable cells was calculated by using the following equation: (A_{570} of cells treated with LF, PA83, and inhibitor) − (A_{570} of cells treated with LF and PA83) (A_{570} of cells treated with LF alone) − (A_{570} of cells treated with LF and PA83). The TPRARRRKKRT peptide alone when incubated with cells in concentrations up to 0.5 mM had no effect on cell viability.

Animal Experiments with Anthrax Spores and Pseudomonas Toxin—To protect the peptide from proteolysis *in vivo*, the TPRARRRKKRT peptide sequence was amidated at the C terminus and had β-Ala at the N terminus. Purification of anthrax spores and the inhalation model of anthrax using A/J mice was described previously (17, 18). A/J mice (8 mice/group) received *B. anthracis* Sterne spores (4×10^5/animal in 20 μl of phosphate-buffered saline). On the day following infection, mice received the TPRARRRKKRT peptide (12.5 mg/kg intraperitoneal) in phosphate-buffered saline and then continued to receive injections once daily for the remainder of the experiment. Control mice received an equal volume of phosphate-buffered saline. Mice treated with ciprofloxacin (Cipro) received 25 mg/kg subcutaneous treatments daily beginning on the fourth day following infection.

C57/BL6 mice (5 mice/group) received one intramuscular injection of PEx (500 ng/animal, 2× LD_{50}) (19). Mice received one injection of the TPRARRRKKRT peptide (12.5 mg/kg intraperitoneal) either 24 h prior to toxin injection or simulta-

neously with toxin injection. An additional group of mice, after receiving one injection of the peptide 24 h prior to toxin injection, continued to receive daily injections of the peptide for the remainder of the experiment.

Peptides Synthesis—A 96-well format centrifugal synthesizer and purification and characterization of the peptides were described earlier (20–22). Peptide synthesis was performed in wells of a 96-well flat bottom polypropylene microtiter plate (Evergreen Scientific). The peptides were amidated at the C terminus. In addition to the C-end amidation, peptides used for their attachment to silica nanoparticles (SiNPs) exhibited hydroxylaminoacetic acid at the N terminus (prepared by attachment of *t*-butoxycarbonyl-NHOCH$_2$-COOH at the last step of the synthesis). The purity of the peptides was confirmed by use of reversed-phase high-performance liquid chromatography and by mass spectrometry.

The peptide for the cell-based assays and *in vivo* studies was synthesized manually in a plastic syringe equipped with a frit (CSPS Pharmaceuticals) using Rink resin (1 g, 0.45 mmol/g, Novabiochem). Diisopropylcarbodiimide was used for coupling (2 × 1 h) and 20% 4-methylpiperidine (20, 23) for Fmoc (*N*-(9-fluorenyl)methoxycarbonyl) group deprotection. Final deprotection and cleavage from the resin was performed by using Mixture K (82.5% TFA, 5% phenol, 5% H_2O, 5% thioanisoee, 2.5% ethanedithioe) (24). The peptide sample was precipitated and washed (5×) in ether, dissolved in 0.1 M HCl, and lyophilized. The peptide was then dissolved in 10 ml of 0.1 M HCl and purified on a Sephadex LH-20 column equilibrated in 0.1 M HCl. Fractions containing the peptide were pooled and lyophilized. High-performance liquid chromatography (μBondapak C18, Waters, 10-μm particles, 125-Å pore size, 3.9 × 150 mm, gradient 0.05% trifluoroacetic acid in H_2O to 40% acetonitrile, 0.05% trifluoroacetic acid in 15 min, flow rate 1.5 ml/min, detection by UV at 217 nm) of the peptide determined the purity of the material to exceed 95%. Mass spectrometry analysis of the synthesized peptide confirmed the identity of the product (calculated molecular weight, 1495.81; found M + H, 1497).

Protease Assays with Fluorescence Peptides—The assay for PC activity was performed using a Pyr-RTKR-AMC substrate (24 μM). The concentrations of the catalytically active proteinases were measured using a fluorescence assay by titration against a standard DEC-RVKR-CMK solution of a known concentration. The buffer for furin cleavage reactions was 100 mM HEPES, pH 7.5, containing 1 mM $CaCl_2$ and 0.5 mg/ml bovine serum albumin. The buffer for PACE4, PC4, PC5/6, and PC7 was 20 mM Tris-HCl, pH 6.5, supplemented with 1 mM $CaCl_2$. The total assay volume was 0.1 ml. Enzyme concentrations were 10 nM. Increasing concentrations of the inhibitory peptides were preincubated with the enzymes for 30 min. The steady-state rate of substrate hydrolysis was monitored continuously (λ_{ex} = 360 nm and λ_{em} = 460 nm) using a fluorescence spectrophotometer at 37 °C. The IC_{50} values were derived from fitting the V_0 *versus* log $[I]_t$ plots with sigmoidal dose-response curves, and the inhibition constant (K_i) was derived using the Cheng-Prusoff equation: $K_i = IC_{50}/(1 + [S]/K_m)$, where V_0 is the steady-state velocity of substrate hydrolysis, $[I]_t$ is the total inhibitor concentration, [S] is the substrate concentration, K_m is the Michaelis-Menten constant, and K_i(app) is the apparent inhibition constant.

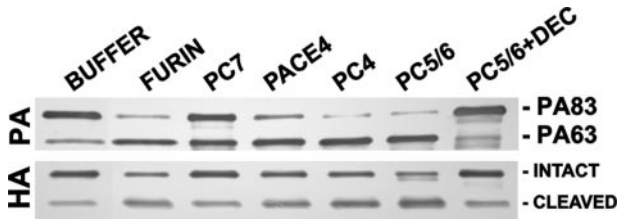

FIGURE 1. **Processing of PA83 and the HA precursor by furin and related PCs.** PA83 and HA precursor (HA0) (500 ng each) were cleaved by furin and PCs (1 activity unit each), and the reactions were analyzed by gel-electrophoresis. *DEC*, DEC-RVKR-CMK (20 μM).

Preparation of SiNPs and Immobilization of Peptides—A cyclohexane, Triton X-100, and *n*-hexanol 24.8-ml mixture (volume ratio, 4.2:1:1) was converted to a nanoemulsion by stirring at room temperature for 1 h. Water (940 μl) and tetramethyl orthosilicate (100.5 μl) were added. The mixture was sonicated for 1 h to facilitate the diffusion of tetramethyl orthosilicate into the encapsulated water droplets in the nanoemulsion. 28% NH_3 in water (59 μl) was added to catalyze the hydrolysis of tetramethyl orthosilicate and condensation to form the SiNPs. The reaction mixture was stirred for 24 h, followed by the addition of tetramethyl orthosilicate (10.05 μl) and then, in 30 min, aminopropyl trimethoxysilane (11.8 μl). The mixture was stirred for an additional 24 h, and then the amino-SiNPs were precipitated by 25-ml acetone washed with water and anhydrous ethanol. The presence of amino groups on SiNPs was confirmed by using fluorescamine in methanol followed by sonication of the sample for 5 min at room temperature and fluorescence analysis (λ_{ex} = 390 nm, λ_{em} = 475 nm). An aliquot of SiNPs in ethanol was placed on the lacey carbon film covering a 300-mesh copper grid (Ted Pella), and ethanol was then allowed to evaporate. Transmission electron microscopy images showed the uniform, 15 ± 1 nm diameter, amino-SiNPs. Because the density of the SiNPs is equal to pure silica (1.96 g/cm^3), the molecular weight of SiNPs was calculated to be 2000 kDa. 4-Formylbenzoyl chloride/triethylamine (1:3 molar ratio) was allowed to react with amino-SiNPs in dimethyl formamide for 40 min at 0 °C and then at room temperature overnight. Aldehyde-SiNPs were separated by the addition of water to the sample and extensively washed in water. To accomplish the binding of the peptides to aldehyde-SiNPs, a suspension of aldehyde-SiNPs (~0.2 mg/0.1 ml) was co-incubated for 48 h in a shaker with 1 mM solution of the peptides (which exhibited a hydroxylamine group) in 1 M citrate buffer, pH 5.1-Me_2SO mixture (1:1, v/v). Beads were then centrifuged and washed with water.

RESULTS

Derivatization of the Furin Cleavage Sequence—Furin and related PCs are directly implicated in many pathogenic states, because they process membrane fusion proteins and pro-toxins of a variety of pathogenic bacteria and viruses, including anthrax and the highly pathogenic H5N1 avian influenza. Our results show that both PA83 and the HA precursor (HA0) from the H5N1 influenza virus (13, 14) are sensitive to the processing by several individual PCs as opposed to furin alone (Fig. 1).

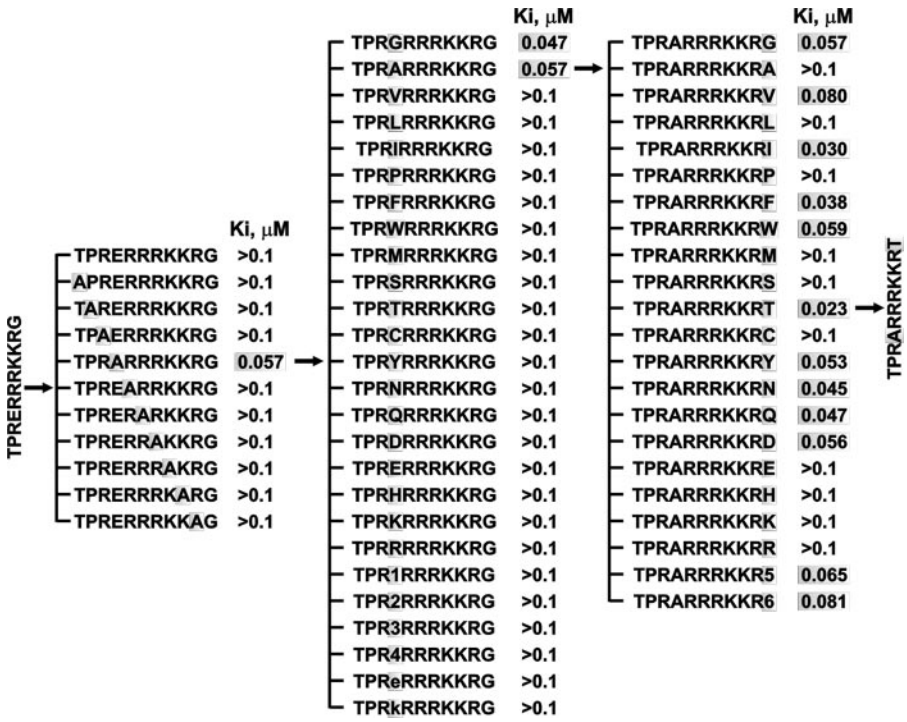

FIGURE 2. **Peptides derived from the cleavage motif of HA inhibit furin and related PCs.** Peptide sequence and the K_i values of the peptides against furin. Peptides exhibited the free N terminus, whereas the C terminus was amidated. The assay for PC activity was performed using a Pyr-RTKR-AMC substrate. Mutant amino acid positions and the most efficient K_i values are shown in *brackets*. *E*, D-Glu; *K*, D-Lys; *1*, β-Ala; *2*, ϵ-aminohexanoic acid; *3*, aminocyclopentanecarboxylic acid; *4*, citrullin; *5*, Cys(Me); and *6*, Nle.

TABLE 1

K_i values of the inhibitory peptides against PCs

The assay for PC activity was performed using a Pyr-RTKR-AMC substrate. The varied C-terminal amino acid is underlined.

Peptide	K_i				
	Furin	PACE4	PC4	PC5/6	PC7
			μM		
TPRARRRKKRI	0.030	0.267	0.562	0.492	0.135
TPRARRRKKRT	0.023	0.162	0.441	0.232	0.152
TPQRARRRKKRT	0.033	0.296	0.515	0.188	0.206
TPQRARRRKKRW	0.034	0.192	0.952	0.433	0.172
TPQRARRRKKRF	0.038	0.602	0.772	0.806	1.133
TPQRARRRKKRY	0.047	1.020	0.624	0.649	1.220

PA83 was converted to PA63 by furin and also by PC4 and PC5/6 (1 activity unit each) with an ~90% efficiency, whereas PACE4 and PC7 (1 activity unit each) accomplished a PA83-to-PA63 conversion with an ~70 and 40% efficiency, respectively. Both furin and PC5/6 were efficient in cleaving HA, whereas PACE4 and PC4 and, especially PC7, were much less efficient.

The pathogenicity of H5N1 correlates with the extended furin cleavage motif, TPQRERRRKKR↓GL, within the HA sequence (12). Following furin cleavage, the resulting activated HA becomes competent to initiate fusion with the host membrane. We used the extended furin cleavage sequence of HA as the starting point to obtain uncleavable peptide sequences that competitively inhibit cleavage of a fluorescent peptide substrate by furin (15). Alanine-scanning mutagenesis using single, double, and triple substitutions (A, AA, and AAA, respectively) was used to modify the peptide sequence. The inhibitory potency of the synthesized peptides was measured in the cleavage reaction with a fluorescent peptide substrate. The presence of the Gln residue at position P9 of the TPQRERRRKKRG cleavage motif was not necessary for inhibition. Mutagenesis of TPRERRRKKRG led us to a potent inhibitor of furin (TPRARRRKKRG, K_i = 57 nM). The sequences and the K_i values of the peptides are shown in Fig. 2, Table 1 and in supplemental Table S1. The inhibitory potency of TPRARRRKKRG against furin and other purified PCs (PACE4, PC4, PC5/6, and PC7) was improved further by substitution of the P1′ C-terminal glycine by several other amino acid residues, including threonine (TPRARRRKKRT, K_i = 23 nM) (Fig. 2 and supplemental Table S2). Other PCs (PACE4, PC4, PC5/6, and PC7) were also inhibited but with less efficiency (Table 1). Overall, peptides with aromatic C-terminal residues (Phe or Tyr) were more selective for furin, whereas TPQRARRRKKRT and TPRARRRKKRT were potent pan-inhibitors of PCs (K_i = 150–300 nM) (Table 1). Co-incubation of the peptides with furin followed by mass spectrometry analysis showed that the inhibitory peptides were resistant to furin proteolysis (not shown).

Cell-based and in Vivo Activity Tests—We next determined if the HA-derived peptides could inhibit intoxication by two unrelated pathogens, anthrax and *Pseudomonas* toxins. Host cleavage of anthrax PA83 by PCs is a prerequisite for the translocation of the toxic enzymes, LF and edema factor, into the host cell cytosol (4). It is well established that, following its binding with the cell receptor, furin cleavage of PA83 occurs directly at the cell membrane rather than in the intracellular milieu (25). In our tests, U251 cells, which in addition to furin, PC5/6, and PC7 express sufficient levels anthrax toxin receptor (26), were allowed to bind and process PA83. The amounts of cell-associated PA83 and PA63 were determined by Western blotting.

Thus, using a cell-based assay in U251 cells, we determined that at a 20 μM concentration TPRARRRKKRX peptides with C-terminal Phe, Trp, Thr, and Tyr accomplished a near complete inhibition of PA83 processing by cellular PCs (Fig. 3*A*). Consistent with inactivation of cell surface PCs and subsequent PA83 processing, the TPRARRRKKRT peptide inhibited delivery of the PA63·LF complex into the cytosol and protected cells from LF-induced cytotoxicity (Fig. 3*B*) with an efficiency similar to that of GM6001 (16). Because of its inhibitory activity (27), GM6001, a hydroxamate inhibitor of the LF metalloproteinase (2–5 μM), also rescued cells from LF intoxication and was used as a control. The peptide alone at concentrations ≤0.5

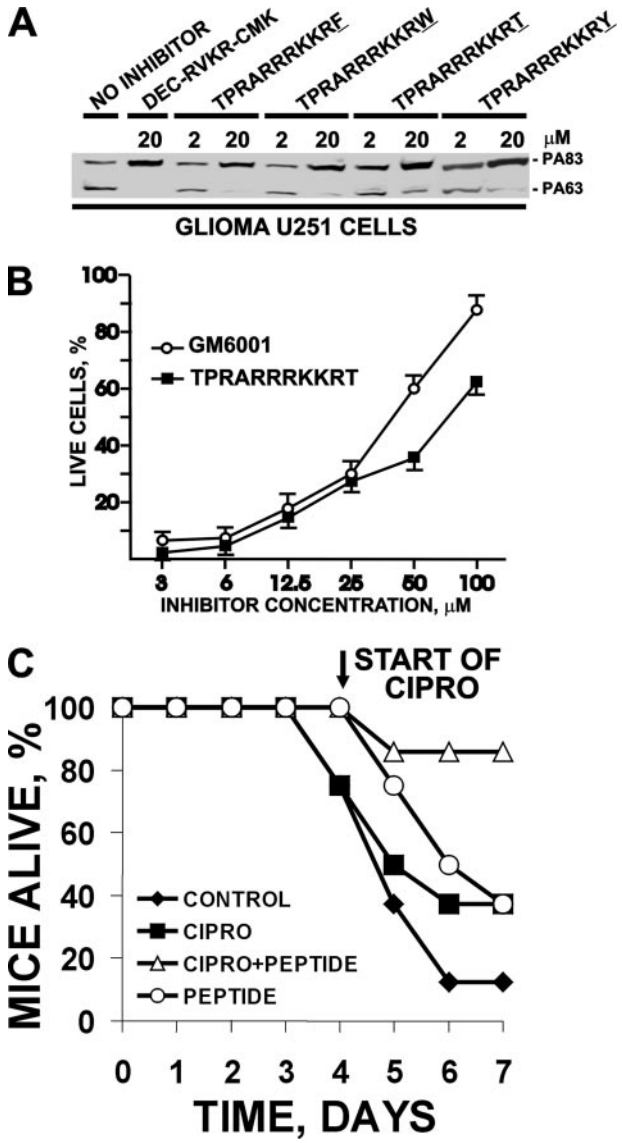

FIGURE 3. **Peptides derived from the cleavage motif of HA inhibit PC-dependent processing of PA83 in cell-based assays and protect mice from post-exposure inhalation anthrax.** *A*, peptides inhibit the processing of PA83 (1 μg/ml) in glioma U251 cells. *B*, peptide inhibitors protect macrophage RAW264.7 cells against PA-LF cytotoxicity. Cells were co-incubated with PA83 (400 ng/ml) and LF (25 ng/ml). Indicated concentrations of the inhibitors were added to the cells. The residual viable cells were measured by adding MTT. To protect the peptide from proteolysis, the TPRARRRKKRT peptide sequence was amidated at the C terminus and had β-Ala at the N terminus. *C*, the β-Ala-TPRARRRKKRT-amide peptide and Cipro protect A/J mice from anthrax. Mice (8 animals/group) were infected intranasally with 4×10^5 *B. anthracis* Sterne spores. Treatment with the peptide (12.5 mg/kg intraperitoneal) was started 24 h post-exposure and continued for the next 6 days. On the fourth day following infection, mice were given daily injections of Cipro (25 mg/kg subcutaneously). Untreated mice were used as a control. The Cipro plus peptide group had the longest survival time (mean ± S.E. 7.00 ± 0.18 days), followed by the peptide group (6.63 ± 0.14 days), the Cipro group (6.00 ± 0.17 days), and the control group (5.38 ± 0.14 days).

mM displayed no toxicity and had no effect on cell viability (not shown).

We next tested the peptide in a mouse model of inhalation anthrax. A/J mice (8 mice/group) received *B. anthracis* Sterne spores (4×10^5/animal). On the day following infection, mice received the TPRARRRKKRT peptide (12.5 mg/kg intraperitoneal) and then continued to receive injections once daily for the remainder of the experiment. Mice treated with antibiotic Cipro received 25 mg/kg subcutaneous treatments daily beginning on the fourth day following infection. This post-exposure peptide plus Cipro regimen protected 90% of the infected mice from disease, compared with 40% using either the peptide or Cipro alone (Fig. 3*C*).

We carried out a similar set of experiments with an unrelated toxin, *Pseudomonas* exotoxin A, the processing of which occurs in the intracellular milieu. Consistent with the earlier data (28–30), PEx was resistant to PC cleavage at pH 7.5 but following unfolding at pH 5.5 PEx (66 kDa) was readily processed by furin, PC4, and PC5/6 to produce the 28-kDa N-terminal fragment and the toxic 37-kDa C-terminal fragment (Fig. 4*A*). As expected, furin proteolysis of PEx was inhibited by the TPRARRRKKRT peptide in the cleavage reaction *in vitro* (data not shown). To demonstrate the efficacy of the peptide *in vivo*, C57/BL6 mice (5 mice/group) received one intramuscular injection of PEx (500 ng/animal, $2\times$ LD_{50}) (19) and one injection of the TPRARRRKKRT peptide (12.5 mg/kg intraperitoneally) either 24 h prior to toxin injection or simultaneously with toxin injection. Another group of mice, after receiving one injection of the peptide 24 h prior to toxin injection, continued to receive daily injections of the peptide for the remainder of the experiment. Daily injections of the peptide provided protection (60% survival) from the lethal action of PEx, demonstrating efficacy against a second, otherwise unrelated, furin-dependent pathogen (Fig. 4*B*).

Immobilization on the Peptides on Silica Nanoparticles—Given that cell surface-associated PCs in bronchial epithelial cells are the first to encounter inhaled pathogens, we suggest the development of an inhalation drug that could be used for acute treatment or for prophylactic use in civilian or battlefield settings. We investigated peptide immobilization on SiNPs, which have been widely used for biosensing and catalytic applications (31, 32). When peptides with either the GGG or the GGGGGG and GAGAGA linkers were immobilized on 15 nm diameter 4-formylbenzoyl chloride-activated SiNPs with a density of ~100 peptide molecules/particle (Fig. 5), the inhibitory efficacy of the immobilized peptides against furin was similar on a molar basis to that of the soluble peptides. Immobilization without a linker reduced the inhibitory efficacy (Table 2). Similar to soluble peptides, the immobilized TPRARRRKKRT peptide inhibited PA83 processing by furin (Fig. 6). SiNPs showed no cell toxicity, even at high concentrations (*e.g.* 50 nM SiNPs (3×10^{17} SiNP particles)/100,000 cells).

DISCUSSION

Furin is a multidomain protease of animal cells, the catalytic domain of which is similar in structure to bacterial subtilisin. Furin is enriched in the Golgi apparatus and also on cell surfaces where it functions to cleave a number of functionally important cellular proteins, including proteinases, integrins, signaling receptors, growth factors, hormones, and neuropeptides, into their respective mature forms. In addition to furin, six additional, albeit less characterized, furin-related PCs are known in humans. In addition to processing cellular precursor proteins, PCs are also utilized by a number of pathogens. Pathogens or their toxins, including viruses and bacterial toxins,

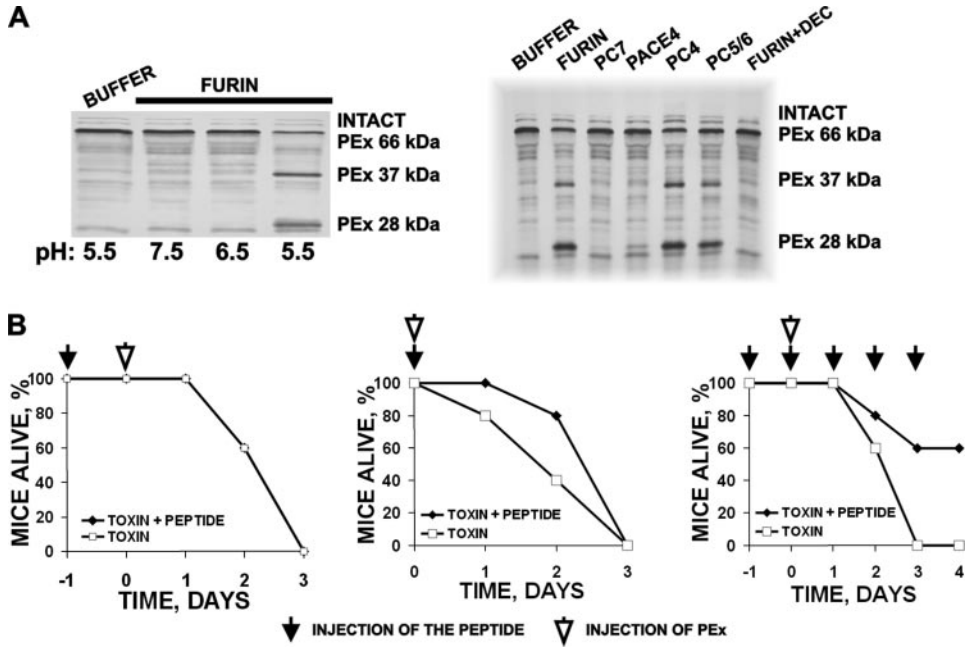

FIGURE 4. **The TPRARRRKKRT peptide protects mice from *Pseudomonas* PEx.** In *A*: *Left*, furin cleaves the exposed cleavage site of PEx at pH 5.5 to produce the 28-kDa N-terminal and the 37-kDa C-terminal fragments. *Right*, furin, PC4, and PC5/6 cleave PEx at pH 5.5. *DEC*, DEC-RVKR-CMK (20 μM). *B*, animal experiments with PEx and the TPRARRRKKRT peptide. *Left*, C57/BL6 mice (5 mice/group) received an injection of the peptide (12.5 mg/kg intraperitoneal) 1 day before injection of PEx (500 ng/animal, 2× LD_{50}). *Middle*, C57/BL6 mice (5 mice/group) received an injection of the peptide (12.5 mg/kg intraperitoneal) simultaneously with an injection of PEx (500 ng/animal). *Right*, C57/BL6 mice (5 mice/group) received an injection of the peptide (12.5 mg/kg intraperitoneal) 1 day before an injection of PEx (500 ng/animal) and then animals received daily injections of the peptide for the remainder of the experiment.

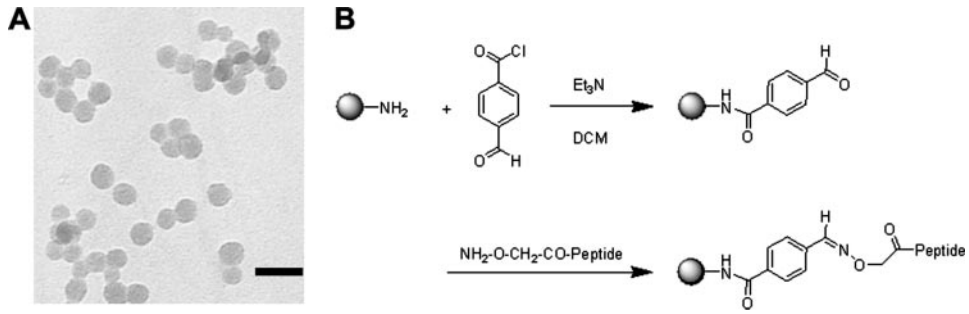

FIGURE 5. **SiNPs.** *A*, transmission electron microscope image of the amino-functionalized SiNPs. *Scale bar*, 30 nm. *B*, coupling of 4-formylbenzoyl chloride and peptide inhibitors to amino-SiNPs. *DCM*, dimethyl formamide; *Et_3N*, triethylamine.

TABLE 2

K_i values of the soluble and immobilized peptides against furin

The assay for PC activity was performed using a Pyr-RTKR-AMC substrate. The K_i values for SiNPs were calculated based on the total amount of the immobilized peptide. The K_i values based on the 2000-kDa molecular mass of the beads and the used concentrations of the beads were ~2000-fold less. The varied C-terminal amino acid is underlined.

	Peptide	N-terminal linker, K_i			
		None	GGG-	GGGGGG-	GAGAGA-
				μM	
Peptide alone	TPRARRRKKRT	0.023	0.039	0.066	0.047
	TPRARRRKKRF	0.038	0.067	0.045	0.056
	TPRARRRKKRY	0.047	0.042	0.054	0.057
	TPQRARRRKKRW	0.034	0.067	0.088	0.127
Peptide on nanobeads	TPRARRRKKRT	4.9	1.99	2.32	2.57
	TPRARRRKKRW	3.85	4.28	9.09	ND[a]

[a] ND, not determined.

exploit host PCs to become fully functional and to allow entry into host cells and to cause disease onset. The low pathogenicity viral subtypes have mutations in the cleavage site sequence and thus a reduced sensitivity to furin (12). Overall, proteolytic processing by furin is an important determinant in the pathogenicity of viruses and bacterial toxins.

To develop sharply focused and specific antagonists of pathogen entry, we developed nanomolar range peptide inhibitors of host cell furin and furin-related PCs. For these purposes, we modified the sequence of the extended furin cleavage sequence of avian influenza A H5N1 HA. HA is synthesized as a precursor molecule (HA0), which undergoes proteolytic processing into two subunits (HA1 and HA2), which are held together by disulfide bonds (33). Without proteolysis, the acid-triggered conformational change of HA that occurs in the endosomes and that exposes the fusion peptide cannot occur, and the virus is non-infectious.

The resulting competitive inhibitors TPRARRRKKRX with C-terminal Phe, Trp, Thr, and Tyr were highly potent not only against furin but also against related PCs, including PACE4, PC4, PC5/6, and PC7. These inhibitors were capable of efficiently inhibiting furin proteolysis of anthrax PA83 and avian influenza H5N1 HA *in vitro*. The peptide inhibitors protected cells from LF-induced cytotoxicity. Most importantly, we then confirmed the efficacy of the inhibitory peptides in mice *in vivo* against two unrelated toxins, anthrax and *Pseudomonas* exotoxin. Because cell surface-associated PCs in bronchial epithelial cells are the first to encounter inhaled pathogens, including influenza A H5N1 (bird flu), we developed an inhaled, nanoparticle-immobilized drug to minimize potential side-effects and optimize delivery. The specific furin inhibitors we designed are superior relative to D-Arg-peptides, which have been shown to cross-react with multiple host and pathogen targets, including both furin and anthrax lethal factor (6).

In summary, we have shown that peptides based on the cleavage motif of avian influenza H5N1 HA are efficient inhibitors of host cell furin and related PCs and that these inhibitors inhibit manifestation of toxicity by PC-depend-

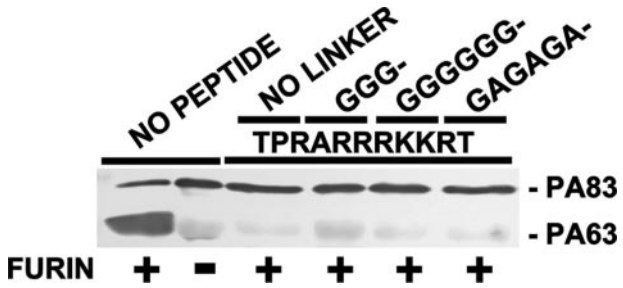

FIGURE 6. **SiNPs with the immobilized peptides inhibit furin.** SiNPs with the immobilized TPRARRRKKRT peptide inhibit furin processing of PA83 (500 ng). A 500 nM concentration of SiNPs (molecular mass, 2000 kDa) was used in the reactions.

ent, but otherwise unrelated, pathogens. Our results support and extend the earlier, albeit less conclusive, observations by other authors (6–9, 34). Because furin is likely essential for normal cell functions in adults, we suggest that our results represent a proof-of-principal from which novel, short-term therapeutics and prophylactics of furin-dependent acute disease pathogens, including anthrax, bird flu, Marburg, Ebola, and flaviviral infections will emerge (35).

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