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How Immune Peptidases Change Specificity: Cathepsin G Gained Tryptic Function but Lost Efficiency during Primate Evolution

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Cathepsin G is a major secreted serine peptidase of neutrophils and mast cells. Studies in Ctsg-null mice suggest that cathepsin G supports antimicrobial defenses but can injure host tissues. The human enzyme has an unusual “Janus-faced” ability to cleave peptides at basic (trypsin) as well as aromatic (chymotryptic) sites. Tryptic activity has been attributed to acidic Glu226 in the primary specificity pocket and underlies proposed important functions, such as activation of prourokinase. However, most mammals, including mice, substitute Ala226 for Glu226, suggesting that human cathepsin activity may be anomalous. To test this hypothesis, human cathepsin G was compared with mouse wild-type and humanized active site mutants, revealing that mouse primary specificity is markedly narrower than that of human cathepsin G, with much greater Tyr activity and selectivity and near absence of tryptic activity. It also differs from human in resisting tryptic peptidase inhibitors (e.g., aprotinin), while favoring primary specificity pocket and underlies proposed important functions, such as activation of prourokinase. Phylogenetic analysis reveals that the Ala226Glu missense mutation appearing in primates 31–43 million years ago represented an apparently unprecedented way to create tryptic activity in a serine peptidase. We propose that tryptic activity is not an attribute of ancestral mammalian cathepsin G, which was primarily chymotryptic, and that primate-selective broadening of specificity opposed the general trend of increased specialization by immune peptidases and allowed acquisition of new functions. The Journal of Immunology, 2010, 185: 000–000.

Cathepsin G is a nonclassical endopeptidase of granulated immune cells. It is highly expressed in mast cells and neutrophils and to lesser extents in monocytes and dendritic cells (1, 2). In human mast cells, cathepsin G is abundant in secretory granules that contain histamine, chymase and tryptases (3, 4). In neutrophils, it resides with elastase in azurophil granules, where it is released into phagolysosomes and helps to kill microbes (5, 6). Cathepsin G and elastase also are released extracellularly, where they can resist antiproteases, neutralize toxins, and kill bacteria (7, 8). High concentrations of uninhibited peptidase are present where neutrophils accumulate in large numbers, as in Pseudomonas-infected airways in humans with cystic fibrosis (9–11).

Cathepsin G belongs to a family of immune serine peptidases, with its closest relatives in humans being granzyme B and mast cell chymase. Genes for these enzymes arose by duplication and divergence of an ancestral chymase-like gene and are clustered on chromosome 14q11.2 (12, 13). Cathepsin G- and granzyme B-like genes separated early in evolution of placental mammals (13). Although phylogenetically related, these peptidases differ radically in substrate specificity. Human granzyme B has caspase-like affinity for substrate Asp residues (14), and chymase is chymotryptic, hydrolyzing after Phe, Tyr, Trp, or Leu (15). Cathepsin G is less selective, with unusual combined ability to hydrolyze chymotryptic and tryptic (especially Lys-containing) substrates (16–18). Tryptic activity is thought to be responsible for activating proteinase-activated receptors (19), C3 (17), and prourokinase plasminogen activator (20). Despite its tryptic activity, cathepsin G has an active site that differs from known tryptic serine peptidases, most of which, like trypsin and trypstatine, have a highly conserved “specificity triad” configuration of Asp189, Gly216, and Gly226 (chymotrypsin numbering). Crystal-derived structures of human cathepsin G (21) suggest that accommodation of basic side chains in tryptic substrates and inhibitors is due to Glu226 at the base of the primary specificity pocket. The side chain carboxylate of Glu226, which is nearly unique at this site among known peptidases, serves the charge–charge coupling function of Asp189 in classic tryptic peptidases. In a similar fashion, with flip-flopping of charges, Arg226 determines specificity for acidic side chains (Asp-ase activity) in granzyme B (14). Although human cathepsin G activity is exceptionally broad, it is also comparatively weak, with specificity constants (kcat/Km) toward its best substrates being much lower than those of chymase (16, 22). Some functions may be independent of proteolytic activity; indeed, cathepsin G-derived peptides have antibacterial properties (23). Nonetheless, peptidase-dependent properties include secretagogue, angiotensin II-generating, metallopeptidase-activating, and hepatocyte growth factor-inactivating functions (24–28).

Studies in Ctsg−/− mice suggest that cathepsin G is important for surviving fungal and bacterial infections, as from i.v. Aspergillus fumigatus (29) and Staphylococcus aureus (5). Immune

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Abbreviations used in this paper: Ang, angiotensin; hCG, human cathepsin G; mCG, mouse cathepsin G; n, norleucine; 4NA, 4-nitroanilide; N.I., no inhibition; prouPA, prourokinase plasminogen activator; suc, succinyl.
delicts are even more pronounced when cathepsin G deficiency is combined with deficiency of neutrophil elastase and may be due to ineffective microbial killing by neutrophils (5). Cathepsin G-deficient mouse neutrophils also respond defectively to activation by immune complexes (30). However, compared with wild-type mice, Ctg−/− mice have lower bacterial counts in a model of bacterial bronchitis produced by tracheal inoculation with *Pseudomonas aeruginosa*-embedded beads (31), suggesting that cathepsin G interferes with airway defenses (although without a demonstrated effect on inflammation or mortality). In a noninfectious model of renal ischemia-reperfusion injury, Ctg−/− mice are protected from death and have less inflammation and tissue damage (32). Thus, mouse models suggest that cathepsin G contributes to antimicrobial defenses and to survival postinfection but can harm the host and actually increase mortality. Recent data reveal that dual chymase–cathepsin G inhibitors reduce pathology associated with allergic and neutrophilic inflammation (33, 34).

Insights concerning contributions of human cathepsin G to host defense derive mostly from in vitro data. These studies suggest that the enzyme can contribute to host defense by cleaving bacterial virulence factors (35) or detract from host defense by inactivating antimicrobial collectins (36) and neutrophil chemokine receptors (11). Humans with Papillon-Lefèvre syndrome, which is characterized by hyperkeratosis and destructive periodontitis, are deficient in active cathepsin G and other immune peptidases (37, 38) due to defects in dipeptidyl peptidase I, which is the major activator of cathepsin G and related peptidases from proenzyme forms (39, 40).

The present study was prompted by structural comparisons of mouse and human cathepsin G suggesting that the mouse enzyme differs from the “dual-specificity” trypic–chymotryptic human enzyme in key specificity-determining residues, instead resembling chymotryptic mast cell chymases. These predictions regarding functions of the heretofore uncharacterized mouse enzyme were tested by comparing substrate preferences of recombinant wild-type and humanized mutant forms of mouse cathepsin G with those of human cathepsin G and by tracking evolution of primary specificity-determining amino acids in mammals from inferred ancestral forms. The findings suggest that mouse and ancestral mammalian cathepsin G, unlike the human enzyme, are purely chymotryptic and that a small number of active site mutations in primate ancestors of human cathepsin G dramatically altered activity, inhibitor sensitivity, and substrate specificity, causing, most notably, acquisition of trypsin-like ability to hydrolyze substrates after lysine residues and new targeting functions.

**Materials and Methods**

**Phylogenetic analysis**

Full amino acid sequences of cathepsin G not already published or annotated were obtained by data mining, including Basic Local Alignment Search Tool searches of high-throughput genome sequence and whole-genome shotgun databases at the National Center for Biotechnology Information (Bethesda, MD) using human and mouse cathepsin G genes and cDNAs as query sequences. Marmoset sequence (*Callithrix jacchus*, Contig 30.531) was obtained from a search of genomic sequence archived at the Washington University Genome Sequencing Center (St. Louis, MO). Previously unreported amino acid sequences of cathepsin G were predicted from genomic DNA using existing cathepsin G gene structures as a template following standard rules for placement of intron–exon boundaries. Cathepsin G amino acid sequences were aligned using Geneious software (Biomatters, Auckland, New Zealand). A likely evolutionary path was constructed from mutations in specificity triad codons using established branching dates for primate ancestors and presuming that mutations accumulated in a stepwise fashion. Specificity triad codons in ancestral mammalian cathepsin G were predicted by identifying the most parsimonious path from putative ancestral sequence to known extant mammalian cathepsin G sequences.

**Production of wild-type mouse cathepsin G**

Mouse cathepsin G catalytic domain cDNA was PCR-amplified from Integrated Molecular Analysis of Genomes and their Expression Consortium (http://image.hudsonalpha.org) clone BC125513 with the addition of an overhang sequence to permit ligation-independent cloning into pHE-3 (EMD Chemicals, Gibbstown, NJ). The original expressed construct containing an N-terminal GST tag was insoluble. Therefore, the GST sequence was removed from the plasmid by restriction digestion, and the signal sequence was ligated in-frame with the downstream enterokinase cleavage site using a linker. The resulting expression plasmid, after confirmation of sequence, was transfected into adherent S97 cells with Insect Gene Transfer (Novagen). Secreted recombinant procathepsin G was purified from supernatant collected from a 75 × 750 mm Heparin-5 PW column (Tosoh Bioscience, King of Prussia, PA) equilibrated in 20 mM Tris-HCl (pH 7.4) containing 50 mM NaCl and 2 mM CaCl2 with procathepsin G eluting at a concentration of ~450 mM NaCl. Peak fractions were desalted and concentrated to ~0.05 ml with 5k NMW centrifugal filters (Biomax) and incubated for 4 h at 25 °C with 0.16 U enterokinase (Novagen), which then was removed on a Mono S 5/5 HR cation exchange column eluted with a gradient of NaCl. Activated cathepsin G eluted at a concentration of ~900 mM NaCl.

**Production of humanized mutants of mouse cathepsin G**

Specificity site mutants were generated from the modified pLEX-3 wild-type mouse procathepsin G plasmid using QuikChange II site-directed mutagenesis kits (Agilent Technologies, Santa Clara, CA). Single-site mutant Ala226Glu was constructed using QuikChange-designed primers (http://www.stratagene.com/shmdesigner). Mutant plasmid sequence was verified in both directions. A Ser189→Ala/Ala226Glu double mutant then was generated using primers targeting the Ser189 codon on the Ala226Glu plasmid. Primers were as follows: Ala226Glu forward 5′-CAACAATGTT AACCTC-CAG AGGTAATCAC CAAAATCCAG AG-3′, reverse 5′-AAGCGAACAAT GTGAAACCTC CAGCTGTATT CACCAAAATC CAGAGCTT-3′. Other primers for this study are available on request. Determination of P1 substrate preferences

To determine the level of active peptidase, recombinant, purified wild-type mouse cathepsin G was titrated with human α1-proteinase inhibitor (α1-antitrypsin, EMD Chemicals) in PBS containing 0.01% Triton X-100 and 0.05% DMSO. Residual activity was measured by addition of cathepsin G substrate succinyl (suc)-L-Val-Pro-Phe-4-nitroanilide (4NA) (1 mM) and monitoring change in absorbance at 410 nm on a Synergy 2 microplate spectrophotometer (BioTek, Winooski, VT). The original expressed construct of mouse cathepsin G contained a cleavage site using a linker. The resulting expression plasmid, after confirmation of sequence, was transfected into adherent S97 cells with Insect Gene Transfer (Novagen). Secreted recombinant procathepsin G was purified from supernatant following standard rules for placement of intron–exon boundaries. A Ser189Ala/Ala226Glu double mutant then was generated using primers targeting the Ser189 codon on the Ala226Glu plasmid. Primers were as follows: Ala226Glu forward 5′-CAACAATGTT AACCTC-CAG AGGTAATCAC CAAAATCCAG AG-3′, reverse 5′-AAGCGAACAAT GTGAAACCTC CAGCTGTATT CACCAAAATC CAGAGCTT-3′. Other primers for this study are available on request. Determination of D1 substrate preferences

To probe the influence of the D1 residue at the site of hydrolysis, human (0.5 M) and recombinant mouse cathepsin G (0.5 M) were used to screen a >1-proteinase inhibitor (α1-antitrypsin, EMD Chemicals) in PBS containing 0.01% Triton X-100 and 0.05% DMSO. Residual activity was measured by addition of enzyme...
and monitored fluorometrically with excitation at 380 nm and emission at 450 nm.

Hydrolysis of synthetic substrates, angiotensin, casein, and prourokinase plasminogen activator

Chymotryptic and trypsinic activity of the enzymes first were compared using peptide, colorimetric substrates. Chymotryptic activity was assessed using N-terminally blocked peptide 4NAs with Phe in the P1 position at the site of hydrolysis. Standard assays monitored an increase in absorbance at 410 nm of 1 mM substrate at 37°C in PBS containing 0.01% Triton X-100 and 0.05% DMSO spectrophotometrically in 96-well plates. Turnover number \( k_{\text{cat}} \) and Michaelis constant \( K_{\text{m}} \) were calculated using Prism 5 software (GraphPad, La Jolla, CA) from substrate hydrolysis rates determined over a range of substrate concentrations bracketing \( K_{\text{m}} \). For selected substrates, kinetic constants also were determined in high ionic strength conditions (0.45 M Tris-HCl [pH 8], 1.8 M NaCl, and 10% DMSO). Tryptic activity was assessed using N-carbenzoyl-3-lys-thiobenzoylester (0.1 mM) at 37°C in PBS containing 0.01% Triton X-100 and 0.05% DMSO. Generation of free thiol by substrate hydrolysis was detected by inclusion of 0.1 mM 5, 5'-dithio-bis(2-nitrobenzoate) in the reaction mixture and monitoring the change in absorbance at 412 nm. Angiotensin-cleaving activity of wild-type mouse and human cathepsin G was compared with that of recombinant human mast cell chymase (produced as described in Ref. 43) by incubating enzymes with 19 mM angiotensin I for 40 min at 37°C in PBS containing 0.01% Triton X-100. Hydrolyzed fragments were detected by SDS-PAGE and staining with Coomassie brilliant blue. Human prourokinase plasminogen activator (prouPA; Landing Biotech, Newton, MA) activation by cathepsin G was detected via change in absorbance at 410 nm for 2 h at 37°C in PBS containing 0.01% Triton X-100, 0.05% DMSO, 10 mg/ml heparin (bovine lung; Sigma-Aldrich, St. Louis, MO), and 1 mM benzoyl-L-Val-Gly-Arg-4NA (Sigma-Aldrich), which is cleaved by active urokinase plasminogen activator but not by the forms of cathepsin G in this study.

Determination of inhibitor susceptibility

Inhibitory constants \( (K_i) \) for wild-type (Lys^189) aprotinin with mouse cathepsin G mutants and human cathepsin G were determined by assaying hydrolysis of 0.037–1 mM succ-t-Val-Pro-Phe-4NA in 0.45 M Tris-HCl (pH 8) containing 1.8 M NaCl and 10% DMSO in the presence of 12.5 and 25 mM aprotinin for mouse mutants and 1 and 2 mM Lys^189-apatinin for human cathepsin G. Observed \( K_m \) in the presence of each inhibitor was derived using Prism 5 software (GraphPad) by nonlinear regression fit of the velocity versus substrate concentration curve. \( K_i \) was calculated from observed \( K_m \) (\( K_{\text{m}} \) observed), and \( K_m \) was obtained without inhibitor according to the equation \( K_i = \frac{[I]}{K_m(\text{observed}/K_{\text{m}}) - 1} \), where \( I \) is the inhibitor concentration.

Results

Prediction of mammalian cathepsin G protein sequence

Twenty mammalian sequences containing the complete catalytic domain were identified by in silico translation of genomic sequence. No sequences identifiable as cathepsin G were found in DNA from nonmammalian genotypes. Accession numbers (http://www.ncbi.nlm.nih.gov/genbank/) for cathepsin G sequences identified and compared in this work (Fig. 1) are as follows: human NP_001099511; chimpanzee (Pan troglodytes) XP_522810; gorilla (Gorilla gorilla gorilla) CABD01205422; rhesus (Macaca mulatta) XP_001114339; galago (Otolemur garnettii) AAQ06159072; mouse (Mus musculus) NP_031826; Norway rat (Rattus norvegicus) NP_001099511; kangaroo rat (Dipodomys ordii) ABRO01262720; dolphin (Tursiops truncatus) ABRRN0179956; cattle (Bos taurus) XM_587908 (1) and XM_587826 (2); pig (Sus scrofa) XP_001926799; little brown bat (Myotis lucifugus) AAEPP1464601; cat (Felis catus) ACBE0102053; dog (Canis lupus familiaris) AAEX02019056; giant panda (Ailuropoda melanoleuca) ACTA01131456; tenrec (Echinosorex telfairi) AA01076445; rocky hyrax (Procavia capensis) ABQQ0119103; armadillo (Dasypus novemcinctus) AAGV020373271; and elephant (Loxodonta africana) AAGU03084767.

Human cathepsin G specificity triad is doubly mutated compared with that of ancestral cathepsin G

As shown by the mammalian sequences in Fig. 1, two of the three primary specificity-determining ["specificity triad" (46)] residues differ in human cathepsin G relative to those of nonprimate cathepsin Gs. In comparison with mouse cathepsin G specifically, human cathepsin G replaces Ser with Ala at position 189 and Ala with Glu at position 226. The third triad residue (Gly^216) is invariant. The mouse triad (Ser^189/Gly^216/Ala^226) is typical in that it matches cathepsin G consensus sequence at all three positions. It also matches the human chymase triad, even though chymase is less closely related in overall sequence than human cathepsin G and belongs to a distinct clade distinct from mammalian cathepsin G (45). As shown in Fig. 2, residue 189 and 226 codons reveal origins of differences between humans and extant mammals in these specificity-determining amino acids. The Ser^199Ala change is absent in our closest mammalian relative, the chimpanzee, and thus occurred within the past 7 million years, which is when humans and chimpanzees are thought last to have shared a common ancestor (47). The Ser^189Ala conversion resulted from a single change (T → G) in the first base of the Ser^189 codon, which is otherwise highly conserved. The T → A change at the same site in marmoset DNA, which yields a conservative Ser^189Thr change, appears to have arisen independently after separation of ape and new world monkey lineages. The more dramatic Ala^226Glu change occurred earlier in primate evolution than the Ser^189Ala change, because although the former mutation is observed in humans, chimpanzee, and old world monkey (rhesus macaque), it is absent from more distantly related primates (marmoset and galago) and from nonprimates. Compared to marmoset and galago, humans have a single change (C → A) in the second base of the Ala^226 codon causing missense conversion to Glu. Thus, Ala^226Glu conversion arose by point mutation in the primate lineage 31–43 million years ago, between the time humans last shared a common ancestry with old and new world monkeys, respectively (47). Mouse and rat cathepsin G have the same residues in positions 189 and 226 as most mammals, excepting humans, chimpanzees, and marmosets, as noted. However, the base in the wobble position for Ala^226 has undergone an A → T synonymous change (Fig. 2). Mice and rats form the only group of mammals with such
a change, which thus appears to have arisen independently. Similarly, domestic dogs and cats have a synonymous, independent change in the Ser189 codon. From the data summarized in Fig. 2, we conclude that ancestral mammalian cathepsin G had the following specificity triad amino acid sequence and codons: Ser189 (TCT)/Gly216 (GGA)/Ala226 (GCA). Thus, the human specificity triad, compared with the ancestral sequence, is modified more extensively than in any other identified mammal, with changes in amino acid sequence arising from two nucleotide mutations, each of which was introduced at a different time point in primate evolution.

Mouse cathepsin G is more active than human cathepsin G toward chymotryptic substrates and lacks tryptic activity

As shown in Fig. 3, the preferences of mouse cathepsin for substrate residues in the P1 position at the site of hydrolysis are markedly restricted compared with those of the human enzyme. Human cathepsin G has broad chymotryptic activity, cleaving after Trp, Phe, and Tyr, with little preference for Tyr versus Phe. It also has substantial Leu-ase and Met-ase activity, with little or no ability to cleave after P1 acidic residues (granzyme B-like Asp-ase activity) and small aliphatic residues (neutrophil elastase-like activity). Its most unique feature, however, is tryptic activity, which is as strong as its Tyr-cleaving chymotryptic activity and is largely Lys-specific. By contrast, the mouse enzyme lacks the tryptic, Leu-ase and Met-ase activity of the human enzyme, and even its chymotryptic profile is narrower, showing preference for Tyr over Phe and little inclination to cleave after Trp. Furthermore, the maximal activity of mouse cathepsin G is much higher than that of human cathepsin G. After normalization for differences in enzyme concentration used in the combinatorial assay, the P1 Tyr substrate-hydrolyzing activity is 19-fold greater for mouse versus human cathepsin G, even though maximal activity for both enzymes was achieved with substrates containing Tyr in the P1 position. As revealed in Figs. 3 and 4, wild-type human and mouse cathepsin G both cleave a variety of peptide-4NA chymotryptic substrates with Phe at the site of cleavage. Suc-l-Val-Pro-Phe-4NA and suc-l-Phe-Pro-Phe-4NA are the best identified substrates for both enzymes, suggesting that subsite P3 is similar for both enzymes. As shown in Table I, $K_m$ for suc-l-Val-Pro-Phe-4NA is substantially and significantly lower for mouse than for human cathepsin G at each of the two buffer conditions


(p = 0.0001 and p < 0.01 in 1.8 M NaCl and PBS, respectively), possibly because the mouse enzyme better accommodates binding of the P1 Phe side chain, as suggested by modeling of the primary specificity pocket (data not shown). Neither enzyme shows activity toward the human chymase-optimized substrate acetyl-L-Arg-Glu-Thr-Phe-4NA (48), indicating that the mouse enzyme, although it has a chymase-like specificity triad lining its primary (P1) specificity pocket, does not resemble chymase in its extended substrate binding fold. Although mouse cathepsin G is more active than human cathepsin G toward most of the surveyed chymotryptic substrates, the mouse enzyme is remarkable for reduced or absent trypsin-like activity, as reflected by minimal to no ability to cleave tetrapeptide substrates with basic amino acids in the P1 position (Fig. 3) and by lack of Lys-thioesterase activity (Fig. 5).

**Humanized mutants of mouse cathepsin G acquire trypsin-like activity**

As shown in Fig. 5, Lys-thioesterase activity appears in the humanized mutants of mouse cathepsin G, suggesting particularly that the Ala226Glu mutation contributes to trypsin-like activity in the human enzyme. Key modifications of the active site in human cathepsin G proposed to result in trypsin-like activity are modeled in Fig. 6.

**Mouse cathepsin G preferentially destroys but human cathepsin G activates angiotensin I**

As revealed by chromatograms in Fig. 7A, wild-type human chymase and human and mouse cathepsin G exhibit distinct patterns of angiotensin I hydrolysis. Recombinant human chymase, as reported (43), cleaves angiotensin I rapidly and highly selectively at Phe8 to generate vasoactive angiotensin II. Human cathepsin G also hydrolyzes selectively at Phe8, exhibiting very low level hydrolysis at Tyr4, but is much weaker than human chymase overall in attacking angiotensin I. In contrast, mouse cathepsin G preferentially hydrolyzes at Tyr4, which is an inactivating event in that it prevents angiotensin I from being activated to angiotensin II by hydrolysis at Phe8. Under these conditions, Phe8/Tyr4 selectivities for mouse cathepsin G, human cathepsin G, and human chymase are 0.31, 12, and 460, respectively. Although mouse cathepsin G hydrolyzes angiotensin I at Tyr4 3.2 times as often as at Phe8, it is 8.5-fold more active than human cathepsin G in generating angiotensin II, because it is more active overall, as also observed with chymotryptic 4NA substrates (Fig. 4, Table I). The mouse enzyme’s preference for cleaving angiotensin at Tyr4 is consistent with its observed preference for tetrapeptide substrates with P1 Tyr versus Phe (Fig. 3).

**Mouse and human cathepsin G are general proteinases**

As shown by SDS-PAGE in Fig. 7B, wild-type mouse and human cathepsin G, as well as humanized mouse mutants, exhibit general cysteine proteinase activity. This contrasts with human mast cell chymase, which cleaves casein more selectively, suggesting that the general proteinase activity is not specifically a function of its specificity triad mutations, even though they broaden specificity.

**Discussion**

This work reveals that cathepsin G substrate specificity underwent major changes during evolution of primates. These changes broadened specificity to include one of human cathepsin G’s most unusual characteristics (namely, trypsin-like activity) while reducing catalytic efficiency toward chymotryptic substrates. The phylogenetic analysis reveals that these transformations were generated by successive missense mutations in codons for key residues in the primary specificity pocket accommodating the substrate side chain at the site of hydrolysis. Consequently, as reflected by the identity of specificity triad residues 189 and 226, the human cathepsin G active site deviates substantially from that of the last ancestral cathepsin G shared by humans and new world monkeys, and indeed, its triad differs from that of any known serine peptidase. Mouse cathepsin G, which supports immune function as suggested by phenotypes of mice lacking cathepsin G (5, 29, 50), differs from the human enzyme in two of three triad residues.

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**Table I. Comparison of kinetics of chymotryptic (suc-L-Val-Pro-Phe-4NA-hydrolyzing) activity**

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Buffer</th>
<th>k&lt;sub&gt;cat&lt;/sub&gt; (s&lt;sup&gt;-1&lt;/sup&gt;)&lt;sup&gt;a&lt;/sup&gt;</th>
<th>K&lt;sub&gt;m&lt;/sub&gt; (mM)&lt;sup&gt;a&lt;/sup&gt;</th>
<th>k&lt;sub&gt;cat&lt;/sub&gt;/K&lt;sub&gt;m&lt;/sub&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mouse cathepsin G</td>
<td>1.8 M NaCl</td>
<td>41 ± 2</td>
<td>0.12 ± 0.02</td>
<td>330</td>
</tr>
<tr>
<td></td>
<td>PBS</td>
<td>33 ± 10</td>
<td>0.20 ± 0.12</td>
<td>170</td>
</tr>
<tr>
<td>Ala&lt;sup&gt;226&lt;/sup&gt;Glu Mouse cathepsin G</td>
<td>1.8 M NaCl</td>
<td>22 ± 2</td>
<td>3.10 ± 0.35</td>
<td>7.1</td>
</tr>
<tr>
<td></td>
<td>PBS</td>
<td>12 ± 2</td>
<td>0.63 ± 0.05</td>
<td>19</td>
</tr>
<tr>
<td>Ser&lt;sup&gt;189&lt;/sup&gt;Ala&lt;sup&gt;226&lt;/sup&gt;Glu Mouse cathepsin G</td>
<td>1.8 M NaCl</td>
<td>16 ± 2</td>
<td>1.88 ± 0.29</td>
<td>8.5</td>
</tr>
<tr>
<td></td>
<td>PBS</td>
<td>9 ± 0</td>
<td>0.37 ± 0.05</td>
<td>24</td>
</tr>
<tr>
<td>Human cathepsin G</td>
<td>1.8 M NaCl</td>
<td>100 ± 7</td>
<td>1.73 ± 0.19</td>
<td>58</td>
</tr>
<tr>
<td></td>
<td>PBS&lt;sup&gt;b&lt;/sup&gt;</td>
<td>14 ± 0</td>
<td>0.69 ± 0.12</td>
<td>20</td>
</tr>
<tr>
<td>Human chymase</td>
<td>1.8 M NaCl</td>
<td>230 ± 35</td>
<td>0.32 ± 0.12</td>
<td>720</td>
</tr>
<tr>
<td></td>
<td>PBS&lt;sup&gt;b&lt;/sup&gt;</td>
<td>17 ± 0</td>
<td>0.29 ± 0.07</td>
<td>59</td>
</tr>
</tbody>
</table>

<sup>a</sup>Mean ± SD, derived from three independent measurements at each of four substrate concentrations.

<sup>b</sup>As previously determined in Ref. 48.
Instead, it has the predicted ancestral configuration. Thus, substrate preferences of the mouse enzyme, including lack of tryptic activity, more likely represent those of the ancestral form.

The mutagenesis results suggest that acquisition of tryptic activity was mainly due to the Ala$^{226}$Glu change. Leaving aside the question of whether this change was beneficial, the tryptic anomaly in human cathepsin G is intriguing biochemically because it is, to our knowledge, a novel solution to the problem of generating tryptic specificity. The crux of that problem is to accommodate positively charged tips of basic amino acid side chains in the generally hydrophobic interior of the globular catalytic domain. In serine peptidases (including immune peptidases) specialized to cleave substrates exclusively at tryptic sites, the specificity triad is universally Asp$^{189}$/Gly$^{216}$/Gly$^{226}$ (Fig. 6). In classic tryptic peptidases, the anionic Asp$^{189}$ side chain carboxylate at the base of the primary specificity pocket forms a charge–charge complex with the substrate Lys or Arg side chain. Probably the closest parallel with the human cathepsin G configuration is that of bovine duodenase, which also has dual tryptic and chymotryptic specificity but with specificity triad Asn$^{189}$/Gly$^{216}$/Asp$^{226}$, with Asp$^{226}$ proposed to serve the function of Asp$^{189}$ in classic tryptic serine peptidases (51). Duodenase is related to the chymase-cathepsin G-granzyme B family but forms its own clade, is absent in humans and mice, and is prominent in ruminant mammals, which also contain chymase and cathepsin G. The specificity triad of both types of cattle (Bos taurus) cathepsin G is identical to that of mouse and predicted ancestral cathepsin G and thus is expected to lack tryptic activity. The ancestors of duodenase thus achieved dual specificity independently, but because duodenase and cathepsin G are thought to share a chymotryptic ancestor (13, 46), the starting point was apparently the same. It is tempting to consider that duodenase in cattle plays a role similar to cathepsin G in humans, but not enough is known about roles and sources of these enzymes to inform speculation about functional parity. It may be significant that duodenase and cathepsin G (along with chymases and granzyme B-related peptidases) belong to the subset of immune peptidases that form only three disulfide linkages within the catalytic domain (13), the fewest such linkages known in the extended trypsin/chymotrypsin family. It is proposed that absence of particular disulfide pair (Cys$^{191}$/Cys$^{226}$) in the vicinity of the active site (and otherwise highly conserved in serine peptidases) allows structural plasticity (46, 52) such that changes in residues lining the pocket are better tolerated than in peptidases with the disulfide pair. This may explain how primate cathepsin G and perhaps duodenase were able to acquire tryptic activity with as little as a single amino acid change, even though changing chymotrypsin into a tryptic enzyme requires exchange of many more residues, including loops (53).

Although the mouse Ser$^{189}$/Ala/Ala$^{226}$Glu double mutant specificity triad matches human, the Ala$^{226}$Glu single mutant specificity triad matches rhesus macaque (an old world monkey) and the great apes gorilla and chimpanzee. Because tryptic activity of
the single mutant lies between that of the mouse wild-type and the double mutant, as reflected by Lys15-aprotinin $K_i$ and by rates of Lys-thioester hydrolysis (Fig. 5), tryp tic activity of macaque and chimpanzee cathepsin G may be intermediate between that of mouse and human wild-type enzymes. However, prouPA activation, which occurs at Lys158 (20) is less robust in the double than mouse and human wild-type enzymes. However, prouPA activation, which occurs at Lys158 (20) is less robust in the double than mouse and human wild-type enzymes.

The comparisons of caseinolytic activity suggest that despite differences in ability to cleave peptidic substrates all of the tested forms of cathepsin G have general proteinase activity and may be less selective than human chymase, which cleaves casein and albumin (15) at fewer sites. It should be noted that the recent discovery of mast cell protease 4 chymase appears to be the major source of serine peptidase-derived angiotensin II-generating activity in uninflamed mouse tissues (43, 55). However, our in vitro assays show that mouse cathepsin G generates approximately one molecule of active angiotensin II for every three molecules of angiotensin I, as indicated. B. Results of SDS-PAGE of casein after incubation with peptidases mouse cathepsin G (mCG), Ala226Glu and Ser189Ala/Ala226Glu mutants, and human cathepsin G (hCG). Size in kilodalton and elution positions of marker proteins are indicated.

FIGURE 7. Peptidase and general proteinase activity. A, HPLC chromatograms of angiotensin (Ang) I after incubation with human chymase, human cathepsin G, and wild-type mouse cathepsin G. Peaks (as detected by monitoring absorbance at 210 nm) correspond to dipeptide HL and active octapeptide product Ang II (both resulting from hydrolysis at Phe8), in-active tetrapeptide DRVY and hexapeptide IHPFHL (resulting from hydrolysis at Tyr4), and uncleaved Ang I, as indicated. B, Results of SDS-PAGE of casein after incubation with peptidases mouse cathepsin G (mCG), Ala226Glu and Ser189Ala/Ala226Glu mutants, and human cathepsin G (hCG). Size in kilodalton and elution positions of marker proteins are indicated.

in rates of hydrolysis of tetra- and tripeptidyl substrates with invariant P1 Phe. For both enzymes, this is also revealed by very low rates of hydrolysis of benzoyl-L-Phe-4NA, for which there are few contacts outside of the primary specificity pocket. These considerations likely explain why mouse cathepsin G, despite having a primary specificity pocket more similar to human chymase than human cathepsin G, lacks the selectivity of angiotensin II-generating (Phe-hydrolyzing) activity that is prominent in both human enzymes, for which surface topography, charge, and hydrophilicity outside of the primary specificity pocket are important determinants of angiotensin hydrolysis (44, 54). The finding that mouse cathepsin G preferentially destroys angiotensin I may explain why mast cell protease 4 chymase appears to be the major source of serine peptidase-derived angiotensin II-generating activity in uninflamed mouse tissues (43, 55). However, our in vitro assays show that mouse cathepsin G generates approximately one molecule of active angiotensin II for every three molecules of angiotensin I that it inactivates. In settings where cathepsin G is released in high concentrations, as in pneumonia, local generation of angiotensin II by cathepsin G may be important.
to Leu-ase activity (45). Although cathepsin G appears to be microbicidal in mice (6), in the context of chronic airway infection in humans with cystic fibrosis, cathepsin G interferes with the killing of certain bacteria (11). Potentially, differences in the nature of immune deficits in mice and humans with dypeptidyl peptide I deficiency/Papillon-Lefèvre syndrome are in part due to differences in specificity and immune roles of cathepsin G in the two species. Whether the changes in substrate preferences caused by specificity triad mutations in cathepsin G fundamentally alter host defense functions in humans remains to be determined. Similarly, the importance to homeostasis of mutation-enabled capabilities, such as modulation of fibrinolysis by activating prouPA, will require further investigation and may be modeled inadequately by mice.

Disclosures
The authors have no financial conflicts of interest.

References


