A Novel HLA-A*0201 Restricted Peptide Derived from Cathepsin G Is an Effective Immunotherapeutic Target in Acute Myeloid Leukemia

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Abstract

Purpose: Immunotherapy targeting aberrantly expressed leukemia-associated antigens has shown promise in the management of acute myeloid leukemia (AML). However, because of the heterogeneity and clonal evolution that is a feature of myeloid leukemia, targeting single peptide epitopes has had limited success, highlighting the need for novel antigen discovery. In this study, we characterize the role of the myeloid azurophil granule protease cathepsin G (CG) as a novel target for AML immunotherapy.

Experimental Design: We used Immune Epitope Database and in vitro binding assays to identify immunogenic epitopes derived from CG. Flow cytometry, immunoblotting, and confocal microscopy were used to characterize the expression and processing of CG in AML patient samples, leukemia stem cells, and normal neutrophils. Cytotoxicity assays determined the susceptibility of AML to CG-specific cytotoxic T lymphocytes (CTL). Dextramer staining and cytokine flow cytometry were conducted to characterize the immune response to CG in patients.

Results: CG was highly expressed and ubiquitinated in AML blasts, and was localized outside granules in compartments that facilitate antigen presentation. We identified five HLA-A*0201 binding nonameric peptides (CG1-CG5) derived from CG, and showed immunogenicity of the highest HLA-A*0201 binding peptide, CG1. We showed killing of primary AML by CG1-CTL, but not normal bone marrow. Blocking HLA-A*0201 abrogated CG1-CTL–mediated cytotoxicity, further confirming HLA-A*0201-dependent killing. Finally, we showed functional CG1-CTLs in peripheral blood from AML patients following allogeneic stem cell transplantation.

Conclusion: CG is aberrantly expressed and processed in AML and is a novel immunotherapeutic target that warrants further development.

Clinical Cancer Research; 19(1); 247–57. ©2012 AACR.
Acute myeloid leukemia (AML) is an aggressive and clinically challenging malignancy. Although hematopoietic stem cell transplantation (HSCT) can be curative in AML, it carries a high rate of treatment-related mortality and morbidity. To minimize the toxicity of HSCT while taking advantage of the graft-versus-leukemia effect, leukemia-associated antigens (LAA) have been identified and targeted successfully with immunotherapy. However, because of leukemia heterogeneity and tumor antigen loss, the latter a mechanism of immune evasion by malignant cells, it is highly unlikely that any single antigen will be consistently expressed in all leukemias. This highlights the need for leukemia antigen discovery. In this study, we characterize a novel LAA, cathepsin G (CG). We show that CG is aberrantly expressed and processed by AML blasts and stem cells and that it can be targeted effectively in AML. These results provide preclinical evidence for the development of immunotherapeutic strategies to target CG in AML.

Translational Relevance

Acute myeloid leukemia (AML) is an aggressive and clinically challenging malignancy. Although hematopoietic stem cell transplantation (HSCT) can be curative in AML, it carries a high rate of treatment-related mortality and morbidity. To minimize the toxicity of HSCT while taking advantage of the graft-versus-leukemia effect, leukemia-associated antigens (LAA) have been identified and targeted successfully with immunotherapy. However, because of leukemia heterogeneity and tumor antigen loss, the latter a mechanism of immune evasion by malignant cells, it is highly unlikely that any single antigen will be consistently expressed in all leukemias. This highlights the need for leukemia antigen discovery. In this study, we characterize a novel LAA, cathepsin G (CG). We show that CG is aberrantly expressed and processed by AML blasts and stem cells and that it can be targeted effectively in AML. These results provide preclinical evidence for the development of immunotherapeutic strategies to target CG in AML.

Materials and Methods

Patients, cells, and cell lines

Patient and healthy donor samples were obtained after appropriate informed consent through an institutional review board approved protocol at the University of Texas MD Anderson Cancer Center. The AML samples were collected between 2006 and 2012 and were selected based on their AML subtype, percent blasts, sample viability, and HLA status. U-937 (myelomonoblastic leukemia) and T2 (B-cell/T-cell hybridoma) cell lines were obtained from American Type Culture Collection. Cell lines were cultured in RPMI-1640 with 25 mmol/L HEPES-L-Glutamine (HyClone) supplemented with 10% FBS (Gemini Bio-Products), Penicillin [100 U/mL]/Streptomycin [100 μg/mL] (Cellgro), and were kept in 5% CO2 at 37°C. Cell lines were authenticated by DNA finger-printing at MD Anderson Cancer Center within 6 months of use in experiments. Healthy individual and patient peripheral blood mononuclear cells (PBMC), bone marrow, and granulocytes, were enriched using standard Histopaque 1077 or 1119 (Sigma) gradient centrifugation. Patient leukemia blast samples were collected at the time of original diagnosis.

Western blotting and immunoprecipitation

Whole cell lysates (WCL) from AML samples were generated using standard methodology with radioimmunoprecipitation assay buffer [50 mmol/L TrisHCl (pH 8); 150 mmol/L NaCl; 1% NP-40; 0.1% SDS; 0.5% sodium deoxycholate]. Purified CG (Sigma) and P3 (Athens Research and Technology) were used as positive controls; U-937 WCL was used as NE positive control. For IP reactions, anti-CG antibody (Abcam) was added to precleared WCLs and incubated overnight at 4°C. WCL and IP products were separated by electrophoresis on 10% SDS gels under reducing conditions, transferred onto polyvinylidene difluoride membranes, blocked with 5% milk and probed with anti-CG (Abcam), anti-NE (Santa Cruz), anti-P3 (NeoMarkers), anti-ubiquitin (Santa Cruz), or anti-actin (Millipore) antibodies. Chemiluminescence was captured on Kodak film and digitally using Molecular Imager ChemiDoc XRS+ (BIO-RAD).

CG peptide binding

Immune epitope database (IEDB) binding algorithms were used to identify CG peptides with highest binding affinities (www.immuneepitope.org). Peptide binding was subsequently confirmed using standard peptide-T2
binding assays (25, 26). Briefly, T2 cells were washed and then incubated at 37°C in serum-free media containing increasing concentrations of CG-peptides (BioSynthesis; Supplementary Table S1) or PR1 peptide. After 90 minutes, cells were washed and stained with the FITC-conjugated anti-HLA-A*0201 antibody BB7.2 (Becton-Dickinson [BD]) to determine the stabilization of peptide/HLA-A*0201 on the T2 cell surface. Flow cytometry was conducted using the BD fluorescence-activated cell sorting (FACS) Canto II (BD). Data were analyzed using FlowJo software (Tree Star Inc.).

The affinity of CG1 for HLA-A*0201 and the relative stability of the peptide-HLA complexes were measured using the iTopia Epitope Discovery System (Beckman Coulter), following the manufacturer’s protocol. Both assays use a FITC-conjugated anti-HLA antibody that binds to the correctly folded HLA-peptide complex and a positive control peptide (FLPSDFPPSV) for comparison with the test peptide. For the affinity assays, peptides were incubated in HLA-A*0201 coated wells at concentrations ranging from 10^-4 to 10^-6 M at 21°C overnight, in the presence of the anti-HLA antibody. After washing the wells to remove unbound antibody and peptide, fluorescence was read on a Synergy 2 microplate reader (BioTek) with the excitation set at 485 nm and emission detected at 528 nm. Results were graphed relative to the binding of the positive control peptide at 10^-6 M, and the ED50 was determined using GraphPad Prism’s nonlinear regression “log (agonist) versus response – variable slope (4 parameter)” curve. For the off-rate assay, peptides were incubated in HLA-A*0201 coated wells at a concentration of 11 μmol/L at 21°C overnight, then washed and incubated at 37°C to allow the peptides to dissociate. Wells were washed again at the times indicated on the graph to remove dissociated peptide and antibody, and fluorescence was read on the microplate reader. Results were graphed relative to the positive control peptide as 100% binding at each time point. The t1/2 was calculated using GraphPad Prism’s nonlinear regression, “dissociation – 1 phase exponential decay” curve (27).

Fluorescent confocal microscopy and flow cytometry analysis

To determine intracellular CG expression, cells were washed, fixed with 4% paraformaldehyde, permeabilized, and stained with Alexa-647 directly conjugated anti-CG antibody (Santa Cruz); we used the Alexa-647 conjugation kit (Invitrogen) to conjugate anti-CG to fluorophore. Aqua live/dead stain (Invitrogen) was used to assess viability in flow cytometry experiments. For confocal imaging, after staining, cells were resuspended in Prolong Gold antifade reagent with dapi (Invitrogen). Confocal imaging was conducted using Leica Microsystems SP2 SE confocal microscope (Leica) with ×10/25 air, ×63/1.4 oil objectives. Leica LCS software (version 2.61) was used for image analysis. Flow cytometry was conducted using the Cytometry CyAn flow cytometer (Dako) and analyzed using FlowJo software (Tree Star Inc.).

Before intracellular CG staining of stem cells, leukemia and normal donor samples were stained with antibodies targeting CD34, CD38, and the lineage (Lin) markers CD3, CD14, CD16 (all from BD), and CD19 (eBioscience). Lin−CD34+ CD38− stem cells (28) were sorted using Influx cell sorter (BD). Because of their low frequencies, normal stem cells (NSC) were FACS sorted from 1 normal donor bone marrow and pooled with sorted stem cells from 3 granulocyte colony-stimulating factor (G-CSF) mobilized normal donor apheresis samples.

To determine the location of CG within AML and normal granulocytes (i.e., granular vs. extragranular) and the level of CG expression in stem cells, after staining for CG cells were imaged using BD Pathway 435 (BD) cell imager with a 60× Olympus objective, and then analyzed using AttoVision software (BD). To determine the intracellular distribution of CG, regions of interest (ROI) were drawn around each cell. The ratio of the dimmest:brightest 10% of pixels per cell was calculated (29). To determine CG staining intensity, mean fluorescence intensity in each ROI was measured.

Peptide-specific CTL lines

Peptide-specific CTLs were expanded by stimulating PBMCs from healthy HLA-A*0201 individuals with peptide in vitro, as previously described (3, 30). Briefly, T2 cells were washed in serum-free RPMI 1640 medium and incubated with CG1 or negative control peptide PR1 at 20 μg/mL for 90 minutes at 37°C. Peptide-loaded T2 cells were irradiated with 7500 cGy, washed, and cultured with freshly isolated PBMCs at a 1:1 ratio in RPMI 1640 medium supplemented with 10% human AB serum. Cultures were restimulated with peptide-pulsed T2 cells on days 7, 14, and 21, and the following day 20 IU/mL of recombinant human interleukin-2 (rHL-2; Invitrogen) was added.

Cell-mediated cytotoxicity assay

A standard calcein AM cytotoxicity assay was used to determine specific lysis as described previously (31, 32). Briefly, 1,000 target cells in 10 μL (1.0 x10^5 cells/mL) were stained with calcein-AM (Invitrogen) for 90 minutes at 37°C, washed 3 times with RPMI-1640 and then coincubated with 10 μL of peptide-specific CTL at varying effector to target (E:T) ratios. After a 4-hour incubation period at 37°C in 5% CO2, 5 μL of Trypan blue was added to each well and fluorescence was measured using an automated CytoFluor II plate reader (PerSeptive Biosystems). For HLA-A*0201 blocking experiments, target cells were incubated with BB7.2 antibody before the addition of effector CTLs. Percent specific cytolysis was calculated as follows: [(FluorescenceTarget+Effectort Target alone – FluorescenceTarget alone) x 100].

Cytokine flow cytometry and major histocompatibility-dextramer staining

T2 cells were pulsed with 20 μg/mL of CG1 peptide for 90 minutes, irradiated, and incubated with PBMC from HLA-A*0201 leukemia patients at a 1:1 ratio for 6 hours at 37°C.
in 5% CO₂. Brefeldin A (Sigma) was added after the first hour of incubation. After coincubation of T2 and PBMC, media was removed, the cells were washed with PBS, and stained with aqua live/dead stain (Invitrogen) for 20 minutes on ice. Cells were then washed with PBS, fixed, and permeabilized using FACS Lyse and PermII solutions (BD).

The following fluorescently conjugated MHC dextramer and antibodies were added to each sample: PE-CG1/HLA-A*0201 dextramer (Immudex); APC/PP65/HLA-A*0201 dextramer (Immudex); APC/H7-anti-CD8; lineage (Lin) markers including Pacific blue-anti-CD4, CD14, CD16 (BD), and CD19 (Biolegend); and PE-Cy7 anti-interferon (IFN)-γ and PerCP Cy5.5-anti-tumor necrosis factor (TNF)-α (both from BD). The cells were washed, fixed, and analyzed using an LSRII Fortessa flow cytometer (BD). Live, Lin−, CD8+, dextramer+ cells were then enumerated for IFN-γ and TNF-α production. Unpulsed T2 cells were used as negative stimulator controls. Fluorescence minus 1 (FMO) controls were conducted for each sample and background staining was subtracted from each experimental group.

**Statistical analysis**

GraphPad Prism 5.0 software was used to conduct statistical analyses and P values less than 0.05 were used to establish significance.

**Results**

**CG is aberrantly expressed in primary AML and is ubiquitinated**

We first examined the expression of CG by AML from patient samples with high peripheral blood blasts that were obtained at the time of original diagnosis. We initially examined 12 patient samples for CG expression and we present the immunoblots from 8 AML patient samples representing various AML subtypes. We conducted western immunoblots on primary patient AML blasts, which showed CG expression in a number of AML subtypes (Fig. 1A; Supplementary Table S2). We also examined these samples for expression of NE and P3, the 2 azurophil granule proteases from which the PR1 peptide is derived and that share a common promoter (3, 31, 32). Our data show lower expression of NE and P3 in the samples we used in our studies, compared with CG. Furthermore, there was no correlation between CG expression and NE or P3 expression. Because CG is located on a different chromosome (chromosome 14) than NE and P3 (33, 34), which are both located on chromosome 19 (35, 36), and as CG is expressed later than NE and P3 during the maturation of the myeloid progenitor under the regulation of a different promoter than NE and P3 (20, 37), it is not surprising that levels of NE and P3 did not correlate with CG expression. Furthermore, we show higher expression of CG in primary AML than in normal granulocytes (Fig. 1B).

Because protein ubiquitination facilitates proteasomal degradation of antigens for processing on MHC class I (38, 39), we investigated whether CG was also ubiquitinated in AML, thereby facilitating CG-derived peptide presentation on the leukemia cell surface. IP of AML WCLs with anti-CG antibody and subsequent probing with anti-ubiquitin show ubiquitination of CG in AML, but not in healthy granulocytes (Supplementary Fig. S1). Furthermore, because cytosolic proteins are favored for antigen processing, as they have direct access to the proteasome (40), we studied the subcellular localization of CG in AML and normal neutrophils. Our data show that CG is diffusely localized in AML in contrast with normal granulocytes, where it is located primarily in granules, as evidenced by distinct foci of staining in the normal granulocyte samples.
A was confirmed to have a high binding affinity to HLA-binding and iTopia assays, the CG1 peptide (FLLPTGAEA) surface of leukemia cells (Supplementary Fig. S2). Using T2 CML (21), and because of our work confirming CG1 on the report showing that CG1 is a naturally processed peptide in #5 n

A time for half-maximal dissociation of CG1 from HLA-binding epitopes are derived from CG

Five CG derived nonameric peptides were identified using IEDB and SYFPEITHI binding algorithms (Supplementary Table S1 and Fig. 3A). Although we identified 5 CG-derived peptides with high binding affinities to HLA-A*0201, we focused our experiments on CG1 peptide because of a prior report showing that CG1 is a naturally processed peptide in CML (21), and because of our work confirming CG1 on the surface of leukemia cells (Supplementary Fig. S2). Using T2 binding and iTopia assays, the CG1 peptide (FLLPTGAEA) was confirmed to have a high binding affinity to HLA-A*0201 (CG1 IC50 = 1.1 μmol/L) in comparison with other CG derived peptides and with the control peptide FLPSDFPSV (Fig. 3A and B). Furthermore, using iTopia assays we measured the off-rate for CG1 and calculated the time for half-maximal dissociation of CG1 from HLA-A*0201 (t1/2) to be approximately 14 hours.

CG1-CTL lyse CG-expressing HLA-A*0201 AML

To determine the ability of CG1-CTL to lyse primary AML blasts, we conducted calcine AM cytotoxicity assays (31, 32). We first show dose-dependent specific killing of AML blasts by CG1-CTL, with minimal killing of HLA-A*0201 normal bone marrow (Fig. 4A). The low level of cytotoxicity seen in the HLA-A*0201 normal bone marrow sample may be due in part to a low level of expression of CG1 peptide by normal bone marrow myeloid cells. As CG expression is highest in the early stages of myeloid cell development (20), CG1 may be presented by HLA-A*0201 on subsets of normal early myeloid progenitor cells in the bone marrow, as we previously reported for the LAA PR1 (41); this low-level expression could account for the low cytotoxicity seen in normal HLA-A*0201 bone marrow sample. There was no killing of HLA-A*0201 negative bone marrow consistent with CG1 being HLA-A*0201 restricted. Furthermore, we confirmed HLA-A*0201 dependency of CG1-CTL–mediated killing, as blocking HLA-A*0201 with the BB7.2 antibody abrogated CG1-CTL killing of HLA-A*0201 AML and CG1-pulsed T2 cells (Fig. 4B).

As we showed HLA-A*0201 restricted specific cytotoxicity of AML blasts by CG1-CTL, we next examined CG1-CTL cytotoxicity using 5 HLA-A*0201 (Patients 1–5) and 1 HLA-A*0201 negative AML patient samples (Patient 6; Fig. 4C). Our data show variable lysis of HLA-A*0201 AML samples by CG1-CTL, but not the HLA-A*0201 negative sample. Furthermore, at some of E:T ratios, we observed higher specific lysis in some of the AML samples that had higher CG expression. However, there was some variability seen in killing of the AML samples independent of CG expression.
suggesting that there may be differences in antigen presentation by the AML target cells that could account for differences in CG1/HLA-A*0201 presentation (Fig. 4C and Supplementary Fig. S3). Moreover, although we were unable to assess mean fluorescence intensity (MFI) of CG expression of Patient 5 using flow cytometry because of sample limitation, immunoblotting of this patient sample showed relatively high CG expression (see AML#8 Fig. 1A).

**CG expression is higher in CD34**\(^+\) CD38**–** LSC in comparison with normal stem cells

As the expression of target antigen is ideally absent or lower in normal cells compared with malignant counterparts, we investigated the expression of CG in normal and leukemia stem cells. We stained Lin**–** CD34**+** CD38**–** leukemia stem cells (LSC; ref. 28) sorted from 2 different AML patients for intracellular CG. Because of their low frequency, sorted Lin**–** CD34**+** CD38**–** stem cells from 4 different normal donors were combined and stained for CG. Confocal imaging shows higher expression of CG in LSC in contrast with NSC (Fig. 5A). Using a high throughput bioimaging system (BD Pathway 435 cell imager), we confirmed significantly higher expression of CG in cells from 2 different LSC samples (LSC 1: \(n = 234\) cells; LSC 2: \(n = 570\) cells) in comparison with NSC (\(n = 357\) cells; Fig. 5B). As we had to combine NSC from 4 different healthy donors, there may be variability in the expression of CG in NSC from different individuals, which may not be reflected in the mean values presented (Fig. 5B). However, the median and range pixel intensity values of LSC 1 (median = 620; range = 82–2,474), LSC 2 (median = 62; range = 46–2,550), and NSC (median = 48; range = 45–497) together suggest higher expression of CG in LSC in comparison with NSC. Furthermore, a significant difference was also observed between the 2 LSC samples, which can be attributed to leukemia heterogeneity.

**Functional CG1-CTL are detected in AML patients following allo-SCT**

As we showed CG expression in AML and lysis of CG-expressing AML by CG1-CTL in vitro, we next investigated whether immunity to CG1 can be detected in AML patients
Following allo-SCT, CG1/HLA-A*0201 dextramer was used to stain PBMC samples from patients with AML. We show the presence of CG1-CTL in AML patient peripheral blood following allo-SCT (range, 0.07%–0.44%) at similar frequencies to what was previously detected for PR1- and WT1-CTL (Table 1; refs. 3, 16). The gating strategy used and the specificity of CG1/HLA-A*0201 dextramer for CG1-CTL is shown in Supplementary Fig. S4. Furthermore, we show functionality of patient CG1-CTL using a CFC assay measuring IFN-γ and TNF-α response following CG1-CTL stimulation with CG1-pulsed T2 cells. Although responses were detected in 4 of the 5 AML patient samples that were analyzed indicating functional CG1-CTL, they were highly variable ranging from 0.6% to 11%. The absence of a response in one of the samples (Patient 2) could be attributed to the lack of full immune reconstitution seen early following allo-SCT (day 30), as the other patient samples analyzed were collected at later time points following allo-SCT (Range, 205–1,162 days).

Discussion

We report the discovery of a novel immunogenic epitope derived from the myeloid azurophil granule protease CG. We show high expression and ubiquitination of CG in AML blasts as well as aberrant CG localization outside azurophil granules, which could facilitate CG antigen presentation by leukemia. In addition, CG is highly expressed in LSC but not normal hematopoietic stem cells. We identify 5 CG-derived nonameric peptides that bind with high affinity to HLA-A*0201 and show that the CG1 peptide (FLLPTGAEA) is a naturally processed immunogenic HLA-A*0201 epitope. Moreover, we show that CG1-CTL lyse HLA-A*0201-resorted CG-expressing targets, with minimal killing of HLA-A*0201 normal bone marrow. Importantly, we detected evidence of active immunity targeting CG in AML patients following allo-SCT.

Because of the heterogeneity of antigen expression in myeloid leukemia (42), targeting a single antigen is unlikely to provide adequate therapeutic efficacy unless a universal leukemia antigen is discovered. Moreover, expression of LAA by normal tissues, including hematopoietic stem cells, and the failure to elicit immune responses against LAA in some patients, together limit the clinical utility of targeting individual LAA and highlight the need for further antigen discovery. Considering these factors, CG is an ideal LAA, as it is highly expressed by numerous AML subtypes in comparison with normal granulocytes (Fig. 1) and is a naturally processed peptide in myeloid leukemia (Supplementary Fig. S2). Although it is expressed by normal...
granulocytes and stem cells, we show a different pattern of expression in normal tissues. Specifically, we show lower expression in normal granulocytes and LSC, aberrant localization in myeloid leukemia outside granules and ubiquitination in AML blasts, but not normal granulocytes, together indicating preferential processing of CG in AML (43–45). The distinct expression and processing of CG in AML is further supported by the specific killing of HLA-A*0201 AML by CG1-CTL, with minimal killing of HLA-A*0201 normal bone marrow (Fig. 4). Together, these data highlight the potential role for CG as a novel target in AML immunotherapy.

Our results corroborate 2 previous reports showing a potential role for targeting CG in leukemia. In the first report by Papadopoulos and colleagues, a high copy number of CG1 peptide was eluted from the surface of CD34+ blasts from 1 patient with CML using high-performance liquid chromatography purification and sequencing (21). Furthermore, they showed higher expression of CG mRNA in CD34+ CML blasts versus normal CD34+ cells. However, the authors did not investigate immunity against CG1 in the patient that was studied. We expand on these findings by showing that in AML, the CG protein is highly expressed and processed by AML blasts and Lin−/CD34+CD38−/LSC and that the CG1 epitope is naturally presented on the cell surface. Furthermore, we show specific immunity targeting the CG1 peptide in vitro and in patients with AML. In the second report, Fujiwara and colleagues showed a generalized IFN-γ response to P3, NE, or CG in 4 patients with CML and 1 patient with AML using CD40 ligand (L)-activated B cells transfected with expression vectors encoding P3, NE, and CG (46). In our study, we further characterize the anti-CG immune response in AML and show that CG1 is a naturally processed CG-derived epitope that is likely responsible for the immunity against CG. This epitope, along with CG2 and CG3 (Supplementary Table S1 and Fig. 3) are all derived from the signal peptide of CG. Because cleavage of the signal peptide occurs in the endoplasmic reticulum and golgi (47, 48), 2 compartments that are involved in MHC class I antigen processing, the presence of the cleaved signal peptide in these compartments may facilitate processing for presentation on MHC class I.

Table 1. Functional CG1-specific cytotoxic T lymphocytes are detected in AML patient peripheral blood following allogeneic SCT

<table>
<thead>
<tr>
<th>Sample</th>
<th>Diagnosis</th>
<th>Days post-SCT</th>
<th>% CG1 dextramer post-SCT</th>
<th>% Cytokine+ CG1-CTLs post-SCT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient 1</td>
<td>MDS RAEB-I</td>
<td>1,162</td>
<td>0.13</td>
<td>11</td>
</tr>
<tr>
<td>Patient 2</td>
<td>AML-FAB M2</td>
<td>30</td>
<td>0.08</td>
<td>0</td>
</tr>
<tr>
<td>Patient 3</td>
<td>AML treatment related</td>
<td>366</td>
<td>0.11</td>
<td>0.6</td>
</tr>
<tr>
<td>Patient 4</td>
<td>AML-unspecified</td>
<td>205</td>
<td>0.12</td>
<td>2.3</td>
</tr>
<tr>
<td>Patient 5</td>
<td>AML-FAB M2</td>
<td>545</td>
<td>0.07</td>
<td>9.7</td>
</tr>
<tr>
<td>Patient 6</td>
<td>AML-FAB M1</td>
<td>171</td>
<td>0.33</td>
<td>ND</td>
</tr>
<tr>
<td>Patient 7</td>
<td>AML-FAB M2</td>
<td>31</td>
<td>0.20</td>
<td>ND</td>
</tr>
<tr>
<td>Patient 8</td>
<td>AML-FAB M6</td>
<td>181</td>
<td>0.44</td>
<td>ND</td>
</tr>
</tbody>
</table>

Abbreviations: CTL, cytotoxic T lymphocytes; MDS, myelodysplastic syndrome; RAEB, refractor anemia with excess blasts; FAB, French–American–British classification; ND, not determined.

aGating strategy for CG1/HLA-A*0201 dextramer is shown in Supplementary Fig. S4.

b% cytokine+ CG1-CTL refers to the sum percentages of dextramer positive CTLs that produced either IFN-γ, TNF-α, or both in response to CG1-pulsed T2 stimulator cells.
Furthermore, although ubiquitination is an important step in antigen degradation during the process of antigen presentation (38, 39), it may not be significant in the processing of CG1-CG3 peptides, as these are naturally found within the signal domain of CG, which is normally cleaved during CG intracellular processing. Whether other CG-derived epitopes (i.e., CG2-CG5) are also immunogenic is the subject of ongoing research in our laboratory.

Furthermore, we studied whether there was a correlation between the expression of CG and the primary granule serine proteases NE and P3. This was investigated to determine whether targeting CG will add to the existing immunotherapeutic approaches that target PR1 peptide, which is a nonameric peptide derived from NE and P3 that has shown clinical efficacy in vaccine trials of patients with AML, CML, and MDS (16). The lack of a correlation between CG expression and NE or P3, as shown in Fig. 1, adds to the significance of CG as an immunotherapeutic target in AML. Unlike NE and P3, CG is located on chromosome 14 and has a promoter region that differs from NE and P3 (49, 50). Because of the distinct expression and regulation of CG that is independent of NE and P3 expression, CG may prove to be an effective target in AML that may be resistant to PR1 therapy because of low NE and P3 expression. In addition, because of the heterogeneity among the leukemia subclones within an individual patient (9), which could account for variable expression of LAA by the leukemia cells, targeting CG could be used in combination with other LAA in a multipepptide immunotherapeutic approach to broaden the immune response, as was previously shown for a combined WT1 and PR1 vaccine in myeloid leukemia (16).

Despite our promising data highlighting the immunogenicity of CG in AML and as AML represents a heterogeneous group of diseases (9, 51), we realize that more samples representing the various AML subtypes, including AML subgroups expressing different mutations and cytogenetic abnormalities, are needed to more conclusively determine the broad applicability CG-targeting immunotherapy in AML. For example, Jin and colleagues showed that the fusion protein AML1-ETO directly targets and suppresses CG in t(8;21) AML, suggesting a mechanism for leukemia escape from intracellular surveillance whereby the lack of CG prevents the cell from degrading abnormal proteins that may play role in leukemogenesis (52). This same mechanism of CG silencing in t(8;21) AML subtype may also contribute to leukemia evasion of the anti-CG immune response, which would also further promote leukemia escape as was shown for other tumor-associated antigens (53). Additional investigations are currently underway to more fully characterize CG expression in different subtypes of AML.

In addition to AML, which we show here, and CML (46), targeting CG may prove beneficial in nonmyeloid hematopoietic malignancies. In a recent study, Gorodkiewicz and colleagues showed a significant amount of CG protein expression in 3 chronic lymphocytic leukemia (CLL) patient samples, which was lower than CG expression in 2 AML patient samples and higher than CG expression detected in leukemia cells from 1 chronic phase CML patient (54). In addition to CLL, Fujiwara and colleagues showed immunity to CG in 3 patients with acute lymphoblastic leukemia (46). Collectively, these 2 reports highlight a potential role for targeting CG in nonmyeloid hematologic malignancies.

Taken together, our results identify CG as a novel target in AML. CG is highly expressed by some AML subtypes and is aberrantly located in cellular compartments that facilitate antigen presentation. Immunity targeting CG was elicited 
vitro, was specific for malignant cells with minimal effects on normal cells, and was detected in AML patient samples following allo-SCT. Thus, our findings show a promising role for CG targeting immunotherapy in AML.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Acknowledgments
The authors thank Kimberly J. Acklin, Ting Qiang, and Erik B. Puffer for their technical assistance and expertise in cell imaging.

Grant Support
This work was supported in part by the MD Anderson Cancer Center Leukemia SPORE grant, CA100632, a grant from the Leukemia Research Foundation, and direct start-up funds from the MD Anderson Cancer Center (to G. Alatrash). Research was also supported by National Institutes of Health (NIH) grants R01CA133244 (to E.A. Mittendorf), and NIH grant K23TR000084 (to P.M. Armistead). The Flow Cytometry and Cellular Imaging core is supported by Cancer Center Support Grant NCI P30CA16672.

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Received August 22, 2012; revised October 4, 2012; accepted October 23, 2012; published OnlineFirst November 12, 2012.

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