Enriched HLA-E and CD94/NKG2A Interaction Limits Antitumor CD8+ Tumor-Infiltrating T Lymphocyte Responses

Megat Abd Hamid1,2, Ruozheng Wang3,4, Xuan Yao1,2, Peiwen Fan3,4, Xi Li1,2, Xue-Mei Chang3,4, Yaning Feng3,4, Stephanie Jones5, David Maldonado-Perez5,6, Craig Waugh7, Clare Verrill5,6, Alison Simmons1,2, Vincenzo Cerundolo1,2, Andrew McMichael1, Christopher Conlon1, Xiyan Wang2,4, Yanchun Peng1,2, and Tao Dong1,2,3

Abstract

Immunotherapy treatments with anti-PD-1 boost recovery in less than 30% of treated cancer patients, indicating the complexity of the tumor microenvironment. Expression of HLA-E is linked to poor clinical outcomes in mice and human patients. However, the contributions to immune evasion of HLA-E, a ligand for the inhibitory CD94/NKG2A receptor, when expressed on tumors, compared with adjacent tissue and peripheral blood mononuclear cells, remains unclear. In this study, we report that epithelial-derived cancer cells, tumor macrophages, and CD141+ conventional dendritic cells (cDC) contributed to HLA-E enrichment in carcinomas. Different cancer types showed a similar pattern of enrichment. Enrichment correlated to NKG2A upregulation on CD8+ tumor-infiltrating T lymphocytes (TIL) but not on CD4+ TILs. CD94/NKG2A is exclusively expressed on PD-1high TILs while lacking intratumoral CD103 expression. We also found that the presence of CD94/NKG2A on human tumor-specific T cells impairs IL2 receptor–dependent proliferation, which affects IFNγ-mediated responses and antitumor cytotoxicity. These functionalities recover following antibody-mediated blockade in vitro and ex vivo. Our results suggest that enriched HLA-E/CD94/NKG2A inhibitory interaction can impair survival of PD-1high TILs in the tumor microenvironment.

Introduction

Avoidance of immune destruction is a hallmark of cancer. Tumor employs diverse mechanisms to escape antitumor immunity such as by enhancing the immune checkpoint expression of PD-1 on tumor-infiltrating T lymphocytes (TIL) and by down-regularing the MHC-Ia surface expression on cancer cells (1–3). These changes reduce the efficacy of tumor-localized T-cell priming, leading to impaired antitumor immunity and increased tumor progression. Although past clinical studies of checkpoint blockade using anti-PD-1 or anti-CTLA-4 have shown improvement in some patients, these treatments failed to improve overall response rates in many anti-PD-1 treated cancer patients (4–7). Various studies have associated an enrichment of the nonclassical MHC-Ib molecule, HLA-E, with poorer clinical outcome in patients with cancer (8–13). For example, high numbers of patients with head and neck cancer were found to have HLA-E–enriched carcinomas, corresponding to lower survival rates as tumor progresses. On the other hand, lymphoma-treated Qa-1b–knockout mice (Qa-1b− is the murine HLA-E homologue) have better tumor regression (12, 13). Nevertheless, whether HLA-E is enriched specifically in carcinoma compared with adjacent tissue or blood of patients and whether this enrichment negatively affects antitumor T-cell responses in humans remains unclear.

Although MHC-Ia molecules help in cancer cell recognition through the T-cell receptor, HLA-E can be recognized by the inhibitory heterodimeric CD94/NKG2A ligand (14). This interaction inhibits NK-cell cytotoxic functions and prevents autoimmunity, but is also exploited by cytomegalovirus to evade antiviral immunity (15–19). In a phase II human clinical trial, treatment of patients with head and neck cancer with anti-NKG2A in combination with anti-EGFR demonstrated improvement in overall response rates in the majority of the patients (12).
However, it is still unknown in other human cancers whether the HLA-E:CD94/NKG2A inhibitory machinery could also be exploited by cancer to impair TIL priming capacity and inhibit antitumor T-cell responses.

The efficacy of T-cell priming in cancer relies on the uptake and presentation of neoantigen by antigen-presenting cells (APC) via the MHC-Ia molecules. For example, tumor-localized CD141+ conventional dendritic cells (cDC) enable prolonged tissue-localized cross-priming of T-cell activation and maintenance (20, 21), whereas tumor-infiltrating macrophages treated with anti-CD47 showed improved phagocytosis and antigen priming capacity in murine model (22). However, studies using DC vaccines that solely targeted the recovery of MHC-Ia surface expression on tumor APC failed to improve outcomes in mice and patients with cancer (23–25). This is thought to be due to the expression of inhibitory receptors, such as PD-1, on tumor-localized APCs that affected the efficacy of MHC-Ia–T-cell priming and contributed to further tumor growth (26–28). It is therefore likely that an enriched inhibitory HLA-E presence in tumor could also interfere with efficient DC presentation of tumor neoantigens by dampening and masking MHC class Ia–T-cell priming via the CD94/NKG2A interaction.

Thus, in this study, we sought to investigate with human tissues and cells, the correlation between HLA-E and CD94/NKG2A expressions, as well as the phenotype of CD94/NKG2A+ T cells from paired tumor, paratumor, and peripheral blood mononuclear cell (PBMC) samples of patients with cancer. In addition, we investigated the potential of enriched HLA-E:CD94/NKG2A interaction to impair human antitumor T-cell function. We found that HLA-E enrichment on carcinoma tissue derives from epithelial-derived cancer cells, tumor-localized DCs, and macrophages. Effector CD8+ TILs but not regulatory CD4+ TILs have enriched CD94/NKG2A presence that is associated with PD-1+ expression but antagonistic to tissue resident CD103 marker expression. We found that the enriched presence and interaction of HLA-E with CD94/NKG2A significantly impairs IL2 receptor–dependent proliferation of tumor-specific T cells that contributed to reduced cytotoxicity and cytokine production, which improved following antibody-mediated blockade treatment in vitro and ex vivo. Altogether, our work highlights the inhibitory role of enriched HLA-E and CD94/NKG2A on antitumor T-cell functions and the overall exhaustion nature of TILs, which makes them a good target for human cancer immunotherapy in various gastrointestinal cancer types.

**Materials and Methods**

**Study subjects**

This study was approved by the Oxford Radcliffe Biobank research ethics committee (reference number: 09/H0606/5+5) and the Ethics Committee of the Third Affiliated Tumor Hospital of Xinjiang Medical University (Xinjiang, China, reference number: K-201403), based on the guidelines of the Declaration of Helsinki. The average age of the patients was 58.18 years (range 39–81 years). Similar sizes of tissues samples were collected from each patient. Samples were of adenocarcinoma without metastasis, with resection volume no less than 0.5 cm³. Tumor was confirmed using immunohistopathology. Written informed consent was obtained from all subjects prior to inclusion in the study. General stratification of patients is described in Supplementary Table S1.

**Isolation of lymphocytes from paired blood and tissues**

PBMC were isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation. Mononuclear cells were isolated from tumor and paratumor tissues using Millenyi tumor dissociation kit as commercially described. Lymphocytes were isolated using Ficoll-Hypaque density gradient centrifugation.

**Generating antigen-specific T-cell lines**

Antigen-specific T-cell lines were generated as described previously (29). Briefly, isolated lymphocytes from blood and tissues were stimulated with either cancer SSX241–49–specific K9 peptide (KASEKIFVY) or CMV pp65495–503–specific NV9 peptide (NLVPQAVYV) and cultured in RPMI1640 supplemented with 10% v/v heat-inactivated human AB serum (National Blood Service), 2 mmol/L L-glutamine and 1% v/v (500 U/mL) penicillin–streptomycin (Sigma-Aldrich), and recombinant human IL2 (PeproTech) at 37°C. After 14 days, antigen-specific T cells were purified with peptide-MHC Class I tetramer (HLA-A2 K9 or HLA-A2 NV9) using BD Aria II (BD Biosciences) and later expanded in vitro. The cell lines were confirmed for antigen-specificity using tetramer staining by flow cytometry and all functional assays were performed using peptide-specific stimulation.

**Generation of HLA-Ehigh EBV-transformed B-cell line**

An HLA-A2+ Epstein-Barr virus–transformed B-cell line (BCL) was generated in the laboratory in 2005 and maintained in RPMI1640 supplemented with 10% v/v FCS (Sigma Aldrich), 2 mmol/L L-glutamine, and 1% v/v (500 U/mL) penicillin–streptomycin (Sigma-Aldrich) at 37°C. Surface expression of CD19 and HLA-A2 on this BCL was assessed regularly by flow cytometry staining. Lentiviruses expressing either HLA-E0101 or HLA-E0103 allele were generated using the three plasmids system by cotransfection of 293T cell line cultured in DMEM supplemented with 10% v/v FCS (Sigma-Aldrich), 2 mmol/L L-glutamine, and 1% v/v (500 U/mL) penicillin–streptomycin (Sigma-Aldrich) at 37°C, as described previously (29). After 48 hours, supernatant containing lentivirus was collected, filtered, and later concentrated using Lenti-X Concentrator (Clontech) according to the manufacturer’s instruction. The HLA-A2+ BCL was then transduced with either HLA-E0101 or HLA-E0103 lentivirus and cultured for 5 days at 37°C before sorting for HLA-Ehigh expression using BD Aria II (BD Biosciences) and grown in complete media at 37°C. After 7 days, HLA-E expression was confirmed using flow cytometry, with wild-type HLA-A2+ BCL as negative control. All cell lines were tested for Mycoplasma monthly.

**Ex vivo flow cytometry staining**

Cells isolated from tissues and PBMC were first stained with LIVE/DEAD Fixable Aqua Dead Cell Stain Kit (Thermo Fisher Scientific), then stained with conjugated antibodies, with incubation at each step for 20 minutes at 4°C. Tetramer staining was performed as described previously (29). Briefly, cells were stained with either HLA-A2 K9 or HLA-A2 NV9 tetramer for 20 minutes at 37°C before continuing with above mentioned staining process. All samples were acquired on BD LSR Fortessa (BD Biosciences) flow cytometer and analyzed using FlowJo v.10 software (Tree Star Inc.).

Antibody specificities and coupled labels used for surface staining included: Alexa Fluor 488-MHC-1a (clone W6/32; Bio-Rad; RRID: AB_322094), PE-HLA-E (3D12; BioLegend; RRID:AB_1659249).
T-cell proliferation assay

HLA-E<sup>high</sup> BCL (generated as mentioned above) or commercially available HCT116 colorectal cancer cell line (CCL-247; ATCC) were stimulated in vitro with specific peptides at different concentrations. Ex vivo TILs were stimulated with 1 μmol/L Staphylococcal enterotoxin B (SEB; Sigma-Aldrich) for 1 hour at 37°C. T-cell lines were stained with 0.5 μmol/L carboxyfluorescein diacetate succinimidyl ester (CFSE) before being cocultured with peptide-stimulated HLA-E<sup>high</sup> BCL or HCT116 for another 5 hours at 37°C. Cells were then fixed with Cytofix/Cytoperm (BD Biosciences) prior to coculture with peptide-stimulated HLA-E<sup>high</sup> BCL.

For the intracellular cytokine staining assay, HLA-E<sup>high</sup> BCL and HCT116 were stained with 0.5 μmol/L CFSE before being stimulated by peptides at different concentrations and cocultured with antigenspecific T-cell lines at 1:1 E:T ratio at 37°C for 6 hours. Cells were then stained with 7-AAD and assessed by the CFSE®/7-AAD® population present. Evaluation of response was assessed using the abovementioned process of antibody-mediated blocking treatment.

**Statistical analysis**

All graph generation and statistical analyses were conducted using GraphPad Prism v.7 software. Unless stated otherwise, data are summarized as median ± SEM. All statistical details of experiments can be found in figure legends and results sections. Number of patients used for each analysis is as mentioned in the figure legends. All in vitro T-cell experiments were performed three times for each type of experiments. Statistically significant differences between two groups were assessed using a two-tailed paired t test, with Wilcoxon adjustments for nonparametrically distributed variable. For comparisons between more than two paired groups of tissues or treatments, one-way ANOVA with Tukey multiple comparison test was performed. Comparisons between different blocking treatments on different T-cell lines and of the difference in TILs populations across different tumor–node–metastasis (TNM) stages were carried out using two-way ANOVA with Tukey multiple comparisons test. Correlation analysis was performed using nonparametric Spearman test. All tests were two-sided, and differences were considered statistically significant at P < 0.05.

**Results**

HLA-E expression is upregulated on specific cell populations in tumor

Previous studies have highlighted enrichment of HLA-E across cancer tissue sections (10–13), but it remains uncertain on whether specific cell populations in cancer actually contributed toward the enrichment. We first look into whether HLA-E upregulation could be contributed by a specific subpopulation of cancer cells, such as the epithelial cell adhesion molecule (EpCAM)-specific cancer cells, as past studies have demonstrated the commonality of EpCAM overexpression on a majority of carcinomas from tumors of gastrointestinal origin (15, 30–32). Following exclusion of immune cells from our flow cytometry analysis (Supplementary Fig S1A), we confirmed that carcinomas do indeed have EpCAM<sup>high</sup> cells, which are absent in paired
paratumor tissue and PBMC, indicating that EpCAM<sup>high</sup> cells in tumor are specifically epithelial cancer cells (Fig. 1A). In addition, the proportion of EpCAM<sup>high</sup> tumor-derived cells (average: 50.8%) are lower than the EpCAM<sup>dim</sup> paratumor-derived cells (average: 74.4%; Fig. 1A), which is consistent with past studies on overexpression of EpCAM on tumor epithelial cells undergoing tumorigenesis and therefore identifying EpCAM<sup>dim</sup> paratumor cells as normal epithelial cells (15, 30–32).

Upon evaluation of HLA-E on these populations, we observed higher HLA-E<sup>r</sup> population of EpCAM<sup>high</sup> epithelial cancer cells (average = 81%), compared with the EpCAM<sup>dim</sup> tumor-derived cells (average 41.3%) and the EpCAM<sup>dim</sup> paratumor-derived/tumorigenic epithelial cells (average 21%; Fig. 1B). This is consistent with significantly higher HLA-E surface expression (average median fluorescence intensity (MFI) = 750) observed on the EpCAM<sup>high</sup> epithelial cancer cells (P < 0.01; Fig. 1C). In contrast, MHC-Ia surface expression is downregulated on EpCAM<sup>high</sup> epithelial cancer cells (Fig. 1D). Similar patterns of gradual HLA-E upregulation from EpCAM<sup>dim</sup> tumor-derived tumorigenic cells to the EpCAM<sup>high</sup> epithelial cancer cells were found across different cancers of gastrointestinal origin, namely esophageal, gastric, and colorectal cancers (Supplementary Fig. S1B).

In addition to cancer cells, the immunosuppressive tumor microenvironment is well known to dysregulate the functionality of tumor-infiltrating immune cells (26–28). We thus decided to assess whether the dysfunctionality could also be due to upregulation of HLA-E expression on macrophages, cDC subsets, and plasmacytoid DC (pDC) residing in solid tumors (gating strategy and identification of APC subpopulations as per Supplementary Fig. S2A and S2B). In particular, we found that tumor-localized CD141<sup>r</sup> cDC have significantly reduced MHC-Ia expression (average of 2- to 4-fold) but increased HLA-E expression (average of 2-fold) compared with the same population derived from paired paratumor tissue and PBMC (r<sup>2</sup> = 0.9747; P < 0.01; Fig. 1E; Supplementary Fig. S2C). Other professional APC subsets in tumor, namely CD1c<sup>r</sup> cDC, pDC, and inflammatory macrophages, were also found to have an inverse correlation between the increase in HLA-E expression and the decrease in MHC-Ia expression (r<sup>2</sup> > 0.9000; P < 0.01; Fig. 1E). Although the frequencies of paratumor-derived and PBMC-derived APC subpopulations were higher, their HLA-E expression was reduced compared with HLA-E expression on the smaller subpopulations of tumor APCs (Supplementary Fig. S2D). Nonprofessional APCs, such as B cells, further demonstrated significant increase of its HLA-E and reduction of MHC-Ia expressions in solid tumors (Supplementary Fig. S2E).

A similar pattern of HLA-E upregulation on tumor-derived DCs was observed across the three different cancers of gastrointestinal origin, as well as in kidney cancer (Fig. 1F). This therefore suggests that HLA-E upregulation is not only enriched on cancer cells but also on other tumor-residing cells such as on APCs, indicating a potential contributory role of HLA-E in evading antitumor cell responses in cancer.

Inhibitory CD94/NKG2A ligand is upregulated on CD8<sup>r</sup> TILs

Given the upregulation of HLA-E in the tumor microenvironment, we then investigated whether the inhibitory receptor of HLA-E, the heterodimeric CD94/NKG2A, displayed a similar pattern of enrichment in the same set of patients with cancer from paired tumor, paratumor, and PBMC samples. We observed significant CD94 and NKG2A coexpression and heterodimeric CD94/NKG2A<sup>r</sup> T-cell population in carcinoma, but minimal CD94/NKG2A population and coexpression on T cells derived from paratumor tissue and PBMC (Fig. 2A and B). In contrast, we did not observe any heterodimeric CD94/NKG2A<sup>r</sup> T-cell population from tumor, paratumor, or PBMC (Fig. 2C). The enrichment of CD94/NKG2A<sup>r</sup> TILs population is directly correlated with the enrichment of HLA-E on both epithelial cancer cells (r<sup>2</sup> = 0.9241; P < 0.001) and tumor-derived CD141<sup>r</sup> cDCs on the same patients with cancer (r<sup>2</sup> = 0.8860; P < 0.001; Fig. 2D).

Effect-based immune cells such as CD8<sup>r</sup> T cells, NKT cells, and NK cells were the ones that have significantly higher CD94/ NKG2A<sup>r</sup> population in tumor, whereas regulatory-based cells such as CD4<sup>r</sup> T cells lack any CD94/NKG2A<sup>r</sup> population in any of the tissue sites evaluated (Fig. 2E and F). The enrichment of the CD94/NKG2A<sup>r</sup> population in tumor was similarly observed across different types of gastrointestinal cancers, namely esophageal, gastric, and colorectal tumors (Supplementary Fig. S3A). We observed that patients with gastrointestinal cancer with later TNM stage of cancer size (indicative of tumor progression) have a significantly gradual increment of CD94/NKG2A<sup>r</sup> TILs population (Fig. 2G), suggesting the preferential selection of CD94/NKG2A<sup>r</sup> and especially HLA-E overexpression during tumor growth in human cancers.

In assessing the maturation phenotype of TILs in tumor, we found that CD94/NKG2A<sup>r</sup> TILs are primarily of late-stage effector memory phenotype (CD27<sup>r</sup> CD45RA<sup>r</sup> CCR7<sup>r</sup>), in contrast to the predominantly early-stage effector phenotype of the CD94/NKG2A<sup>r</sup> population (CD27<sup>r</sup> CD45RA<sup>r</sup> CCR7<sup>r</sup>; Fig. 2H).

This matured phenotype is characteristic of the tumor-derived CD94/NKG2A<sup>r</sup> population as the CD94/NKG2A<sup>r</sup> population from paratumor tissue is primarily early-stage effector memory (CD27<sup>r</sup> CD45RA<sup>r</sup> CCR7<sup>r</sup> and the CD94/NKG2A<sup>r</sup> population from PBMC is mostly early-stage central memory phenotype (CD27<sup>r</sup> CD45RA<sup>r</sup> CCR7<sup>r</sup>; Supplementary Fig. S3B). The highly matured phenotype of CD94/NKG2A<sup>r</sup> TILs population suggest that these TILs in tumor are antigen-experienced T cells that could be selected to upregulate inhibitory CD94/NKG2A expression to impair and exhaust antitumor TIL responses.

CD94/NKG2A<sup>r</sup> and PD-1 are coexpressed on CD8<sup>r</sup> TILs

PD-1<sup>r</sup> T cells are dysfunctional in solid tumors (33), and thus we evaluated whether the CD94/NKG2A<sup>r</sup> TILs could also have high PD-1 expression (Supplementary Fig. S4). We found that CD8<sup>r</sup> T cells are enriched for the PD-1<sup>r</sup> population (Fig. 3A and B). Specifically, the PD-1<sup>r</sup> CD94/NKG2A<sup>r</sup> population is present in tumors (average of 37% of total CD8<sup>r</sup> T cells; P < 0.001) at a greater frequency, compared with paired paratumor tissue and PBMC (Fig. 3A and C).

A similar pattern of PD-1 and CD94/NKG2A coexpression on TILs was found in patients with either colorectal or gastric cancers (Fig. 3D). In contrast, BTLA and KLRG-1 was found not to be coexpressed on CD94/NKG2A<sup>r</sup> TILs (Fig. 3E), thus suggesting that the exclusive coexpression of CD94/NKG2A<sup>r</sup> with PD-1 in carcinoma and this dual coexpression might contribute to the overall dysfunctionality of PD-1<sup>r</sup> TILs.

CD94/NKG2A<sup>r</sup> TILs lack intratumoral CD103 expression

We also found that NKG2A<sup>r</sup> T cells lack CD103 surface expression such that only the CD94/NKG2A<sup>r</sup> TILs population...
Epithelial-derived cancer cells and tumor-residing APCs have higher HLA-E expression but reduced MHC-1a expression. A, Representative contour plots of EpCAM expression on cells isolated from paired tumor (TUMOR), paratumor (PARA), and PBMC, with EpCAM^{high} cells observed only in tumor-derived tissue identified as epithelial cancer cells, whereas EpCAM^{dim} tumor-derived cells as tumorigenic cells and EpCAM^{dim} paratumor-derived cells as normal epithelial cells. B, Representative gating of HLA-E^{+} population on tumor-derived EpCAM^{high} cancer cells (left), tumor-derived EpCAM^{dim} tumorigenic cells (middle), and paratumor-derived EpCAM^{dim} normal epithelial cells (right). The HLA-E expression (C) and MHC-1a expression (D) by MFI on three different populations of EpCAM-expressing populations. N, number of patients = 10 (esophageal cancer, n = 3; gastric cancer, n = 4; and colorectal cancer, n = 3); one-way ANOVA with Tukey post hoc analysis; F-values, degree of freedom: 5.852,9 (left); 4.163,9 (right).

E, Correlative expression of HLA-E and MHC-1a by MFI on CD141^{+} cDC, CD1c^{+} cDC, pDC, and inflammatory macrophages derived from paired tumor, paratumor, and PBMC. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7); correlative analysis of non-parametric Spearman test of r^2 = 0.9747, P < 0.01 for CD141^{+} cDC; r^2 = 0.8174, P < 0.05 for CD1c^{+} cDC; r^2 = 0.9764, P < 0.01 for pDC; and r^2 = 0.9085, P < 0.01 for inflammatory macrophages. F, HLA-E expression by MFI on DC subsets from paired tumor, paratumor, and PBMC samples in four different cancer types. (N, number of patients with esophageal cancer = 7; gastric cancer n = 8; colorectal cancer n = 7; and kidney cancer n = 5); one-way ANOVA with Tukey post hoc analysis. Horizontal line, median; interval, 95% confidence; connecting lines, samples from the same patients. *, P < 0.05; **, P < 0.01; *** P < 0.001; ns, not significant. Data represent with median ± SEM.
Figure 2.
CD94/NKG2A expression and presence is higher on tumor-infiltrating immune cells. A, Representative contour plots on CD94 and NKG2A staining on CD3⁺ T cells from paired tumor, paratumor, and PBMC samples from 1 patient with cancer (proportion of CD94/NKG2A⁺ T cells in tumor = 17.9%; in paratumor = 1.27%; and in PBMC = 0.3%). B, Correlative analysis on NKG2A and CD94 expression by MFI on tumor-derived CD3⁺ T cells. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7); correlative analysis of nonparametric Spearman test, $r^2 = 0.9064; P < 0.001$. C, The frequency of CD94/NKG2C⁺ T cells from paired tumor (TUMOR), paratumor (PARA), and PBMC samples. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7). D, Correlative analysis between the frequency of CD94/NKG2A⁺ CD3⁺ TILs with the HLA-E expression by MFI on EpCAM-specific tumor cells (left) and the HLA-E expression by MFI on tumor-derived CD141⁺ cDC (right). N, number of patients = 10 (esophageal cancer, n = 3; gastric cancer, n = 4; and colorectal cancer, n = 3); correlative analysis of nonparametric Spearman test, $r^2 = 0.9241, P < 0.0001$ (left); $r^2 = 0.8860, P < 0.0001$ (right). (Continued on the following page.)
are able to express CD103 in tumor ($P < 0.001$; Fig. 4A and B), suggesting antagonistic expression between both markers on TILs. Patients with later TNM stage of cancer size had gradually increasing CD94/NKG2A $^+$ CD8$^{+}$ TIL populations but with steadily decreasing CD103$^+$ CD8$^{+}$ TIL populations (Fig. 4C). This is consistent with the higher CD103$^+$ T-cell population but a reduced NKG2A$^+$ population in paratumor tissue compared with the paired carcinoma (Fig. 4D). In comparison with the tissue-localizing CD103$^+$ CD94/NKG2A$^+$ T cells in PBMC, a significant presence of circulating CD103$^+$ CD94/NKG2A$^+$ T cells (average $= 4\%$) was observed in some patients with cancer (Fig. 4E), suggesting impaired antitumor cellular responses, which might occur prior to further tumor expansion, also exist in the blood of the patients with cancer.

CD94/NKG2A$^+$ antigen–specific T cells have impaired proliferation capacity

To investigate the potential role of HLA-E:CD94/NKG2A interaction on immune responses, we isolated CD94/NKG2A$^+$ and CD94/NKG2A$^-$ populations of PBMC-derived HLA-A2–restricted tumor-associated antigen (TAA)-specific CD8$^+$ T cells and cocultured with HLA-A2–matched allogeneic HCT116 human cancer cell line (HCT116, which expresses HLA-E at steady state; Supplementary Fig. S5A). We observed reduced proliferation in the CD94/NKG2A$^+$ TAA-specific T-cell population compared with the CD94/NKG2A$^-$ population ($60\%$ vs. $7\%$; $P < 0.001$; Fig. 5A). Upon anti-CD94/NKG2A–mediated blocking treatment, most cells of the CD94/NKG2A$^+$ population have reduced CFSE expression that is indicative of higher proliferation, compared with the isotype and no blocking treatments (Fig. 5B). Similar improvement of proliferation was also observed on tumor-derived antigen-specific T cells following antibody treatment (Fig. 5C).

The improvement in T-cell proliferation was contributed by the increase in IL2 receptor (CD25) expression on CD94/NKG2A$^+$ cells following the antibody blocking treatment, reaching a similar high receptor expression as of the CD94/NKG2A$^+$ population (Fig. 5D). This is again observed on the tumor-derived antigen-specific T cells following antibody treatment (Fig. 5E). As expected, the upregulation of IL2 receptors (CD25) on the antibody-treated CD94/NKG2A$^+$ T-cell population corresponded to the increment in IL2 cytokine production and the proportion of IL2-producing cells (Fig. 5F and G; Supplementary Fig. S5B). The recovery of IL2 receptor–dependent proliferation following antibody-mediated treatment suggested that enriched HLA-E and CD94/NKG2A interaction on tumor-specific T cells can impair the proliferation capacity, which might subsequently affect its antitumor T-cell responses.

Impaired responses recovered after CD94/NKG2A antibody blockade

We next investigated whether the reduced proliferation of CD94/NKG2A$^+$ T cells can affect its antitumor killing ability. We found that CD94/NKG2A$^+$ population of TAA-specific T cells have poor killing ability when cocultured with HCT116 cancer cell line compared with the CD94/NKG2A$^-$ population (Fig. 6A). The poor killing ability is evident from the significant improvement of cytotoxicity observed on CD94/NKG2A$^+$ TAA-specific T-cell population when treated with the anti-CD94/NKG2A–blocking antibody and is sensitive up to 0.3 μmol/L antigen stimulation of HCT116 and up to 0.1 μmol/L antigen stimulation of HLA-E$^{high}$ BCL (Fig. 6B and C). Similar pattern of T-cell cytotoxic recovery was also observed on tumor-derived CD94/NKG2A$^+$ antigen-specific T cells, again up to 0.1 μmol/L antigen stimulation of HLA-E$^{high}$ BCL (Fig. 6C).

In addition, the CD94/NKG2A$^+$ TAA-specific T-cell population has significantly impaired IFN$\gamma$ production compared with the CD94/NKG2A$^-$ population (Fig. 6D). This corresponded to the significantly reduced number of IFN$\gamma$-expressing cells of the CD94/NKG2A$^+$ population, when cocultured with either HCT116 or HLA-E$^{high}$ BCL, even at high antigen stimulation of 1 μmol/L (Fig. 6E). Similar to the recovery in proliferation and cytotoxicity, IFN$\gamma$ production and expression recovered following anti-CD94/NKG2A–mediated blockade treatment (Fig. 6F and G; Supplementary Fig. S5B). However, no differences were observed in TNF$\alpha$ and MIP-1β responses following the anti-CD94/NKG2A blockade treatment. Only the chemotactic CCL5 was significantly elevated 48 hours later (Supplementary Fig. S6A–S6G). Taken altogether, these in vitro data suggest that enriched HLA-E and CD94/NKG2A interaction, particularly on tumor-specific T cells, affected the survivability of T cells through their proliferation capacity, antitumor cytotoxicity, and cytokine responses.

To corroborate the in vitro observations, we then performed ex vivo study by isolating cell mixtures from tumors of 4 patients with gastric cancer with confirmed presence of at least 5% of CD94/NKG2A$^+$ TILs and stimulated with SEB before being treated with anti-CD94/NKG2A–blocking antibody. Consistent with our in vitro findings, we confirmed that the frequency of IFN$\gamma$-expressing cells and the amount of IFN$\gamma$ produced were significantly improved following antibody-mediated treatment compared with the isotype and no blocking treatments (Fig. 7A and B; Supplementary Fig. S7). Furthermore, more stages of cell proliferation were observed after the anti-CD94/NKG2A–blocking treatment (Fig. 7C), corresponding to significantly elevated IL2 receptor (CD25) expression on CD8$^+$ TILs 48 hours later (Fig. 7D). The IL2 receptor–dependent proliferation was vital in the recovery of CD8$^+$ TILs ex vivo after antibody treatment, as the IL2 expression and production were also found to be significantly elevated on CD8$^+$ TILs (Fig. 7E and F; Supplementary Fig. S7).

Altogether, our in vitro and ex vivo observations indicated that the enriched presence and interaction between HLA-E and CD94/NKG2A, particularly on tumor-specific T cells, can negatively affect antitumor T-cell immune responses and contribute to the exhaustive and dysfunctional nature of TILs in patients with gastrointestinal cancer.

(Continued.) E, The proportion of CD94/NKG2A$^+$ populations of CD3$^+$ T cells, CD8$^+$ T cells, NKT cells, and NK cells from paired tumor, paratumor, and PBMC. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7); one-way ANOVA with Tukey post hoc analysis. F, The proportion of CD94/NKG2A$^+$ population of CD4$^+$ T cells derived from paired tumor, paratumor, and PBMC. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7); two-way ANOVA with Tukey post hoc analysis. G, The proportion of CD94/NKG2A$^+$ CD8$^+$ TILs (left), CD94/NKG2A$^+$ CD8$^+$ TILs (middle), and total CD8$^+$ TILs (right) according to maturation phenotype expression of CD27, CD45RA, and CCRI in carcinoma. N, number of patients = 22 (esophageal carcinoma, n = 7; gastric carcinoma, n = 8; and colorectal carcinoma, n = 7); one-way ANOVA with Tukey post hoc analysis. Horizontal line, median; interval, 95% confidence; connecting lines, samples from the same patients; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ns, not significant. Data represent with median ± SEM.
Figure 3.
CD94/NKG2A+ TILs exclusively coexpressed PD-1. A, Representative contour plots of PD-1 and NKG2A expression on CD8+ T cells derived from paired tumor (TUMOR), paratumor (PARA), and PBMC, according to PD-1 high, intermediate, or negative expression. B, The proportion of CD94/NKG2A+ CD8+ TILs expressing either PD-1high, PD-1int, or PD-1−/−. N, number of patients = 22 (esophageal cancer, n = 5; gastric cancer, n = 6; colorectal cancer, n = 6; and lung cancer, n = 5); one-way ANOVA with Tukey post hoc analysis. C, Proportion of CD94/NKG2A+ PD-1high CD8+ T cells from paired tumor, paratumor, and PBMC. N, number of patients = 22 (esophageal cancer, n = 7; gastric cancer, n = 8; and colorectal cancer, n = 7); one-way ANOVA with Tukey post hoc analysis. D, The proportion of CD94/NKG2A+ PD-1high CD8+ T cells from paired tumor, paratumor, and PBMC according to cancer types; patients with colorectal cancer n = 7 (left) and patients with gastric cancer n = 8 (right); one-way ANOVA with Tukey post hoc analysis. E, Proportion of CD94/NKG2A+ CD8+ TILs expressing either BTLA, KLRG-1, or PD-1 according to cancer types; patients with colorectal cancer n = 7 (left) and patients with gastric cancer n = 8 (right). Horizontal line, median; interval, 95% confidence; connecting lines, samples from the same patients; *, P < 0.05; **, P < 0.01; ***, P < 0.001; ns, not significant. Data represent with median ± SEM.
Discussion

Using comparison between paired tumor, paratumor, and PBMC from mainly patients with gastrointestinal cancer, we reported on enrichment of HLA-E in carcinoma that is contributed not only by the epithelial cancer cells but also by tumor dendritic cells and macrophages. The HLA-E enrichment paralleled the increment in the inhibitory CD94/NKG2A⁺CD8⁺ TIL population that is exclusively associated with PD-1 high expression in solid tumors, but minimally present in paired paratumor tissue and absent in PBMC of patients with cancer.

Studies by Andre and colleagues, as well as by van Manfoort and colleagues highlighted the improvement in survival rates and tumor control in anti-NKG2A–treated murine cancer models and the increased disease stability of combinatory anti-NKG2A and anti-EGFR–treated patients with head and neck cancer of a phase II clinical trial (12, 13). Our current study reveals mechanisms by which enriched presence and interaction of HLA-E with CD94/NKG2A could impair antitumor T-cell responses in human cancer. The improvement of IL2 receptor–dependent proliferation and antitumor killing by tumor-specific T cells treated with anti-CD94/NKG2A revealed the inhibitory effect of enriched CD94/NKG2A presence on human TILs, which contribute toward worse clinical outcomes in patients as tumor progresses.

In addition, past studies indicating abundance of HLA-E in cross-sectional cancer tissue analysis lack corresponding comparison with paired paratumor tissue and blood of the patients and did not examine the types of cells that contribute to this
abundance. Here, we showed that HLA-E enrichment occurs on epithelial cancer cells and on tumor-residing APCs. Tumor-residing APCs help in tissue-localized antigen presentation and maintenance of antitumor T-cell responses (20–22). However, other murine studies have also shown that tumor APCs can be dysregulated to become tolerogenic, a process driven by immunosuppressive factors such as IL10 and β-catenin (26, 27, 34, 35). For instance, the inhibitory PD-1/PD-L-1 axis was upregulated on murine tumor APC and contributed to progressively growing tumor (28, 36, 37). We further demonstrated that not only can HLA-E be upregulated on tumor-residing APC, but its inhibitory CD94/NKG2A ligand on TILs is also upregulated within larger tumors. This in turn could elucidate the reasons that past DC-based vaccines that solely targeted recovery of tumor neoantigen presentation on MHC-Ia of tumor DC were not successful at improving recovery in murine cancer models and patients with cancer (23–25). The enriched HLA-E and CD94/NKG2A presence and interaction between tumor–APCs and CD8$^+$ TILs could overpower and dampen the activating MHC Class Ia–T-cell receptor signaling, causing ineffective antitumor priming and anergic T-cell activation.

The corresponding increment of CD94/NKG2A on TILs in patients with gastrointestinal cancer is antagonistic to the downregulation of the intratumoral CD103 expression. CD103$^+$ T cells are T-cell mediators of long-lived protection against viral infections in peripheral tissues such as intestines and lung (38, 39). In the cancer setting, the presence of CD103 aids T-cell infiltration into intraepithelial murine tumors, whereas the accumulation of CD103 contributed to extensive granzyme B degranulation in the immunologic synapse, leading to better killing of cancer cells.
Figure 6. Impairment of IFNγ response and cytotoxicity by CD94/NKG2A+ HLA-A2–restricted antigen-specific T cells, which recovers following antibody-mediated blocking treatment in vitro. A, The proportion of lysed cancer cells following CD94/NKG2A+ or CD94/NKG2A– TAA-specific T cells cocultured with HCT116. N, number of experimental repeats, n = 3; paired student t test with Wilcoxon adjustments; F-values, degree of freedom: 47.3, 2. B, The proportion of lysed cancer cells following CD94/NKG2A+ TAA-specific T-cell population coculture with HCT116, following either CD94/NKG2A antibody blockade, isotype, or no blocking treatments at five different concentration of antigen stimulation. N, number of experimental repeats, n = 3; two-way ANOVA with Tukey post hoc analysis. C, The proportion of lysed cancer cells following coculture of CD94/NKG2A+ population of PBMC-derived TAA-specific T cells (left) and tumor-derived CMV-specific T cells (right) with HLA-Ehigh BCL. N, number of experimental repeats, n = 3; two-way ANOVA with Tukey post hoc analysis. D, The IFNγ production of CD94/NKG2A+ or CD94/NKG2A– TAA-specific T cells following coculture with HLA-A2–matched HLA-Ehigh BCL. N, number of experimental repeats, n = 3; paired Student t test with Wilcoxon adjustments; F-values, degree of freedom: 33.9, 2. E, The proportion of IFNγ+ cells of CD94/NKG2A+ or CD94/NKG2A– TAA-specific T cells following coculture with either HCT116 or HLA-Ehigh BCL. N, number of experimental repeats, n = 3; paired Student t test with Wilcoxon adjustments. The proportion of IFNγ+ cells (F) and IFNγ production (G) of CD94/NKG2A+ population of PBMC-derived TAA-specific T cells and tumor-derived CMV-specific T cells following either CD94/NKG2A antibody blockade, isotype, or no blocking treatments. N, number of experimental repeats, n = 3; one-way ANOVA with Tukey post hoc analysis. P value, 95% confidence; *, P < 0.05; **, P < 0.01; ***, P < 0.001. Data represent with median ± SEM.
in vitro (40, 41). The observation of gradual loss of CD103 in progressively growing gastrointestinal tumors suggests that CD103 absence is detrimental toward cancer survival and that cancer preferentially upregulates inhibitory markers such as CD94/NKG2A and PD-1 expression as a mechanism to avoid antitumor immunity. Our observation of antagonistic expression is contradictory to the coexpression of NKG2A with CD103 on TILs observed by van Manfoort and colleagues on patients with human papilloma virus–positive cervical carcinoma (13). It is most likely that any NKG2A coexpression with CD103 could be present on viral-specific tumor-infiltrating T lymphocytes, whereby another study has highlighted the overabundance of bystander viral-specific T cells in tumor that do not recognize tumor neoantigens and therefore might not have antitumor immune capacity in carcinoma (42).

Patients with PD-1 high T cells have demonstrated good responses to anti-PD-1 treatment due to their impaired functionality and characteristics (33). Although anti-PD-1 treatment in various clinical studies has supported recovery toward prolonged survival in patients with cancer, there is still a sizeable portion of patients that lacked major improvement (6, 7). We demonstrated here that PD-1 high TILs in patients with gastrointestinal cancer have enriched CD94/NKG2A expression, which is consistent with findings in studies in patients with head and neck cancer (12, 13). As we further show that the enriched CD94/NKG2A+ tumor-specific T cells lack efficient proliferation capacity, this can therefore lead to detrimental outcome on the long-term survivability of antitumor T cells. Subsequently, the reduced proliferation of TILs could eventually contribute toward the impaired antitumor cytotoxicity and responses against cancer, albeit even after being treated with anti-PD-1 treatment. The commonality of HLA-E and CD94/NKG2A enrichment across different cancer types, together with the exclusivity of PD-1 high expression highlights the key role of CD94/NKG2A as a compensatory exhaustive marker of TILs that limits the effectiveness of antitumor TILs.

In light of cancer immunotherapy, targeting the inhibitory CD94/NKG2A signaling pathways on TILs and their interaction with HLA-E in tumors could prove beneficial to patients with HLA-E and PD-1 enriched tumors. Targeting CD94/NKG2A could improve the long-term survivability of effector cells such as CD8+ T cells with better cytotoxic functions following combinatory anti-PD-1 treatment, especially in patients with early-stage cancer.

Disclosure of Potential Conflicts of Interest
A. McMichael reports receiving speakers bureau honoraria from the Chinese Academy of Medical Sciences and is a consultant/advisory board member for Oxford Vacmedix Ltd. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions
Conception and design: M. Abd Hamid, A. McMichael, Y. Peng, T. Dong
Development of methodology: M. Abd Hamid, X. Li, T. Dong
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): M. Abd Hamid, R.-Z. Wang, X. Yao, P. Fan, X. Li, X.-M. Chang, Y. Feng, S. Jones, D. Maldonado-Perez, C. Waugh, C. Verrill
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): M. Abd Hamid, X. Li, T. Dong

Figure 7.
Recovery of CD8+ TILs functions following anti-CD94/NKG2A–mediated blocking treatment ex vivo. The proportion of IFN-γ+ cells (A) and IFNγ production (B) of CD8+ TILs stimulated with 0.1 μmol/L SEB stimulation following either CD94/aNKG2A antibody blockade, isotype, or no blocking treatment. N, number of patients with gastric cancer, n = 4; one-way ANOVA with Tukey post hoc analysis. C, Representative histogram plot of CFSE-based proliferating cells of CD8+ TILs following different treatments. The IL2 receptor (CD25) geometric MFI expression (D), proportion of IL2+ cells (E), and IL2 production (F) on CD8+ TILs following different treatments. N, number of patients with gastric cancer, n = 4; one-way ANOVA with Tukey post hoc analysis. P value, represent 95% confidence; *, P < 0.05; **, P < 0.01. Data represent with median ± SEM.
References


Enriched HLA-E and CD94/NKG2A Interaction Limits Antitumor CD8⁺ Tumor-Infiltrating T Lymphocyte Responses


Updated version Access the most recent version of this article at:
doi:10.1158/2326-6066.CIR-18-0885

Supplementary Material Access the most recent supplemental material at:
http://cancerimmunolres.aacrjournals.org/content/suppl/2019/06/18/2326-6066.CIR-18-0885.DC1

Cited articles This article cites 42 articles, 20 of which you can access for free at:
http://cancerimmunolres.aacrjournals.org/content/7/8/1293.full#ref-list-1

Citing articles This article has been cited by 2 HighWire-hosted articles. Access the articles at:
http://cancerimmunolres.aacrjournals.org/content/7/8/1293.full#related-urls

E-mail alerts Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions To request permission to re-use all or part of this article, use this link
http://cancerimmunolres.aacrjournals.org/content/7/8/1293.
Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.