CEACAM1-3S Drives Melanoma Cells into NK Cell-Mediated Cytolysis and Enhances Patient Survival

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Abstract

CEACAM1 is a widely expressed multifunctional cell–cell adhesion protein reported to serve as a poor prognosis marker in melanoma patients. In this study, we examine the functional and clinical contributions of the four splice isoforms of CEACAM1. Specifically, we present in vitro and in vivo evidence that they affect melanoma progression and immune surveillance in a negative or positive manner that is isoform specific in action. In contrast with isoforms CEACAM1-4S and CEACAM1-4L, expression of isoforms CEACAM1-3S and CEACAM1-3L is induced during disease progression shown to correlate with clinical stage. Unexpectedly, overall survival was prolonged in patients with advanced melanomas expressing CEACAM1-3S. The favorable effects of CEACAM1-3S related to enhanced immunogenicity, which was mediated by cell surface upregulation of NKG2D receptor ligands, thereby sensitizing melanoma cells to lysis by natural killer cells. Conversely, CEACAM1-4L downregulated cell surface levels of the NKG2D ligands MICA and ULBP2 by enhanced shedding, thereby promoting malignant character. Overall, our results define the splice isoform-specific immunomodulatory and cell biologic functions of CEACAM1 in melanoma pathogenesis.

Introduction

Melanoma is one of the most aggressive types of cancer, and its prevalence has risen faster than any other malignant disease in the western world. Tumor progression starts very early, resulting in a median survival of 6 to 12 months in patients with advanced melanoma (1). Melanoma progression is a complex multistep process orchestrated by a variety of cellular factors, including dysregulation of cell adhesion molecules (2). Evidence has amassed that expression of the multifunctional carcinoembryonic antigen (CEA)-related cell adhesion molecule 1 (CEACAM1) may be involved during this process (3). CEACAM1 belongs to the CEA family within the immunoglobulin superfamily (4) and is expressed in human epithelial (5, 6), endothelial (7), and hematopoietic cells (8, 9). Downregulation of CEACAM1 has been reported in colon (10), prostate (11), and breast cancer (12). Melanocytes are CEACAM negative (13), while high expression levels of CEACAM1 have been detected in melanoma (14) and adenocarcinoma (15). CEACAM1 was reported to inhibit cell proliferation in several tumor entities, excepting melanoma (13, 16, 17). On the tumor cell surface, the CEACAM1 protein has been shown to interact directly with CEACAM1 on immune cells, leading to functional inhibition of those cells (18–21), or to indirectly modulate cancer cell immunogenicity by downregulating their cell surface expression of MHC class I-related molecule A and B (MICA/B) and UL16-binding protein1 (ULBP; ref. 22), both ligands for the natural killer (NK) gene complex group 2 member D (NKG2D) receptor expressed on malignant cells (23, 24).

Although 12 different splice variants of the human CEACAM1 gene have been reported, only four are shown to be expressed at mRNA level (25, 26). The CEACAM1-4 variants consist of four, CEACAM1-3 of three heavily glycosylated extracellular domains. Both isoforms are trans-membrane anchored and carry either the long (L, 73 aa) or short (S, 10 aa) cytoplasmic domain (27).

CEACAM1 has been controversially discussed as tumor suppressor and driver of invasion (28, 29). Most studies contributing to this discussion were focused on total CEACAM1 or CEACAM1-4L/S. In 2002, Thies and colleagues showed that the CEACAM1 protein expression in primary cutaneous melanoma predicts the development of metastatic disease (30). Furthermore, levels of soluble CEACAM1 in sera from melanoma patients have been shown to inversely correlate with overall survival (31, 32). This spurred discussion of CEACAM1 as a more specific and sensitive biomarker than those currently used, including melan-A, S100β, and HMB45, and has implicated CEACAM1 as a potential novel therapeutic target (14). Nevertheless, none of these studies addressed the impact of the four CEACAM1 splice variants.
Furthermore, the clinical impact and the precise mechanism by which the four CEACAM1 variants modulate melanoma progression are completely unknown. Our present study analyzed the biologic function and clinical relevance of the individual CEACAM1 splice variants in human melanoma biopsies of increasing disease stages and in cell lines, established from patient’s metastases. We show for the first time that CEACAM1-3S, CEACAM1-3L, CEACAM1-4S, and CEACAM1-4L differentially affects cellular function and melanoma progression. Furthermore, we demonstrate that the expression of CEACAM1-3S correlates significantly with the clinical stage and strikingly with a prolonged patient overall survival. Finally, we provide strong evidences that CEACAM1-3S triggers melanoma cells for NK cell-mediated cytolysis by upregulating cell surface expression of MICA and ULBP2, whereas CEACAM1-4L causes the contrary effect due to enhanced shedding of both NKG2D ligands (NKG2DL).

Materials and Methods

Some Materials and Methods are detailed in the Supplementary Data.

Tissues and cell culture

Malignant melanoma cell lines and biopsies were obtained from the Skin Cancer Biobank of the Dermatology Department, University Hospital Essen, Germany. Informed patient consent and the appropriate Institutional Review Board approval were obtained for all patients. Clinical information including age, gender, stage of disease, tumor load, and survival time was documented and retrieved from the electronic database (Achiver Anyware Medical, Achiver Software). Disease staging was performed according to the staging criteria of the American Joint Committee on Cancer (AJCC; ref. 33). Cell lines were established from malignant melanoma as described before (34, 35). RPMI-1640 supplemented with 10% FCS, 1% penicillin/streptomycin, and 1% l-glutamine (all from PAA Laboratories) was used as culture medium. All cell lines were maintained at 37°C and 5% CO2 and regularly tested for mycoplasma infection.

Plasmid constructs and transfection

The coding sequences for CEACAM1-3L (NM_001184813.1), CEACAM1-3S(NM_001184816.1), CEACAM1-4L(NM_0017124.4), and CEACAM1-4S (NM_001024912.2) were cloned into the pcDNA3.1(−) Neo plasmid (Invitrogen) and verified by sequencing. Constructs were transfected into the Ma-Mel-86a cell line using Metafectene (Biontex) according to the manufacturer’s protocol, and single clones selectively grown in medium containing 1 mg/mL G418 (Carl Roth).

xCELLigence System

The Real-Time Cell Analyzer System was used to analyze cellular functions (36) and cytotoxicity (37). The experiments were performed as described by the manufacturer’s instructions. In short, the half-maximum cell index (IC50) between 0 hour and 70 hours (CI70) was used for determination of statistical differences calculated by the Student t test. Cytotoxicity results are presented as percentages of cytosis determined from normalized cell index (nCI): % of specific lysis = [nCI (no effector) – nCI (effector)]/nCI (no effector) × 100. Experiments were performed in duplicates.

Please refer to the detailed Supplementary Experimental Procedures.

Immunofluorescence

Melanoma cells on coverslips were grown to 90% confluency. Cells were fixed either with methanol or 4% PFA, blocked with 3% BSA/PBS, then incubated at 4°C overnight with primary antibodies in 1.5% BSA/PBS. Primary antibodies were visualized by fluorescent labeled secondary antibodies. Nuclei were counterstained with DAPI (Carl Roth), and fluorescence microscopy was conducted on a Leica SP8 confocal microscope (Leica), Zeiss AxioObserver.Z1 with Apotome and Zeiss ELYRA PS.1 using SIM technology (Zeiss). Antibody information is provided in Supplementary Materials and Methods section.

Flow cytometry

Surface expressions were analyzed using a FACSscilab flow cytometer and the CellQuest Pro software (BD Biosciences). Gallios system (Beckman Coulter) equipped with FlowJo software and Accuri C6 flow cytometer (BD Biosciences). Cells were harvested, incubated with primary antibodies and fluorescence-conjugated secondary antibodies. Isotype matched control antibody staining served as negative control. Dead cells were excluded from measurements by propidium iodide staining. Antibody information is provided in Supplementary Materials and Methods section.

MICA ELISA

Soluble MICA (sMICA) was quantified, using the DuoSet ELISA Development System (R&D Systems) according to the manufacturer’s protocol. Melanoma cells were starved for 24 hours. Supernatant was collected and centrifuged to remove cellular debris. Levels of sMICA were normalized to cell number at time of harvesting.

Enrichment of primary polyclonal NK cells

CD3~CD56~ NK cells were enriched from PBMCs of healthy donors using MACS technology (Miltenyi Biotec) according to the manufacturer’s protocol. Enrichment of CD3~CD56+ NK cells was confirmed by flow cytometry and ranged between 90% and 95%. NK cells were cultured in the presence of 200 IU/ml IL2 (Chiron) before analyses.

FACS-based cytotoxicity assay

To determine specific lysis of melanoma cells by NK cells, flowcytometric analysis was performed (38). In brief, melanoma cells (5 × 106 cells/mL) were labeled with 2 nmol/L CFSE for 10 minutes (Invitrogen). Then antibody pretreated NK cells were added to 5 × 104 of CFSE-labeled melanoma cells at various effector to target ratios for 3 hours. 7-AAD (Cayman Chemicals) was added to each sample according to the manufacturer’s protocol. Probes were measured directly in a Gallios flow cytometer (Beckman Coulter). Gating strategy was used as described in Heinemann and colleagues (38).

Statistical analysis

Quantitative expression values between two groups were compared using Wilcoxon-Mann-Whitney tests. In the case that comparisons were to a group with no observable
expression values (stage I/II of CEACAM1-3S), we applied the one-sided t test (against an expected value of 0). We used the Student t test to compare two experimental conditions in functional experiments. Spearman correlations (p) were used to assess associations between gene expression levels and tumor stages. Time-to-event data (from melanoma diagnoses until death or the last observation in case of censoring) were displayed using the method of Kaplan–Meier. Given the problems of selecting an appropriate cutoff/cut point value, which is often data driven, we decided to display our results for the “presence of any transcripts” in contrast to “no transcripts.” Subgroups in Kaplan–Meier plots were compared using log-rank statistics; in addition, we used Cox regression to the related estimate HR. All reported P values are nominal and two sided. We applied a significance level of 5% and did not adjust for multiple testing.

Results

Analysis of CEACAM1 variants in malignant melanoma identified correlation of CEACAM1-3S with patient clinical stage and overall survival

Total CEACAM1 expression has been shown to be significantly higher in melanomas compared with benign nevi (39). To examine the presence of CEACAM1-3S, CEACAM1-3L, CEACAM1-4S, and CEACAM1-4L in melanoma, we analyzed 46 cell lines established from human melanoma metastases using RT-PCR. We detected CEACAM1 variant expression in 33 of 46 cell lines (72%, Supplementary Table S1). Remarkably, all CEACAM1-positive cell lines expressed CEACAM1-4L in combination with other variants. We assessed relative variant expression by densitometric quantification. For each case (both CEACAM1-4 and CEACAM1-3), the longer (L)-variant was expressed at a higher level in the melanoma cell lines (Supplementary Table S1).

Next we assessed the impact of CEACAM1 splice variants during melanoma progression, by analyzing variant expression in 51 biopsies from melanoma patients that spanned stages I–IV according to the AJCC. First, in 45 of 51 (88%) biopsies, we observed CEACAM1 variant expression (Table 1 and Supplementary Table S2). Surprisingly, both CEACAM1-3 variants were absent in stage I/II melanomas, with only one exception that expressed CEACAM1-3L (Fig. 1A and Supplementary Table S2). CEACAM1-3S and CEACAM1-3L expression was induced during melanoma progression, and significantly positively correlated with clinical stage, reaching the highest expression levels in stage IV tumors (CEACAM1-3S stage III: P = 0.031, stage IV: P = 0.002; CEACAM1-3L stage III: P = 0.002, stage IV: P < 0.0001 vs. stage I/II; Fig. 1A). Furthermore, expression of both CEACAM1-3 isoforms was even higher in late-stage melanoma (stage IV) compared with stage III biopsies (CEACAM1-3S P = 0.004; CEACAM1-3L P = 0.015; Fig. 1A). CEACAM1-4S expression was detected in 40 of 51 (78%) biopsies but did not vary according to stage (Fig. 1A and Supplementary Table S2). CEACAM1-4L expression was detected in all CEACAM1-positive patient biopsies (88%; Supplementary Table S2) and was significantly induced during early disease progression from stages I/II to stage III (P = 0.030, Fig. 1A). Moreover, CEACAM1-4L was either expressed alone or in combination with other isoforms, while no other isoform was expressed without CEACAM1-4L (Supplementary Table S2). In correspondence to our in vitro observations, CEACAM1-3S exhibits the lowest expression intensities, whereas CEACAM1-4L was predominantly expressed (Fig. 1A and Supplementary Table S2).

Then we applied the CEACAM1 isoforms data to analyze the prognostic power. Surprisingly, patients with advanced melanomas expressing CEACAM1-3S showed significantly (P = 0.039) prolonged overall survival compared with patients with melanomas lacking CEACAM1-3S expression (HR, 0.43; 95% confidence interval, 0.19–0.98; Fig. 1B), whereas expression of CEACAM1-
CEACAM1 variants localize to different intracellular compartments in melanoma cells

To explore CEACAM1 isoform functionality, we stably transfected CEACAM1-3S, CEACAM1-3L, CEACAM1-4S, or CEACAM1-4L, respectively, into the CEACAM-negative cell line Ma-Mel-86a, established from a stage III metastases (Fig. 2). Empty vector Ma-Mel-86a-transfection served as a negative control. Expression of exogenous CEACAM1 isoforms was identified by RT-PCR (Fig. 2A), Western blot analysis (Fig. 2B), and flow cytometry (Fig. 2C).

Next, we investigated the subcellular localization of each CEACAM1 isoform using IHC. Beside their surface expression, the CEACAM1-3S and CEACAM1-3L isoforms were primarily detected in vesicle-like structures that accumulated around the nucleus (Fig. 3A, I and II), whereas the CEACAM1-4S and CEACAM1-4L isoforms were predominantly localized to sites of cell–cell contact on the cell surface (Fig. 3A, III and IV, arrowheads). No CEACAM1 staining was detectable in control cells transfected with empty vector (data not shown). Interestingly, CEACAM1-3S- and CEACAM1-3L-positive vesicle-like structures were arranged like a "string of pearls" orientated toward sites of cell–cell contact (Fig. 3A, I and II, arrows), pointing to a recruitment of both variants to areas of cellular interactions. To analyze how this linear orientation is achieved, CEACAM1-3L and CEACAM1-3S transfectants were immunostained for total CEACAM1 and F-actin. Costaining of CEACAM1-3S transfectants revealed that CEACAM1-positive vesicular structures associated with F-actin fibers in cell protrusions extending toward contact points with adjacent cells (Fig. 3B). Similar observations were made in CEACAM1-3L transfectants (data not shown). Taken together, all CEACAM1 isoforms were predominantly expressed at cell–cell contacts, but cellular localization of the CEACAM1 isoforms varied and was dependent on the presence of the extracellular A2 domain.
CEACAM1 isoforms differently affect migration and invasion of melanoma cells

CEACAM1-4L expression has been shown to enhance the migratory capacity and invasive potential of melanoma cells without affecting cell proliferation (13). We found that expression of the different CEACAM1 isoforms transfected into Ma-Mel-86a did also not alter proliferation (data not shown). To investigate the specific contributions of each CEACAM1 isoform to cellular motility, we monitored the CEACAM1 transfectants in real time by using xCELLigence impedance measurement. Expression of CEACAM1-4S (P = 0.009) and CEACAM1-4L (P = 0.025) had the strongest migration enhancing influence on melanoma cells, compared with control cells (Fig. 4A and B). Also, CEACAM1-3L significantly increased migratory capacity, but to a lesser extent (P = 0.023, Fig. 4A and B). In accordance to this finding, expression of CEACAM1-4S (P = 0.006) and CEACAM1-4L (P = 0.005) resulted in enhanced invasive behavior, which was only slightly increased by CEACAM1-3L (Fig. 4C and D). Interestingly, CEACAM1-3S expression significantly decreased both cell migration (P = 0.031, Fig. 4A and B) and invasion (P = 0.020, Fig. 4C and D) compared with control cells. Analyses of a second set of independently generated CEACAM1 transfectants confirmed these results (data not shown). Now we hypothesized that activity of matrix metalloproteinases (MMP), enzymes known to be key regulators of invasive potential in melanoma cells (40, 41), could be involved in modulating the cellular function of the individual CEACAM1 isoforms. Consequently, we treated our CEACAM1 transfectants with the MMP inhibitor marimastat (42–44), and reassessed invasive capacity after inhibition of MMP activity. In accordance to our hypothesis, marimastat treatment impaired the invasive promoting effect of CEACAM1-4S or CEACAM1-4L (Fig. 5).

CEACAM1-3S and CEACAM1-4L direct tumor immunogenicity by deregulating MICA and ULBP2 expression

It has been reported that the CEACAM1 expression influences the immunogenicity of cancer cells by modulating the surface expression of NKG2D ligands. These data prompted us to analyze the impact of the four CEACAM1 isoforms on the expression of NKG2D ligand MICA and ULBP2 by flow cytometry. Although expression of CEACAM1-3L or CEACAM1-4S did not modulate MICA and ULBP2 expression, significant upregulation of MICA (P = 0.006) and ULBP2 (P = 0.011) on CEACAM1-3S transfectants was detected compared with control cells (Fig. 6A and B). Remarkably, expression of CEACAM1-4L resulted in damped cell surface expression of MICA (P = 0.020) without affecting ULBP2 levels (Fig. 6A and B).
was consistent with the analysis. MICA and ULBP2 expression in whole-cell lysates of Mel-86a-cell surface (Fig. 6C). Parallel we analyzed ligand expres-

sion of NKG2D ligands, MICA and ULBP2 expression was more, we con-

Figure 3. CEACAM1 splice variants localize to different cellular compartments. A, immunofluorescence-based assessment for cellular localization of CEACAM1 (green) in the indicated CEACAM1 isoform transfectants. Nuclei were counterstained using DAPI (blue). White arrowheads, CEACAM1 staining at cell-cell contact sites; white arrow, CEACAM1-positive vesicles arranged in a line toward cell-cell contacts. B, double staining for total CEACAM1 (mAb 4/3/17, green) and F-actin (phalloidin, red) in CEACAM1-3S transfectants; nuclei were counterstained using DAPI (blue). Similar results were observed in CEACAM1-3L cells (data not shown). Representative images show maximum z-projection of confocal optical sections. Analyses were repeated three times by using different passages of each transfectant. Scale bar, 10 μm.

To verify whether CEACAM1-3S indeed affected cell surface expression of NK2D ligands, MICA and ULBP2 expression was determined by confocal microscopy. Expression of CEACAM1-3S resulted in enhanced recruitment of MICA and ULBP2 to the Ma-Mel-86a-cell surface (Fig. 6F). Parallel we analyzed ligand expression levels in the CEACAM1 transfectants using Western blot analysis. MICA and ULBP2 expression in whole-cell lysates of CEACAM1-3, CEACAM1-3S, and CEACAM1-4S transfectants was consistent with the flow-cytometric data (Fig. 6D). Furthermore, we confirmed that CEACAM1-3S-transfected cells upregulated MICA and ULBP2 expression (Fig. 6D). Unexpectedly, CEACAM1-4L expression did not alter the total protein expression of MICA and enhanced ULBP2 protein expression compared with control cells (Fig. 6D). These data did not correlate with our flow-cytometric findings, unless the reduced MICA and ULBP2 surface levels in CEACAM1-4L–positive cells would appear due to shedding. Accordingly, we examined the levels of soluble MICA (sMICA) and ULBP2 (sULBP2) in media conditioned by the CEACAM1 transfectants using Western blot analysis, and exclu-

sively detected enhanced amounts of sMICA and sULBP2 in conditioned medium obtained from CEACAM1-4L–expressing cells (Fig. 6E). Quantification of sMICA by ELISA revealed an approximately 2-fold elevation \( (P = 0.033) \) in conditioned medi-

um from CEACAM1-4L–expressing cells compared with control cells (Fig. 6F). Noteworthy, marimastat treatment reduced the level of soluble MICA \( (P = 0.0034) \) to the control level (Fig. 6G)."
synergistic effects and reduced the NK cell-mediated lysis of both target cell lines to a comparable level (CEACAM1-3S: 26%; control: 21.6%, Supplementary Fig. S2B, 2 hours after NK cell addition, E/T = 1:1).

Discussion

Tumor progression is a complex multistep process orchestrated by a variety of cellular factors, such as cell adhesion molecules, but also influenced by host-derived microenvironmental cell populations including cells of the immune system. Most recent studies discussed CEACAM1 as a novel promising target for immunotherapy of malignant melanoma patients (3, 45).

Here, we report CEACAM1-3S, CEACAM1-3L, CEACAM1-4S, and CEACAM1-4L expression in melanoma cell lines and biopsies. The isoform expression pattern differed during malignant progression. Early in tumor establishment (stage I/II), CEACAM1-4L and CEACAM1-4S were exclusively expressed in 50% of melanoma biopsies, whereas CEACAM1-4L was expressed to a higher extend in metastatic melanoma compared with primary tumors. Interestingly, CEACAM1-3L was predominately and CEACAM1-3S was solely expressed in progressed...
Figure 6.
CEACAM1-3S enhances the immunogenicity of melanoma cells by upregulating cell surface expression of NKG2D ligands. A, MICA and ULBP2 cell surface expression of control cells compared with CEACAM1 transfectants by flow cytometry. Representative histograms are shown: background fluorescence of control cells (thin black line) or of indicated CEACAM1 transfectants (thin gray line), expression for NKG2D ligands of control cells (thick black line), or of CEACAM1 isoform transfectants (dashed black line). (Continued on the following page.)
melanoma (stage III/IV). Previously, Gambichler and colleagues reported elevated CEACAM1 expression in melanoma compared with benign nevi (39). The data we present suggest that the enhanced CEACAM1 expression levels observed by Gambichler and colleagues in primary melanomas were due to changes in the expression of CEACAM1-4S/L. Thus, they seemed to have underestimated the impact of individual biologic functions of the four CEACAM1 isoforms on melanoma progression and metastasis whose importance has been implicated by our study. The lack of CEACAM1-3S expression in early melanoma (stage I/II) followed by the dramatic increase in de novo expression for both CEACAM1-3 variants (86%) in later stages (stage III/IV) identified CEACAM1-3 and, in particular, CEACAM1-3S as potential novel biomarker for disease progression. This finding, however, requires a prospectively planned longitudinal evaluation.

Cellular functions of CEACAM1 require its localization at the cell surface and CEACAM1 has been shown to be recruited to sites of cell–cell contacts (46). Interestingly, by selective expression of individual CEACAM1 isoforms in melanoma cells, we identified variant-specific cellular localizations that are determined by the extracellular domain. However, CEACAM1-4 variants were primarily membrane associated, whereas CEACAM1-3 isoforms were predominantly localized in vesicular-like structures that accumulated around the nucleus. Schumann and colleagues (47) has previously reported that CEACAM1-8 binds to F-actin. Together with our data, this leads to the speculation that CEACAM1-3L and CEACAM1-3S–positive vesicular structures move toward sites of cell–cell contact via association with actin fibers. No evidence currently exists in the literature to identify which specific motor proteins would mediate this process. Sadakova and colleagues described localization of CEACAM1 in lamellipodia, suggesting a potential role in cell motility (48). However, it is still not understood if and how the extracellular domains of CEACAM1 affect downstream effectors, which modulate subsequently the localization of CEACAM1.

Early studies reported enhanced cell migration and invasion after transfection of CEACAM1-L into human melanoma cells, whereas overexpression of the CEACAM1-S variant had no effect (13). Contrary to this report, our data precisely show that CEACAM1-4L and CEACAM1-4S trigger the migratory capacity and invasive potential of melanoma cells, whereas CEACAM1-3S diminishes these cellular properties. In this context, Ebrahimnejad and colleagues has proposed that Tyr-488 within the ITIM domain of the CEACAM1 long cytoplasmic domain is essential for the invasive and migratory effect in CEACAM1-transfected melanoma cells (13). The fact that our study show that the expression of CEACAM1-3L (also containing Tyr-488) influenced migratory and invasive potential less strongly than CEACAM1-4L and CEACAM1-4S, argues against the hypothesis. Moreover, the here shown contradictory effects of CEACAM1-4S and CEACAM1-3S on cell motility, implicate that the modification of function occurs independent of the long cytoplasmic domain. To our knowledge, this is the first report showing that the extracellular domain of CEACAM1 has the potential to modulate cellular functions. The migratory behavior and invasive potential of cancer cells are, of course, multifaceted and strongly influenced by the tumor microenvironment. In this context, our in vitro experiments implicated the involvement of MMPs in regulating CEACAM1-4L and CEACAM1-4S-mediated invasion.

Recently, it was shown that CEACAM1-3L and CEACAM1-3S dampen antitumor immunity by downregulating the surface expression of ligands for the activating NK cell receptor NKG2D in colon cancer cells (22). Contrastingly, our data clearly point to a differential isoform-specific function of CEACAM1 in melanoma cells. In our experiments, CEACAM1-3S expression triggered enhanced expression of the NKG2D ligands MICA, ULBP2, and DNAM-1 ligand CD155 on the melanoma cell surface, which drove these cells to NK cell-mediated cytolysis. In contrast, expression of CEACAM1-4L resulted in reduced cell surface expression of MICA, ULBP2, CD155, and CD112, whereas the lower surface expression of NKG2D ligands was mediated by enhanced shedding of these ligands.

Our differing data on the impact of CEACAM1-4L for NK cell-mediated tumor cell cytolysis could be caused by donor-specific variations. In line with this idea, Markel and colleagues presented data that melanoma patient-derived NK cells show an irregular phenotype and lower levels of NKp46, NKp30, and CD16 while the expression NKG2D was not altered (31). Furthermore, they showed that NK cells from healthy donors behaved differently than patient-derived NK cells. Thus, utilizing melanoma patient-derived NK cells expressing increased amounts of CEACAM1 on their cell surface, could result in stronger interaction with CEACAM1-4L on melanoma cells (Fig. 3A) and consequently show higher susceptibility to CEACAM1-mediated inhibition of NKG2D-triggered lysis.

Interestingly, treatment with marimidast reverting the soluble level of MICA in medium conditioned by CEACAM1-4L–expressing melanoma cells almost back to the level of control cells. These data implicate a possible involvement of MMPs in the regulation of NKG2D ligand shedding by CEACAM1-4L in melanoma cells. Data from Liu and colleagues strengthen our hypothesis. They could show that MMP mediates MICA shedding independent of disintegrin; other MMPs and ADAMs (49). Our data implicate the possibility that CEACAM1-4L–expressing melanoma cells reduce the tumor–immune response by MMP-mediated shedding of NKG2D. But further studies are clearly needed to unravel the involvement of all the players in this process. Taken together, our results provide for the first time evidence that the expression of CEACAM1-3S, CEACAM1-3L, CEACAM1-4S, and CEACAM1-4L differentially affect disease progression in malignant melanoma. Importantly, we clearly demonstrated that CEACAM1 variants
differentially modulate attenuation of immune surveillance by regulating ligand expression for the NKG2D receptor on tumor cells in malignant melanoma. These findings are of major interest, since CEACAM1 is discussed for use in clinical applications of immunotherapy. Caused by the fact that CEACAM1-3S potentially inhibits melanoma cell migration and invasion, and drives these cells through NK cell-mediated cytolysis, whereas CEACAM1-4L is acting in the opposite direction by supporting tumor progression, it is indispensable to define the impact of different CEACAM1 variants to secure therapeutic efficiency. Hence, determination of all four CEACAM1 isoforms opens up new possibilities for diagnosis and prognosis of melanoma patients.

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

Authors’ Contributions
Conception and design: N. Ullrich, A. Heinemann, I. Scheffrann, D. Schaden-dorf, B.B. Singer, I. Helfrich
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): N. Ullrich, A. Heinemann, I. Scheffrann, J. Klode, B.B. Singer, I. Helfrich
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): N. Ullrich, A. Heinemann, I. Scheffrann, A. Scherag, B.B. Singer, I. Helfrich

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