HEPATOLOGY

HEPATOLOGY, VOL. 69, NO. 3, 2019

Deficient Natural Killer Cell NKp30-Mediated Function and Altered NCR3 Splice Variants in Hepatocellular Carcinoma

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The activating natural cytotoxicity receptor NKp30 is critical for natural killer (NK) cell function and tumor immune surveillance. The natural cytotoxicity receptor-3 (NCR3) gene is transcribed into several splice variants whose physiological relevance is still incompletely understood. In this study, we investigated the role of NKp30 and its major ligand B7 homolog 6 (B7-H6) in patients with hepatocellular carcinoma (HCC). Peripheral blood NK cell phenotype was skewed toward a defective/exhausted immune profile with decreased frequencies of cells expressing NKp30 and natural killer group 2, member D and an increased proportion of cells expressing T-cell immunoglobulin and mucin-domain containing-3. Moreover, NKp30-positive NK cells had a reduced expression of NCR3 immunostimulatory splice variants and an increased expression of the inhibitory variant in patients with advanced tumor, resulting in deficient NKp30-mediated functionality. Tumor-infiltrating lymphocytes showed a prevalent inhibitory NKp30 isoform profile, consistent with decreased NKp30-mediated function. Of note, there were significant differences in the cytokine milieu between the neoplastic and the surrounding non-neoplastic tissue, which may have further influenced NKp30 function. Exposure of NK cells to B7-H6-expressing HCC cells significantly downmodulated NKp30, that was prevented by small interfering RNA–mediated knockdown, suggesting a role for this ligand in inhibiting NKp30-mediated responses. Interestingly, B7-H6 expression was reduced in HCC tissue and simultaneously augmented as a soluble form in HCC patients, particularly those with advanced staging or larger nodule size. *Conclusion:* These findings provide evidence in support of a role of NKp30 and its major ligand in HCC development and evolution. (Hepatology 2019;69:1165-1179).

Natural killer (NK) cells play a significant role in innate immune responses to cancer cells through recognition of germline-encoded ligands of positive and negative signaling receptors. Lysis of tumor targets occurs through reduction of inhibitory signals and a simultaneous increase in

Abbreviations: ADAM, a disintegrin and metalloprotease; ADCC, antibody-dependent cellular cytotoxicity; B7-H6, B7 homolog 6; BCLC, Barcelona Clinic for Liver Cancer; HBV, hepatitis B virus; HC, healthy controls; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; IFN-γ, interferon-γ; IL, interleukin; LIL, liver-infiltrating lymphocytes; MFI, mean fluorescence intensity; NCR, natural cytotoxicity receptor; NK, natural killer; NKG2D, natural killer group 2, member D; PBMC, peripheral blood mononuclear cells; PCR, polymerase chain reaction; sB7-H6, soluble B7-H6; siRNA, small interfering RNA; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobin and immunoreceptor tyrosine-based inhibition motif domains; TIL, tumor-infiltrating lymphocytes; and Tim-3, T-cell immunoglobulin and mucin-domain containing-3.

Received January 24, 2018; accepted August 21, 2018.
Additional Supporting Information may be found at onlinelibrary.wiley.com/doi/10.1002/hep.30235/suppinfo.
Supported by the Italian Ministry of Health, Bando Giovani Ricercatori (GR-2011-02349273) (to B.O.).
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View this article online at wileyonlinelibrary.com.
DOI 10.1002/hep.30235

Potential conflict of interest: Nothing to report.

activating signals that are necessary for NK cell triggering.[1-3] Activating receptors include DNAM-1, natural killer group 2, member D (NKG2D), and the natural cytotoxicity receptors (NCR), whose ligands consist of both major histocompatibility complex (MHC)-like and non-MHC molecules. The NCR family includes NKp30 (NCR3), NKp44 (NCR2) and NKp46 (NCR1), which are type I transmembrane glycoproteins consisting of one (NKp30 and NKp44) or two (NKp46) immunoglobin-like extracellular domains.[4] The NCR3 gene is transcribed into three major isoforms (NKP30a, NKp30b, and NKp30c) of the NKp30 protein that are generated by alternative splicing and that have different biological functions. The NKp30a and NKp30b isoforms are considered to be immunostimulatory, as they induce cytotoxicity and Th1 cytokine secretion, respectively, whereas the NKp30c isoform shows an immunosuppressive activity triggering interleukin (IL)-10 release. Furthermore, the relative abundance of the mRNA encoding the NKp30c isoform compared with isoform a or b can negatively affect the prognosis and evolution of different malignancies and might be associated with advanced liver disease in hepatitis C virus (HCV)-infected patients.[5-8] Moreover, the expression of different NCR3 splice variants by NK cells delineates functionally distinct subsets and is governed by the cytokine-defined microenvironment.[9,10] The NKp30 receptor recognizes the human leukocyte antigen–B-associated transcript 3, the human cytomegalovirus pp65 tegument protein, and the cell surface protein B7 homolog 6 (B7-H6), a member of the B7 family of receptors.[11-13] Interestingly, B7-H6 is not expressed by normal human tissues but is selectively expressed on stressed cells, including both solid and transformed blood cells, which can up-regulate B7-H6 expression and enhance tumor susceptibility to NK cell lysis.[14-16] The interaction of B7-H6 on tumor cells with NKp30 on NK cells results in interferon-γ (IFN-γ) production and tumor cell killing, suggesting that the NKp30–B7-H6 axis can be exploited for cancer immunotherapy.[17] In addition, B7-H6 can also be induced as a stress protein by viral infections closely linked to carcinogenesis, such as hepatitis B virus (HBV).[18] Current evidence indicates that malignant cells can also bypass the NK surveillance by releasing B7-H6 as soluble proteins that block NKp30 activity, suggesting that this may be an immune escape mechanism of tumor cells from NK cell-mediated killing.[19] It is clear from the aforementioned that the NKp30-B7-H6 axis represents an important pathway in chronic inflammation leading to tumor development. One such example is hepatocellular carcinoma (HCC), which may develop in the setting of advanced chronic HBV and chronic HCV virus infections.[20]

In this study we investigated the NKp30-B7-H6 axis in patients with HCC. We showed that peripheral and tumor-infiltrating NKp30+ NK cells have deficient NKp30-mediated functionality and altered expression of NCR3 splice variants. Moreover, B7-H6 expression was reduced in HCC tissue and simultaneously augmented as a soluble form in the serum

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of HCC patients, particularly those with advanced staging or larger nodule size. These findings provide evidence in support of a role of NKp30 and its major ligand in HCC development and evolution.

Materials and Methods

Complete technical details are reported in the Supporting Information. Briefly, paired blood and tissue-infiltrating lymphocytes were obtained from patients undergoing surgical liver resections for HCC (Supporting Table S1) and prepared for phenotype determination and redirected functional analysis through NKp30 ligation, RNA extraction, and real-time quantitative polymerase chain reaction (PCR) to detect NKp30 isoforms. Primary HCC cell cultures were established as described in the Supporting Information. Liver samples from HCC and cirrhotic patients were retrospectively examined as described in the Supporting Information. NKp30 down-regulation experiments using B7-H6-expressing cells and B7-H6 small interfering RNA (siRNA) knockdown are also described in the Supporting Information.

Statistical analysis was performed using the GraphPad Prism 6 software (GraphPad, La Jolla, CA). The nonparametric Wilcoxon matched-pairs signed rank test or Mann-Whitney U test as well as parametric paired or unpaired *t* test were used as appropriate. The Dunn's multiple comparison test was used to compare more than two groups of data. The Pearson test was used to examine correlations. A P value ≤ 0.05 was deemed statistically significant.

Results

PERIPHERAL NK CELLS SHOW AN EXHAUSTED PHENOTYPE IN HCC PATIENTS, AND NKp30-EXPRESSING NK CELLS ARE ENRICHED IN TUMOR-INFILTRATING LYMPHOCYTES

We investigated the frequency of circulating NK cells in HCC patients and HC, according to the gating strategy shown in Supporting Fig. S1, and found that frequencies of total peripheral NK cells and of the $CD56^{bright}$ and $CD56^{dim}$ subsets (Fig. 1A) were comparable in HCC patients and healthy controls (HC). The frequency of peripheral NK cells carrying NKp30 receptor and its expression were instead significantly lower in patients with HCC compared with HC (Fig. 1B,C). There were no differences in NKp30 expression according to liver disease etiology (not shown). The frequency of the immunomodulatory T-cell immunoglobulin and mucin-domain-containing molecule-3 (Tim-3) receptor was significantly higher in HCC patients' NK cells, compared with HC NK cells (Fig. 1D). Moreover, there was a statistically significant reduction in the proportion of NKG2D+ (Fig. 1E) and a significant increase in the proportion of CD69+ (Fig. 1F) NK cells from patients with HCC compared with controls. At the same time, no statistically significant differences were noted in the proportion of programmed death receptor 1 (PD-1), NKG2A, Fas ligand, T-cell immunoreceptor with immunoglobin and immunoreceptor tyrosine-based inhibition motif domains (TIGIT), and NKp46 (Supporting Fig. S2A-E) expressing NK cells compared with HC. We further investigated intrahepatic NK cell receptors in HCC patients and found a lower frequency of total NK cells in tumor-infiltrating lymphocytes (TIL) compared with liver-infiltrating lymphocytes (LIL) (Fig. 2A), as shown by others.[21,22] However, the proportion of NKp30+ NK cells and the mean fluorescence intensity (MFI) of the NKp30 receptor were significantly higher in TIL-NK compared with LIL-NK cells (Fig. 2B-D). There was a higher frequency of NKp30+ NK cells in the $CD56^{bright}$ subset in TIL compared with LIL (Fig. 2E). In contrast, the proportion of NKp46+ NK cells and the NKp46 MFI were similar in tumor and non-tumor NK cells (data not shown).

DEFICIENT NKP30-MEDIATED FUNCTIONALITY AND ALTERED NKp30 ISOFORM PROFILE IN HCC PATIENTS

Altered expression of NKp30 receptor in HCC patients prompted us to study the NKp30-mediated cytolytic potential and cytokine production of peripheral and intrahepatic NK cells of HCC patients, using an *ex vivo* redirected functional (ADCC) assay. Peripheral blood mononuclear cells, TIL, and matched LIL were incubated overnight with or without IL-15 and subsequently co-cultured with the FcγR+ P815 murine cell line in the presence of anti-NKp30 monoclonal antibody. Patients with chronic HCV

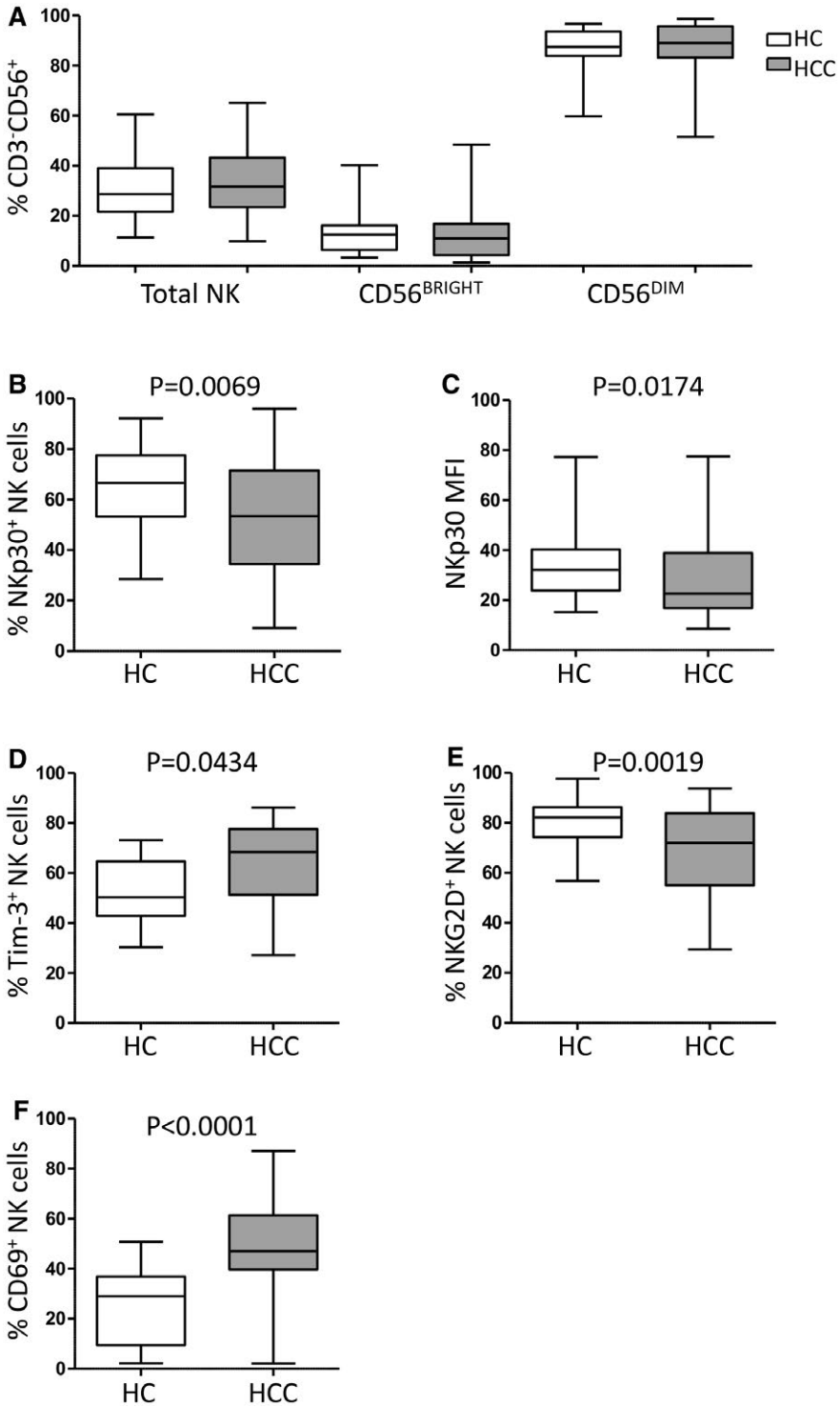

FIG. 1. Peripheral NK cells of HCC patients show an exhausted phenotype in HCC patients, and NKp30-expressing NK cells are enriched in tumor-infiltrating lymphocytes. Frequencies of circulating NK cells, $CD56^{bright}$ and $CD56^{dim}$ subsets (A), and NKp30+ NK cells and NKp30 MFI (B-C) in HCC patients (n = 55) and HC (n = 39). Frequencies of circulating Tim-3 (D), NKG2D (E), and CD69 (F) expressing NK cells in HCC patients (n = 14, n = 47 and n = 44, respectively) and HC (n = 10, n = 38 and n = 34, respectively). Middle bars represent the median values; box plots are 25% and 75% percentiles; and whiskers are minimum and maximum values. The Mann-Whitney U test or the unpaired *t* test were used to compare data.

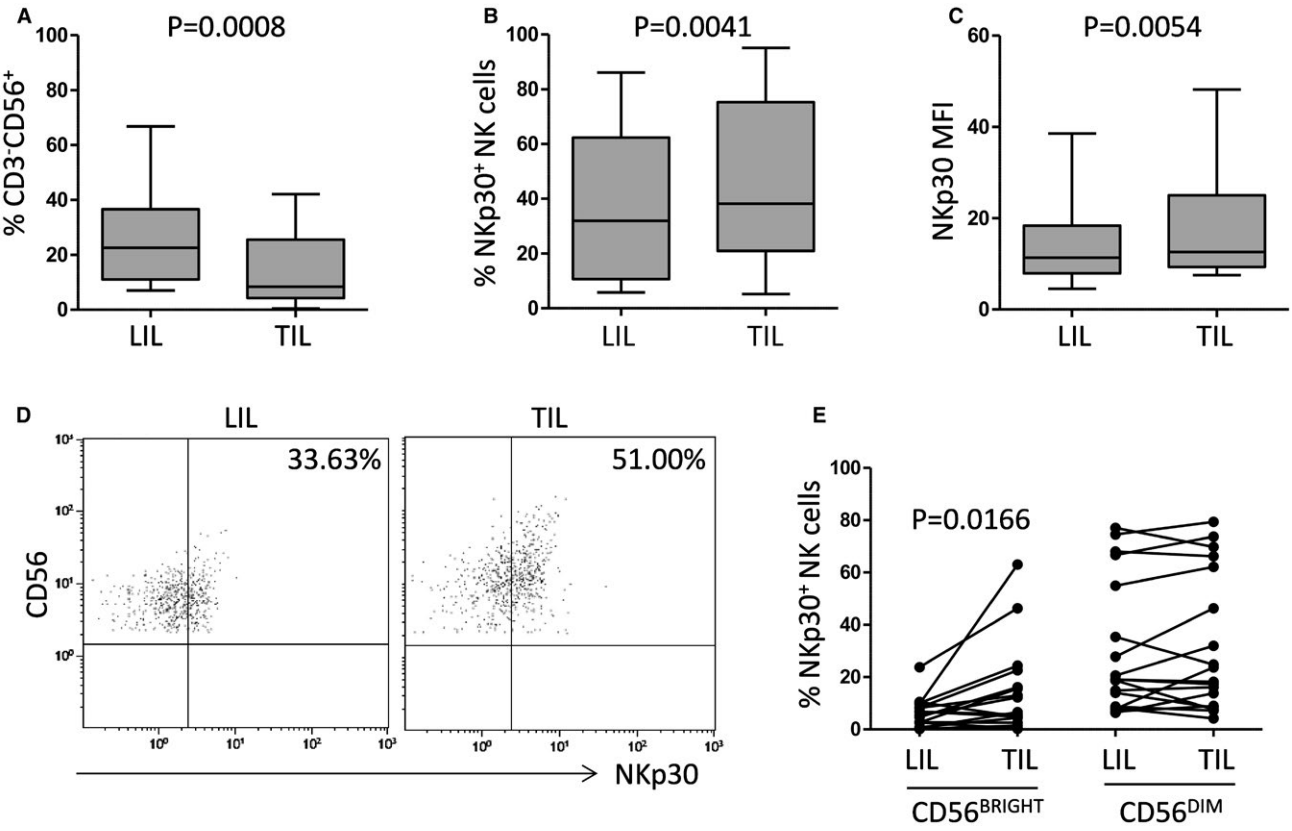

FIG. 2. Increased proportion of NKp30 receptor-positive NK cells and NKp30 density in TIL-NK cells of HCC patients. The frequency of total NK cells in TIL (n = 23) was lower compared with matched LIL (A), with a relative increase of NKp30+ NK cells (B) and NKp30 receptor density (C). (D) Representative dot plots show the frequencies of NKp30-positive NK cells in LIL and matched TIL. (E) Frequency of NKp30-expressing LIL-NK and TIL-NK cells within the $CD56^{bright}$ and $CD56^{dim}$ subsets (n = 18). Middle bars represent the median values; box plots are 25% and 75% percentiles; and whiskers are minimum and maximum values. The Wilcoxon matched-pairs signed rank test or paired *t* test were used to compare data.

infection without HCC were added as disease controls. There was no difference in peripheral NKp30-mediated cytotoxicity between patients with HCC, patients with chronic HCV infection, and HC (Fig. 3A). NKp30 expression was reduced in the HCV+ disease control group (not shown) compared with HC, in keeping with previously published data from our laboratory.[8] After IL-15 stimulation, NKp30-mediated cytotoxicity was significantly augmented in HCV+ patients compared with HC, whereas HCC patients displayed a lower cytotoxic potential compared with HCV+ patients (Fig. 3A). NKp30-mediated IFN-γ production was significantly reduced in peripheral blood NK cells from both HCC and HCV+ patients compared with HC, which was maintained in HCC patients also after IL-15 stimulation (Fig. 3B). There was a trend toward a more profound reduction in IFN-γ secretion for HCC patients compared with non-HCC, HCV+ controls (Fig. 3B). The NKp30-mediated functional dichotomy exhibited by peripheral blood NK cells in chronic HCV infection (i.e. increased degranulation and poor cytokine production) is consistent with previous findings from our own and other laboratories.[23,24]

When we analyzed the intrahepatic compartment, we found that the NKp30-mediated degranulation ability of TIL-NK cells tested by reverse ADCC was significantly reduced compared with matched LIL-NK cells (Fig. 3C). IL-15 stimulation was unable to rescue NKp30-mediated degranulation in TIL-NK cells, despite being able to boost NKp30 expression (data not shown). No statistically significant differences in IFN-γ (and TNFα, not shown) production were noted following NKp30 ligation (Fig. 3D).

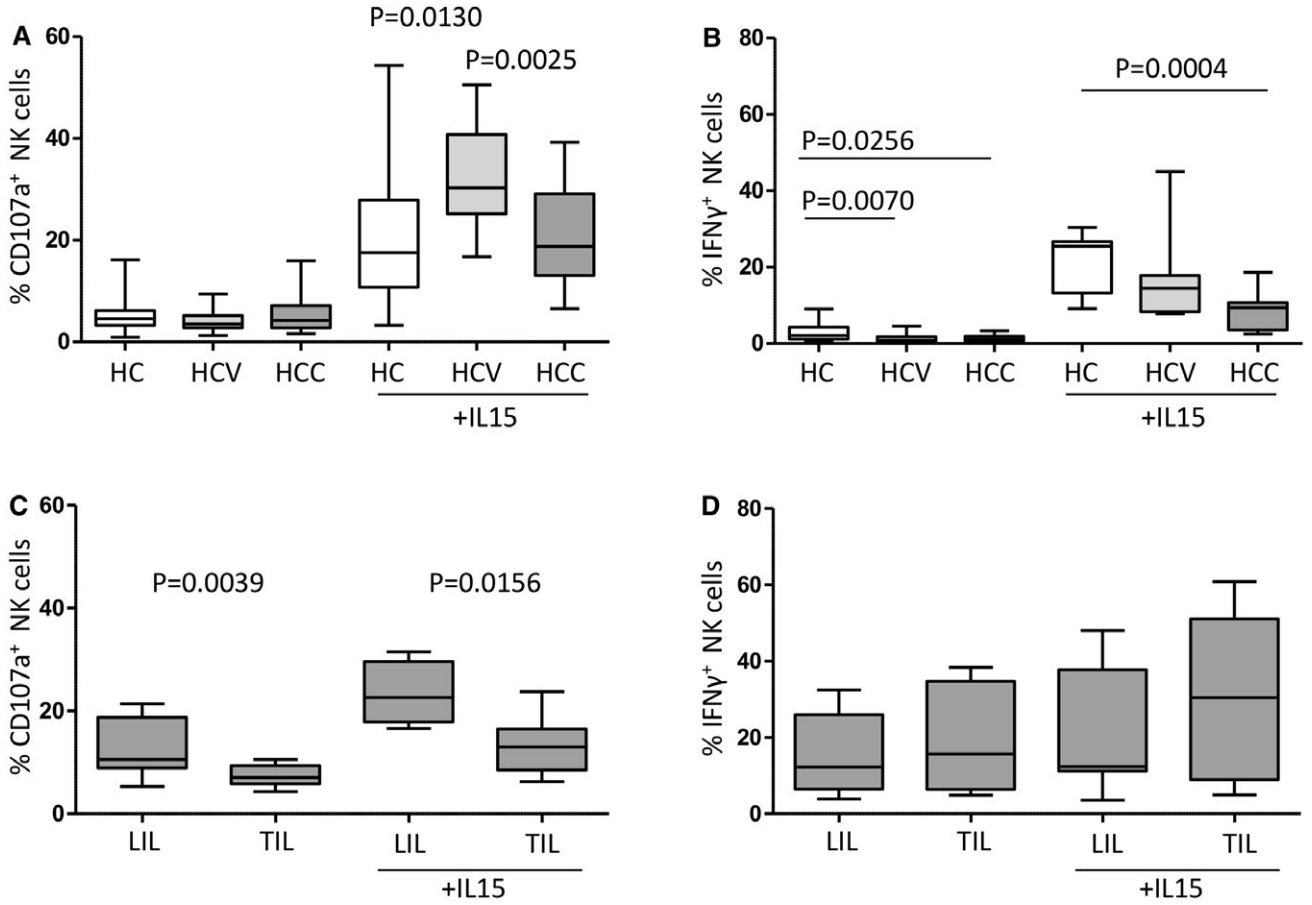

FIG. 3. Deficient NKp30-mediated function in HCC patients. (A) NKp30-mediated degranulation in unstimulated or IL15-stimulated PBMC of HCC patients (n = 30), HC (n = 29), and HCV+ patients (n = 11). (B) NKp30-mediated cytokine production in unstimulated or IL-15-stimulated PBMC of HCC patients (n = 11), HC (n = 15), and HCV+ patients (n = 11). NKp30-mediated degranulation (C) and NKp30-mediated cytokine production (D) in unstimulated or IL-15-stimulated LIL-NK and matched TIL-NK cells (n = 13). Middle bars represent the median values; box plots are 25% and 75% percentiles; and whiskers are minimum and maximum values. The Mann-Whitney U test, unpaired *t* test, or the Wilcoxon matched-pairs signed rank test were used to compare data.

Recent studies have shown that the NKp30 isoform expression pattern affects the NK cell functionality, the prognosis and evolution in the settings of cancer and infection.[6-8] We investigated whether alternatively spliced variants of the NCR3 gene might explain the reduced NKp30-mediated cytokine production of peripheral-blood NK cells in HCC patients. To this end, we quantified the three major NKp30 isoforms (NKp30a, b, and c) in freshly isolated PBMC of patients and HC using real-time quantitative PCR. The relative expression of the immunostimulatory NKp30a and NKp30b isoforms was significantly lower in HCC patients than in HC (Fig. 4A). In agreement with the low NKp30a and b transcripts, the Δac and Δbc ratio values were lower in NK cells from patients with HCC compared with HC (Fig. 4B). Interestingly, when HCC patients were analyzed according to the Barcelona Clinic for Liver Cancer (BCLC) staging classification, we found that the immunosuppressive NKp30c isoform was increased in patients with advanced tumor (Fig. 4C). Notably, there was a statistically significant positive correlation between the NKp30a/c isoform ratio and IFN-γ by NK cells, providing further evidence in support of the immunostimulatory function of the NKp30a isoform (Fig. 4D).

In consideration of the inhibitory function of NKp30[25] and the potential role of microenvironment cytokines in influencing the NCR3 splice

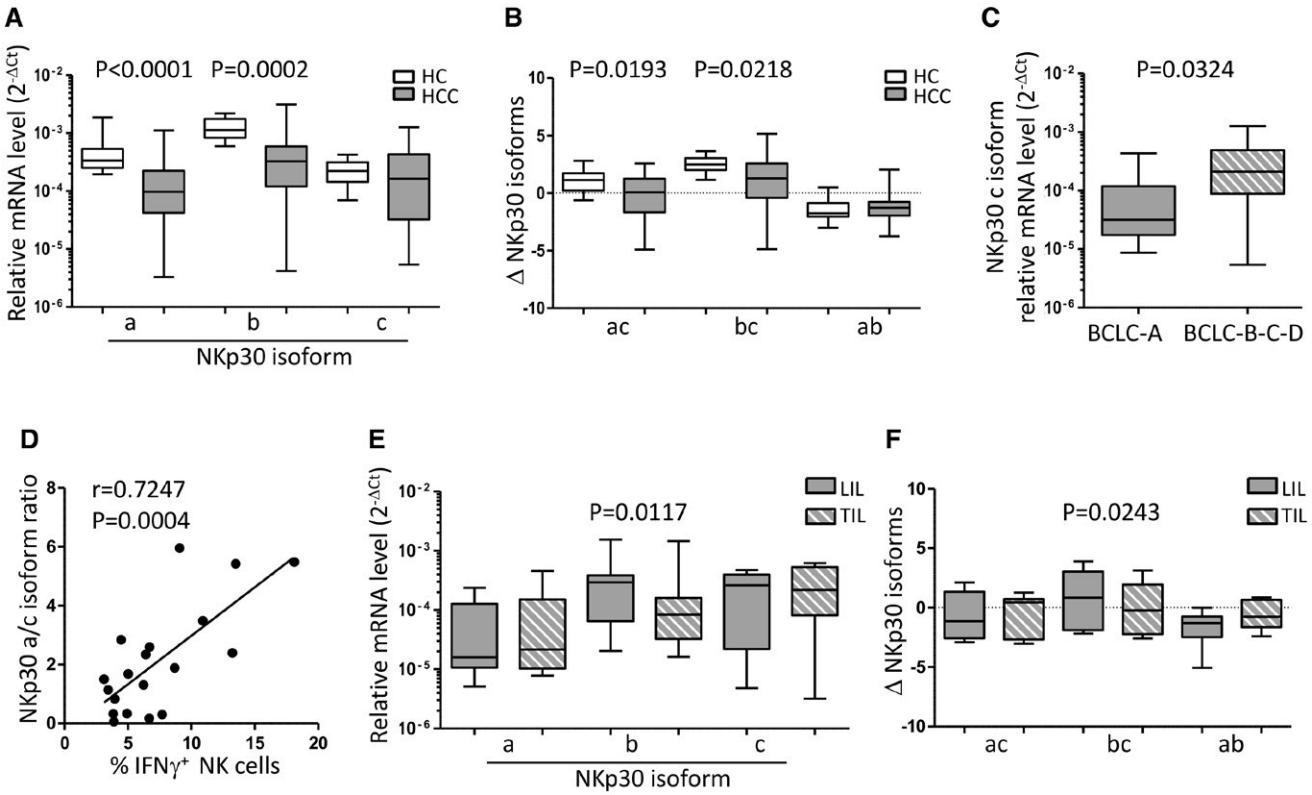

FIG. 4. Altered NKp30 isoform balance in HCC patients. Relative expression of NKp30 isoforms (A) and NKp30 Δac, Δbc, and Δab ratios (B) in the PBMC of 15 HC and 33 HCC patients. (C) NKp30c isoform expression in HCC patients was stratified according to BCLC staging classification. (D) The Pearson correlation coefficient was used to examine dependence between the NKp30a/c isoform ratio and the NKp30-mediated IFN-γ production on IL-15 stimulation in 19 HCC patients. The relative expression of NKp30 isoforms (E) and the NKp30 Δac, Δbc, and Δab ratios (F) were determined in LIL-NK and matched TIL-NK cells from 19 HCC patients.

variants,[9] we explored whether a switched NKp30 isoform profile could explain the deficient degranulation efficiency of TIL-NK cells in HCC patients. To this end, we quantified the three major NKp30 isoforms in freshly isolated LIL and matched TIL-NK cells. As shown in Fig. 4E, the relative expression of the immunostimulatory NKp30b isoforms was significantly lower in TIL-NK cells than in LIL-NK cells. TIL-NK cells exhibited a reduced Δbc ratio compared with the matched non-tumor liver counterpart, suggesting a prevalent inhibitory NKp30-mediated signaling (Fig. 4F). This difference in tissue-specific NKp30 isoform profile and NK cell functionality prompted us to examine changes in the cytokine content in the neoplastic and the surrounding non-neoplastic liver tissue. To this end, we analyzed mRNAs of selected cytokines that were previously shown to be involved in the necroinflammatory process leading to advanced fibrosis and liver carcinogenesis[26-31] as well as in NK cell regulation.[32] There was a reduced mRNA content of certain cytokines, including IL-6, IL-8 and IL-10, in the tumor compared with the non-neoplastic tissue, whereas no statistically significant differences were observed for IL-18 and transforming growth factor (TGF)-β mRNAs (Fig. 5).

NKp30 RECEPTOR IS DOWN-REGULATED AFTER EXPOSURE TO B7-H6 EXPRESSING HCC CELLS

To assess whether NKp30 expression could be influenced by B7-H6 contact, we performed co-culture experiments with the HCC Huh7.5 cell line expressing the B7-H6 ligand. As shown in Fig. 6A, B7-H6 expression was higher on HCV-infected Huh7.5 cells than on uninfected cells. The frequency of NK cells carrying the NKp30 receptor and its expression was

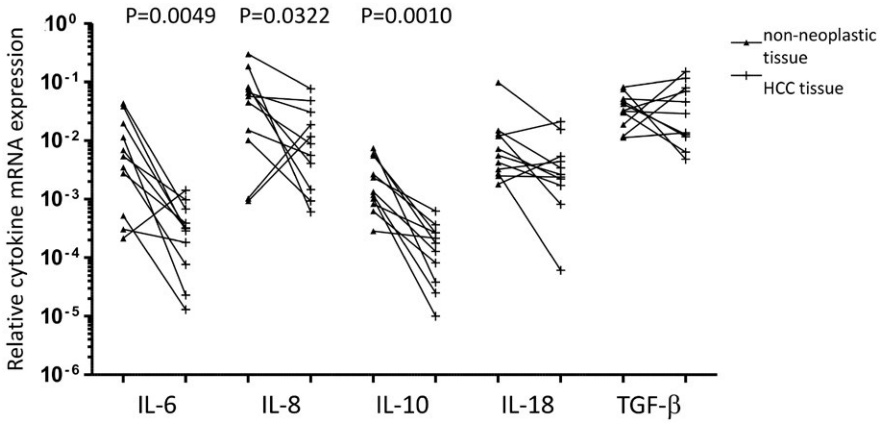

FIG. 5. Cytokine profile in HCC and non-neoplastic tissue. IL-6, IL-8, IL-10, IL-18, and TGF-β mRNA expression on HCC tissues compared with matched non-neoplastic surrounding tissue (n = 11). The Wilcoxon matched-pairs signed rank test was used for comparison.

down-regulated after exposure of PBMC from HC to uninfected Huh7.5 cells, expressing low levels of B7-H6. A stronger down-regulation was shown when PBMC were incubated with HCV-infected Huh7.5 cells, expressing higher levels of B7-H6, both as percentage and MFI (Fig. 6B,C). In contrast, NKp46 expression remained unchanged (data not shown). Representative dot plots showing NKp30+ and NKp46+ NK cell frequencies after B7-H6 exposure are shown in Supporting Fig. S3. B7-H6-induced NKp30 down-regulation was also confirmed by siRNA-mediated knockdown. Surface B7-H6 expression was evaluated on HepG2 cells after transfection with B7-H6 and/or siRNA-negative control by flow cytometry and real-time quantitative PCR (Fig. 6D and Supporting Fig. S4). As shown in Fig. 6D, siRNA-mediated knockdown of B7-H6 was able to reduce B7-H6 expression in HepG2 cells. The frequency of NK cells carrying the NKp30 receptor and its expression were higher after exposure of PBMC from HC to siRNA-B7-H6-transfected HepG2 cells compared with siRNA-negative control (Fig. 6E,F). B7-H6-induced NKp30 down-regulation was also confirmed after PBMC exposure to the breast carcinoma cell lines MCF-7/VC or MCF-7/B7-H6, retrovirally transduced with pMX-neo or pMXneo-CD8L-Myc tag-B7-H6, respectively (Supporting Fig. S5). Furthermore, to assess whether NKp30 expression could be influenced by soluble B7-H6 (sB7-H6), we performed experiments incubating PBMC from HC with the heterologous serum of HC and HCC patients. No statistically significant differences were observed, suggesting that NKp30 down-regulation requires B7-H6 to be cell-associated (Supporting Fig. S6).

B7-H6 PROTEIN EXPRESSION IS REDUCED IN TUMOR TISSUE OF HCC PATIENTS

Expression of the NKp30 ligand B7-H6 was evaluated in HCC biopsy specimens by immunohistochemistry and compared with cirrhotic livers. B7-H6 was highly expressed in cirrhotic livers and was significantly less expressed in HCC tissue stratified according to the degree of differentiation: well, moderately, and poorly differentiated tissue (Fig. 7A). Interestingly, we found that poorly differentiated tumor cells showed a trend toward lower B7-H6 expression compared with better differentiated HCC tissues. Immunohistochemical staining showed that B7-H6 was mainly localized in the cytoplasm and on the membrane of hepatocytes as shown in Fig. 7B. To investigate whether different levels of B7-H6 protein expression by immunohistochemistry *in situ* were caused by a decrease in gene transcription, we analyzed B7-H6 mRNA levels in HCC tissues along with matched non-tumor specimens, but we were unable to detect significant differences (Fig. 7C), suggesting that decreased B7-H6 protein expression did not result from reduced transcript levels, and might have occurred through other post-transcriptional mechanisms. Schlecker et al. demonstrated a mechanism

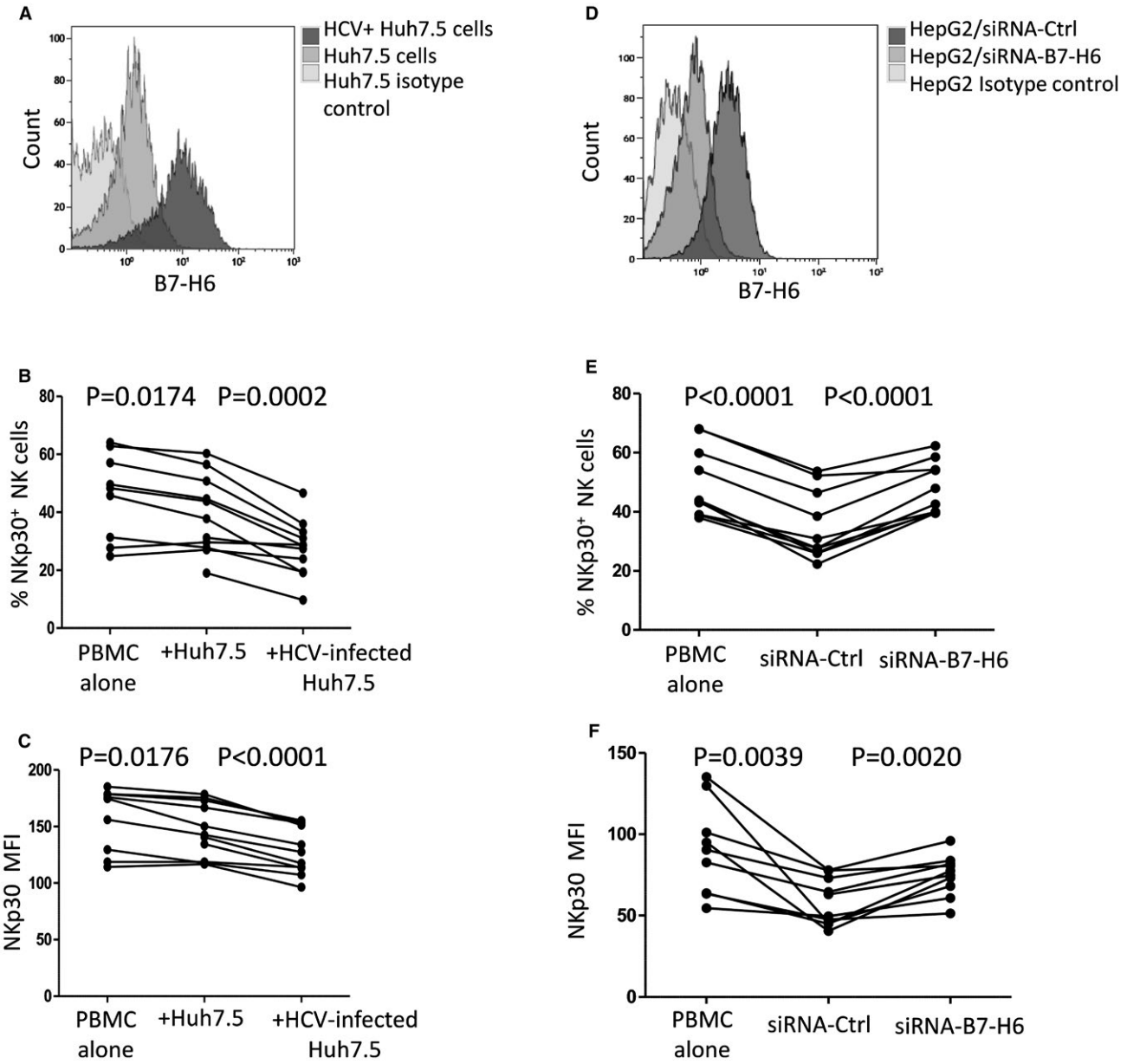

FIG. 6. NKp30 is down-regulated after co-culture with a B7-H6-positive HCC cell line. (A) B7-H6 expression on uninfected or HCV-infected Huh7.5 cell line. (B) Frequency of NKp30+ NK cells (B) and NKp30 MFI (C) in HC PBMC (n = 11) cultured alone or co-cultured with uninfected or HCV-infected Huh7.5 cell line. (D) B7-H6 expression on HepG2 cells transfected with B7-H6 and/or control siRNA. The frequency of NKp30+ cells (E) and NKp30 expression (F) after exposure of PBMC from 10 HC to siRNA-B7-H6-transfected HepG2 cells, siRNA control–transfected HepG2 cells, and medium alone. The paired *t* test was used to compare data.

of immune escape in which tumor cells impede NK cell recognition by metzincin-mediated shedding of B7-H6.[33] To address whether this mechanism plays a role in B7-H6 down-regulation on HCC patients, we treated HCC primary cell lines with different a disintegrin and metalloprotease (ADAM)-specific inhibitors. B7-H6 surface expression was measured by flow cytometry on untreated HCC primary cell lines or after exposure to ADAM-10 and ADAM-17 inhibitors LT4 or MN8 or to solvent alone dimethyl sulfoxide (DMSO) for 24 hours. As shown in Supporting Fig. S7, there was a modest and not always consistent increase in B7-H6 surface expression only after exposure of HCC cells to MN8.

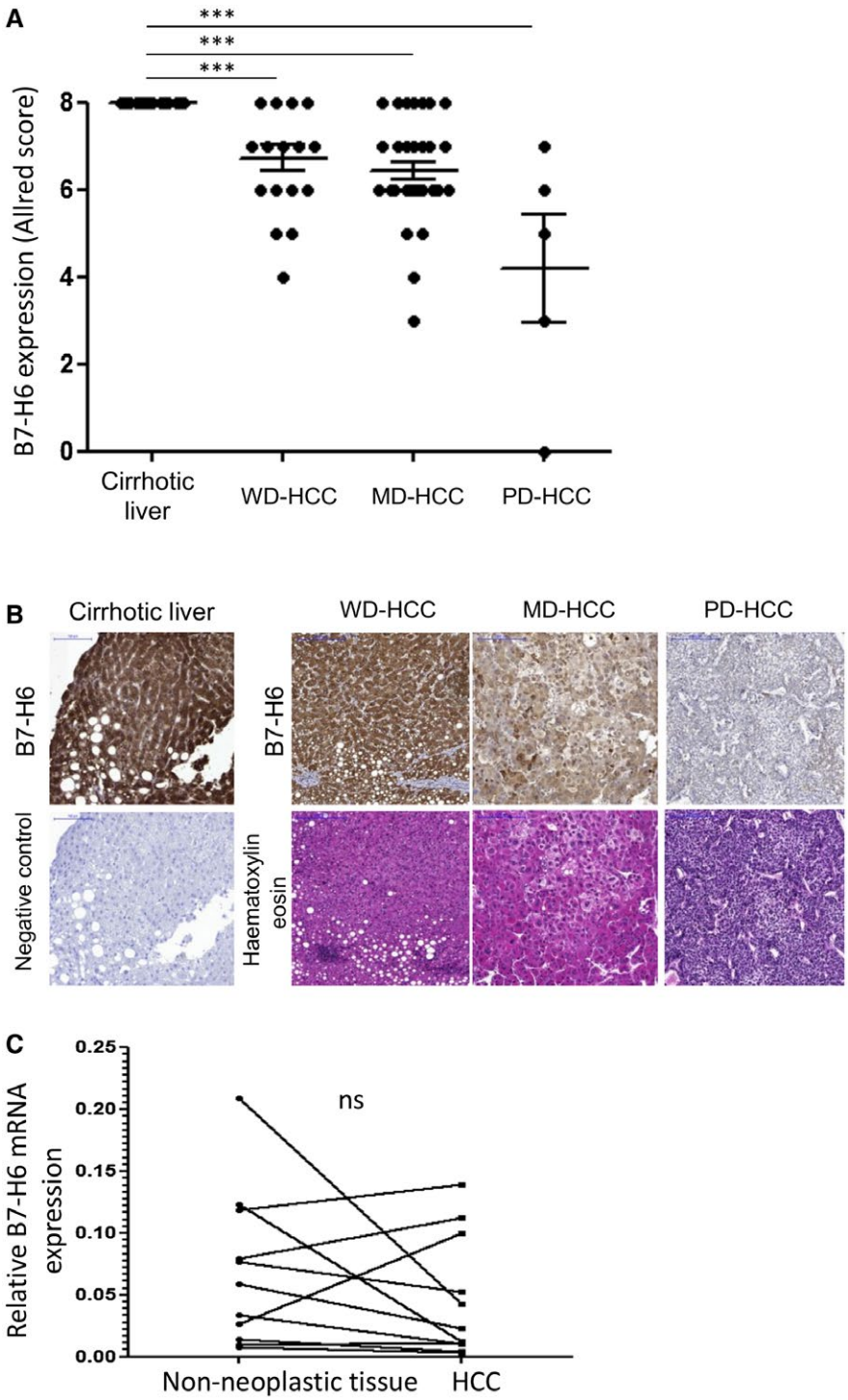

FIG. 7. B7-H6 protein expression is reduced on neoplastic tissue in HCC patients. (A) Immunohistochemical analysis of B7-H6 protein expression on HCC tissue stratified according to degree of differentiation compared with cirrhotic livers (n = 28). Data are presented as mean values ± SEM. The Dunn's multiple comparison test was used to compare data (***$P < 0.001$; WD-HCC, well differentiated HCC [n = 18]; MD-HCC, moderately differentiated HCC [n = 34]; PD-HCC, poorly differentiated HCC [n = 5]). (B) Representative B7-H6 and matched negative control immunohistochemistry or hematoxylin and eosin staining on cirrhotic samples and HCC tissue classified as WD-HCC, MD-HCC, and PD-HCC (×100 magnification). (C) mRNA B7-H6 expression on HCC tissues along with matched non-neoplastic specimens (n = 11). The Wilcoxon matched-pairs signed rank test was used. Abbreviation: ns, not statistically significant.

SOLUBLE B7-H6 SERUM CONCENTRATIONS ARE ELEVATED IN HCC PATIENTS WITH INTERMEDIATE AND ADVANCED TUMORS AND CORRELATE WITH CLINICAL PARAMETERS

Based on *in situ* expression of B7-H6 in HCC, we next investigated whether sB7-H6 was detectable in patients' sera by enzyme-linked immunosorbent assay. As shown in Fig. 8A, higher serum B7-H6 levels were detected in HCC patients with intermediate and advanced tumor, classified according to the BCLC staging classification, compared with early-stage tumors (BCLC-A) and to HC and patients with cirrhosis. Differences among HC, cirrhosis, and HCC remained highly significant when HCC were not stratified according to BCLC stage (not shown). There were no significant differences in sB7-H6 levels when HCC patients were stratified according to etiology or tumor grading (data not shown). Moreover, there were positive correlations between sB7-H6 levels and HCC nodule size and serum alpha fetoprotein values (Fig. 8B,C).

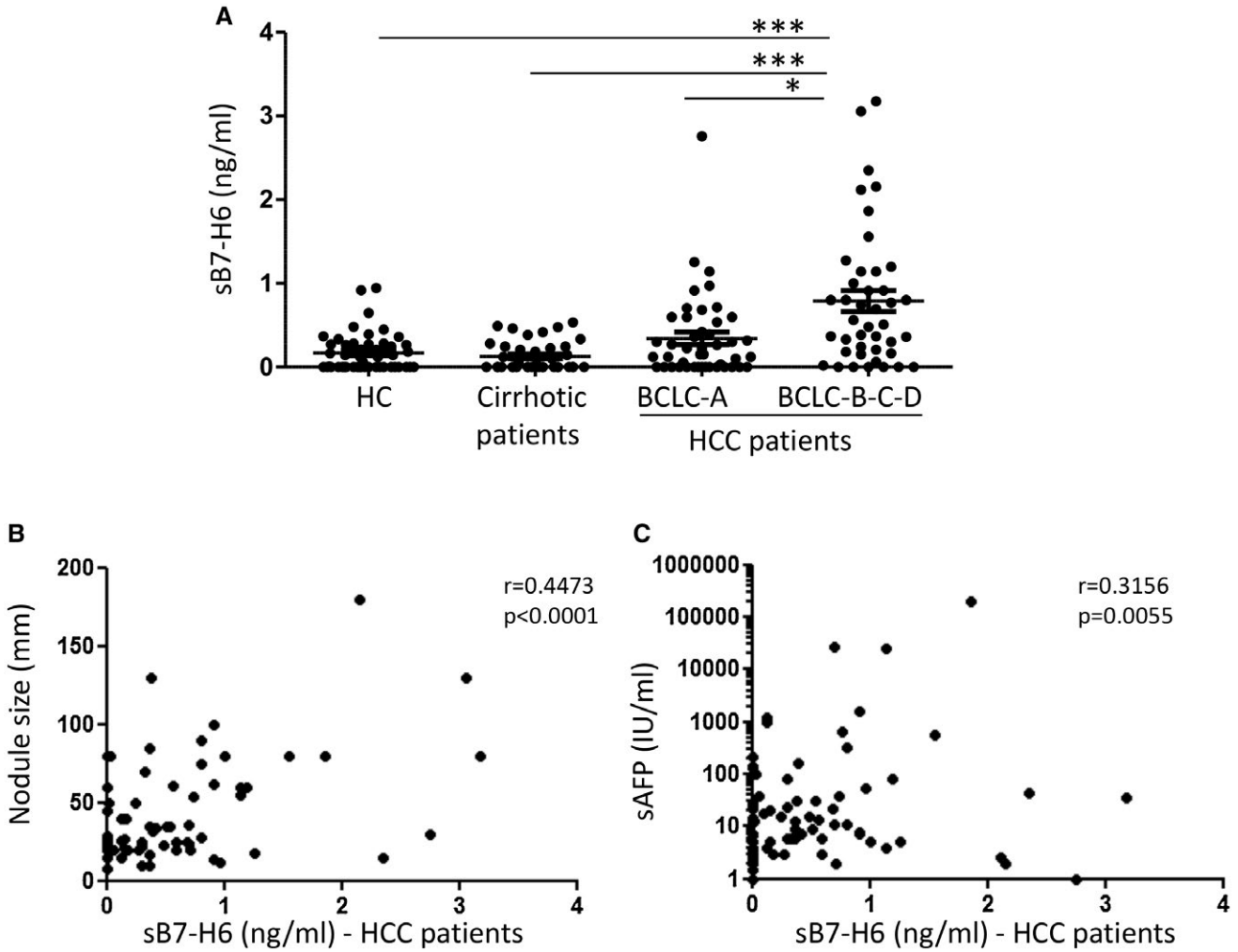

FIG. 8. Soluble B7-H6 protein correlates with clinical parameters and is higher in patients with BCLC stage ≥ B. (A) Serum B7-H6 concentrations in HCC patients stratified according to BCLC stage (n = 87), patients with cirrhosis (n = 39), and HC (n = 48). Data are presented as mean values ± SEM. The Dunn's multiple comparison test was used to compare data. $^{*}P < 0.05$; $^{***}P < 0.001$. The Pearson correlation coefficient was used to examine dependence between sB7-H6 protein (B) and maximum nodule size or serum alpha-fetoprotein (C) in HCC patients.

Discussion

Functional deficiencies of circulating and intralesional NK cells have been demonstrated in various human cancers, including HCC.[21,22,25,34,35] Nevertheless, the mechanisms responsible for altered NK cell effector function and their association with disease progression remain largely unexplored. Previous studies found a reduction in the proportion of peripheral blood NK cells and of $CD56^{dim}$ phenotype in HCC patients,[21,22,35] which could contribute to reduced immune surveillance, whereas no differences were found in our study between patients and controls. These discrepancies might be a consequence of patient selection, as our patients had an overall more advanced disease, a larger proportion of them being categorized as BCLC-B, C or D, whereas the vast majority of patients in Cheung et al.[22] and Cariani et al.[35] were classified as BCLC-A. An altered NK cell phenotype may reflect NK cell anergy; however, this does not always correlate with altered expression of activating and inhibitory receptors on NK cells in HCC patients. Relevant to this statement are controversial data regarding the frequencies of NK cells carrying NKG2D and NKG2A receptors in circulating and intrahepatic NK cells.[21,22,35] Interestingly, phenotypic analysis of our patients with HCC showed decreased frequencies of NK cells expressing NKp30 and NKG2D activating receptors, together with an increased frequency of Tim-3, suggesting that innate immunity is skewed toward exhausted antitumor immune responses, despite an increased proportion of NK cells expressing the CD69 early activation marker. Recent studies have reported conflicting data about Tim-3 function in NK cells.[36-38] Ndhlovu et al. showed that Tim-3 inhibits NK cell–mediated cytotoxicity,[36] whereas another study suggested that Tim-3 may instead enhance IFN-γ production.[37] Both studies focused on healthy donors and not patients with chronic diseases, such as cancer. In cancer patients, da Silva et al. showed that Tim-3 could function as an NK-cell exhaustion marker in advanced melanoma and that its blockade reverses the NK-exhausted phenotype.[38] Functional NK cell deficiency might also be associated with an increased regulatory T-cell frequency, an altered dendritic cell function, and an increased proportion of myeloid-derived suppressor cells.[21,25,39] Apart from those mechanisms, alternative splicing of the NCR3 gene has been shown to profoundly influence NKp30-dependent function and has been correlated with the prognosis and evolution in gastrointestinal stromal tumor patients as well as other cancers, viral infections, and miscarriage.[5-10] However, no information is currently available on NCR3 splice variant profile and function in liver cancer. In the present study we showed that in HCC patients' NK cells displayed reduced NKp30 expression as well as NKp30-mediated cytokine secretion and cytotoxicity. We also showed that peripheral and tumor-infiltrating NKp30-expressing NK cells displayed altered expression of the major NKp30 isoforms (NKp30a, NKp30b, and NKp30c), which is compatible with defective NKp30-mediated tumor immune surveillance in HCC patients. Indeed, the PBMC of HCC patients displayed a lower mRNA expression level of the NKp30a and b immunostimulatory isoforms compared with HC, and in those patients with advanced tumor, expression of the inhibitory NKp30c isoform was clearly increased. Furthermore, NK cells displaying a reduced NKp30 a/c isoform ratio exhibited a reduced NKp30-mediated cytokine production. Moreover, considering the relative expression of the different NCR3 alternative splice variants, there was a bias toward a prevalent inhibitory NKp30 isoform profile in the liver compartment, consistent with decreased NKp30-mediated function. This sheds light on the role for the NKp30 receptor in HCC surveillance. In line with this interpretation, NKp30-mediated cytokine production by circulating NK cells was found to be reduced in HCC patients compared with controls, in keeping with a lower frequency of NKp30+ NK cells and a lower density of NKp30 receptor expression in HCC compared with HC. These findings somehow differ from those obtained in the intrahepatic compartment, in which NKp30-mediated NK cell degranulation was reduced despite higher relative frequency of NKp30+ cells and higher density of the NKp30 receptor in neoplastic compared with non-neoplastic adjacent tissues. In this respect, NKp30-mediated responses may be influenced by differences in the cytokine milieu between the neoplastic and non-neoplastic tissue, as shown in previous studies supporting an epigenetic role for certain cytokines, such as TGF-β, IL-15 and IL-18, which are enriched in a specific microenvironment, to convert the NCR3 splice variant profile of NK cells and to affect the NK cytolytic behavior.[9,10] In line with these findings, our data showing a reduced pro-inflammatory

cytokine (IL-6, IL-8) mRNA content and a concomitant inhibitory signal delivered by unaltered TGF-β mRNA expression in the neoplastic tissue support the existence of an inhibitory microenvironment affecting NK cell responses. Thus, the evidence gathered in this study pointed to peculiar characteristics of the neoplastic tissue in patients with HCC, in whom the NKp30 isoform analysis was compatible with an inhibitory profile, despite an increased relative proportion of NKp30-positive NK cells.

Our data clearly emphasized the role of B7-H6 in regulating NKp30 expression. Interaction of B7-H6 with NKp30 on NK cells leads to efficient NK cell activation and target cell killing.[40] The absence of B7-H6 transcripts in normal tissues and the presence in tumor cells, on inflammatory monocytes during sepsis and in viral infections, define B7-H6 as an example of a stress-induced self-molecule.[18,41,42] Until now, hepatic B7-H6 expression remained poorly explored. Zou et al. investigated B7-H6 protein expression on HBV-induced acute on chronic liver failure and another study investigated B7-H6 expression at the transcriptional level in HCC[18,43]; however, the non-neoplastic liver was only poorly explored. In the former study, B7-H6 expression, assessed by immunohistochemistry, was found to be markedly enhanced on HBV-infected hepatocytes compared with the healthy liver, and its expression positively correlated with the severity of liver injury in this clinical setting.[18] In addition, Fiegler et al. observed elevated B7-H6 mRNA levels in HCC tissue compared with normal liver controls.[43] Importantly, our results compared tumor tissue and cirrhotic liver showing a significantly reduced B7-H6 expression in HCC tissue by immunohistochemistry. Notably, the HCC tissue exhibited different intensity of B7-H6 expression according to tumor differentiation status, the ligand being less expressed, although not significantly so, in poorly differentiated HCC. Decreased B7-H6 expression was not caused by altered gene transcription, as tumor B7-H6 mRNA levels were not significantly different from those of the surrounding non-neoplastic tissue, suggesting that other mechanisms might be involved. Similarly to other members of the B7 family, B7-H6 was also identified in a soluble form capable of binding to NKp30 receptor and to prevent NKp30-mediated NK cell triggering. Release of sB7-H6 was shown to be at least in part compatible with a metzincin-mediated shedding mechanism, as ADAM-specific inhibitors slightly increased B7-H6 surface expression on primary HCC cell lines, in agreement with data in melanoma patients.[33] The role of soluble B7-H6 in HCC is not entirely clear, as a short incubation with heterologous serum containing cell-free B7-H6 was unable to decrease the proportion of NKp30+ NK cells *in vitro*, whereas cell-associated B7-H6 clearly was. Instead, a competing role for B7-H6 has convincingly been shown in ovarian carcinoma, in which down-modulation of the NKp30 receptor expression and function on tumor-associated NK cells were associated with the presence of its ligand B7-H6 as a surface/cytosolic molecule in tumor cells as well as a soluble molecule.[19] In line with this observation, and in agreement with our data showing a clear ligand-induced receptor down-modulation, higher NKp30 expression observed in TIL compared with LIL may be due to an absent down-regulatory effect caused by reduced ligand-receptor interaction. Evidence in support of this hypothesis comes from our data showing decreased expression of B7-H6 ligand in HCC tissues. Moreover, significantly elevated levels of sB7-H6 were detected in the sera of HCC patients with intermediate and advanced tumor compared with HC and patients with cirrhosis, suggesting a potential inhibitory role for this soluble ligand on NKp30 expression and NKp30-mediated NK cell activity. Our data suggesting that B7-H6 is released by sheddases from neoplastic cells are compatible with larger amounts of soluble ligand being shed from larger neoplastic nodules or advanced HCC. This may represent an evasion mechanism from the host immune surveillance.

In conclusion, our study provides evidence in support of an alteration of the NKp30/B7-H6 axis in HCC and reveals several mechanisms that can be exploited for immunotherapeutic approaches for liver cancer. It may be envisaged that beyond restoring cytotoxic T lymphocyte activity with checkpoint inhibitors, such as PD-1/PD-L1-specific monoclonal antibodies,[44] it could also be possible to associate specific immune interventions to modulate altered NK cell activity. Moreover, it is of interest that sorafenib, which for years was the only systemic treatment available for patients with advanced HCC,[45] primes proinflammatory responses of macrophages located within the HCC microenvironment and induces anti-tumor NK cell responses in a cytokine-dependent fashion, providing insights for immune stimulatory treatments.[46]

Acknowledgment: A.L. was aided by the Nuovo-Soldati Cancer Foundation.

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