Virus-induced hepatocellular carcinomas cause antigen-specific local tolerance

Gerald Willinsky,1,2 Karin Schmidt,1 Christoph Loddenkemper,3 Johanna Gellermann,4 and Thomas Blankenstein1,2

1Institute of Immunology, Charité Campus Benjamin Franklin, Berlin, Germany. 2Max Delbrück Center for Molecular Medicine, Berlin, Germany. 3Institute of Pathology, Charité Campus Benjamin Franklin, Berlin, Germany. 4Clinic for Radiation Medicine, Charité Campus Berlin Buch, Berlin, Germany.

T cell surveillance is often effective against virus-associated tumors because of their high immunogenicity. It is not clear why surveillance occasionally fails, particularly against hepatitis B virus– or hepatitis C virus–associated hepatocellular carcinoma (HCC). We established a transgenic murine model of virus-induced HCC by hepatocyte-specific adenovirus-induced activation of the oncogenic SV40 large T antigen (TAg). Adenovirus infection induced cytotoxic T lymphocytes (CTLs) targeted against the virus and TAg, leading to clearance of the infected cells. Despite the presence of functional, antigen-specific T cells, a few virus-infected cells escaped immune clearance and progressed to HCC. These cells expressed TAg at levels similar to HCC isolated from neonatal TAg-tolerant mice, suggesting that CTL clearance does not select for cells with low immunogenicity. Virus-infected mice revealed significantly greater T cell infiltration in early-stage HCC compared with that in late-stage HCC, demonstrating progressive local immune suppression through inefficient T cell infiltration. Programmed cell death protein-1 (PD-1) and its ligand PD-L1 were expressed in all TAg-specific CD8+ T cells and HCC, respectively, which contributed to local tumor-antigen-specific tolerance. Thus, we have developed a model of virus-induced HCC that may allow for a better understanding of human HCC.

Introduction

T cell surveillance is often effective against virus-induced tumors because of their high immunogenicity (1, 2). It remains unclear why surveillance occasionally fails, e.g., against hepatitis B virus–associated (HBV-associated) or hepatitis C virus–associated (HCV-associated) hepatocellular carcinoma (HCC). Possible reasons could be an initial failure to induce effective T cells (3–5), T cell exhaustion due to chronic antigen stimulation (6, 7), tumor-induced tolerance (8), immune escape by loss of immunogenicity (9), or tumor development in tolerogenic organs, e.g., the liver (10). In humans, T cell responses appear to be more efficient in those individuals who completely cleared the virus (11, 12); however, it is difficult to identify individuals in the acute infection phase (4, 12). HCC progresses in a great proportion of individuals with chronic HCV infection in the presence of virus-specific CD8+ T cells (13–15). On the other hand, impaired HCV-specific T cell responses have been observed in PBMCs or liver biopsies obtained from patients with chronic HCV infection (4, 16–18). Heterogeneity within individuals, difficulties in analyzing local T cell responses, and the need of in vitro manipulation and expansion for functional analysis of HCV-specific T cells make firm conclusions difficult. Likewise, in chimpanzees, no strict correlation between virus clearance and vigorous T cell responses was observed (19, 20).

Several HCV transgenic mouse lines with constitutive or inducible HCV expression and models that allow infection of hepatocytes by HCV have been generated (21–28). While these models have yielded important information about viral pathogenesis, the mice were either tolerant for viral antigens or did not develop HCC with reliable, high frequency. Thus, the endogenous T cell response to virus-induced HCC throughout the course of the disease has not been analyzed. To overcome the problem of T cell tolerance to viral antigens, T cells from HBV-immunized wild-type mice were transferred into HBV transgenic mice. The data showed that CD8+ T cells were mainly responsible for hepatitis and that viral replication was abolished by cytolytic and noncytolytic mechanisms (29). The chronic necroinflammatory T cell response was suggested to contribute to HCC development (30). On the other hand, HCC developed in some HCV transgenic mice independent of inflammation (25), and it is not clear whether the fate of adoptively transferred CD8+ T cells recapitulates that of the endogenous T cell pool following viral infection. Here, we established a model of virus-induced HCC, in which a viral oncogene, SV40 large T antigen (TAg), was activated in hepatocytes through viral infection of a host, LoxP-TAg mice, that can efficiently respond to TAg. In LoxP-TAg mice, Cre recombinase–encoding adenoviruses (Ad.Cre) with high tropism for the liver deleted a stop cassette, suggested to contribute to HCC development (30). On the other hand, HCC developed in some HCV transgenic mice independent of inflammation (25), and it is not clear whether the fate of adoptively transferred CD8+ T cells recapitulates that of the endogenous T cell pool following viral infection. Here, we established a model of virus-induced HCC, in which a viral oncogene, SV40 large T antigen (TAg), was activated in hepatocytes through viral infection of a host, LoxP-TAg mice, that can efficiently respond to TAg. In LoxP-TAg mice, Cre recombinase–encoding adenoviruses (Ad.Cre) with high tropism for the liver deleted a stop cassette, which prevented TAg expression. Previously, we have shown that these mice have retained CD8+ T cells against peptide IV (pIV), the dominant epitope of TAg, which could be induced by prophylactic immunization for protection from sporadic tumors that occur late in life (8, 31). In contrast to mice with virus-induced HCC reported here, mice with sporadic lesions readily developed TAg-specific CD8+ T cell tolerance.

Results

Virus-induced oncogene activation and HCC development. LoxP-TAg mice allow activation of the dormant TAg oncogene by Cre/loxP recombinase–mediated stop cassette deletion (Figure 1A). Based on Ad.Cre infection of the liver we established a model for virus-induced HCC. LoxP-TAg mice were injected i.v. with Ad.Cre and monitored for tumor development by MRI, palpation, and determination of liver enzymes alanine aminotransferase (ALT) and aspartate transaminase (AST). By MRI, tumors of around 2.5 mm in size were...
detected in the liver 8–16 weeks after virus infection (Figure 1B). Elevated ALT and AST levels were detected 1 week after virus infection, indicating liver damage (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI64742DS1). After 4 to 6 weeks, ALT/AST values returned to slightly elevated levels, when compared with those of control mice, and subsequently increased proportionally to HCC development. The virus-induced TAg activation induced multinodular HCC of classical type, resembling hepatocytes with a predominantly trabecular (plate-like) architectural pattern within 8 to 24 weeks (in some

Figure 1
LoxP-TAg transgenic mice develop HCC after i.v. injection of Ad.Cre. (A) Cre recombinase–mediated TAg activation. (B) For induction of HCC, 8- to 12-week-old LoxP-TAg mice were injected i.v. with 1 × 10⁹ PFUs of Ad.Cre, and HCC development was detected by MRI and palpation. Representative MR images (left) and macroscopically visible tumors of livers 10 (middle) and 20 weeks (right) after Ad.Cre injection are shown. MR image and liver photograph (middle) are from the same mouse. Arrows indicate tumor nodules. (C) LoxP-TAg mice that received Ad.Cre (red line, n = 14) and double-transgenic LoxP-TAg × Alb-Cre (DTg) mice (blue line, n = 15) were monitored for HCC development. Nontreated LoxP-TAg mice (black line; n = 10) served as control. Time after adenovirus injection is given for Ad.Cre-injected mice, and age is given for double-transgenic LoxP-TAg × Alb-Cre mice. (D) Immunohistology of liver tissue sections of LoxP-TAg mice at different time points after Ad.Cre injection as indicated. Tissues were stained with antibodies specific for TAg and Ki-67 and counterstained with hematoxylin. Scale bar: 100 μm. At least 3 mice were analyzed for each time point, and a representative staining is shown. Schematic drawings show an overview of the cumulative data of the average tumor number and progression not considering inter-mouse variability.
mice 35 weeks) (Figure 1, C and D, and Supplemental Figure 2). In comparison, neonatal TAg-tolerant LoxP-TAg × albumin-Cre (Alb-Cre) mice that express the Cre recombinase by the albumin promoter and activate TAg in the liver early in life developed HCC within 7 to 14 weeks of age (Figure 1C). Upon liver tumor development, LoxP-TAg mice showed an increase of ALT/AST values that stayed elevated until mice succumbed to HCC and cholangiocellular carcinoma (Supplemental Figure 3). Nontreated LoxP-TAg mice did not develop HCC or pathological abnormalities in the liver during the more than 12-month observation time, as assessed by MRI, histology (data not shown), and determination of liver enzymes ALT and AST (Supplemental Figure 4). TAg expression was abundantly detected throughout the liver 1 week after viral infection (Figure 1D). Ki-67 expression often mirrored TAg expression, indicating abundant cell proliferation in TAg-expressing hepatocytes. Within the next 3 weeks, TAg+ cells were almost completely eliminated, leaving behind few microscopically small TAg lesions, which then progressed to HCC (Figure 1D).

**Tag recognition during viral infection induces T cell immunity.** Our model is based on the assumption that the stop cassette is deleted and TAg is activated in virus-infected liver cells and that TAg is recognized by the adaptive immune system concomitant with a strong antiviral immune response. Within 3 weeks after Ad.Cre infection, LoxP-TAg mice developed high anti-TAg IgG antibody titers, demonstrating that TAg was rapidly recognized by the adaptive immune system and suggested functional CD4+ T cell activation (Figure 2A). Neither Ad.Cre infection of C57BL/6 (B6) mice nor luciferase-encoding adenovirus (Ad.Luc) infection of LoxP-TAg mice induced anti-TAg antibodies. Bioluminescence (BL) imaging of Ad.Luc-infected LoxP-TAg mice confirmed the high tropism for the liver (Supplemental Figure 5). The TAg-specific IgG antibodies were of IgG1, IgG2a, and IgG2b isotypes (Figure 2B). Because
the IgG1 isotype was not observed in LoxP-TAg mice with sporadic tumors. TAg recognition in the viral context apparently induced functionally different CD4+ T cells. During subsequent HCC progression, anti-TAg IgG serum titers increased to dramatically high levels (Figure 2A). In order to directly assess the role of T cells during HCC development, CD4+ and CD8+ T cell–deficient LoxP-TAg mice were infected with Ad.Cre. The absence of both CD4+ T cells and CD8+ T cells substantially reduced the latency of virus-induced HCC in comparison with that in T cell competent–LoxP-TAg littermates (Figure 2C). Similarly, strongly accelerated HCC development was observed in combined Rag-2/IL-2 receptorγ chain–deficient LoxP-TAg mice, which lack T cells, B cells, and NK cells (Figure 2D). Because the immune deficiency also might have abolished antiadenoviral T cell responses and clearance of virus-infected cells, HCCs were induced by viral infection in villin-Cre (Vil-Cre) × LoxP-TAg double-transgenic mice. Due to constitutive stop cassette deletion and TAg activation in epithelial cells of the gastrointestinal tract, these mice had developed neonatal cytotoxic T lymphocyte (CTL) tolerance for TAg but were otherwise immune competent (32). Virus-induced HCC developed with similar reduced latency in Vil-Cre × LoxP-TAg mice as in T cell–deficient mice (Figure 2E). Collectively, the data indicate that virus-induced TAg activation in hepatocytes led to T cell immunity, which inhibited but did not prevent HCC development long term. Furthermore, TAg-specific T cells were mainly responsible for impairing HCC progression.

Virus-induced HCCs “sneak through” despite persistently functional CTLs. In LoxP-TAg mice with sporadic tumors, anti-TAg IgG antibodies predicted TAg-specific CTL tolerance (31). In contrast, in vivo CTL assays in Ad.Cre-infected LoxP-TAg mice revealed that functional CTLs directed against the immunodominant TAg pIV were induced as early as 2 weeks after virus infection (Figure 3, A and B). Remarkably, pIV-specific CTLs persisted in the presence of progressing TAg+ HCC (Figure 3B). The strongest pIV-specific CTL
activity was detected in mice with large tumor burdens, suggesting that the progressing HCC upregulated CTL activity in the spleen (Figure 3B, white circles). CTLs specific for the adenovirus protein DNA-binding protein 43 (dbp43) were also induced upon Ad.Cre infection and were detectable by in vivo kill analysis throughout the experiment (Figure 3C).

As a more rigorous test for functional pIV-specific CTLs, HCC-bearing LoxP-TAg and — as controls — Rag2−/− mice, young LoxP-TAg mice, and old LoxP-TAg mice with sporadic tumors were challenged s.c. with the TAg-expressing tumor cell line 16.113 (Table 1). Whereas in Rag2−/− mice tumors grew, most LoxP-TAg mice infected with viruses 4, 8, and 24 weeks before 16.113 (Table 1) rejected the transplanted tumor cells, while the primary TAg+ tumor cells that had been injected with Ad.Cre when they were 8–12 weeks old (Tg). Tumor growth was followed using caliper measurement. The number of mice with challenge tumor per mice in experiment is shown. Mice were observed until they had to be sacrificed because of primary HCC or challenge tumor grew to an average size of at least 6 mm in diameter (for these mice, time to growth of transplanted tumor cells is given in brackets). Young LoxP-TAg mice observed for the indicated time were tumor free.

Virus-induced HCCs induce antigen-specific local tolerance. The previous experiments raised the question of how the HCCs, regressors upon transplantation, could progress in the presence of functional pIV-specific T cells. Histopathological examination of livers from nontreated and Ad.Cre-infected LoxP-TAg mice at different time points thereafter revealed moderate infiltration of the tumor nodules by CD3+ T cells (Figure 5A). Quantitative analysis of CD3+ T cell infiltration revealed significantly higher infiltration of small tumor nodules that developed 6–10 weeks after Ad.Cre infection in comparison with that of end-stage HCCs in mice 12–35 weeks after Ad.Cre infection. Peritumoral CD3+ T cell infiltration in end-stage tumors was only slightly higher (statistically not significant) than intratumoral infiltration (Supplemental Figure 6). Whereas FoxP3+ cells were not detected (Figure 5A), F4/80+ cells, comprising macrophages and Kupffer cells, were equally distributed in the livers of naive and virus-infected mice (Figure 5A, weeks 0–4) but were decreased in cancerous tissue (Figure 5A, weeks 6–10 and 12–35). Solid tumors are supposed to create an immune-suppressive environment. We detected CD163+ M2 macrophages, FAP+ stromal cells, and CD11b+/Gr-1+ immature myeloid cells in end-stage HCC (Supplemental Figure 7). Therefore, these components potentially could contribute to local immune suppression. To analyze local T cell function in HCC, 16.113 cells, transduced to express luciferase (Fluc) and EGFP (16113gl), were injected into the livers of virus-induced HCC-bearing LoxP-TAg mice, and mice were observed until they had to be sacrificed due to primary HCC burden. Histological analysis of liver sections revealed the growth of 16.113gl tumors with the typical ductal appearance of this (gastrointestinal-derived) tumor, TAg-specific staining, and absence of the liver/HCC-specific marker HepPar1 in both HCC-bearing LoxP-TAg and Rag2−/− mice (Figure 5B). Age-matched tumor-free LoxP-TAg mice rejected 16.113gl cells injected into the liver (data not shown). Because 16.113 cells were rejected in HCC-bearing mice at a s.c. injection site (Table 1), the data demonstrate local tolerance in HCC-bearing LoxP-TAg mice.

16.113 cells were transduced to express luciferase and EGFP (16113gl) not only to visualize tumor growth but also to express foreign antigens in the tumor cells. This allowed us to ask whether tolerance in the tumor microenvironment was specific for TAg, the dominant transplantation rejection antigen in TAg-transformed tumors (8), or whether CTLs were suppressed independent of their specificity. First, 16113gl cells were injected s.c. to analyze whether variants that lost the marker proteins (or the coexpressed selectable markers neomycin and hygromycin) could be selected in suitable hosts. In Rag2−/− mice, tumors grew and retained Fluc expression, as detected by BL imaging (Figure 5C). In LoxP-TAg × Alb-Cre mice, which are TAg tolerant but generate normal CTL responses to other antigens (31), Fluc (and EGFP; data not shown) signals became undetectable within 2 to 3 weeks (Figure 5, S and D), while TAg+ tumors progressed after a short selection phase (Figure 5D). In young LoxP-TAg mice, 16113gl tumors were rejected. Compatible with previous experiments, in old LoxP-TAg mice with sporadic tumors, which had developed TAg tolerance and CTL hyporesponsiveness to unrelated antigens (31), 16113gl...
tumors grew progressively, while retaining the Fluc signal, albeit at reduced level (Figure 5, C, and D). These data show that antigen loss variants can be selected but not in mice with nonvirus-induced sporadic cancer, leading to impaired CTL responses against unrelated antigens. Remarkably, if 16113gl cells were injected intrahepatically (i.h.) into LoxP-TAg mice with virus-induced HCC, Fluc signals were lost within 2 to 3 weeks (Figure 5E and Supplemental Figure 8), and antigen loss variants progressed (Figure 5B). These results demonstrate that, in LoxP-TAg mice with virus-induced HCC, local tolerance is specific for the tumor transplantation rejection antigen TAg and that foreign antigens were still selected against in the tumor microenvironment.

Local tolerance is mediated by PD-1/PD-L1 dependent and independent mechanisms. pIV-specific CD8+ T cells in livers and spleens of LoxP-TAg mice with virus-induced HCC were analyzed with Kβ/IV tetramers. A high frequency of the CD8+ T cells in the livers of HCC-bearing LoxP-TAg mice were pIV specific (14%–31% Kβ/IV-tetramer+ cells of the CD8+ T cells) but not in age-matched nontreated LoxP-TAg mice (Figure 6A). The frequency of Kβ/IV-tetramer+ CD8+ cells in the spleens of HCC-bearing LoxP-TAg mice was 5%–6%, whereas it was undetectable in the control mice. Importantly, programmed cell death protein-1 (PD-1) receptor was expressed on almost all Kβ/IV-tetramer+ CD8+ T cells in the liver (Figure 6B). PD-1 expression was higher on liver compared with that on spleen pIV-specific CD8+ T cells (Supplemental Figure 9). All virus-induced HCC cell lines investigated expressed the ligand PD-L1, whereas hepatocytes from noninfected LoxP-TAg mice did not (Figure 6C). In addition, immunohistochemical analysis of livers from HCC-bearing LoxP-TAg mice showed PD-L1 expression on TAg-positive carcinoma cells and TAg-negative stromal cells (Supplemental Figure 10). Notably, intrahepatic CD11c+, CD68+, and Gr-1+ cells showed upregulation of PD-L1 when HCC-bearing LoxP-TAg mice 10–20 weeks after Ad.Cre infection were compared with untreated age-matched LoxP-TAg mice (Supplemental Figure 11). The sporadic tumor cell line 16.113 that grew in livers of HCC-bearing mice also expressed PD-L1 (Figure 6C).

Figure 4
Transplanted Ad.Cre-induced HCCs from LoxP-TAg mice are as immunogenic as those from TAg-tolerant LoxP-TAg × Alb-Cre mice. (A) Similar TAg expression in HCC lines derived from Ad.Cre-treated LoxP-TAg mice and LoxP-TAg × Alb-Cre mice. Western blot analysis of TAg expression in primary HCC lines derived from Ad.Cre-treated LoxP-TAg mice (Ad.56, Ad.451, Ad.434) and LoxP-TAg × Alb-Cre mice (Alb.7, Alb.14). Sporadic TAg+ tumor line 16.113 was used as a control. 20 μg protein was separated by SDS-PAGE gel, blotted onto nitrocellulose membrane, and incubated with anti-TAg antibodies. After autoradiography, the membrane was stripped and reprobed with anti-β-actin antibodies as loading control. The lanes were run on the same gel but were noncontiguous. (B) TAg+ HCC lines induced pIV-specific CTLs. 1 × 10^6 cells of tumor lines 16.113 and HCC lines as indicated were injected s.c. into B6 mice, and 10 days later pIV-specific in vivo kill was assayed. Experiments were performed as described in Figure 3. The percentage of specific killing of peptide-loaded cells is indicated. Each symbol represents 1 mouse; bars indicate mean values. The P value represents overall significance of the graph calculated by Kruskal-Wallis test. In a separate experiment, 1 × 10^6 TAg+ HCC and, as a control tumor line, 16.113 cells, were injected s.c. into untreated 8- to 12-week-old Rag2- and immunocompetent B6 mice. Tumor growth was followed using caliper measurement. Shown is the number of mice that rejected challenge tumor per mouse in experiment. Mice were observed until challenge tumors grew up to an average size of at least 10 mm in diameter. Mice that rejected the transplanted tumor cells were observed for at least 90 days.
7 weeks after viral infection (Supplemental Figure 14B) was similarly effective as that after 12 weeks (Figure 6, E and F). Together, both PD-1/PD-L1-dependent and –independent mechanisms appear to contribute to local tolerance. Furthermore, PD-1+CD8+ T cells have the potential to eliminate HCC in conditioned hosts.

Discussion

We established a model that recapitulates several features of virus-induced HCC in humans. A strong viral antigen, for which the mice were not tolerant at young age, was activated and recognized by T cells during viral infection of hepatocytes. The virus infection induced an antivirus response concomitant with a rapid and strong response against Tag, the cancer-driving oncogene, due to stop cassette deletion in the infected hepatocytes. T cell recognition resulted in hepatitis and clearance of the infected Tag cells, at least the vast majority. Because adenoviruses do not replicate in mice, we ensured that the very few remaining Tag+ hepatocytes escaped elimination and were not induced by virus spread. It remains enigmatic why these few Tag+ hepatocytes survived, while neighboring infected Tag+ cells were eliminated. They could have expressed less Tag during the effector CTL response (35), deleted the stop cassette when effector CTLs already went through the contraction phase (36), or reflected a subtype of hepatocytes that are resistant to elimination (37, 38). Strikingly, the few Tag+ hepatocytes that sneaked through, despite functionally activated Tag-specific CTLs, were recognized at some point and upregulated systemic tumor immunity, at least at sites distant from the primary tumor, while progressing to lethal HCC. Sneaking through has been described previously in tumor transplantation models, in which low numbers of injected tumor cells remained unrecognized for too long by T cells (39). Sneaking through had not been demonstrated before in a primary tumor context; had not been demonstrated before in a primary tumor model in the presence of functionally activated CTLs.

Our data illustrate the fundamentally different immune response to sporadic and virus-induced tumors, directed against the same antigen in the same mouse model. If left untreated, LoxP-Tag mice develop in a stochastic manner sporadic tumors late in life after a long premalignant phase (8, 31). Tag recognition in mice with premalignant lesions, as detected by the generation of anti-Tag IgG antibodies, induced CTL tolerance, and no transient phase of functional activation was detected (31). In sharp contrast, if Tag was recognized by T cells during viral infection, anti-Tag antibodies were of partially different IgG subtype, indicating already the qualitatively different adaptive immune response. More importantly, in the viral context, CD4+ and CD8+ T cells were functionally activated and substantially delayed HCC progression. The response was primarily directed against Tag, because Tag-tolerant mice rapidly succumbed to HCC. In contrast to (nonvirus-induced) sporadic tumors, the virus-induced HCC needed to escape immune control. Immune escape did not involve systemic CTL tolerization or the apparent selection of low immunogenic variants. However, the observation that HCCs, progressors in the primary host with systemic tumor immunity, were regressors in transplantation experiments raises doubts about the ability of this assay to measure immune selective processes in the primary host.

There is ample evidence that solid tumors create an immune-suppressive microenvironment (40, 41). Therefore, it may not be surprising that transplanted Tag+ tumor cells, which were rejected at a distant site, a phenomenon termed concomitant immunity (42), grew in the livers of HCC-bearing mice. Because most described immune-suppressive mechanisms, e.g., those mediated by indoleamine 2,3-dioxygenase, TGF-β1, FAP-expressing cells, M2 macrophages, or CD11b+Gr1+ cells (43–47), act nonspecifically, one would have expected that tumor-unrelated T cell responses were also suppressed within the suppressive tumor microenvironment. Remarkably, transplanted tumor cells were selected against expression of foreign antigen but not Tag in the livers of HCC-bearing mice, demonstrating local tolerance specifically for the rejection antigen of HCC. Tolerance required the presence of HCC, because young untreated LoxP-Tag mice rejected Tag+ tumor cells injected into the liver. Our data contrast those obtained in a tumor transplantation model, suggesting that tumors are a privileged site for bacterial growth (48). Because of the rapid growth of the transplanted tumor, bacterial accumulation could be observed for only 6 days after intratumoral injection. Therefore, it is not clear whether an innate or adaptive immune response was impaired and whether the bacteria would have been eliminated at a later time point. This model is also difficult to compare to ours, because the bacteria, Listeria monocytogenes, reside inside macrophages and CD4+ T cells are mainly responsible for protection.

The virus-induced HCC used at least 2 independent mechanisms of local tolerance, each of which was necessary for unimpaired progression. PD-1, expressed by almost all Tag-specific CD8+ T cells in HCC-bearing mice, and PD-L1, expressed by the HCC, together with the observation that a brief treatment with anti–PD-L1 blocking antibodies substantially delayed HCC progression, reveal the first immune escape mechanism. We cannot exclude a contribution of PD-L1 expression by tumor stroma cells for T cell inhibition. This appears even likely, because various tumor stroma cell types expressed PD-L1 (49–52). PD-1 expression by CD8+ T cells has been associated with cellular exhaustion in models of persistent viral infection (6, 53). Even though we cannot rule out some functional impairment of the Tag-specific PD-1+CD8+ T cells (5), they exhibited undiminished CTL activity in vivo, rejected Tag+ tumor cells injected at a s.c. site and, importantly, inhibited autochthonous HCC progression upon transfer into sublethally irradiated mice. In fact, CTL activity was upregulated as HCC progressed and antigen amount was increased. Thus, while PD-1/PD-L1 interaction was clearly involved in local immune suppression, it was not sufficient to constrain HCC progression. We found additional inhibitory receptors, Lag3, CD160,
research article

A

B

C

D

E

F

K/IV Tet

Gate: CD8+

Percent survival

Weeks after in vivo antibody treatment

P = 0.038

Rat IgG2b

Anti-PD-L1

Percent survival

Weeks after spleen cell transfer

P = 0.002

@ Spleen cells

Percent survival

Weeks after CD8+ T cell transfer

P < 0.001

@ CD8+ T cells
and, occasionally, Tim-3, being expressed on pLV-specific T cells in the liver that could further contribute to T cell dysfunction in the liver (54–56). T cell accessibility of the HCC appeared to be a second mechanism impeding tumor immunosurveillance. It has been proposed that infiltration of adoptively transferred T cells in an autoimmune hepatitis model was facilitated by irradiation (57). Consistent with these data, the transfer of CD8+ T cells from HCC-bearing mice, which contained TAg-specific CD8+ T cells that basically all expressed PD-1, into irradiated HCC-bearing mice also substantially inhibited HCC progression. Virus-induced HCC in untreated mice contained fewer CD3+ T cells in comparison with sporadic premalignant lesions of LoxP-TAg mice that had already developed CTL tolerance (31). Collectively, our data suggest a 2-stage immune evasive mechanism of HCC: T cells can only poorly infiltrate HCC, and the few infiltrating T cells are locally inhibited in their function. Blocking functional inhibition (through anti-PD-L1 antibodies) or allowing better T cell infiltration (through irradiation) overcomes local tolerance, albeit not long term.

While it has long been accepted that virus-associated cancers are under effective immunosurveillance (58), the mechanism of escape from immunosurveillance may be manifold and depend on the experimental or clinical situation. This is nicely illustrated by comparison of our model with a model published recently, in which lentivirus was used to deliver neoantigens into cells, simultaneously compared with that of the lentivirus may explain the different results. Thus, the adenovirus may act as stronger adjuvant to activate TAg-specific T cells compared with the lentivirus that helps the activation of the chosen model antigens SIY and ovalbumin (59, 60). Two reasons may explain the different mechanisms of immune escape in the HCC model (retention of the target antigen/high immunogenicity and local tolerance) versus the sarcoma model (loss of target antigen and selection for low immunogenicity).

Sequences introduced into cells by viral infection may be silenced easier by epigenetic mechanisms than sequences introduced into the germline. More importantly, in the HCC model, the T cell response was directed against the cancer-driving oncogene, which cannot be easily selected against (61), while, in the sarcoma model, the T cell response was directed against surrogate antigens, which better reflect passenger mutations and can be easily selected against (60).

Because HCC progresses in a great proportion of patients with chronic HCV infection, despite the presence of HCV-specific CD8+ T cells (15–17, 62), and the liver-infiltrating CD8+ T cells in these patients expressed PD-1 (63), we think that our model encompassing both initial anti-virus immune response and HCC development bears high similarity to the human disease.

**Methods**

*Mice.* LoxP-TAg, Alb-Cre × LoxP-TAg, and Vii-Cre × LoxP-TAg transgenic mice were described previously (8, 31, 32). Rag2−/− mice (B6.129S6-Rag2tm1Wtsi/J) and Rag2−/− RAG2+ mice (B6.129S2-Rag2tm1Wtsi/J) were purchased from The Jackson Laboratory; B6 mice were obtained from Charles River; and CD45.1 congenic mice were bred in our animal facilities.

**Immunization/tumor cell transplantation.** For TAg-specific immunization, mice were injected i.p. with 5 × 10^6 to 10 × 10^6 TAg+ 16.113 tumor cells. Adenovirus-specific immunization was performed by i.v. injection of 1 × 10^7 PFUs of Ad.Cre. For tumor challenge experiments and analysis of TAg-specific CTL response, mice were injected s.c. with 1 × 10^6 cells of the indicated cell lines: 16.113 is a tumor cell line that developed spontaneously in the gastrointestinal tract of a LoxP-TAg mouse (8), HCC cells line Ad.56/Ad.451/Ad.434 were obtained from LoxP-TAg mice 5–6 months after Ad.Cre administration, and HCC cell lines Alb.7/Alb.14/Alb.346 were isolated from 3-month-old LoxP-TAg × Alb-Cre mice (31). For analysis of local tolerance in the liver, 16.113 cells were retrovirally transduced with pLGSN and subsequently transfected with pCAG-Fluc generating cell line 16.113αβ. For selection of transduced and transfected clones neomycin and hygromycin resistance markers were used, respectively. 1 × 10^6 16.113αβ cells (bulk culture) expressing EGFP and Fluc were injected into the liver parenchyma, and growth of 16.113αβ cells was determined by histology of liver tissue sections. Tumor volume in mice injected s.c. with 1 × 10^6 16.113αβ cells into the flank was determined by caliper measurement of the tumor parameters (x,y,z) according to the formula (x^2yz/2). Animals that rejected the challenge tumors were monitored for at least 60 days.

**In vivo kill assays.** CTL activity against the TAg-specific pLV (VYD-FLKL; ref. 8) was analyzed in vivo separately or simultaneously with the adenovirus dbp43 (FALSNAEDL; ref. 64). Single pLV-specific in vivo kill assay was performed as previously described (8). For simultaneous detection of CTL activity against pLV and dbp43, nonloaded (Ø) and pLV- and dbp43 peptide-loaded (1 μM each) CD45.1+ congenic spleen cells (1 × 10^7)
each) were labeled with CFSE in a final concentration of 0.75 μM (CFSElo), 0.075 μM (CFSEint), or 0.0075 μM (CFSELo), respectively. A total of 3 x 10⁷ mixed cells at a 1:1:1 ratio were injected i.v. into the indicated mice. 18 hours later, spleens of recipient mice were stained with APC-labeled anti-CD45.1 antibodies (A20, BD Pharmingen) to separate CFSE-labeled cells. The ratios among the 3 populations were determined by flow cytometry, and the specific cytolytic activity was calculated as follows: percentage of specific killing = 1 – [ratio of control mice/ratio of immunized] or 1 – [ratio of control mice/Ad.Cre-injected mice] x 100, where the ratio is the percentage of CFSE/Lo/CFSEint or CFSELo/CFSEint.

**ELISA.** Serum samples from individual mice were collected. For detection of anti-TAg antibody, ELISA plates, coated with TAg protein, were used as described previously (8). Mouse TAg antibody (PAb100; BD Pharmingen) was used as standard. TAg-specific IgG1, IgG2a, IgG2b, and IgG3 were determined in serum samples, obtained from individual mice. The mouse immunoglobulin screening/isotyping kit (Zymed Laboratories Inc.) was used according to the manufacturer’s instructions.

**Histology and immunohistochemistry.** During autopsies of LoxP-TAg mice, whole organs or macroscopically detectable tumor tissues were embedded in paraffin. Serial sections (2–4 μm) were mounted on slides and stained with hematoxylin and eosin. For immunostaining, consecutive slides were subjected to a heat-induced epitope retrieval step before incubation with the following antibodies: mouse anti-SV40 large T, small t antigen (PAb108; BD Pharmingen), Ki-67 (TEC-3, Dako), CD3 (N1580, Dako), FoxP3 (FJK-16s, eBioscience), F4/80 (BM8, eBioscience), CD163 (M-96, Santa Cruz Biotechnology), fibroblast activation protein (FAP; Abcam), and HepPar1 (OCH1E5.2.10, Dako). For detection, the Streptavidin-AP Kit (K5005, Dako) alone or biotinylated donkey anti-rat (Dianova) or rabbit anti-rat (Dako) secondary antibodies were used followed by the Streptavidin-AP Kit or the EnVision Peroxidase Kit (K 4010, Dako). Alkaline phosphatase (AP) and peroxidase were developed by Fast Red as chromogen or diaminobenzidine chromogen substrates, respectively. For double immunofluorescence staining, 5-μm cryosections were incubated first with FITC-labeled mouse anti-SV40 large T, small t antigen (PAb108; BD Pharmingen) antibody. After washing 3 times in PBS, sections were incubated with anti-mouse PD-L1 (10F.9G2; Bio X Cell) and rat IgG2b isotype control (LTF-2; Bio X Cell) were incubated i.p. into the indicated mice every third day for 2 weeks as described previously (7), and HCC development was monitored.

**Adoptive immune cell transfer.** For adoptive cell transfer, splenic CD8⁺ T cells were purified by use of the CD8 T Cell Isolation Kit II (Miltenyi Biotec). 1 x 10⁶ purified CD8⁺ T cells (80%–95% purity) were injected i.v. into irradiated (5 Gy) HCC-bearing LoxP-TAg mice. For spleen cell transfer, single cell suspensions were prepared, and 5 x 10⁶ cells were transferred i.v.

**Statistics.** Statistical analyses were performed using SPSS and Prism (GraphPad) Software. The overall significance of each graph was calculated with the Kruskal-Wallis test. Comparisons of 2 groups were done by Mann-Whitney U test. Survival curves were compared by Gehan-Breslow-Wilcoxon test. P values of less than 0.05 were regarded as statistically significant.

**Study approval.** Animal experiments were performed according to and with approval of Landesamt für Gesundheit und Soziales, Berlin, Germany.

**Acknowledgments**
We thank K. Borgwald, S. Horn, K. Retzlaff, D. Barthel, S. Speckermann, M. Roesch, A. Gaertner, and C. Westen for technical assistance. This work was supported by grants from the Deutsche Forschungsgemeinschaft (TR36, TR54, and SFB633), the “Alliance” program of the HGF (HA-202), and the clinical cooperation program of the Max Delbrück Center for Molecular Medicine Berlin (to G. Willinsky and J. Gellermann).

Received for publication May 10, 2012, and accepted in revised form December 6, 2012.

Address correspondence to: Thomas Blankenstein, Max Delbrück Center for Molecular Medicine, Robert-Rössle Str. 10, 13092 Berlin, Germany. Phone: 49.30.9406.2816; Fax: 49.30.9406.2453; E-mail: tblanke@mdc-berlin.de. Or to: Gerald Willinsky, Institute of Immunology, Charité Campus Berlin Buch, Lindenberger Weg 80, 13125 Berlin, Germany. Phone: 49.30.450.513607; Fax: 49.30.450.7513607; E-mail: gerald.willinsky@charite.de.