Preventing tumor escape by targeting a post-proteasomal trimming independent epitope

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Adoptive T cell therapy (ATT) can achieve regression of large tumors in mice and humans; however, tumors frequently recur. High target peptide-major histocompatibility complex-I (pMHC) affinity and T cell receptor (TCR)-pMHC affinity are thought to be critical to preventing relapse. Here, we show that targeting two epitopes of the same antigen in the same cancer cells via monospecific T cells, which have similar pMHC and pMHC-TCR affinity, results in eradication of large, established tumors when targeting the apparently subdominant but not the dominant epitope. Only the escape but not the rejection epitope required postproteasomal trimming, which was regulated by IFN-γ, allowing IFN-γ-unresponsive cancer variants to evade. The data describe a novel immune escape mechanism and better define suitable target epitopes for ATT.

INTRODUCTION
Adoptive T cell therapy (ATT) can be highly effective in treating individuals with late stage cancer. Treating metastatic melanoma with in vitro expanded tumor-infiltrating lymphocytes achieved objective response rates (49–72%), depending on the preconditioning regimen (Rosenberg et al., 2011). This represents one of the most effective therapies of metastatic melanoma for patients amenable to ATT. Nevertheless, in 74/93 patients, tumors recurred within 3 yr after treatment (Rosenberg et al., 2011). Tumor recurrence can be attributed to the transferred T cells, the cancer, or the host. Metastatic melanoma trials suggested loss of the target antigen (Melan-A/Mart-1) as escape mechanism (Yee et al., 2002; Mackensen et al., 2006), likely because of the poor binding of Melan-A/Mart-1 epitope to MHC class I (MHC-I) restriction element (HLA-A*0201), a factor that predicts tumor escape (Engels et al., 2013). In other cases, loss of the β2-microglobulin (β2m) gene and concomitant loss of MHC-I cell surface expression was suggested (Restifo et al., 1996; Paschen et al., 2003; Chang and Ferrone, 2007). The β2m gene is in close vicinity to a tumor suppressor gene frequently deleted in cancer (15q21.1; Feenstra et al., 1999; Leal et al., 2008), and loss of MHC-I appears to confer a growth advantage for cancer cells unrelated to immune effects (Garrido et al., 2012). Therefore, it is unclear whether MHC-related genetic lesions are the result of immune escape or simply increased malignancy. Such a cause-and-effect relationship is difficult to address in the clinic, mainly because of the limited number of patients in which the T cell pressure might be sufficiently strong and persistent that the cancer cells indeed needed to escape. In most cases, the transferred T cells were specific for self-antigens and derived from the autologous repertoire, skewed toward low-avidity T cells (Lyman et al., 2005).

Cancer cells could evade T cell recognition by several other mechanisms. Defects in the proteasome or transporter associated with antigen processing could cause altered or impaired peptide generation (Androlewicz et al., 1993; Rock et al., 1994; Suh et al., 1994). IFN-γ responsiveness by the cancer cells favors their rejection (Dighe et al., 1994; Kaplan et al., 1998). It also increases MHC-I expression and induces components of the immunoproteasome, leading to a broader peptide pool (Kloeetzl and Ossendorp, 2004). However, many MHC-I ligands are produced in the form of extended precursors that require the removal or trimming of amino acids to adapt to the constraints of the MHC-I peptide-binding site (Weimershaus et al., 2013). This trimming is mainly per-
formed by the endoplasmic reticulum–resident aminopeptidase ERAAP (the human homologue is ERAP1), which is also IFN-γ inducible (Saric et al., 2002; Serwold et al., 2002).

Target cell recognition by T cells is the result of a tripartite interaction between the peptide, the presenting MHC molecule, and the TCR. Targeting peptide–MHC-I complexes (pMHC) with high affinity led to eradication of large established tumors, whereas targeting pMHC with low affinity selected antigen loss variants (Engels et al., 2013). Similarly, high but not low TCR affinity for pMHC resulted in effective T cell responses with high affinity TCRs typically deriving from the nontolerant and low affinity TCRs from the tolerant repertoire (Theobald et al., 1995). Thus, if pMHC and pMHC-TCR affinities were similar for two peptide epitopes, T cells might be similarly effective or ineffective in rejecting tumors. Therefore, it was critical when comparing the usefulness of different peptide epitopes as targets for ATT to keep the model constant for all but one factor. To this end, we introduced TCRs into monospecific TCR transgenic CD8+ T cells specific for an antigen not expressed by the host or the cancer cells, which ensured that the CD8+ T cells redirected with different TCRs had identical phenotype at the time of transfer. The TCRs were originally isolated from antigen-negative hosts, i.e., the unskewed repertoire. By targeting two different epitopes of the same tumor antigen in the same cancer cells, we excluded the amount of antigen, frequency of variant clones, and tumor-induced immune suppression as possible factors for differential immune escape. Arguably, genetic instability of cancer cells and tumor burden are the highest risk factors for immune escape. Therefore, we treated tumors grown for several weeks to ∼1 cm diam (∼500 mm³), which corresponds to a clinically detectable mass of ∼10⁹ tumor cells (Yu et al., 2006).

We targeted two different epitopes of SV40 large T (T-Ag) in tumors whose growth depended on T-Ag (Anders and Blankenstein, 2013). The H2-Kb–presented peptide IV (pIV) is dominant, with ∼11% of the CD8+ T cells in T-Ag immunized wild-type mice being pIV specific, demonstrating that the epitope is efficiently processed and presented under vaccinal conditions (Mylin et al., 2000). The H2-Db–presented peptide I (pI) is sub-dominant, with ∼3% specific CD8+ T cells at peak levels. Nevertheless, pI-specific CD8+ T cells can eradicate large established tumors (Anders et al., 2011; Charo et al., 2011) and pIV-specific CD8+ T cells were shown to control autochthonous pancreatic or prostate carcinomas (Garbi et al., 2004; Otahal et al., 2007; Bendle et al., 2013). However, in these cases tumor burden at the time of ATT was probably too low to allow for the generation of escape variants. Here, we show that pI and pIV bind with similar affinity to MHC-I, and that pI- and pIV-specific TCR-redirected CD8+ T cells (TCR-I and TCR-IV, respectively) have similar affinity to the cognate pMHC. Both rejected large established tumors expressing high amounts of MHC-I molecules but tumors with low MHC-I were eradicated only by TCR-I T cells. TCR-IV T cells selected IFN-γ–unresponsive escape variants, which was possible because pIV, but not pI, required postproteasomal trimming by ERAAP for efficient T cell recognition, suggesting that IFN-γ–independent epitopes are better targets for ATT.

RESULTS

TCR-I and TCR-IV redirected T cells have similar avidity

To maximize the correct chain pairing and surface expression upon T cell transduction, the α and β genes of TCR-I and TCR-IV, respectively, were connected by the P2A element (β-P2A-α), codon optimized, and integrated into retroviral vectors (Fig. 1). To generate monospecific T cells, TCR–transgenic CD8+ T cells derived from Rag−/− mice specific for lymphocytic choriomeningitis virus gp33 (P14) or ovalbumin (OT-1) were transduced with TCR-I or TCR-IV. Both TCRs were equally well expressed (Fig. 2A). The mean expression on CD8+ T cells derived from P14 mice was 76%
(SD ± 3%; n = 4) and 77% (SD ± 3%; n = 4) for TCR-I and TCR-IV, respectively. The expression levels, although similar between the two TCRs, were generally lower on OT-1 T cells (46%; SD ± 18% for TCR-I; n = 4; and 40%; SD ± 16% for TCR-IV; n = 4). We next compared the avidity of TCR-I and TCR-IV T cells by labeling them with pMHC multimers, which can be dissociated into monomers, termed MHC Streptamers. The dissociation of MHC Streptamers from the T cell surface accurately measures $k_{\text{off}}$-rates and was followed by confocal microscopy (Nauerth et al., 2013). The pMHC $k_{\text{off}}$-rate was comparable for the two TCRs (36 s, SD ± 13 s for TCR-I; 46 s, SD ± 7 s for TCR-IV); if anything, the $T_{1/2}$ was longer for TCR-IV T cells ($P = 0.002$; Fig. 2B). When we compared the functional avidity of TCR-I and TCR-IV T cells by measuring the levels of secreted IFN-γ upon recognition of peptide-loaded, transporter associated with antigen processing–deficient RMA-S cells, we found that both TCR-I and TCR-IV T cells recognized lower peptide concentrations equally well (Fig. 2 C). These data exclude differences in TCR affinity as a major variable in our system.

**Tet-TagLuc and 16.113p cells have similar T-Ag levels, whereas pl and IV have similar pMHC affinity and pMHC-I levels on the cell surface**

To characterize the two T-Ag+ cancer cell lines used in this study, Tet-TagLuc and 16.113p (Anders et al., 2011; Charo et al., 2011), we evaluated factors that can influence the likelihood of tumor recurrence, such as pMHC affinity (Spiotto et al., 2004; Engels et al., 2013) and antigen expression levels. Tet-TagLuc and 16.113p cells expressed similar levels of T-Ag (Fig. 3 A). The affinity of pl and pIV for MHC-I was analyzed in a cell-free peptide competition assay. The peptide concentrations needed for replacing 50% of the indicator peptides bound to H2-Db and H2-Kb, respectively, were quite similar (IC$_{50}$, 31 and 76 nM for pl and pIV, respectively; Fig. 3 B). Because the functional avidity was similar for TCR-I and TCR-IV T cells (Fig. 2 C), co-culturing these T cells with T-Ag+ cancer cells could indirectly answer whether the two epitopes are equally well presented on the cancer cell surface. To maximize the surface expression of pl and pIV, we stimulated Tet-TagLuc and 16.113p cells with IFN-γ for 48 h. TCR-I and TCR-IV T cells recognized both cell lines equally well (Fig. 3 C), thus we conclude that the levels of surface expression was similar for both epitopes.

**TCR-I and TCR-IV T cells reject Tet-TagLuc tumors, but 16.113p tumors escape TCR-IV T cell pressure**

Because MHC-I expression influences the amount of peptide presented on the cell surface, we analyzed MHC-I expression by Tet-TagLuc and 16.113p cells. MHC-I expression (H2-Kb/Dd) was lower for 16.113p (Kb/Db MFI, 10.5/4.8; SD ± 9.9/2.3; n = 3) compared with Tet-TagLuc cells (Kb/Db MFI, 21.9/14.7; SD ± 21.3/6.3; n = 3), even after IFN-γ stimulation (Kb/Db MFI, 79.3/30; SD ± 60.9/10.8 and 162.5/62.1 SD ± 137.1/29.4; n = 3, for 16.113p and 16.113p).
The importance of epitope choice in T cell therapy | Textor et al.

To analyze whether the difference in MHC-I has an impact on ATT depending on the targeted epitope, we compared the ability of TCR-I and TCR-IV T cells to reject large, established Tet-TagLuc and 16.113p tumors. Rag\(^{−/−}\) mice bearing ∼4-wk-old established Tet-TagLuc or 16.113p tumors received 5 × 10\(^4\) TCR-I, TCR-IV, or mock T cells. The mean tumor volume at the day of treatment was ∼500 mm\(^3\) (497 mm\(^3\); SD ± 111 mm\(^3\)) for Tet-TagLuc and ∼400 mm\(^3\) (358 mm\(^3\); SD ± 60 mm\(^3\)) for 16.113p tumors. Tet-TagLuc tumors were rejected in all cases whereas TCR-IV T cells favored escape.

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Figure 3. **Similar Ag levels for Tet-TagLuc and 16.113p cells, and similar pMHC affinity for pl and pIV.** (A) Histogram shows T-Ag expression measured in T-Ag-negative cells (MCA-205), Tet-TagLuc, and 16.113p tumor cells by intracellular T-Ag staining. One representative of two experiments is shown. (B) The concentration of pl and pIV necessary for yielding 50% binding inhibition [IC\(_{50}\)] of the indicator peptides to MHC-I (pI/H2-D\(^b\), pIV/H2-K\(^b\)). One representative of three experiments is shown. (C) IFN-γ values obtained by 24-h co-culturing of 10\(^5\) TCR-I or TCR-IV T cells with indicated numbers of Tet-TagLuc or 16.113p tumor cells. The target cells were incubated with 100 ng/48 h IFN-γ before co-culture. The values are given as a percentage of maximum, which was calculated by taking the T cell response to the highest tumor cell number as 100% (maximal value), and then calculating the percentage of for each value as percentage of maximum. One representative of two experiments is shown.

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Figure 4. **TCR-I and TCR-IV T cells reject MHC-I high Tet-TagLuc tumors, but only TCR-I reject MHC-I low 16.113p, whereas TCR-IV T cells favor escape.** (A) H2-D\(^b\) and H2-K\(^b\) surface expression for Tet-TagLuc and 16.113p tumor cells stimulated with IFN-γ or left untreated and corresponding isotype controls are shown in the histograms. One representative of three experiments is shown. (B) Tet-TagLuc tumor volumes over time for Rag\(^{−/−}\) mice receiving TCR-I, TCR-IV, or mock-transduced P14/Rag\(^{−/−}\) CD8\(^+\) T cells. Each line represents the mean value of indicated numbers of mice receiving the same therapy. Error bars correspond to SD. Total mouse numbers from four experiments are shown in the table. (C) 16.113p tumor volumes of indicated number of Rag\(^{−/−}\) mice are shown for TCR-I and mock (error bars correspond to SD), and each line represents a single mouse for TCR-IV (n = 4) treatment. Total mouse numbers from five experiments are shown in the table.
by TCR-I and TCR-IV T cells, whereas in mock-treated mice tumors progressed (Fig. 4 B). In contrast, TCR-I T cells eradicated 16.113p tumors, whereas in 3/4 mice receiving TCR-IV T cells tumors eventually relapsed after initial regression (Fig. 4 C). In total, 12/16 16.113p tumors recurred in TCR-IV T cell–treated mice and in 0/17 mice receiving TCR-I therapy (Fig. 4 C), suggesting that pMHC and pMHC–TCR affinities are not sufficient parameters to predict rejection epitopes. We next investigated whether TCR-IV T cell tumor recognition was impaired in vivo. We treated 16.113p tumor-bearing mice with Renilla Luciferase (RLuc) expressing TCR-I and TCR-IV T cells (Charo et al., 2011) to monitor T cell accumulation at the tumor site by bioluminescent imaging. The signal for both TCR-I and TCR-IV T cells appeared at a similar time in the tumor and peaked at day 10 (Fig. 5 A), indicating that tumor infiltration and proliferation of TCR-IV T cells was not impaired. To examine whether TCR-IV T cells were still functional in mice with recurrent tumor, we performed an in vivo kill assay. We injected those mice with unpulsed and pI- and pIV-pulsed splenocytes labeled with different CFSE concentrations and, after 16 h, analyzed for specific kill of pIV-pulsed population. Naive and 16.113-immunized C57BL/6 mice served as negative and positive controls. Unlike naive mice, immunized C57BL/6 mice effectively killed both pI- and pIV-pulsed but not unpulsed cells. The specific pIV kill was 2.6% (SD ± 0.9%; n = 3) for naive and 90.1% (SD ± 9.7%; n = 4) for immunized C57BL/6 mice (Fig. 5 B). TCR-IV T cells in mice with recurrent 16.113p tumors were still functional, as they lysed the pIV-pulsed splenocytes with 99.5% (SD ± 0.5%; n = 5) specific kill (Fig. 5 B), but not pI-pulsed or unpulsed splenocytes.

16.113p tumors escape TCR-IV T cells by disrupted IFN-γ signaling

Because TCR–IV T cells remained functional despite progressively growing tumors, seven escape variants were isolated from TCR-IV T cell–treated mice and analyzed for the mechanism of escape. We analyzed them for MHC-I and IFN-γ receptor (IFNγR) expression, and several other IFN-γ–inducible genes, and all seven escape variants showed similar results. The expression of H-2/Dβ and Kk molecules on the escape variants was lower when compared with the parental 16.113p cells and could not be clearly detected with individual antibodies (Fig. S1 A). Therefore, we amplified the MHC-I signal by using biotinylated pan MHC-I (anti-H-2/Db/Kb) antibody (Ab) and fluorochrome-coupled streptavidin. Without IFN-γ stimulation, MHC-I expression was a bit lower for the 999 escape variant compared with the parental 16.113p cells (16.113p/999 MFI: 16.113p/999 MFI: 56.6/18.8; SD ± 2.8/1.7; n = 2; Fig. 6 A). Upon IFN-γ stimulation, parental 16.113p cells up-regulated MHC-I expression (16.113p/999 MFI: 547/18.6; SD ± 124.5/0.8; n = 2), indicating that variants with acquired IFN-γ unresponsiveness had been selected under TCR-IV T cell pressure (Fig. 6 A and Fig. S1 B). Despite the IFN-γ unresponsiveness, 999 cells still expressed the IFNγR (16.113p/999 MFI, 1,214/1,924.5; SD ± 687.3/1,966.5; n =...
Recognition of pIV, but not pl, is dependent on IFN-γ signaling

To understand why the IFN-γ–unresponsive escape variants occurred only upon TCR-IV, but not TCR-I, T cell therapy, we analyzed their recognition by TCR-I and TCR-IV T cells in vitro and in vivo. For in vitro recognition, the parental 16.113p cell line and seven escape variants were incubated with TCR-I or TCR-IV T cells. In contrast to parental 16.113p cells, the recognition of the escape variants was impaired for TCR-IV but not TCR-I T cells (Fig. 7 A and Fig. S2 C), indicating that unlike for pIV, the recognition of pl did not require IFN-γ signaling. TCR-IV T cells recognized 16.113p without IFN-γ pretreatment (Fig. 7 A), suggesting that a small amount of pIV was produced in the absence of IFN-γ, enough to stimulate the T cells to secrete IFN-γ and further stimulate epitope production, leading to better recognition and more IFN-γ secretion. To obtain independent evidence that pIV was dependent on IFN-γ, we treated mice bearing Tet-TagLuc tumors, which are normally rejected by TCR-IV T cells (Fig. 4 B), with IFNγ−/− TCR-I, IFN−γ−/− TCR-IV T cells to ask whether under these conditions tumors escaped. Mice with ∼4-wk-old established tumors (309 mm³; SD ± 216 mm³) received 5 × 10⁵ IFN−γ−/− TCR-I, IFN−γ−/− TCR-IV, or mock (OT-1) T cells. Tumors progressed in mock-treated cells and were rejected in most of the IFN−γ−/− TCR-I–treated mice (1/5 mice had a late relapse; Fig. 7 B). In contrast, Tet-TagLuc tumors in IFN−γ−/− TCR-IV T cell–treated mice regressed, in some cases completely, but finally resumed growth in 6/7 mice (9/10 tumors from two experiments; Fig. 7 B), confirming the critical role of IFN-γ for targeting pIV but not pl.

IFN-γ regulates pIV production through ERAAP

To elucidate the mechanism by which IFN-γ regulates pIV generation, we analyzed the processing of pl and pIV by the
constitutive proteasome and the immunoproteasome. No qualitative and no major quantitative differences were observed between the relevant cleavage products generated by either constitutive or immunoproteasomes (Fig. 8 and Fig. S3). Both, standard and immunoproteasome efficiently generated the T-Ag206-215 epitope (pI) from T-Ag196-225 polypeptide (Fig. 8 A and Fig. S3 A), and produced minor amounts of potential epitope precursor peptides plus the corresponding N-terminal flanking cleavage products (Fig. 8 A and Fig. S3 A). The precise minimal T-Ag204-411 epitope (pIV) was difficult to detect and proteasomes generated only minor amounts of this minimal epitope (Fig. 8 B and Fig. S3 B). In contrast, N-terminally extended potential epitope precursor peptides plus their corresponding N-terminal flanking cleavage products were generated prominently (Fig. 8 B and Fig. S3 B). Additionally, we detected N-terminally extended cleavage products with methionine as C-terminal residue (Fig. 8 B and Fig. S3 B). This cleavage results indicated that efficient production of pIV required post-proteasomal trimming. Because up-regulation of ERAAP was impaired in the 16.113p escape variants (Fig. 6 C), we asked whether ERAAP was responsible for pIV generation. An escape variant was transduced with retrovirus containing ERAP1-GFP or only GFP, and GFP sorted. The GFP expression of sorted cells was stable over time for the cells that were transduced with GFP only, but not for ERAP1-GFP–transduced cells (Fig. 9 A). Therefore, three stably transduced clones were GFP selected from ERAP1-GFP–transduced cells, where clone 1 and 4 over-expressed ERAP1, whereas clone 2 was negative (Fig. 9 B). The GFP selected clones were similar to the original escape variant when other IFN-γ–inducible genes were compared (Fig. 9 B). We next compared the in vitro recognition of these cells by TCR-I and TCR-IV T cells. Because TCR-I T cells already recognize the original escape variants, introduction of ERAP1 in the escape variant did not affect TCR-I T cell recognition (Fig. 9 C). For TCR-IV T cells, the recognition of the escape variant was restored by introduction of ERAP1 (Fig. 9 C), demonstrating that ERAAP facilitates the IFN-γ–regulated generation of pIV. However, the levels of secreted IFN-γ were a bit lower in comparison to the values obtained upon recognition of parental 16.113p cells. This was not surprising considering that all the other IFN-γ–inducible proteins contributing to pMHC T cell recognition were still down-regulated in the selected clones.

IFN-γ–resistant variants appear only in established tumors despite the presence of endogenous T cells

Current models often use therapy a few days after cancer cell inoculation, which does not compare to tumors detected in the clinic. Assuming genetic instability and tumor burden as critical factors for generation of variants, we treated mice with 16.113p tumors grown for a short or long time period. Mice bearing large established tumors (533 mm³, SD ± 293 mm³) grown for ~30 d or small tumors grown for ~10 d (36 mm³, SD ± 21 mm³) were treated with 5 × 10⁵ TCR-IV or mock T cells. In mock-treated mice, tumors progressed for both small and large tumors (Fig. 10 A). As expected, large established tumors regressed, but then recurred in all TCR-IV–treated mice; however, small 16.113p tumors were rejected and did not relapse during a 3-mo observation time (Fig. 10 A). These data suggest that variants occurred with low frequency and were present only in large tumors. Therefore, the IFN-γ–resistant variants likely also occurred in mice treated with TCR-I T cells, but were recognized and eliminated, which makes IFN-γ–independent epitopes better targets for ATT. Nevertheless, we cannot exclude
the possibility that these variants would not have developed in
the presence of functional endogenous T cells, as it is known that
ERAP1 deficiency can lead to an altered peptide pool and im-
munogenicity (Hammer et al., 2007; James et al., 2013). To clar-
ify this, we challenged T-Ag tolerant (LoxP-TagLuc-pA/CM2)
mice (Buschow et al., 2010; Anders et al., 2012) with 16.113p
cells to allow tumor growth in the presence of endogenous T
cells. ~3 wk later, when the tumors were large enough to pos-
sibly contain the variants (201.9 mm³; SD ± 120.6 mm³), mice
were irradiated and treated with 5 × 10⁵ TCR-IV T cells (one
mouse received irradiation only). In the mouse which received
irradiation only, the tumor progressed, whereas in the mice with
irradiation and TCR-IV T cell transfer, tumors were rejected in
2/6 mice (Fig. 10 B). In the other four mice, tumors initially
regressed, but later recurred (Fig. 10 B). We isolated those tumors
and analyzed whether they were still responsive to IFN-γ.
In 1/4 tumors, MHC-I expression was up-regulated upon IFN-γ
stimulation (Fig. 10 C). It could be that the T cells became tolerant
in this mouse because the LoxP-TagLuc-pA mice express low
levels of T-Ag in normal tissues (Buschow et al., 2010). However,
the remaining three tumors were IFN-γ unresponsive and could
not up-regulate MHC-I (Fig. 10 C), demonstrating that similar
escape variants also occur in immunocompetent mice.

**DISCUSSION**
As ATT becomes widely applicable and efficacy will con-
tinuously increase, tumor recurrence of escape variants will
remain a major problem. Because too many factors can cause
tumor recurrence, a reductionist approach is most suitable to
firmly uncover the underlying mechanisms. Previous stud-
ies in which the peptide epitope was the only variable had
shown that high pMHC affinity is a critical factor to prevent
tumor recurrence (Engels et al., 2013). Compatible with these
data, both pI and pIV with relatively high pMHC affinity
served as rejection epitopes in the Tet-TagLuc tumor model.
However, pMHC affinity was not sufficient to predict the
“rejection epitope” when 16.113p tumors expressing low
levels of MHC-I were targeted. TCR-I T cells targeting the
subdominant epitope pI rejected large established tumors,
whereas tumors in most cases escaped TCR-IV T cells target-
ing the dominant epitope pIV. Thus, immunodominance does
not predict rejection epitopes, reminiscent of murine virus
models, in which T cells against subdominant but not domi-
nant epitopes were protective (Gallimore et al., 1998). In the
clinic, mainly dominant epitopes have been targeted, because
subdominant epitopes are difficult to identify.

Just as the antigen amount determines the efficiency
of ATT, with higher antigen levels preventing tumor recur-
rence (Spiotto et al., 2004), the MHC-I level might have a
similar role because the actual amount of the surface pre-
sented epitope is influenced by it (Cormier et al., 1999). With
16.113p cells inherently expressing lower levels of MHC-I,
the TCR-IV T cells might not have acquired as much stim-
uli as with Tet-TagLuc tumors to produce enough effector

**Figure 8.** Epitope I is produced in sufficient
amounts by the proteasome, whereas epitope IV
requires postproteasomal trimming. Shown are
the relevant cleavage products detected in standard
proteasome digestions of T-Ag196-221 (A) and T-Ag398-417
(B) in three independent experiments. Irrelevant pep-
tide-products are indicated in black, and the epitope
and epitope precursor peptides are indicated in red
and blue, respectively. For pIV, peptide precursors for
an alternative epitope with methionine on the C ter-
minus are shown in green. Thickness of the cleavage
products indicates relative cleavage intensity.
molecules for tumor stroma destruction as a prerequisite for preventing tumor recurrence by escape variants (Spiotto et al., 2004; Zhang et al., 2008; Anders and Blankenstein, 2013). TCR-I T cells rejected the MHC-I high expressing Tet-TagLuc tumors and the MHC-I low expressing 16.113p tumors. Therefore, when targeting a suitable epitope, the levels of MHC-I may not be as an important factor for cancer eradication as previously believed, which is encouraging considering that many tumors express low levels of MHC-I (Bukur et al., 2012). However, the amount of produced epitopes should be sufficiently high to compensate for the low MHC-I levels.

IFN-\(\gamma\) secretion by T cells was essential for tumor rejection in most analyzed models (Zhang et al., 2008; Listopad et al., 2013), probably acting in multiple ways. It needs to act on the tumor stroma to induce vasculature destruction (Qin and Blankenstein, 2000; Briesemeister et al., 2011; Schietinger et al., 2013). Its effect on the cancer cells is controversial. Some studies suggested that tumor rejection required IFN-\(\gamma\) responsiveness by the cancer cells (Dighe et al., 1994; Kaplan et al., 1998), whereas others suggested that IFN-\(\gamma\)-unresponsive cancer cells were rejected at equal levels as the IFN-\(\gamma\)-responsive counterparts (Mumberg et al., 1999; Qin and Blankenstein, 2000). Our data may resolve this discrepancy, as they suggest that effective pIV-targeting requires the cancer cells to respond to IFN-\(\gamma\), whereas pI-targeting does not. IFN-\(\gamma\) action on the cancer cells was suggested to increase T cell recognition by up-regulation of MHC molecules and/or components of the proteasome (Dighe et al., 1994), notably before ERA AP was discovered (Saric et al., 2002; Serwold et al., 2002). Because the immunoproteasome appears to generate quantitatively but not qualitatively different peptides (Mishto et al., 2014), it could not explain why tumors escaped TCR-IV but not TCR-I T cells, especially because pIV as the dominant epitope is usually efficiently generated. In contrast, ERA AP generates qualitatively different peptides (Hammer et al., 2006; York et al., 2006), thus the differential amounts of pI and pIV generated in the IFN-\(\gamma\)-unresponsive variants allowed tumors to escape only under TCR-IV T cell pressure, indicating that IFN-\(\gamma\)-independent epitopes qualify as rejection epitopes if all the other parameters are met. Therefore, any cancer containing variants with loss in genes that play a role in IFN-\(\gamma\) signaling (Abril et al., 1998; Kaplan et al., 1998; van Hall et al., 2006; Respa et al., 2011) could result in tumor escape if the generation of the targeted epitope depended on ERA1.

The impaired recognition of the escape variants by TCR-IV T cells was probably a result of the combined effect of overall down-regulation of IFN-\(\gamma\)-inducible genes.

![Figure 9](image-url)
that contributed to poor epitope presentation which made them therapy resistant and allowed escape. Nevertheless, ERAP1-reconstitution in the escape variants restored TCR-IV T cell recognition, suggesting that efficient epitope IV generation was directly linked to IFN-γ-regulated postproteasomal trimming. However, the inability to up-regulate IFN-γ-inducible genes did not abolish elimination of the escape variants within 16.113p tumors when they were treated by TCR-I T cells, showing that these therapy-resistant variants still produced enough pI epitope.

ERA AP deficiency leads to altered peptide pool which has been associated with increased immunogenicity (Hammer et al., 2007; James et al., 2013). Nevertheless, in our model the IFN-γ-unresponsive variants developed in established tumors independently of the presence of the endogenous T cells, suggesting that IFN-γ-resistant variants can develop naturally without causing immunogenicity.

Although the exact mechanism of escape that we see in our model has not yet been described after ATT in the clinic, a polymorphism in ERAP1 appears to be associated with poor prognosis in human papillomavirus-induced cervical carcinoma (Mehta et al., 2009). Moreover, immune escape caused by ineffective N-terminal trimming by ERAP1 has been described for HIV and CMV infections (Draenert et al., 2004; Kim et al., 2011). Therefore, when selecting rejection epitopes for ATT, it should be taken into consideration whether the epitope production is dependent on ERAP1.

MATERIALS AND METHODS

Mice

All mouse studies were in accordance with institutional, state, and federal (Landesamt für Arbeitsschutz, Gesundheitszusatz und technische Sicherheit, Berlin, Germany) guidelines. The following mice with indicated strain numbers were purchased from Taconic: Rag−/− mice (RAG2), P14 (4138; these mice were additionally backcrossed to Rag−/− to obtain P14/Rag−/− mice), OT-1/Rag−/− mice were provided by T. Schüler (Institute for Molecular and Clinical Immunology, Magdeburg, Germany). LoxP-TagLuc-pA mice (Buschow et al., 2010) were crossed to CM2 mice (Anders et al., 2012) to generate LoxP-TagLuc-pA/CM2 mice. Male or female mice aged 2–8 mo were used in animal experiments.
Cells

RPMI and DMEM media (Gibco) used in cell culture were supplemented with 10% heat-inactivated FCS (PAN Biotech), 50 µg/ml gentamicin (Gibco), and 50 µM mercaptoethanol (Gibco; hereafter referred as RPMI-all and DMEM-all). Hek-T cells were used as packaging cells for retroviral vectors. MCA-205 (Anders et al., 2011) cells were used as T-Ag-negative controls. Tet-TagLuc cells were previously described (Anders et al., 2011) and 16.113p cells (16.113FP; Charo et al., 2011) were generated by one time in vivo passage of 16.113 cells (Willimsky and Blankenstein, 2005) in a P14/Rag−/− mouse. The seven 16.113p escape variants (999, 1004, 1575, 1577, 2100, 2106, and 2099) isolated from Rag−/− mice and the four 16.113p escape variants (29839, 29836, 29840, and 29846) from LoxP-TagLuc-pA/CM2 mice were generated from relapsed tumors when they reached the size of ∼500 mm3. Tumors were excised, cut in small fragments and incubated for 6 h at 37°C in collagenase (1 mg/ml; Invitrogen) supplemented DMEM-all, after which they were cultured for 1 wk in DMEM-all supplemented with 1x antibiotic-antimycotic (Invitrogen), and then only DMEM-all was used. No routine cell line validation or mycoplasma testing was performed.

Gene vectors and transfection

TCR-I (Staveley-O’Carroll et al., 2003) and TCR-IV constructs containing α and β chains separated by the 2A element of porcine teschovirus (β-P2A-α) were designed using Vector NTI software (Invitrogen). TCR-I and TCR-IV were cloned into individual pMP71 vectors using EcoRI and NotI restriction sites. pMCSV vector encoding for GFP (pMIG) was used as mock control. Retroviral supernatants were generated by cotransfecting (1:1) ≥70% confluent Hek-T cells with pMP71-TCR-I, pMP71-TCR-IV, or mock (GFP) plasmids together with pCL-eco vector (Imgenex) using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s protocol. In brief, a total of 3 µg DNA was added to 500 µl OptiMEM medium (Gibco) preincubcated for 5 min at RT with Lipofectamine 2000 (Invitrogen). The mix was incubated for 20 min at RT and subsequently resuspended in 1.5 ml DMEM-all and added to 6-well plate containing ≥70% confluent Hek-T cells. The cells were incubated for 8–15 h, after which the medium was replaced by RPMI-all. Supernatants were collected 48 and 72 h after transfection, filtered (0.45-µm pore size) and used in T cell transduction. ERAP1 was subcloned from pPM-hERAP1-HA (BioCat GmbH) into pMP71-1RES-GFP by NotI and SalI restriction sites, resulting in pMP71-ERAP1-1RES-GFP retroviral vector.

Expansion of T cells and retroviral transduction

Spleens were isolated from P14/Rag−/− or OT-1/Rag−/− mice and prepared as a single-cell suspension with ACK (150 mM NH4Cl [Merck], 1 mM KHCO3 [Roth], and 0.1 mM Na2EDTA [Roth], pH 7.2) lysis of red blood cells. 1–2 × 10⁶ cells were cultured in 24-well plates in 1 ml of RPMI-all supplemented with 1 µg/ml anti (α)-CD3 (clone 145-2C11), 0.1 µg/ml α-CD28 (clone 37.51) purified Ab (BD) and 10 IU/ml IL-2 (Proleukin; Prometheus Laboratories) for 24 h at 37°C in 5% CO2 humidified incubator. After 24-h activation, media was removed from the splenocytes and replaced with 1 ml/well virus supernatant containing 10 µg/ml polybrene (Sigma-Aldrich). The cells were spinoculated for 2 h at 800 g and 32°C. Virus supernatant was removed and replaced with 1 ml RPMI-all containing 10 IU IL-2. Cells were transduced twice, with an interval of 24 h. The level of surface TCR expression was measured 24 or 48 h after the last transduction. Similarly, 10⁶ 1575 escape variant cells were plated on 6-well plates 1 d before transduction. The cells were spinoculated twice with a 24-h interval with 2 ml/well of virus supernatant (pMP71-ERAP1-IRES-GFP or pMP71-1RES-GFP) containing polybrene as described above in this paragraph. After expansion in culture (transduction ratio; ≈10% for pMP71-1RES-ERAP1-GFP) the cells were sorted for GFP and cloned.

Flow cytometry and cytokine release assays

Transduced T cells were stained with α-CD8 Ab (APC; clone 53–6.7) and the TCR cell surface expression was measured by pI- and pIV-specific PE-conjugated H2-Db and H2-Kb tetramers (H2-Db SAINTYQKL and H2-Kb VVY DFL KL [anchor modified, in other assays native peptide was used]; tetramer I and tetramer IV; Beckman Coulter). Up-regulation of MHC-I on the tumor cells was obtained by incubation with 100 ng/ml IFN-γ (Gibco) for 24–48 h. MHC-I expression was measured by staining with α-H2-Db (FITC; clone KH95; BD) and α-H2-Kb (FITC; clone AF6-88.5; BD). Alternatively, subsequent staining with biotinylated α-H-2Kb/Dk Ab (clone 28–8–6; BD) and streptavidin-APC (BD) was used to increase the MHC-I signal. 16.113p and the escape variants were stained for IFNγR by biotinylated α-CD119 Ab (clone 2E2; BD) and streptavidin-APC (BD). The signal was amplified using FASER kit (BD) according to the manufacturer’s protocol. Tet-TagLuc and 16.113p cells were stained for intracellular T-Ag expression using the Cytofix/Cytoperm kit (BD) with α-T-Ag–specific Ab (FITC; PAb108; BD) according to the manufacturer’s protocol. Cells derived from CD45.1 mice were identified from total splenocytes by staining with α-CD45.1 Ab (APC; clone A20; BD). For the cytokine release assay, 10⁵ transduced CD8+ T cells were co-cultured with 5 × 10⁶ of target tumor cells (that were ≥80% confluent at the day of experiment, ±IFN-γ/48 h) in 200 µl RPMI-all media supplemented with 5 IU/ml IL-2 (Proleukin; Prometheus Laboratories) for 24 h on 37°C in 96-well plates (200 µl/well). For functional avidity, 5 × 10⁵ TCR-I and TCR-IV transduced CD8+ T cells were co-cultured with equal numbers of RMA-S cells pulsed with tritiated amounts of freshly dissolved pI or pIV (10⁻⁵–10⁻¹⁵ M). The cell supernatants from the co-cultures were tested 24 h later for cytokine levels by mouse IFN-γ ELISA kits (BD) according to the manufacturer’s protocol.
Generation of reversible MHC Streptamers and koff-rate assay

Peptide I- and IV-specific MHC Streptamers were generated using native peptides (H2-D\(^b\) SAINNYAQLK and H2–K\(^b\) VVYDFLKL). To visualize monomeric pMHC-I on the surface of living T cells, a fluorochrome was conjugated to a cysteine on a linker at the end of the Streptag sequences. For MHC multimerization, 1 µg of Alexa Fluor 488–conjugated MHC-I and 0.75 µg Streptactin-PE were diluted in a final volume of 50 µl FACS buffer for each staining (up to 5 × 10\(^6\) cells), and incubated for at least 45 min. Before MHC Streptamer binding T cells were kept on ice for at least 30 min to minimize the risk of MHC Streptamer internalization. Cells were subsequently resuspended in 50 µl Streptamer solution and incubated on ice in the dark for 45 min after which they were stained with α-CD8 Ab (20 min) and sorted on MoFlo Legacy Cell Sorter (Beckman Coulter).

The koff-rate of monomeric pMHCs from TCRs on living T cells was analyzed as previously described (Nauerth et al., 2013). In brief, cells were kept at 4°C during the whole analysis by a precooled water-cooling device, connected to a Peltier cooler. 1 µl of cells was pipetted into a reservoir built on the inverse microscope and a time series was started on the FL1 channel with a monochrome camera. The time resolution was 10-15 s. To arrest cells and therefore facilitating monitoring of single cells, a polycarbonate membrane and a small metal shimer were added on top of the cells. 4°C cold FACS buffer was added to the cells, the metal shimer was put into the cooling device on the inverse microscope and a timer was started on the microscope, taking one picture every 10 min. By addition of α-biotin after the first picture, which diffuses through the membrane (Optitran BA-S 85 Reinforced NC; Whatman). The final concentration of 0.5 µM at 37°C for 30 min. Subsequently, the three populations were labeled with different concentrations of CFSE (Invitrogen) and incubated at 37°C for 15 min. The final CFSE concentration was 0.025, 0.25, and 2.5 µM for unpulsed, pI-, and pIV-pulsed cells, respectively. The cells were washed three times with PBS, the different populations were mixed at 1:1:1 ratio, and 5–10 × 10\(^6\) cells in 100 µl PBS were i.v. injected into the mice. 16 h later, spleens were isolated and splenocytes were stained with α-CD45.1 Ab and analyzed by flow cytometry.

**WB**

Cells were lysed in 50 mM Tris–HCl (pH 7.5), 50 mM NaCl, 5 mM MgCl\(_2\), 0.1% Triton X–100, and protease inhibitor (cOmplete; Roche). 20 µg of total protein extracts were separated by SDS-PAGE and transferred onto a nitrocellulose membrane (Optitran BA-S 85 Reinforced NC; Whatman). The membrane was incubated in PBS supplemented with 0.4% Tween–20 and 5% dry milk for 1 h. Primary antibodies recognizing Jak1 (6G4; Cell Signaling Technology), Jak2 (D2E12; Cell Signaling Technology), Stat1 (polyclonal; Cell Signaling Technology), Phospho–Stat1 (58D6 [Tyr701]; Cell Signaling Technology), ERAP1 (6H9), MECL (K6512), LMP2 (polyclonal; Abcam), LMP7 (polyclonal; Abcam), or β-Actin (C4; Santa Cruz Biotechnology, Inc.) were diluted in PBS/0.1% Tween–20 and 2.5% dry milk and were applied overnight at 4°C. The membrane was washed three times with PBS/0.1% Tween–20 followed by 1-h incubation with the secondary Ab (0.2 µg/ml goat anti–rabbit IgG H&L chain–specific peroxidase conjugate, rabbit anti–mouse IgG, using the TopCount (Packard Instrument Co.) microscintillation counter. In the case of competitive assays, the concentration of peptide yielding 50% inhibition of the binding of the radiolabeled peptide is calculated. Under the conditions used, where [label]<[MHC] and IC\(_{50}\) ≥ [MHC], the measured IC\(_{50}\) values are reasonable approximations of the true kD values (Cheng and Prusoff, 1973; Gulukota et al., 1997). Each competitor peptide (H2-D\(^b\)–specific SAINNYAQLK and H2–K\(^b\)–specific VVYDFLKL, pI and pIV, respectively) was tested at six different concentrations covering a 100,000-fold dose range, and in three or more independent experiments. As a positive control, unlabelled version of the radiolabeled probe was also tested in each experiment. The indicator peptides used were Adenovirus E1A P7>Y (SGPSNTYPEI) for H2–D\(^b\) and VSV NP\(_{52,59}\) (RGYVFQGL) for H2–K\(^b\).

In vivo kill assay

1 wk before the assay, C57BL/6 mice were immunized by i.p. injection of 10\(^7\) 16.113 cells resuspended in 100 µl PBS to be used as positive controls. Spleen was isolated from a CD45.1 mouse and single-cell suspension was prepared. After red blood cell lysis with ACK buffer for 2 min, splenocytes were washed twice with 1x PBS (Gibco) and divided into three tubes. The cells were either left untreated or incubated with pI or anchor-modified pIV (VVYDFLKL), at a final concentration of 0.5 µM at 37°C for 30 min. Subsequently, the three populations were labeled with different concentrations of CFSE (Invitrogen) and incubated at 37°C for 15 min. The final CFSE concentration was 0.025, 0.25, and 2.5 µM for unpulsed, pI-, and pIV-pulsed cells, respectively. The cells were washed three times with PBS, the different populations were mixed at 1:1:1 ratio, and 5–10 × 10\(^6\) cells in 100 µl PBS were i.v. injected into the mice. 16 h later, spleens were isolated and splenocytes were stained with α-CD45.1 Ab and analyzed by flow cytometry.

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H&L chain–specific peroxidase conjugate, or rabbit anti–
goat IgG H&L chain–specific peroxidase conjugate; EMD
Millipore). The ECL Prime Western Blotting Detection kit
(GE Healthcare) was used for detection. Membranes
were analyzed with the Fusion FX System using FusionCapt Ad-
ance FX7 Software (Peglab).

Tumor challenge and adoptive T cell transfer
Age– and sex-matched mice were injected s.c. into the right
flank with 5 × 10⁶ tumor cells in 100 µl PBS. On the day of
ATT, mice were ranked by tumor size and equal mean tumor
sizes were allocated to different therapy groups. Mice received
5 × 10⁴ or 5 × 10⁵ CD8+ T cells in 100 µl PBS i.v. Tumor
size was measured by caliper, and the mean tumor size was
determined from the measurements along three orthogonal
axes (a, b, and c). Tumor volumes were calculated according to
this formula: V (mm³) = (a × b × c)/2. Mice were sacrificed
when the tumors reached 15 mm mean diameter. Animals
were excluded from analysis if they died from reasons unre-
lated to tumor burden, and the experimenter was not blinded
with respect to treatment groups. No prespecified effect size
was used to determine sample sizes in animal studies.

Biloluminescence imaging
In vivo imaging was performed using a Xenogen IVIS 200
(Caliper Lifescience). A maximum of five anesthetized mice
were imaged at once. Each mouse received an i.v. injection of
freshly prepared coelenterazine ( Biosynth ) that was dissolved
in DMSO ( Sigma-Aldrich ) and diluted in PBS ( 100 µg/100 µl
per mouse; Charo et al., 2011 ). Images were acquired for
1 min using small binning. All data were analyzed using Liv-
ing Image analysis software (Caliper Lifescience). The region
of interest for the measured signal was drawn at the tumor site
identically for all mice and was set anew for each experiment.

Proteasomal isolation, peptide cleavage,
and mass spectrometry (MS)
20S proteasomes were purified from T2, T2.27, or lympho-
blastoid cell lines as previously reported ( Theobald et al., 1998 )
and the purity was verified by SDS-PAGE electrophoresis ( 12.5% poly-acrylamide gel stained with Coomasie
dye ). Synthetic peptides at different concentrations (from 20
to 80 µM) were digested by 1–5 µg 20S proteasomes in 100 µl
TEAD buffer ( 20 mM Tris, 1 mM EDTA, 1 mM sodium azide,
and 1 mM dithiothreitol, pH 7.2 ) for different time periods
(from 1 to 24 h) at 37°C. Digestions were stopped with 0.1
vol of trifluoroacetic acid and frozen. All experiments were
repeated at least twice. In liquid chromatography runs, the
peptide separation was performed on a 1 mm RP column
( Beta Basic-18, 100 mm × 1 mm, 3 mm, 150 Å; Thermo
Fisher Scientific ) using a Surveyor system (Thermo Fisher
Scientific ). The mobile phase (A) was 100% water containing
0.05% (vol/vol) trifluoroacetic acid, and (B) was 70:30 (vol/ vol
acetoni trile / water containing 0.045% (vol/vol) trifluoro-
acetic acid). The elution was performed on binary gradient: 3%
B 10 min, 3–63% B in 32 min. A flow rate of 30 µl/min was
used. Online MS analysis was performed by DECA XP MAX
ontrap instrument (Thermo Fisher Scientific ). MS data were
acquired with a triple scan method in positive ion mode (MS:
mass range, 200–2000 m/z; zoom scan, MS/MS). Analysis
of ESI/MS data were accomplished using Bioworks version 3.3
(Thermo Fisher Scientific ). Database searching was performed
using the following parameters: no enzyme, mass tolerance for
fragment ions 1.5 amu (atomic mass unit). In time-dependent
processing experiments (signal intensity versus time of diges-
tion) the kinetics of the identified peaks was analyzed by using
LCQuan software version 2.5 (Thermo Fisher Scientific ).

Statistics
Statistical analysis was performed on data obtained with k or-
rate assay. Sample groups were compared using a two-sided
Wilcoxon rank sum test. The variances of the two groups were
compared by F-test and were not equal ( p-value = 0.039).

Online supplemental material
Fig. S1 shows low H-2/D/K expression on escape vari-
ants that cannot be up-regulated with IFN-γ despite surface
IFNγR. Fig. S2 shows TCR-IV escape variants are IFN-γ un-
responsive and not recognized in vitro. Fig. S3 describes immu-
noproteasome cleavage products of T-Ag196-221 and T-Ag398-417.

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