Lymphocytes genetically modified to express tumor antigens target DCs in vivo and induce antitumor immunity

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The exploitation of the physiologic processing and presenting machinery of DCs by in vivo loading of tumor-associated antigens may improve the immunogenic potential and clinical efficacy of DC-based cancer vaccines. Here we show that lymphocytes genetically modified to express self/tumor antigens, acting as antigen carriers, efficiently target DCs in vivo in tumor-bearing mice. The infusion of tyrosinase-related protein 2–transduced (TRP-2–transduced) lymphocytes induced the establishment of protective immunity and long-term memory in tumor-bearing mice. Analysis of the mechanism responsible for the induction of such an immune response allowed us to demonstrate that cross-presentation of the antigen mediated by the CD11c+CD8alpha DC subset had occurred. Furthermore, we demonstrated in vivo and in vitro that DCs had undergone activation upon phagocytosis of genetically modified lymphocytes, a process mediated by a cell-to-cell contact mechanism independent of CD40 triggering. Targeting and activation of secondary lymphoid organ–resident DCs endowed antigen-specific T cells with full effector functions, which ultimately increased tumor growth control and animal survival in a therapeutic tumor setting. We conclude that the use of transduced lymphocytes represents an efficient method for the in vivo loading of tumor-associated antigens on DCs.

Introduction

The identification of genes coding for human tumor-associated antigens (TAAs) (1), the characterization of DCs as the most potent APCs (2), as well as the accumulating evidence refining the concept of tumor immunoeediting and immunosurveillance (3) have all renewed interest in the preclinical and clinical aspects of cancer immunotherapy. Indeed, the results of adoptive immunotherapy trials in both solid (4, 5) and hematologic (6, 7) malignancies confirm that immune effectors represent potent anticancer agents and their use may result in clearance of tumor cells. These results suggest that a suboptimal induction phase could be one of the factors responsible for the limited clinical efficacy of most vaccination trials (8). On the other hand, a large variety of immune escape mechanisms adopted by tumors (i.e., the secretion of immune-suppressive factors by large tumor masses, the generation of TAAs and/or HLA loss variants, induction of TAA-specific tolerance by the tumor, and the intrinsic low immunogenicity of several tumor antigens; refs. 9, 10) as well as heavy pretreatments of the patient could limit the efficacy of anticancer vaccines (11). Novel strategies of active vaccination should consider all these aspects in order to become effective.

At present, a major role in eliciting T cell priming is conferred to secondary lymphoid organ–resident (SLO-resident) DCs (12, 13). This suggests that the next generation of DC-based vaccines should target DCs in vivo, thus exploiting their physiological immunostimulatory capabilities. Indeed, promising results have been obtained in murine tumor models by in vivo targeting of SLO-resident DCs with antigen conjugated to DC-specific mAb (14).

Defined subsets of T lymphocytes are known to be able to migrate to SLOs (15) and to induce a Th-independent cytolytic T cell response in vitro (16). Additionally, we and others have recently shown that, in clinical settings of allogeneic bone marrow transplantation, genetically modified lymphocytes (GMLs) can induce a highly specific immune response against the transgene products (i.e., herpes simplex virus thymidine kinase [HSV-TK]) when injected into immunocompetent patients (6, 17, 18). This evidence represents the experimental observation at the basis of our novel vaccination approach. In murine models, we showed that transduced lymphocytes, delivering antigens to host DCs located in SLOs, elicit protective immunity and long-term memory in tumor-bearing mice by cross-presentation.

Results

GMLs expressing the self/tumor antigen tyrosinase-related protein 2 are able to induce tumor-specific immune responses, ultimately controlling the growth of B16F1 melanoma. We and others have obtained evidence that the in vivo administration of HSV-TK–transduced allogeneic lymphocytes, used as donor lymphocyte infusions in clinical trials of allogeneic bone marrow transplantation, could specifically prime the recipient immune system in a vaccine-like mode, inducing TK-specific T cell effectors (6, 17, 18). This unexpected result prompted us to investigate whether lymphocytes genetically modified to express a self/tumor antigen (TAA) were indeed able to elicit TAA-specific effectors. To address this issue, we used the murine self/tumor antigen TRP-2, expressed by normal mela-
nocytes and by the murine melanoma B16F1 (B16) (19). Splenocytes from WT and β2m−/− C57BL/6 (B6) mice were activated and transduced with the TRP-2-CSM retroviral vector, which codes for the TRP-2 tumor antigen and for a cell-surface marker (CSM), the biologically inactive form of the low-affinity nerve growth factor receptor (ΔLNGFr), for purification and in vivo tracing of the transduced cells (20) (Figure 1A). In a large series of experiments, we obtained homogeneous populations of CD3+ lymphocytes, transduced by 69%-90%, evaluated as ΔLNGFr+ cells by FACS analysis at day 10 of culture (Figure 1B). Before the infusion, we measured the rate of apoptosis in the GML populations and found 6% ± 2.4% of cells to be in early apoptosis (annexin V+/propidium iodide [annexin V/PI]), 15.7% ± 0.9% of cells in late apoptosis/secondary necrosis (annexin V+/PI−), and only 0.45% ± 0.5% in necrosis (annexin V/PI+). The vast majority of the cells (75% ± 3.1%) were annexin V/PI+ viable cells. Transduced cells (4 × 106) were then injected i.v. in B6 mice, 3 times at 2-week intervals. Two weeks after the last infusion, B16 melanoma cells were given s.c. Mice treated with mock-transduced GMLs (mock-GMLs) progressively developed melanoma (Figure 1C, squares), whereas mice vaccinated with TRP-2–transduced GMLs (TRP-2–GMLs) from WT animals (circles) controlled tumor growth as efficiently as mice treated with DCs pulsed with two TRP-2–derived peptides (diamonds). The vaccination elicited T cell effectors specific for the TRP-2 tumor antigen. Indeed, following in vitro stimulation with the TRP-2Δ181-188 (19) and TRP-2Δ180-188 (21) peptides, splenocytes from mice vaccinated with TRP-2–GMLs specifically recognized peptide-pulsed RMA cells (Figure 1D). No such cytotoxic T cells could be established from mice treated with mock-GMLs (Figure 1D). To determine whether T cell priming was mediated by endogenous APCs phagocytosing the antigens released by GMLs, mice were treated with TRP-2–GMLs from β2m−/− mice (Figure 1C, triangles). These animals (22) lack MHC class I expression and therefore are unable to present antigens by themselves. The injection of TRP-2–GMLs from β2m−/− mice (Figure 1C) controlled melanoma growth similarly to the other conditions, indicating that the induction of the TRP-2–specific immune response would require cross-presentation by host APCs.

This vaccination approach elicited a stable memory response, since mice challenged 40 days after TRP-2–GML vaccination with B16 tumor cells were able to control tumor growth (Figure 1E).

We then asked whether the infusion of TRP-2–GMLs was able to effectively control tumor growth in a therapeutic setting. B6 mice in which B16 tumors had been established for 3 days were injected i.v. 3 times at 7-day intervals with either 4 × 106 TRP-2–GMLs or 10 × 106 TRP-2–GMLs or with 5 × 106 LPS-activated DCs pulsed with two TRP-2–derived peptides (Figure 1F). We observed a statistically significant prolonged survival in mice treated with TRP-2–GMLs and TRP-2–pulsed DCs. Most importantly, we observed a superior trend of prolonged survival in mice treated with the higher dose of TRP-2–GMLs in comparison to those treated with the optimal dose of TRP-2–GMLs in comparison to those treated with the optimal dose of...
peptide-pulsed DCs. Indeed, 20% of TRP-2–GML–treated mice were still alive 40 days after tumor infusion.

**In vivo migratory ability of GMLs.** Priming of immune effector cells occurs in SLOs (23), where professional APCs expressing defined MHC-peptide complexes encounter and activate host naive T cells (2). To investigate the mechanism(s) responsible for the observed immunization, we first verified whether GMLs were indeed able to reach SLOs upon i.v. infusion. GMLs expressing the CSM ΔLNGFr were infused i.v. into B6 recipients and recovered from SLOs of animals sacrificed at different times. After 24 hours, we detected 6.15% (corresponding to $7.15 \times 10^5$ total cells) of ΔLNGFr+CD3+ GMLs within the spleen and 0.61% (corresponding to $7.36 \times 10^4$ total cells) in 5 pooled LNs (Figure 2A). Within the spleen, the number of GMLs slightly decreased over time (Figure 2A), thus suggesting that the GMLs had undergone cell death, a process associated with the release of antigen, and/or recirculation through peripheral tissues. The ability to migrate to SLOs seems to be a feature of GMLs, since we were unable to detect both the lymphoid cell line RMA and the T cell hybridoma TG40 within SLOs of mice injected with comparable or higher numbers of CSFE-labeled RMA and TG40 tumor cells (data not shown). To evaluate the fine localization of the GMLs within SLOs, we analyzed serial sections of spleen and LNs from mice injected with CFSE-labeled GMLs. Twelve hours after the infusion, CFSE-GMLs were found in the periarteriolar lymphoid sheaths of the spleen and in the paracortical area of the LNs, interspersed with the endogenous CD3+ cells (Figure 2B). These experiments clearly demonstrate that a relevant number of GMLs is capable of trafficking through SLOs.

**Infusion of OVA-GMLs elicits OVA-specific T cell priming.** To dissect the mechanism responsible for GML-mediated T cell priming, we used T cells derived from the OT-I transgenic line, which carry a transgenic TCR specific for the H-2Kb-pOVA257–264 complex, and GMLs transduced with a retroviral vector encoding the model antigen OVA and the CSM ΔLNGFr (Figure 3A, OVA-CSM vector). As for TRP-2, splenocytes from B6 mice were transduced with the OVA-CSM retroviral vector with an efficiency of 55%–90% (data not shown). We transferred CFSE-labeled, OVA-specific, OT-I CD8+ T cells into B6 mice and assessed their activation and phenotypic profile 6 days after the infusion of $4 \times 10^6$ OVA-transduced or mock-transduced GMLs from either WT or β2m−/− mice. In both the experimental settings, FACS analysis of treated mice showed that OT-I T cells had undergone multiple rounds of cell division, evaluated as CFSE dilution, both in LNs (data not shown) and spleen (Figure 3B). Furthermore, proliferating OT-I T cells showed a marked upregulation of CD44, a marker of T cell activation that is regularly overexpressed upon antigen recognition (24), and downmodulation of the SLO-homing receptor CD62L (Figure 3B), a function that allows activated effector cells to leave the SLOs and patrol peripheral tissues (24). Finally, we demonstrated that the induced effectors, once restimulated ex vivo with the OVA257–264 peptide (SIINFEKL), specifically released IFN-γ, maintaining the OVA-specific responsiveness (Figure 3C) without undergoing tolerance or anergy (25).

To evaluate whether our strategy would also elicit sizeable endogenous OVA-specific T cell effectors, we treated mice with OVA-GMLs 3 times at 2-week intervals. Forty days later, spleen and LNs were harvested and stained with H-2Kb/SIINFEKL pentamer and mAbs specific for T cell activation and memory markers (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI30605DS1). In 2 representative experiments, OVA-GML treatment was able to significantly expand endogenous OVA-specific CD8+ T cells (Supplemental Figure 1B). In this experimental setting, the OVA-specific CD8+ T cells showed the phenotype of memory cells (Supplemental Figure 1C).

We therefore evaluated whether the vaccination with OVA-GMLs was able to induce CD4+ T cell responses. We transferred CFSE-labeled, OVA-specific, OT-II CD4+ T cells into B6 mice and
assessed their activation and phenotypic profile 6 days after the infusion of OVA- or mock-GMLs from either WT or β2m−/− mice (Figure 3D and data not shown). In both the experimental settings, FACS analysis of treated mice showed that OT-II T cells had undergone cell division, upregulation of CD44, and downmodulation of CD62L (Figure 3D). However, proliferation was less intense than that observed with OT-I CD8+ T cells.

To further confirm that the vaccination with OVA-GML endowed naive CD8+ OT-I T cells with full effector functions capable of controlling tumor growth in vivo, we performed tumor challenge experiments in mice adoptively transferred with OT-I cells and vaccinated with GMLs. Forty-eight hours after the injection of 5 × 10⁶ B16-OVA melanoma cells, mice were adoptively transferred with OT-I T cells and 24 hours later treated with OVA-GMLs. OT-I T cells do not spontaneously recognize the tumor; consequently, untreated animals failed to control its growth (data not shown).

Only the administration of OVA-GMLs was able to prime in vivo the naive CD8+ OT-I T cells, enabling mice to successfully control tumor growth (Figure 3E). The involvement of the above-described cross-presentation mechanism was also confirmed in this experimental setting by the administration of OVA β2m−/− GMLs that resulted in a comparable control of tumor growth (Figure 3E). As expected, mock-GMLs were ineffective. These results were further confirmed when mice were challenged 40 days after OVA-GML vaccination (Figure 3F). APCs responsible for in vivo T cell priming are bona fide DCs. To prove that DCs were playing a central role in eliciting T cell priming, we took advantage of CD11c-DTR transgenic mice. CD11c+ DCs from these mice express the diphtheria toxin (DT) receptor, and therefore they can be conditionally deleted by administration of DT (26). CD11c-DTR mice were injected with 1.5 × 10⁶ CFSE-labeled OT-I CD8+ T cells. Eight hours later, mice were treated i.p.
with 4 ng/g body weight DT, and the day after they were given $10 \times 10^6$ OVA-GMLs. Seventy-two hours later, spleen and LNs were harvested and analyzed for OT-I proliferation and for the percentage of CD11c+ DCs present in SLOs. Histograms (CFSE dilution on CD45.1-gated OT-I T cells) show sustained OT-I proliferation in untreated CD11c-DTR transgenic mice (48.1%; upper-right panel) compared with that observed in DC-depleted mice (23.9%; lower-right panel). The fraction of actively proliferating OT-I cells was remarkably different in the 2 groups of mice (38.1% vs. 8.2%). Accordingly, we found 2.07% CD11c+ DCs in untreated CD11c-DTR transgenic mice and only 0.7% in the DC-depleted mice (left panels). Data are representative of 2 experiments performed on splenocytes of 2 mice/group. (B) CD11c-purified DCs from mice treated with CFSE-labeled OVA β2m−/− GMLs were analyzed by FACS for CFSE uptake and CD8α expression. Data are representative of 3 independent experiments. (C) Confocal microscopic analysis. CFSE-labeled GML are displayed as green staining. CD11c and CD8α molecules (DCs) are visualized with CD11c-PE and CD8α-Cy5 mAbs and displayed as red and blue staining, respectively. Arrowheads indicate CD11c+CD8α+ DCs engulfed by CFSE-labeled GMLs, shown at higher magnification in the inset. Original magnification, ×40. (D) TUNEL-CFSE+ apoptotic GMLs (red and green staining, respectively) were detected in SLOs of treated mice (left panels, white arrowheads) and displayed as yellow staining in the optically merged confocal image (original magnification, ×40). Right panels show apoptotic CFSE-labeled GMLs phagocytosed by SLO-resident CD11c+ DCs (blue staining). The white arrowhead indicates TUNEL-CFSE+ GML, whereas the yellow arrowhead shows a DC phagocytosing apoptotic bodies (triple staining; original magnification, ×63).
Phagocytosing DCs undergo activation in vivo and in vitro by a cell-to-cell contact mechanism independent of CD40 triggering. To determine the activation status of SLO-resident DCs, we performed a FACS analysis of phagocytosing (CFSE–) and nonphagocytosing (CFSE+) DCs, collected at different time points. The analysis demonstrated that phagocytosing DCs belonged to the CD11c+CD8α+MHC-II+ (CFSE–) subset and showed an activated phenotype, as confirmed by late (72 hours after GML infusion) upregulation of the costimulatory molecules B7.1 (CD80, 72 hours versus 0 hours; \( P < 0.05 \)) and to a lesser extent CD40 (Figure 5A). We did not observe such activation in nonphagocytosing (CFSE+) DCs and in CD11c+CD8α+MHC-II+ (CFSE+) DCs from untreated mice (Figure 5A). To further investigate the mechanism responsible for such activation, we carried out in vitro coculture experiments on bone marrow–derived DCs (Figure 5B) and on CD11c+ DCs harvested from SLOs of naive mice (Supplemental Figure 2). Bone marrow–derived DCs were either left untreated, activated with LPS (1 \( \mu \)g/ml), cocultured with CFSE-labeled GMLs, or cultured with CFSE-labeled GMLs in transwell plates. After 24 hours (data not shown) and 48 hours, LPS-activated DCs upregulated CD80, CD86, and CD40, whereas untreated DCs did not (Figure 5B). Analysis of DCs cocultured with CFSE-labeled GMLs showed that only the phagocytosing (i.e., CD11c+CFSE–) DCs had undergone activation, suggesting that DC activation would require cell-to-cell contacts. This hypothesis was then confirmed by experiments performed in the transwell culture system, which did not allow DC maturation by preventing direct DC-GML interactions (Figure 5B). Interestingly, DCs differentiated from CD40– mice were activated upon coculture with CFSE-labeled GMLs, demonstrating that in our system, DC activation is independent of CD40/CD40L triggering. Similar results were obtained using the CD11c+ DCs harvested from SLOs of naive mice (Supplemental Figure 2).

Upon in vivo phagocytosis, DCs are able to activate naive T cells. To determine whether the above-characterized population was, indeed, responsible for antigen presentation, DCs isolated (95%–98% CD11c+) from spleen and LN of B6 mice harvested 60–72 hours after the infusion of OVA-GMLs from B2m–/– mice were used to stimulate in vitro CFSE-labeled OT-I T cells. Both OVA-specific IFN-γ release (Figure 6A, right panel) and proliferation (Figure 6A, left and right panels) were observed. As expected, there was neither IFN-γ release nor proliferation of CD8+ OT-I T cells incubated with DCs purified from mice treated with mock-transduced B2m–/– lymphocytes (Figure 6A), thus demonstrating that upon in vivo phagocytosis of GML, DCs are able to prime OVA-specific T cells.

TAA delivered by GMLs into SLOs of vaccinated mice persists up to 120 hours. Finally, we evaluated how long the delivered TAA persisted into SLOs of mice treated with the vaccination protocols used in the prophylactic and therapeutic tumor settings (i.e., i.v. infusion of OVA-GML from B2m–/– mice or s.c. injection of peptide-pulsed DCs). CD11c+ DCs were harvested from SLOs of mice at different times (36, 72, and 120 hours) after the treatments and were cocultured with naive OT-I CD8+ T cells. Forty-eight hours later, IFN-γ release was measured. Seventy-two hours after the treatments, DCs from OVA-GML–treated mice induced OT-I T cells to release approximately 2-fold greater levels of IFN-γ than DCs from mice treated with peptide-pulsed DCs (1,869.1 pg/ml vs. 957.9 pg/ml). Notably, 120 hours later, only DCs from GML–treated mice were still able to activate OT-I T cells (IFN-γ release: 197 pg/ml). These results along with data of GML persistence within SLOs (Figure 2A) indicate that GMLs provide SLO-resident DCs with a continuous source of antigen for longer time, resulting in a prolonged T cell activation.

Discussion

In this study we have investigated a novel approach for cancer vaccination, based on the in vivo delivery of TAs directly to SLOs by GMLs. This approach could improve the current DC-based protocols (30), e.g., ex vivo selection and differentiation of the most appropriate DC subset (31), the low number of intradermally injected DCs reaching the draining LNs (32), and the limited half-life of MHC-I–peptide complexes on the DC cell surface (33). In our system, the GMLs constitutively express the antigen (i.e., TRP-2, OVA); therefore, there are no time constraints limiting their migration to SLOs or the transfer of the antigen to DCs. Indeed, up to 60–72 hours after injection of OVA-GMLs, DCs harvested from SLOs were able to produce maximum stimulation. Notably, DCs harvested 120 hours after OVA-GML infusion were still able to activate OVA-specific CD8+ T cells, whereas those from mice treated with peptide-pulsed DCs did not. These results indicate that DC targeting with TAA-GMLs could overcome some of the abovementioned limitations of the DC-based vaccines, particularly the low number of DCs reaching SLOs and the rapid degradation/loss of MHC-I–peptide complexes. Additionally, the constitutive and strong expression of the transgene products, driven by viral promoters, combined with the ability of GMLs to migrate to SLOs might make them similar to virus-infected cells, which produce enormous amounts of antigen within immunological priming sites (34).

This vaccination approach also elicited antigen-specific CD4+ T cells. However, the proliferation of the CD4+ T cell compartment was less sustained than that of the CD8+ T cells. This result is in...
agreement with recent data (35) showing that MHC-I and -II antigen presentation is achieved by different DC subsets. In particular, the CD11c⁺CD8α⁺ subset is responsible for MHC-I presentation, the CD11c⁺CD8α⁻ subset for MHC-II presentation. In our setting we demonstrated (Figure 4) that the majority of the GML-associated antigen is taken up by the CD11c⁺CD8α⁺ subset. Therefore, we hypothesize that the reduced proliferation of CD4⁺ T cells would reflect a lower recruitment of naive T cells due to the limited uptake of GML-associated antigen by the CD11c⁺CD8α⁻ subset (3%–5%). However, in our vaccination setting, the reduced proliferation of TAA-specific CD4⁺ T cells did not dampen the development of an effective antitumor response in vivo. Moreover, in a pivotal clinical study using a similar strategy, we have observed the induction of fully active CD4⁺ effector cells specific for the TAA carried by GMLs (V. Russo et al., unpublished observations).

Mice vaccinated with TRP-2–GMLs were protected from a subsequent tumor challenge as well as those vaccinated with DCs ex vivo pulsed with TRP-2–derived peptides, thus suggesting a comparable efficacy of the 2 approaches. Notably, in a more stringent therapeutic tumor model, we observed a long-term survival benefit of TRP-2–GML vaccination. However, in our opinion, a more stringent and informative comparison between vaccination strategies based on ex vivo and in vivo DC loading could be addressed with genetic modifications of TAA-GMLs to express SLO-homing molecules, and the combined administration of TAA-GMLs and ganciclovir to kill GMLs, could increase antigen availability and therefore improve the treatment.

In conclusion, transduced lymphocytes represent an efficient way for in vivo loading of TAA on DCs and for the induction of effective antitumor responses.

**Methods**

**Mice.** B6 mice (8–10 weeks of age) were obtained from Harlan. B6 β2m⁻/⁻ mice lack MHC class I expression (22). OT-I (Ly 5.1) mice (42) are transgenic for an αβ TCR specific for the H2Kb–restricted OVA257–264 peptide. B6 CD40⁻/⁻ and CD11c-DTR/GFP (CD11c-DTR) mice were obtained from the Centre de Distribution, Typage & Archivage animal, Institut de Transgénose. Mice were housed under pathogen-free conditions. Animal studies were approved by the Institutional Animal Care and Use Committee of the Scientific Institute H. San Raffaele.

**Cell lines and reagents.** The murine RMA lymphoma was kindly provided by M. Bellone (Istituto Scientifico Institute H. San Raffaele). The murine B16 melanoma cell line was purchased from ATCC. DT was purchased from Sigma-Aldrich and used as described by Jung et al. at 4 ng/g body weight (26).

**Flow cytometry, confocal microscopy, and TUNEL assay.** mAbs specific for murine markers were all from BD Biosciences — Pharmingen. Isotype controls from the same manufacturers were used. Before staining, cells were incubated with Fc Block (purified α-CD16/α-CD32 mAbs; BD Biosciences — Pharmingen). Samples were run on a FACScalibur (BD) and analyzed...
by CellQuest software (BD). H2Kbeta–SIINFEKL OVA pentamer-PE was from ProImmune. TUNEL was performed on SLOs from treated mice using the TUNEL TMR-dUTP assay (Roche) according to the manufacturer’s recommendations. For confocal microscopy, B6 mice were injected with CFSE-labeled (Molecular Probes; Invitrogen) OVA-transduced lymphocytes (10^6 to 20 x 10^6). Six, 12, and 24 hours later, spleen and LNs (cervical, axillary, and inguinal) were collected and fixed in 4% paraformaldehyde (Sigma-Aldrich) for 2 hours at room temperature. Lymphoid organs were then washed in PBS and incubated with 30% saccharose overnight at room temperature, washed, embedded in Tissue-Tek OTC (Sakura Finetek), frozen in isopentane cooled by liquid nitrogen, and stored at −20°C until use. Cryosections (10 μm thick) were adhered to poly-L-lysine-coated glass coverslips for 1 hour. Before staining, cryosections were treated with PBS containing 10% FCS and rat IgG (50 μg/ml) for 1 hour at room temperature and then incubated with rat anti-mouse CD3-PE mAb (BD). To visualize DCs, we used CD11c-PE and CD8α-PE-Cy5 mAbs (BD).

**Retroviral vectors and transduction procedures.** The OVA-CSM and TRP-2–CSM retroviral vectors were constructed as previously described (43), with OVA or the murine TRP-2 under the control of the viral LTR. Expression of ALNGFr was driven by the SV40 promoter. Splenocytes (5 x 10^6 cells/ml) from B6 or B2m−/− mice were stimulated in the presence of 100 U of rhIL-2 (Proleukin; Chiron) and 5 μg/ml of concanavalin A (Sigma-Aldrich). Forty-eight hours later, splenocytes were transduced with virus-containing supernatant by 2 rounds of centrifugation (120 minutes, 1,200 g) a day apart, in the presence of 8 μg/ml of polybrene (Sigma-Aldrich). Three days later, splenocytes were analyzed for ALNGFr expression and then expanded for 10–14 days. B16 murine melanoma cells were transduced with the OVA-CSM vector and selected for ALNGFr expression by magnetic beads (Dynabeads M-450; Dynal; Invitrogen) coated with the LNGFr-specific mAb 20.4 (ATCC).

Adoptive transfer, immunization experiments, and ex vivo recall assay. OT-I CD8+ T cells were enriched from spleen and LNs by depletion of B cells with Dynabeads Mouse pan B (B20; Dynal; Invitrogen) and labeled with CFSE. Briefly, cells were incubated at 10 x 10^6 cells/ml in CFSE at a final concentration of 4 μM for 8 minutes at room temperature. The labeling reaction was stopped by adding the same volume of PBS. After washing, 3 x 10^6 CFSE-labeled CD8+ T cells/mouse were injected into the tail vein of sex-matched B6 recipients. After 24 hours recipients were treated i.v. with 4 x 10^6 GMLs. Splenocytes harvested 8 days after vaccination were restimulated in vitro (1:1 ratio) with syngeneic irradiated splenocytes, pulsed with 2 μg/ml OVA257–264 peptide. Four days later, OT-I CD8+ T cells were purified by FACSVantage sorting (BD) using V2/3/8.1-specific mAbs. OT-I CD8+ effectors (1 x 10^6) were then challenged with 2 x 10^3 RMA cells pulsed with OVA257–264. After 24 hours we measured IFN-γ content in the supernatant by ELISA assay (BD Biosciences – Pharmingen) according to the manufacturer’s recommendations. IFN-γ released on unpulsed RMA cells was always subtracted. OT-II CD4+ T cells were purified with the CD4+ T cell isolation kit (Miltenyi Biotec) and labeled with CFSE as described for OT-I CD8+ T cells. CFSE-labeled CD4+ T cells (3 x 10^6) were injected into the tail vein of sex-matched B6 recipients. After 24 hours recipients were treated i.v. with 4 x 10^6 or 10 x 10^6 GMLs. For the induction of OVA-specific endogenous repertoire experiments, B6 mice were treated 3 times at 2-week intervals with OVA-GMLs (4 x 10^6) and DCs (3 x 10^6 to 5 x 10^6) activated with LPS (1 μg/ml) and pulsed with 2 μg/ml OVA257–264 peptide. Forty days later, spleen and LNs were collected, digested, washed, and then stained with the H2Kbeta–SIINFEKL OVA pentamer-PE together with mAbs specific for activation and memory murine markers.

**In vitro cytotoxicity assay.** Splenocytes from vaccinated mice (3 x 10^6/ml) were cultured with 0.5 μM TRP-2 peptides. After 6 days, activated T cells were isolated on a Lymphocyte-M gradient (Cedarlane Laboratories Ltd.) cultured 1 day in the presence of 20 IU/ml hrIL-2. Responder cells were then tested for cytolytic activity in a standard 4-hour ⁵¹Cr release assay. Data are mean ± SD of experiments performed in triplicate of the percentage of specific lysis at the indicated E/T ratios.

**Ex vivo cross-presentation assay and kinetic of TAA persistence within SLOs.** CD11c+ DCs were purified from B6 mice after vaccination with OVA-transduced B2m−/− lymphocytes (10 x 10^6 to 20 x 10^6). Spleen and LNs were digested for 40 minutes at 37°C with 0.5 mg/ml collagenase A, B, and D (Roche Diagnostics) and then resuspended in PBS containing 0.5% BSA, 2 mM EDTA, to disrupt T cell–DC complexes. Purification of DCs (92–98% purity) was performed with rat anti-mouse CD11c mAb (N418)–coupled magnetic MicroBeads on miniMACS columns (Miltenyi Biotec). Purified DCs (1.5 x 10^5) were used as stimulators, whereas OT-I CD8+ T cells (1.5 x 10^5), isolated from LNs of transgenic mice by depletion using PE-conjugated B220, CD11c, CD11b, CD4 mAbs followed by anti-PE MicroBeads incubation, were labeled with 3 μM CFSE and used as responders. Experiments were performed in triplicates in 96-well U-bottom plates. As positive control, DCs from mice receiving mock-transduced B2m−/− lymphocytes were pulsed with 2 μg/ml of OVA257–264 peptide. Forty-eight hours later, supernatants were tested for IFN-γ production by ELISA. Two days later, the cells were counted and stained with rat anti-mouse CD3-FITC, CD45.1-PE, and CD8α–Cy-Chrome mAbs and analyzed by FACS, to evaluate OT-I CD8+ T cell–specific proliferation as a measure of CSFE dilution. For kinetic experiments of TAA persistence into SLOs, mice were treated i.v. with OVA-GMLs (10 x 10^6 to 20 x 10^6) from B2m−/− mice or with DCs (0.5 x 10^6) pulsed with 2 μg/ml of OVA257–264 peptide and injected s.c. Thirty-six, 72, and 120 hours after treatments, DCs (1.5 x 10^6) purified as described above were used as stimulators, whereas purified OT-I CD8+ T cells (1.5 x 10^5), labeled with 3 μM CFSE, were used as responders. Experiments were performed in triplicate in 96-well U-bottom plates. Forty-eight hours later, supernatants were tested for IFN-γ production by ELISA. IFN-γ released by responders and/or stimulators alone was always subtracted.

**In vitro DC activation assay.** CD11c+ DCs were purified from B6 mice with rat anti-mouse CD11c mAb (N418)–coupled magnetic MicroBeads on miniMACS columns (Miltenyi Biotec) (92–98% purity) or differentiated from bone marrow, as described by Camporeale et al. (44).

Purified DCs (3 x 10^6) were left untreated, activated with LPS (1 μg/ml), cultured with CFSE-labeled GMLs in coculture or in transwell plates. Twenty-four hours later and 48 hours later, cells were harvested, washed once, and then stained with mAbs specific for murine CD3, CD11c, CD8α, CD80, CD86, and CD40.

**In vivo experiments of DC depletion.** CD11c-DTR mice were injected with 1.5 x 10^6 CFSE-labeled OT-I CD8+ T cells. OT-I T cells were purified and labeled with CFSE as described above. Eight hours later, mice were treated i.p. with 4 ng/g body weight DT. The day after, adoptively transferred mice were given 10 x 10^6 OVA-GMLs. Spleen and LNs were harvested 72 hours after GML treatment, processed, and analyzed by FACS to evaluate OT-I proliferation and the percentage of CD11c+ DCs. The proliferation of OT-I T cells (CD45.1+ T cells) was evaluated as CFSE dilution.

**In vivo antitumor response against B16 or B16-OVA melanomas.** B6 mice were vaccinated i.v. 3 times at 2-week intervals with either 4 x 10^6 TRP-2–transduced lymphocytes from WT and B2m−/− mice; or with LPS-activated DCs (5 x 10^6 to 10 x 10^6 cells) generated as described by Camporeale et al. (44) and pulsed with 2 μg/ml of TRP-2181–188 (VYDFFVWL) (19) and TRP-2180–188 (SVYDFFVWL) (21) peptides. Two weeks or 40 days after the last vaccination, mice were inoculated s.c. with 5 x 10^5 B16 cells. Tumor size was evaluated by measuring perpendicularly diameters by a caliper. For curative experiments mice were inoculated s.c. with 5 x 10^6 B16 cells. Seventy-two hours later, when the tumor area was approximately 20 mm², mice were randomly assigned to 1 of the following treatments: (a) 3 injections of 4 x 10^6
mock-GMŁs \((n = 7)\), \((b) 4 \times 10^4 (n = 9)\) or \((c) 10 \times 10^3\) TRP-2-GMŁs from \(\beta_{2m^-}/mice (n = 9)\), or \((d) 3\) injections of \(5 \times 10^5\) LPS-activated DCs pulsed with \(2 \mu g/ml\) of TRP-2:1.81-HLA and TRP-2:1.80-HLA \((n = 9)\). The treatments were administered 3 times at 7-day intervals. Results were compared by evaluating survival curves by log-rank test. Mice were adaptively transferred with \(3 \times 10^6\) OT-I CD8\(^+\) T cells and after 42 days vaccinated i.v. with \(4 \times 10^6\) OVA-transduced lymphocytes from WT or \(\beta_{2m^-}/mice.\) B16-OVA cells \((5 \times 10^6)\) were injected s.c. either 48 hours before OT-I infusion for therapeutic experiments or 40 days after vaccination for protection experiments.

Data are reported as the average tumor volume ± SD.

Statistics. Statistical significance \((P < 0.05)\) was determined by 2-tailed Student’s t test and by the log-rank test.

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