Profound Impairment of Adaptive Immune Responses by Alkylationg Chemotherapy

Adam J. Litterman, David M. Zellmer, Karen L. Grinnen, Matthew A. Hunt, Arkadiusz Z. Dudek, Andres M. Salazar and John R. Ohlfest

*J Immunol* published online 17 May 2013
http://www.jimmunol.org/content/early/2013/05/17/jimmunol.1203539

---

Supplementary Material
http://www.jimmunol.org/content/suppl/2013/05/17/jimmunol.1203539.9.DC1

Subscription
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

Permissions
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

Email Alerts
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
Immune-mediated destruction of solid tumors requires the infiltration of adequate numbers of effector lymphocytes into the tumor site (1). Tumors express mutant proteins termed “neoantigens” that result from frameshift, gene fusion, and missense mutations (2). These neoantigens, rather than self-Ags, tend to dominate the naturally occurring immune responses against cancer (3, 4). The immunogenicity and tumor specificity of the neoantigens provide a compelling rationale for their identification and targeting with therapeutic cancer vaccines. Recent bioinformatics advances make prospective identification of neoantigens for personalized cancer vaccines feasible (5). Numerous analyses of individual patients suggest that naturally occurring T cell responses against neoantigens can be associated with dramatic responses and long-term survival (3, 4, 6). Indeed, it was suggested that the generation of endogenous antitumor responses may be required for durable success of conventional therapies (7). This hypothesis has led to much interest in combining immunotherapy with conventional modalities (8), but the effect of conventional chemotherapy vis-à-vis immunotherapy is incompletely understood.

Numerous reports indicate a synergy between conventional chemotherapy and immune therapy. Synergy is mediated by diverse mechanisms, including preferential depletion of regulatory T cells (Tregs) (9–11), liberation of homeostatic or inflammatory cytokines (12, 13), and enhanced immunogenicity of chemotherapy-treated tumors (14, 15). In the context of vaccines targeting self-Ags, chemotherapy given prior to vaccination can yield synergy and enhanced survival (9, 16). Vaccination against tolerized self-Ags may require Treg depletion to access a latent pool of high-avidity self-Ag–specific CD8 T cells, whereas high-avidity neoantigen-specific T cells can be generated by immunization without Treg depletion (10).

The reported synergy between chemotherapy and vaccines is somewhat paradoxical given that the generation of an adaptive immune response is a highly proliferative process, and chemotherapeutic drugs are given for their selective toxicity to rapidly proliferating cells. The generation of a CD8 T cell response to an acute viral infection involves responder cells doubling ~14 times in a week (17), and cancer vaccines that use neoantigens with potent adjuvants can trigger similar levels of CD8 T cell proliferation (18). The number and proliferative potential of infused effectors have been associated with clinical response to adoptive immunotherapy of metastatic melanoma (19), possibly as the result of a requirement for local proliferation of lymphocytes to generate sufficient E:T ratios at the tumor site (20, 21). In adoptive-transfer protocols, the transferred lymphocytes are cultured ex vivo and, therefore, are not exposed to chemotherapy (22). In contrast, cancer vaccines are administered to drive in vivo proliferation of lymphocytes in pretreated patients, and the extent to which chemotherapy inhibits vaccine-driven immune responses remains unclear.

The lack of understanding of the effect of chemotherapeutic drugs on cancer vaccines is particularly problematic with regard to alkylating chemotherapy drugs. Alkylating chemotherapies,
such as temozolomide (TMZ) and cyclophosphamide, covalently modify DNA and inflict cytotoxic damage on exposed cells (23). These drugs are commonly used for their antineoplastic effect to treat malignancies that are frequent targets of cancer vaccines, such as glioblastoma multiforme (GBM) (24) and metastatic melanoma (25), as well as to deplete Tregs prior to vaccination (16, 26). Although case reports suggest that individual patients have benefited from cancer vaccines given after standard alkylating chemotherapy for GBM (24, 27), overall, cancer vaccines administered after TMZ have had a record of failure (28). Alkylating chemotherapeutics have immune inhibitory effects in vitro, specifically via selective toxicity to proliferating lymphocytes (29) and inhibition of differentiation of immune effectors (30). The applicability of these studies to human cancer patients remains unclear: the degree of lymphopenia in TMZ-treated glioblastoma patients is a negative prognostic factor (31), but it also has been associated with greater vaccine-induced Ab responses (32). To examine the impact of clinically relevant doses of alkylating chemotherapeutics on cancer vaccines, we used controlled animal experiments that minimized the numerous complicating factors encountered in human patients.

Materials and Methods

Cells and culture

GL261 and B16-F10 cells were maintained in DMEM supplemented with 10% FBS. The KMs3M14 and O94M2 cell lines were derived from genetically engineered primary murine gliomas and were generated and maintained as described (33). Model Ag-expressing tumors (Quad-GL261 and Quad-KM3M14) were generated by stable transfection with Quad Ag cassette (34), a single coding sequence expressing the OT-I and OT-II epitopes of GL261 and B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL. A total of 75,000 B16-F10 cells was inoculated in the right flank. Glioma-bearing mice were euthanized when they became symptomatic; B16-F10–bearing mice were euthanized when tumors be-

Peptides and in vitro stimulation

SINSEKl and variant peptides (Anaspec) were dissolved in sterile water. All other peptides (New England Peptide) were dissolved in minimal DMSO and diluted in sterile water. Splenocytes were incubated with peptides for 8 h (Nur77ARP induction) or 24 h (elaborated IFN-γ). Elaborated IFN-γ was measured by cytokine bead array (BD) and normalized to the number of Ag-specific T cells enumerated with BD counting beads. For B16-F10 stimulation, B16-F10–pulsed splenocytes were pulsed with 5 μg/ml the mutant peptide mixture or irrelevant control (16- and 18-aa peptides containing the OT-I and OT-II epitopes). Leukocytes from 100 μl blood from B16-F10–bearing animals were incubated with 150,000 Ag-pulsed splenocytes for 72 h for IFN-γ elaboration.

The peptide sequences are as follows: GARC-1: RASAALLNKLYAMCPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL; B16-F10 mutant peptides: Kif18b-mutant: SKPSFQEFVDWENVSGL.

Flow cytometry and ELISA

All Abs, except as indicated, were from eBioscience; phosphorylated ataxia telangiectasia mutated (pATM; phosphor-Ser1981) Ab was from Millipore. An isotype control (PE-conjugated murine IgGl κ isotype control; eBio-
sience) for pATM staining was included as a control for background staining in non-TMZ-treated lymphocytes. K5-OVA peptide–MHC multimer staining was performed with dextramer (Immudex). PE-conjugated Dλ5-GARC-1 tetramer was synthesized by the National Institutes of Health tetramer core facility (Atlanta, GA). Tetramer falloff assay was performed as described (17), with the following modifications: K5-OVA dextramer was used to stain, and free dextramer was bound with biotinylated anti–K5-OVA mAb. Data were acquired using a BD FACScanto II and analyzed using Cytobank software. Relative affinity and Ab titer were determined by ELISA, as described (39).

Results

An intrinsic proliferation defect of lymphocytes exposed to alkylating chemotherapy

To choose clinically relevant doses of TMZ with which to treat mice, we selected doses that yielded an equivalent pharmacokinetic exposure as obtained after oral dosing in humans (40) (J. Gallo, personal communication). Low (25 mg/kg), intermediate (55 mg/kg), and high (80 mg/kg) dosages of TMZ given daily for 5 d led to a transient reduction in lymphocyte counts that were similar in magnitude to that seen in patients treated with TMZ (Supplemental Table I). TMZ significantly inhibited proliferation of splenic T cells (Fig. 1A). This proliferation defect is cell intrinsic, because purified CD8 T cells from TMZ-treated mice demonstrated a similar inhibition of proliferation and activation of the DNA damage response, as assessed by pATM staining (Fig. 1B, 1C).

Quantitative defects in immune responses to cancer vaccines after TMZ treatment

To examine the effects of alkylating chemotherapy on neopan-
tigen cancer vaccines, we vaccinated mice with the model Ag chicken OVA and polyICLC (18). A cluster of four daily s.c. vacci-
nations causes a robust CD8 T cell response, with the percentage of K5-OVA–specific CD8 T cells in the blood expanding from es-
sentially undetectable levels to ∼6% of the CD8 compartment in a week (Fig. 2A). This expansion from a precursor frequency ∼1/150,000 (41) to a frequency of 1/20 represents ∼13 doublings. When followed by weekly boosters, similar to many established clinical protocols, a second peak in K5-OVA–specific T cell percentage was observed a week after the third booster (Fig. 2A). The magnitude of the CD8 T cell response was diminished in a dose-de-
pendent fashion by TMZ treatment (Fig. 2A). The levels of OVA-specific Ab circulating in the blood of TMZ treated mice were also lower in a dose-dependent fashion (Fig. 2B).
Given that TMZ and other alkylating drugs covalently modify DNA and that some of the directly produced DNA-alkyl adducts (42) or indirectly produced DNA lesions (43, 44) are long-lived, we measured the magnitude of immune responses to vaccines given several weeks after TMZ treatment. B6 mice that were given intermediate-dose TMZ had significantly lower percentages of Kb-OVA–specific T cells elicited by a cluster of four vaccinations that began 80 d after the last dose of TMZ relative to untreated, age-matched controls, with a peak frequency ∼1% versus ∼4.5% (Fig. 2C).

Ag-experienced memory T cells have an intrinsic resistance to DNA-intercalating chemotherapy with daunorubicin (45), and tumor-specific T cell clones may be Ag experienced in cancer patients (46). Therefore, we measured the effect of vaccine-driven T cell expansion in an Ag-experienced memory cell population in mice treated with alkylating chemotherapy prior to vaccination. Mice treated with intermediate- or high-dose TMZ after an initial cluster of vaccines had a significant inhibition of Ag-specific T cell proliferation when vaccinated with a second cluster of vaccines (Fig. 2D). The peak percentage of Kb-OVA–specific CD8 T cells was ∼10-fold lower (∼2% versus ∼20%) in mice treated with intermediate doses of TMZ compared with controls, and the percentage of Kb-OVA–specific CD8 T cells decreased immediately following vaccination in mice treated with a high dose (Fig. 2D).

We next quantified the impact of TMZ on the efficacy of vaccines in tumor-bearing animals using both model Ags and mutated tumor-specific neoantigens. B6 mice were implanted orthotopically with the syngeneic, Ag force–expressing Quad-GL261 glioma line (34), a single course of vaccination is a systemic immune responses by TMZ treatment could lead to a failure to reject a highly immunogenic B6 glioma line expressing the SV40 Large T Ag (Supplemental Fig. 1).

To examine the impact of TMZ treatment on mutated self- neoantigens, we inoculated mice with the GL261 cell line. This cell line expresses an immunogenic mutant self-protein, GARC-1, which forms a D8-binding CD8 T cell epitope based on a single amino acid substitution due to a point mutation (50). We vaccinated using a peptide containing the immunogenic amino acid substitution in glioma-bearing mice, with or without TMZ treatment. A significant reduction in the percentage of activated, D8-GARC-1–specific CD8 T cells in blood elicited by vaccination was observed (Fig. 3E).

**DNA damage response induced by high-intensity TCR stimulation following alkylating chemotherapy**

Because we observed activation of the DNA damage response in T cells given a strong stimulation through the TCR (Fig. 1), we hypothesized that the degree of DNA damage response would correlate with TCR signal intensity. To dissect this question, OT-I mice were treated with drugs and then their splenocytes were stimulated with altered peptide ligands that induce varying TCR signal strengths (36). All three peptides induced similar levels of proliferation and minimal DNA damage response in OT-I cells from untreated control animals, as assessed by Ki67 and pATM.
staining, respectively (Fig. 4A). In TMZ-treated animals, the frequencies of Ki67+ OT-I cells were inhibited for all peptides; however, interestingly, the percentage of proliferating cells that had activated the DNA damage response (i.e., were pATM+) increased with increasing strength of TCR stimulation (Fig. 4A, 4B).

To assess the induction of DNA damage response in lymphocytes after treatment with other DNA-damaging cancer therapies, we repeated the above experiments after treatment of OT-I mice with cyclophosphamide, carboplatin, doxorubicin, and gamma radiation. Following treatment with the alkylating chemotherapy cyclophosphamide and gamma radiation, there were significantly more proliferating cells exhibiting DNA damage in response to the strong antigenic peptides SIIQFEKL and SIINFEKL than with the weak antigenic peptide SIIGFEKL or with no peptide (Fig. 4C). The platinum drug carboplatin and the DNA-intercalating agent doxorubicin did not lead to this effect, with similar pATM staining in proliferating cells stimulated with all peptides (Fig. 4D). The induction of the DNA damage response upon stimulation after drug treatment was mirrored by the defect in CD8 T cell responses to vaccines in B6 mice. TMZ and cyclophosphamide led to markedly and significantly lower peak levels of Ag-specific CD8 T cells in the blood following vaccination (Fig. 4E). In contrast, in animals treated with carboplatin and doxorubicin, the percentage of Ag-specific CD8 T cells was incrementally lower and not significantly different from untreated controls. This defect is likely accounted for by responder lymphocytes failing to enter the cell cycle (as in Fig. 4A), as well as undergoing apoptosis as a result of DNA damage response, because a fraction of adoptively transferred OT-I T cells became apoptotic (Annexin V+/-7-AAD+) after vaccination with SIINFEKL peptide in TMZ-treated mice (Supplemental Fig. 2).

Lower affinity for Ag of vaccine responder lymphocytes after TMZ treatment

As a result of the greater DNA damage response that we observed in OT-I T cells stimulated with stronger antigenic peptides, we hypothesized that in vivo vaccine responder cells would be skewed toward lymphocytes with AgRs with lower affinity for cognate Ag. We found that the median fluorescent intensity of peptide–MHC multimer staining of memory CD8 T cells elicited by vaccination was lower in TMZ-treated mice than in controls (Fig. 5A, 5B). The higher initial rate of decay of staining in a multimer falloff assay (17) in TMZ-treated animals also suggested a lower avidity of vaccine-elicited CD8 T cells for Ag (Fig. 5C). Similarly, we measured a lower relative affinity of anti-OVA serum Ig in TMZ-treated animals than in controls (Fig. 5D).

Inferior functional characteristics of vaccine-responder lymphocytes after TMZ treatment

The lower affinity of responder lymphocytes for Ag after alkylating chemotherapy suggests that, post-TMZ, vaccine-responder cells...
are less sensitive toward antigenic targets. We hypothesized that these cells would receive lower-intensity proliferative signals in TMZ-treated mice than controls and display inferior effector function upon stimulation. Using the Nur77GFP TCR signal strength reporter mouse (36), we directly tested this hypothesis by measuring GFP fluorescence intensity in vaccine-expanded CD8 T cells upon antigenic stimulation. Vaccine-expanded Kb-OVA–specific CD8 T cells from untreated control mice displayed high-intensity GFP fluorescence upon culture with SIINFEKL peptide (Fig. 6A, 6B). In TMZ-pretreated mice, Ag-specific GFP fluorescence upon stimulation was significantly lower (Fig. 6B). We next measured IFN-γ elaboration upon antigenic stimulation in culture and enumerated Ag-specific cells/well. We calculated that, in TMZ-pretreated animals, vaccine-activated CD8 T cells elaborated 10-fold fewer IFN-γ molecules on a per-cell basis (Fig. 6C).

Discussion

We found that alkylating chemotherapy has a long-lasting anti-proliferative effect on lymphocytes in mice, and this effect leads to inferior responses to cancer vaccines targeting mutated self-Ags. Animals pretreated with alkylating chemotherapeutic drugs had lower peak numbers of vaccine-responding CD8 T cells and lower Ab titers. This impairment corresponds to the activation of DNA damage responses in proliferating cells, and this activation of DNA damage responses is greatest in responder cells receiving the strongest TCR signals from the vaccine. In turn, this selective toxicity in the cells with the highest affinity for cognate Ag leads to impairment of CD8 T cell and Ab responses. These responses consist of lymphocytes with, on average, lower-affinity AgRs that have inferior effector function. Importantly, these effects were observed even at low, Treg-depleting doses of alkylating chemotherapeutics (9).

**Figure 3.** TMZ exposure leads to inhibition of immune responses in tumor-bearing animals. C57BL/6 mice (n = 5–8/group) were inoculated with Quad-GL261 cell line and, in the indicated groups, were treated on days 6–10 after tumor inoculation with 80 mg/kg of TMZ and vaccinated with OVA and polyICLC on days 12–15, 19, 26, 33, and 40. (A) The percentage of Kb-OVA–specific CD8 T cells in the blood was assessed at the indicated time points before control mice became moribund. Error bars indicate SEM. **p < 0.01, ***p < 0.001. (B) The percentage of surviving mice in each group. Data are representative of two independent experiments with similar results. ***p < 0.001, log-rank test. (C) C57BL/6 mice (n = 5–6/group) were inoculated with Quad-KM3M14 and, in the indicated groups, were treated on days 3–7 after tumor inoculation with 55 mg/kg of TMZ and vaccinated with OVA and polyICLC on days 10–13. Kb-OVA–specific CD8 T cells were assessed by flow cytometry on day 17. Error bars indicate SEM. *p < 0.05, **p < 0.01, ***p < 0.001. (D) The percentage of surviving mice in each group. **p < 0.01, log-rank test. (E) C57BL/6 mice (n = 6–8/group) were inoculated with GL261 tumors and, in the indicated groups, were treated with 55 mg/kg TMZ on days 6–10 after tumor inoculation and vaccinated with GARC-1 peptide and polyICLC on days 12–15. D17-GARC-1–specific activated CD8 T cells were assessed in blood by flow cytometry on day 19. Error bars indicate SEM. Data are representative of two independent experiments with similar results. *p < 0.01.

ns, Not significant (p > 0.05).
The defects that we observed are likely general to all populations of rapidly proliferating immune responder cells expanded by vaccination (e.g., CD4 T cells, B cells). Activated lymphocytes implement a metabolic and antiapoptotic program that allows for sustained synthesis of macromolecules and cell division (51), dividing up to twice a day during the peak of adaptive-immune responses (17). Alkylating chemotherapy covalently modifies DNA with methyl adducts for methylating drugs, like TMZ or dacarbazine (43), or inter- and intrastrand alkyl cross-links for nitrogen mustard derivatives, like cyclophosphamide (52). These lesions cause stalling of replication forks and dsDNA breaks in proliferating cells (53). This DNA damage is detected by proteins, such as ATM, which binds to dsDNA breaks and autophosphorylates, in turn activating numerous downstream effectors involved in cell cycle arrest and apoptosis, such as Chk2 kinase (54) and p53 (55). Therefore, proliferation-driven toxicity in vaccine-responder cells is a side effect of alkylating chemotherapy that must be balanced against its reported immunomodulatory effects. In the case of neoantigen vaccines for which Treg depletion is not required for efficacy, our data suggest that the negative antiproliferative effect of chemotherapy is dominant over the immunomodulatory effect.

We observed that the immune-inhibitory effect of alkylating chemotherapy was long-lived, with significant defects in CD8 T cell priming persisting for up to 10 wk after cessation of TMZ treatment (Fig. 2C). The persistence of this effect could be due to the fact that DNA repair is induced by proliferative signals (56), so quiescent naive lymphocytes may not fully repair DNA damage. This damage is then “activated” by replication fork read through during DNA synthesis in response to proliferative signals, like vaccines. Numerous studies examined the effect of alkylating chemotherapy on immunotherapeutic modalities. The predominant finding reported is depletion of Tregs and induction of lymphopenia (11, 57), although high doses have been associated with peripheral Treg expansion in rodents (58) and humans (32). Several studies
that reported an immunostimulatory effect of alkylating chemotherapy as a result of Treg depletion were conducted using transferred cells not exposed to drug (59–61). The clinical application of this strategy is complicated by the difficulty in generating large numbers of tumor-specific lymphocytes ex vivo for human patients (62), and cancer vaccines are typically administered after standard chemotherapies (7). Conversely, other studies of endogenous antitumor immune responses following Treg depletion focused on self-Ags for which breaking tolerance is required (9, 10, 16, 63) or did not directly compare immune responses in exposed and non-exposed lymphocytes (58, 64).

We focused on tumor-specific neoantigens derived from mutated self-proteins, as well as exogenous model Ags, both of which are inherently immunogenic (i.e., can readily be targeted by vaccination without additional therapy to break tolerance). Such neoantigens are technically challenging to predict from patient tumor samples, but they have been retrospectively identified in several studies in clinically responding patients using tumor cell lines and patient lymphocytes (3). Similarly, clinical experience from vaccination with idiotypic Ig for lymphoma suggests that nongermline-encoded epitopes from hypervariable regions are more immunogenic and stimulate CD4 and CD8 cells preferentially over framework regions (65). Because of their generation de novo in neoplastic cells, such mutant antigenic targets are less likely to cause autoimmune side effects and are not subjected to central tolerance that can cause negative selection of high-avidity T cells (66). Recent advances in bioinformatics have made prospective identification of immunogenic mutations possible and development of this technology to generate personalized cancer vaccines is an active area of research (5). However, the experience of adoptive immunotherapy suggests that the proliferative potential of effector cells is a critical variable (19). For personalized cancer vaccines targeting tumor-specific mutations to be successful, they should be administered in a protocol designed to maximize the quality and proliferative ability of responder lymphocytes.

We demonstrated that the generation of T cell responses against mutated self-proteins by cancer vaccines was inhibited by TMZ in a mouse model of glioma (Fig. 3E), as well as by cyclophosphamide in a mouse model of melanoma (Fig. 7A). In addition, using the model Ag OVA, we found that T cell clones that expanded after alkylating chemotherapy had lower affinity for cognate Ag, as well as lower TCR signal strength and inferior effector function upon antigenic stimulation (Figs. 5, 6). These differences seem sufficient to account for the loss of survival benefit from vaccination that we observed in both TMZ- and cyclophosphamidetreated mice (Figs. 3B, 3D, 7B).
In conclusion, we found that vaccine-driven and spontaneous adaptive antitumor immune responses were inhibited by the direct antiproliferative effect of alkylating chemotherapy. These findings are particularly noteworthy, because alkylating chemotherapy is a standard treatment for several malignancies that have been the target of vaccine immunotherapy, including TMZ for GBM (48) and dacarbazine for metastatic melanoma (25). These findings suggest that easily implemented modifications in conventional clinical protocols for cancer vaccine trials, such as banking unexposed PBMCs prior to chemotherapy for use in later immunotherapy, could yield improved results. It was reported, for instance, that 500 ml of blood contains sufficient numbers of naive precursor CD8 T cells to allow large numbers of T cells specific to multiple tumor and viral Ags to be expanded in vitro (67). Thus, easily extracted quantities of lymphocytes could be frozen and stored, either as source material for the in vitro expansion of antitumor T cells or as a banked pool of nondrug-exposed naive T cells to be infused prior to vaccination.

Furthermore, future trials of immune therapy could use such prognostic markers to stratify patients based on their relative likelihood to benefit from conventional alkylating chemotherapy versus cancer vaccines, as well as prioritize immune therapy over chemotherapy in those most likely to benefit. MGMT promoter methylation status in glioblastoma is prognostic of response to TMZ and is widely measured clinically (49), whereas tumors with the mesenchymal gene-expression pattern have a poor survival prognosis but appear to be more sensitive to active immune therapy than do glioblastomas with other gene-expression patterns.

**FIGURE 6.** CD8 T cells expanded by vaccines following TMZ have inferior functional characteristics. (A) Nur77GFP TCR signal strength reporter mice (n = 4/group) were treated with TMZ, as indicated, and vaccinated daily for 4 d with OVA and polyI:C. Seven days later, splenocytes were plated with the indicated amount of SIINFEKL peptide for 8 h. Ag-specific T cells were identified by staining for Kb-OVA and CD8, and GFP intensity of Ag-specific cells was assessed by flow cytometry. (B) Aggregate data for experiments performed as described in (A). Error bars indicate SEM. Data shown are pooled from two independent experiments with similar results. (C) C57BL/6 mice (n = 3–4/group) were treated with TMZ, as indicated, and vaccinated daily for 4 d with OVA and polyI:C. Seven days later, mice splenocytes were plated for 24 h with the indicated amount of SIINFEKL peptide. Elaborated IFN-γ was measured by cytokine bead array and normalized to Ag-specific T cells, as indicated in Materials and Methods. Error bars indicate SEM. Data shown are pooled data from two independent experiments with similar results. *p < 0.05, **p < 0.01, ***p < 0.001.

**FIGURE 7.** Cyclophosphamide pretreatment is associated with less survival benefit from melanoma vaccines. (A) C57BL/6 mice (n = 9/group) were implanted s.c. with 7.5 × 10⁶ B16-F10 melanoma cells. Mice were given cyclophosphamide, as indicated, on day 2 after tumor inoculation and vaccinated with B16-F10 cell line mutant peptides and polyI:C on days 3–6 and 17–20 after tumor inoculation. On day 10 after tumor inoculation, leukocytes from 100 μl blood were incubated with splenocyte APCs pulsed either with irrelevant (OVA-derived) peptides or B16-F10 mutant peptide mixture. Elaborated IFN-γ was measured by cytokine bead array for all nine mice/group for vaccinated groups and four mice/group for nonvaccinated groups. Error bars indicate SEM. *p < 0.05. (B) Survival of mice in (A). Mice were sacrificed when tumors reached >1000 mm³ in volume; survival is depicted by Kaplan–Meier plot. *p < 0.05, log-rank test. ns, Not significant (p > 0.05).
(24). Altering clinical protocols and basing patient treatment on known prognostic indicators of treatment response could minimize harm of conventional treatments to cancer vaccines and maximize efficacy, leading to improved outcomes for patients treated with these vaccines.

Acknowledgments

We thank D.A. Largaespada, C.A. Pennell, T.S. Griffith, and B.M. Andersen for editorial assistance and critical comments. We thank D.A. Largaespada, C.A. Pennell, T.S. Griffith, and B.M. Andersen for editorial assistance and critical comments. We thank D.A. Largaespada, C.A. Pennell, T.S. Griffith, and B.M. Andersen for editorial assistance and critical comments.

Disclosures

The authors have no financial conflicts of interest.

References


