Predictive Biomarkers and Personalized Medicine

Gene Expression Profile Correlates with T-Cell Infiltration and Relative Survival in Glioblastoma Patients Vaccinated with Dendritic Cell Immunotherapy

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Abstract

Purpose: To assess the feasibility, safety, and toxicity of autologous tumor lysate–pulsed dendritic cell (DC) vaccination and toll-like receptor (TLR) agonists in patients with newly diagnosed and recurrent glioblastoma. Clinical and immune responses were monitored and correlated with tumor gene expression profiles.

Experimental Design: Twenty-three patients with glioblastoma (WHO grade IV) were enrolled in this dose-escalation study and received three biweekly injections of glioma lysate-pulsed DCs followed by booster vaccinations with either imiquimod or poly-ICLC adjuvant every 3 months until tumor progression. Gene expression profiling, immunohistochemistry, FACS, and cytokine bead arrays were performed on patient tumors and peripheral blood mononuclear cells.

Results: DC vaccinations are safe and not associated with any dose-limiting toxicity. The median overall survival from the time of initial surgical diagnosis of glioblastoma was 31.4 months, with a 1-, 2-, and 3-year survival rate of 91%, 55%, and 47%, respectively. Patients whose tumors had mesenchymal gene expression signatures exhibited increased survival following DC vaccination compared with historic controls of the same genetic subtype. Tumor samples with a mesenchymal gene expression signature had a higher number of CD3⁺ and CD8⁺ tumor-infiltrating lymphocytes compared with glioblastomas of other gene expression signatures (P = 0.006).

Conclusion: Autologous tumor lysate–pulsed DC vaccination in conjunction with TLR agonists is safe as adjuvant therapy in newly diagnosed and recurrent glioblastoma patients. Our results suggest that the mesenchymal gene expression profile may identify an immunogenic subgroup of glioblastoma that may be more responsive to immune-based therapies.

Introduction

Glioblastoma is a lethal malignant brain tumor with overall survival (OS) rates of less than 3.3% at 5 years (1). Glioblastoma remains one of the diseases for which there is no curative therapy. Despite advances in the identification of potential targets for glioma therapy and recent clinical trials utilizing biological therapies and newer cytotoxic agents (2–4), the prognosis of patients with primary malignant brain tumors remains dismal. This sobering fact underscores the need to rethink conventional approaches to the treatment of malignant brain tumors and to base therapeutic strategies on continuing advances in our knowledge of tumor biology and immunology.

The potential therapeutic benefit of eliciting an antitumor immune response in cancer patients was first suggested decades ago. Immunotherapy is theoretically appealing because it offers the potential for a high degree of tumor specificity, while sparing normal brain structures (5). One such approach uses professional antigen-presenting cells, known as dendritic cells (DC), cocultured with autologous tumor lysate to immunologically target endogenous tumor antigens. Initial studies of DC-based vaccine therapy for malignant gliomas have shown acceptable safety and toxicity profiles (6–14), and multicenter randomized phase II and III studies are currently underway.

Previous preclinical studies (15, 16) strongly suggested that toll-like receptor (TLR) agonists (e.g., imiquimod, poly-ICLC), could enhance DC activation and migration, and stimulate T-cell–mediated antitumor immune responses in murine glioma models. To translate these findings, a phase I clinical trial was initiated to evaluate the adjunctive use of...
Preparation of autologous tumor lysate

Fresh tumor samples from surgical resection were transported under sterile conditions to the UCLA-Jonsson Cancer Center GMP facility and used to generate autologous tumor lysate, as previously described (8, 17). Tumor tissue was minced, digested in collagenase (Advanced Biofac-tures) and Dnase-1 (Dornase-α; Genentech) for 8 to 12 hours at room temperature. To generate lysates, tumor cell suspensions were subjected to 5 freeze-thaw cycles, centrifuged for 10 minutes at 800 x g, and the cell-free supernatants were obtained. Protein concentrations of each tumor lysate were determined by a Bio-Rad DC protein assay (Bio-Rad Corp.), and lysates with 100 µg of measured protein were used to pulse DC for each injection.

Preparation of autologous dendritic cells and pulsing with glioma lysate

Monocyte-derived DCs were established from adherent peripheral blood mononuclear cells (PBMC) obtained via leukapheresis performed at the UCLA Hemapheresis Unit. Blood was additionally drawn as a source of autologous serum for the DC cultures. All ex vivo DC preparations were performed in the UCLA-Jonsson Cancer Center GMP facility under sterile and monitored conditions. Dendritic cells were prepared by culturing adherent cells from peripheral blood in RPMI-1640 (Gibco) and supplemented with 10% autologous serum, 500 U/mL granulocyte macrophage colony stimulating factor (GM-CSF; Leukine; Amgen) and 500 U/mL of interleukin 4 (IL-4; CellGenix), using techniques described previously (8). Following culture, DCs were collected by vigorous rinsing and washed with sterile 0.9% NaCl solution. The purity and phenotype of each DC lot was also determined by flow cytometry (FACS-can flow cytometer; BD Biosciences). Cells were stained with fluorescein isothiocyanate–conjugated CD83, phycoerythrin-conjugated CD86 and PerCP-conjugated HLA-DR monoclonal antibodies (BD Biosciences). Release criteria were more than 70% viable by trypan blue exclusion, and more than 30% of the large cell gate being CD86+ and human leukocyte antigen-DR+ (HLA-DR+). One day before each vaccination, DC were pulsed (cocultured) with 100 µg of tumor lysate overnight, washed, and the final product was tested for sterility by Gram stain, mycoplasma, and endotoxin testing prior to injection.

Treatment schema

 Newly diagnosed glioblastoma patients underwent surgery and a standard course of external beam radiotherapy with concurrent temozolomide chemotherapy prior to DC vaccination (4). These patients were given 3 biweekly DC vaccinations following standard chemoradiation and before adjuvant temozolomide treatment. Recurrent glioblastoma patients had previous radiation therapy and chemotherapy prior to presenting with tumor recurrence, so they underwent surgical resection of their tumors followed by DC immunotherapy after they had recovered from surgery and were tapered off perioperative steroids. This ranged from 7 to 30 weeks after surgery.
Vaccine administration

On the day of each DC vaccination, a 1 mL vaccine dose was drawn into a sterile tuberculin syringe and adminis-
tered as an intradermal injection (using a 25-gauge need-
le) in the arm region below the axilla, with the side of administra-
tion rotated for each vaccination. Subjects were monitored for 2 hours postimmunization in the UCLA General Clinical Research Center. Eligible patients initially 3 intradermal injections at biweekly intervals. If patients did not develop any toxic side effects from the experimental treatment and had stable disease for more than 3 months, they received booster injections at the same dosage of tumor lysate–pulsed DC concurrently with either 5% imiquimod cream (Aldara, a TLR-7 agonist) or poly-ICLC (Hiltonol, a TLR-3 agonist). Because of initial safety/toxicity concerns of experimental allergic encephalomyelitis (EAE; ref. 18) resulting from the combined use of DC vaccination and TLR agonists, these immune response modifiers were used only in the booster phase of the protocol, after patients had shown accepta-
ble toxicity profiles to DC-lysate vaccinations alone. Booster vaccinations were given at 3-month intervals in between 28-day cycles (5 days on/23 days off) of temo-
zolomide for up to 10 boosters or until tumor progress-

Patient assessment

Toxicity was monitored and graded according to the NCI Common Toxicity Criteria. The overall incidence of adverse events was recorded. Neurologic examinations were performed before and 30 minutes after each vaccination, and at all follow-up visits. Time to tumor progression (TTP) was defined as the interval from surgical resection until the first observation of tumor progression, as evidenced by MRI or clinical deterioration. Tumor progression was also consid-
ered to be nonreversible neurologic progression, perma-
Inmunohistochemical staining

Serious paraffin sections of pretreatment tumor specimens were cut to 3-μm thickness and stained with anti-human antibodies against CD3 (DakoCytomation) and CD8 (Dako Corp.). Sections were baked for 1 hour at 60°C, deparaffinized, and endogenous peroxidase activity quenched by treating with 0.5% H2O2 in methyl alcohol for 10 minutes. Heat-induced epitope retrieval was performed on the slides using 0.01 mol/L citrate buffer, pH = 6.0 (for CD3, CD8) in a vegetable steamer (Black & Decker); slides were heated for 25 minutes, cooled, and washed in 0.01 mol/L phosphate buffered saline. All slides were then placed on a DAKO Autostainer (DAKO Corp.) and then sequentially incubated in primary antibody for 30 to 60 minutes and in rabbit anti-mouse secondary immu-
noglobulins (DAKO Corp.) for 30 minutes. Diaminoben-
zidine and hydrogen peroxide were used as the substrates for the peroxidase enzyme. For the negative controls, mouse isotype or rabbit immunoglobulins (DAKO Corp.) were used in place of the primary antibodies. Positive labeling was evaluated and scored by a board-certified neuropathologist (W.H.Y.) in a blinded fashion.

Microarray studies

Of the 23 glioblastoma patients, 16 patients had suffi-
cient residual tumor tissue for microarray molecular ana-
lysis at the end of the trial. Total RNA was purified from pretreatment, fresh frozen tumor samples by the RNeasy mini kit (Qiagen) and collected as part of the IRB-approved research protocol. cRNA was generated, quantified, and hybridized to U133 Plus 2.0 arrays at the UCLA DNA Microarray Facility by standard Affymetrix protocols. Cell intensity files (CEL files) were normalized by the Saeil Microarray Database (19), with robust multichip average from Bioconductor (version 2.10) relative to 50 samples of the same platform. The hierarchical clustering (HC) classification for each glioma was determined by a gene voting strategy as described previously (20, 21). Briefly, the mean value of each probe set was evaluated from all samples within the U133 Plus 2.0 platform by the 377 gene pro-
beset list and assigned to an HC group (21). Tumors were assigned to an HC group when the number of probes above the normalized mean was greater than 30% of a given probe set. The OS of patients on this phase I clinical trial was compared with the OS of patients from a collection of samples previously assigned to HC groups (21).
Statistical analysis

TTP and OS curves were determined by the Kaplan-Meier method. The log-rank (Mantel-Cox) test was used to compare curves between study and control groups. All P values are 2-tailed, and P<0.05 was considered statistically significant. Statistics were analyzed by GraphPad Prism software.

Results

Patient characteristics

Twenty-three patients with histologically proven WHO grade IV (glioblastoma) were enrolled in this protocol (Table 1): 15 had newly diagnosed tumors, whereas 8 had recurrent disease. There were 16 men and 7 women, with an age range of 26 to 74 years (mean age of 51 years).

DC preparation and phenotype

DCs were generated from adherent PBMC cultured in the presence of 500 U/mL GMP-grade IL-4 and 500 IU/mL of GM-CSF for 1 week prior to harvest, as reported previously (8). All final autologous tumor lysate–pulsed DC preparations consistently contained a high percentage of viable large, granular cells and were free of contamination. Our DC preparations expressed high levels of MHC class I (HLA-A,B,C), MHC class II (HLA-DR), B7.2 costimulatory molecule (CD86), and CD40, but lower expression of CD14 and CD80 (Supplementary Table 1). These DC preparations were partially mature, with less than 45% of the large cells expressing HLA-DR and CD83, as might be expected for a protocol without a dedicated maturation step. Overnight incubation with tumor lysates induced some DC maturation, as evidenced by an increase in the median fluorescence intensity of CD83 (data not shown), similar to previously reported findings (22).

Safety and toxicity

DC vaccinations were well tolerated, with no major adverse events (NCI Common Toxicity Criteria grade 3 or 4) observed in any subject during the vaccine cycles (Table 1). There were no clinical or radiological signs of EAE or other autoimmune reactions in any patient. There were anecdotal cases of transient increased T2/FLAIR and EAE or other autoimmune reactions in any patient. There were no clinical or radiological signs of EAE or other autoimmune reactions in any patient.

Systemic cytokine responses and regulatory T-cell populations following DC vaccination with TLR agonists

Others have assessed systemic immune responsiveness from autologous tumor lysate–pulsed DC vaccination by either delayed type hypersensitivity skin testing (6, 12) or by restimulating PBMC with lysate-pulsed DC in vitro, followed by assessment of IFN-γ (10, 12). However, the correlations with clinical outcome have not been consistent. In this trial, we elected to assess for more global systemic cytokine responses and changes in regulatory T-cell[Treg] frequency that may be induced by our vaccination strategy.

Peripheral blood changes in the frequency of CD3+CD4+Foxp3+ T cells were compared before and after DC vaccination for patients with available pre- and posttreatment PBMC. We observed that glioblastoma patients on this clinical trial possessed increased frequencies of peripheral blood CD3+CD4+Foxp3+ or CD3+CD4+CD25+Foxp3+ lymphocytes compared with normal volunteers (Fig. 2A). However, at the time points measured, there were no relevant changes in the frequency of this lymphocyte population after immunotherapy that statistically correlated with clinical outcome (data not shown).

To assess the cytokine microenvironment after DC vaccination with and without the addition of TLR agonists, we performed CBA from patient serum during the time course of the clinical trial to evaluate Th1- and Th2-type cytokine levels. Detectable increases in serum TNF-α and IL-6 were observed after DC vaccination (Fig. 2B; Supplementary Fig. 1A). However, the serum cytokine levels were variable between patients and the magnitude of changes did not seem to correlate with clinical outcome. Log-fold elevations in serum TNF-α and IL-6 were observed after booster DC vaccinations with either 5% imiquimod cream or 20 μg/kg poly-I:C via injection. Cumulatively, these data suggest a low toxicity profile for autologous tumor lysate-pulsed DC plus TLR agonists at all DC dose levels tested.

Dose escalation

A typical dose escalation scheme was performed with autologous tumor lysate–pulsed DC vaccination, using 1,
### Table 1. Patient characteristics

<table>
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Table 1. Patient characteristics (Cont’d)

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<th>Age (yr)</th>
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<th>KPS (mo)</th>
<th>OS (mo)</th>
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<th>Prevaccination Tx</th>
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Abbreviation: Tx, treatment.
5, and 10 million DC administered intradermally. A fixed amount of lysate (100 μg) was added to the DC and incubated overnight prior to injection. The patient characteristics and survival data for each dose cohort are outlined in Supplementary Table 2. In this dose escalation trial, there was no relationship between increasing DC dose and toxicity or specific adverse events of any kind. There were also no DC dose-dependent differences in immunologic responses tested. As seen in Supplementary Table 2, the median OS was actually longer in the 1 million DC dose cohort compared with the higher dose cohorts. However, these differences in OS were not statistically significant, given the small sample size in each dose cohort and age differences between groups.

Survival analysis
Although this phase I clinical trial was not powered to detect clinical efficacy, tumor response was monitored by clinical and MRI assessments at baseline (within 1 month prior to therapy), and every 8 weeks thereafter as surrogate markers for clinical response and tumor status. Objective clinical data are summarized in the following text and are listed in Table 1. When considering all 23 glioblastoma patients enrolled in this clinical trial (newly diagnosed and recurrent patients), the median TTP was 15.9 months. The median OS time, taken from the date of initial surgical diagnosis of glioblastoma, was 31.4 months. OS from the time of initial diagnosis at 1, 2, and 3 years was 91%, 55%, and 47%, respectively. If we include only those who received the DC vaccine in the newly diagnosed setting (n = 15), the median OS is 35.9 months, with a mean follow-up time of more than 4 years, and 1-, 2-, and 3-year survival rates of 93%, 77%, and 58%, respectively. For recurrent patients that enrolled in our vaccine trial (n = 8), the median OS was 17.9 months from the time of initial glioblastoma diagnosis. OS was significantly longer for those who received DC vaccination at initial diagnosis compared with those who enrolled in this trial at the time of recurrence (P = 0.03; Supplementary Fig. 2).

Microarray gene expression profiling
Because gene expression patterns have been shown to be highly correlated with survival in various cancers, we investigated whether the genetic signature of glioblastomas (20) was associated with clinical outcome in this DC immunotherapy trial. In patients where pretreatment tumor
samples were available, we performed microarray-based
gene expression classification as previously published
(20, 21). As shown in Figure 3, gene expression profiling
of our pretreatment tumor samples produced the typical
proneural (PN), proliferative (Pro) and
mesenchymal (Mes) hierarchical clusters, using probesets previously described
by our group (20, 21). Furthermore, we validated these
hierarchical clusters using the UCSF-Genentech and TCGA
probesets (24, 25), which yielded similar gene expression
signatures for our DC lysate patients (data not shown).

The *mesenchymal* gene expression signature is defined by
overexpression of many inflammatory-associated genes.
Thus, we hypothesized that there might be a difference
in the clinical outcome of patients on our trial that could be
linked to the local microenvironment of the original
tumor. To control for any selection bias that might have
been introduced by the requisite eligibility criteria for
patients receiving the DC vaccine (i.e., subjects needing
to be alive and off steroids long enough for vaccine
preparation and administration), we eliminated any control
patients that died within approximately 250 days of initial
diagnosis for the purposes of our comparative analysis.
We also stratified for patients who received radiation alone
versus radiation plus concurrent temozolomide chemotherapy
after initial surgical resection, and found no
statistical difference in these 2 groups when the early
progressors (OS < 250 days) were eliminated. As shown
in Figure 4, patients enrolled on our trial with the
proneural gene expression signature had an OS that was indistin-
guishable from a set of 60 contemporary
proneural tumors
analyzed from UCLA and 3 other institutions (ref. 21;
*P* = 0.664; Fig. 4A). In contrast to this, patients in our DC
vaccine trial with mesenchymal gene expression signatures
had a significantly extended survival compared with 82
concurrently collected tumors that were found to have these
same gene expression signatures (*P* = 0.0046;
Although these data are not intended to represent efficacy, such information is noteworthy because glioblastoma patients with mesenchymal gene expression patterns typically have the worst prognosis and are the most refractory to current therapies (21, 24, 25).

Gene expression signature and tumor-infiltrating lymphocytes

The density and location of T lymphocyte accumulation within certain solid tumors have been associated with extended survival (26, 27), and recent evidence suggests that such a correlation may exist in malignant glioma (28). However, an association with the subtype of tumor or treatment modality has not been addressed. Because the Mes expression signature includes numerous genes associated with inflammation, and tumor-specific T cells are known to be attracted to proinflammatory signals, we evaluated whether patients on our DC trial with mesenchymal gene expression signatures also had increased TILs. As shown in Figure 5, tumors with a mesenchymal gene expression signature had significantly increased CD3+ and CD8+ TILs compared with PN tumors (P = 0.006). Although our sample size is small, we also found qualitatively increased CD3+ and CD8+ TIL density after DC vaccination in tumors resected at recurrence (Fig. 5B). In post–DC-vaccinated tumors resected/biopsied at the time of recurrence, increases in CD3+ and CD8+ TILs were associated with the mesenchymal gene expression profile, but not necessarily with the dose of DC given. Such findings point to a potential mechanism by which distinct glioblastoma tumor subtypes might be differentially responsive to immune-based therapies.

Discussion

In this phase I study, we report the safety, feasibility, and bioactivity of a vaccine comprised of autologous DC pulsed...
with autologous tumor lysate as an adjuvant following surgical resection with standard chemoradiotherapy. Unlike our previous reported DC vaccination strategy (8) and those reported by other groups (6, 9–13, 29), we included “booster” vaccinations with the innate immune response modifiers, 5% imiquimod (Aldara), or poly-ICLC (Hiltonol) based on our preclinical studies suggesting that proinflammatory innate immune signals could enhance DC activation, trafficking to lymph nodes, and the priming of antitumor antigen-specific T lymphocytes (15). There were no dose-limiting toxicities and no detectable differences in safety or efficacy among the 3 DC dose levels tested. Of note, there was a significant difference in the average age of patients in the 10 million DC cohort compared with the other dose cohorts, which could influence the difference in OS. However, another possible hypothesis is that this trend in the data was a result of a dilutional decrease in antigens available for presentation by DC at the highest DC dose cohort ($10^7$ cells), given that the quantity of lysate was fixed (at 100 μg per dose) despite the increased DC cell dose.

The concomitant administration of 5% imiquimod or poly-ICLC with DC vaccination was also found to be safe and did not result in any additional toxicity or adverse events. To our knowledge, this is the first report of the use of TLR agonists in conjunction with DC vaccination strategies in brain tumor patients. Because TLR agonists were used only in patients in the booster phase, it is unclear whether or to what extent the addition of the TLR agonists contributed to the potential efficacy and OS of these patients. Furthermore, imiquimod and poly-ICLC are two different biological agents, targeting different TLRs. Imiquimod activates TLR-7 whereas poly-ICLC activates TLR-3, but both induce proinflammatory cytokine secretion. These complexities make it somewhat difficult to determine how these innate immune modifiers actually contributed to our study endpoints. Nevertheless, this study establishes the safety of these TLR agonists in conjunction with glioma lysate-loaded DC, and further phase II studies directly comparing these TLR agonists at the time of initial vaccination (not only in the booster phase) are currently underway.

Although the number of glioblastoma patients entered in this phase I clinical trial was not powered to measure efficacy, the clinical results of this trial are still noteworthy. The median OS from the time of initial surgical diagnosis was 31.4 months for all glioblastoma patients ($n = 23$) treated in this study, including both those enrolled as newly diagnosed and recurrent tumor patients. For those treated in the newly diagnosed setting, the OS was 35.9 months; and the OS was 17.9 months for those who received vaccination at recurrence. In addition, we have had 3 patients surviving more than 6 years to date. Such statistics are compelling in the face of the expected median survival for this disease, which is currently still reported as approximately 14 months for newly diagnosed patients that receive standard surgery, radiation, and temozolomide chemotherapy (4, 30, 31). This compares favorably even when compared with published data for the best clinically defined prognostic group of glioblastoma patients (recursive partitioning analysis; RPA class III: age < 50 years and KPS ≥ 90), whose 2-year survivals were 40% and 29% for RPA III and IV patients, respectively, following treatment with standard radiation and temozolomide (31). Such data are also favorable compared with other recent brain tumor DC-based vaccine trials without booster injections and TLR adjuvants, where the OS was reported as 21.4 months (mean, 11 newly diagnosed and 23 recurrent glioblastoma patients; ref. 10) and 9.6 months (median) in a recurrent glioblastoma population (6).
Glioblastomas are primarily identified by histologic features assigned to cytologically malignant, mitotically active, necrosis-prone tumors established by the WHO (32). Such histologic features are generally associated with patient survival, together with performance status, extent of surgical resection, and age. Yet, histologically identical tumors can behave in different ways: a situation that may underlie the biology of this heterogeneous disease. More recently, extensive genetic profiling of these tumors has been able to identify molecular classifiable subgroups of glioblastoma (i.e., PN, Pro, and Mes subtypes; refs. 20, 21, 24, 33–38), which can better predict survival than conventional histopathologic analysis. Such new classification techniques are of interest so that patients can be more appropriately stratified for new treatment strategies (20).

The Mes subgroup of glioblastomas typically have a poorer prognosis than the more common PN subgroup (21, 24). However, in our study, patients with the mesenchymal gene expression signatures had significantly extended survival compared with a large, multi-institutional cohort (n = 82) of glioblastoma samples of the same molecular subgroup treated with various other therapies. No such survival difference was observed in patients from this clinical trial with proneural signatures, compared with other control glioblastoma subjects of the PN subgroup (n = 60). Admittedly, such comparisons with concurrent and historic controls are not meant to imply efficacy, because this phase I trial did not have a prospectively matched, placebo-controlled arm. Although some prognostic factors, such as age and Karnofsky performance status, were relatively matched in our comparison groups, the extent of surgical resection was not directly compared between the patients in this trial and our concurrent/historic controls. Because we need adequate amounts of tumor (>2 g) to generate the autologous vaccines, tumor resectability was taken into account in the eligibility criteria. Therefore, it is possible that the extent of surgical resection may have been greater in our DC-vaccinated patients compared with concurrent/historic controls, which could have influenced our survival results. Nevertheless, the median OS (31.4 months) of our DC-vaccinated patients is still noteworthy, when compared with large series of glioblastoma patients who underwent gross total tumor resections and were treated with concomitant chemoradiotherapy, where the median survival was reported to be 18.6 months (31).

It is unclear whether the extended survival of our patients with mesenchymal gene expression signatures is a direct result of the vaccine effects, or good responses to follow-up therapies after failing the vaccine. Because Mes signatures represent glioblastoma subgroups that are more resistant to conventional therapy, it can be speculated that DC vaccination somehow makes these tumors more susceptible to subsequent treatments (39). Because adjuvant temozolomide treatment was coordinated into the schedule of the DC booster vaccinations, this is a difficult distinction to make from our study design. Nevertheless, our results suggest that mesenchymal gene expression signatures express elevated inflammatory gene transcripts and possess an increased density of tumor-infiltrating CD3⁺ and CD8⁺ lymphocytes compared with glioblastomas expressing other genetic signatures. As such, we hypothesize that the expression of inflammatory genes (e.g., IL-1R, TNF-α signaling factors, and chemokines) may facilitate the priming and trafficking of tumorspecific T cells into the tumor parenchyma, which might be enhanced by DC vaccination and innate immune response modifiers. Hence, the mesenchymal gene expression signature may have a direct impact on the bioactivity of the vaccine itself, irrespective of postvaccine therapy. Prospectively designed, randomized, multicenter phase III clinical trials will be required to validate such hypotheses and proof of clinical benefit remains to be established.

Overall, the results reported here may provide novel insights for prospective patient selection in future immunotherapy studies and lend additional credence for the ability of genetic expression signatures to impart relevant data for personalized cancer treatment. On the basis of the results of this phase I trial, we will continue developing more advanced clinical trials with this particular approach. We currently are planning a randomized, multicenter phase II/III clinical trial of DC vaccination for newly diagnosed glioblastoma (DCVax-Brain), which will hopefully help to further define which subgroups of patients may respond to tumor vaccination strategies. This in turn may lead to further optimization and refinements of related trials of DC-based vaccines for patients with glioblastoma, with the ultimate goal of developing novel immunotherapeutic strategies for brain cancer patients.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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