Activation of the PD-1 Pathway Contributes to Immune Escape in EGFR-Driven Lung Tumors

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ABSTRACT

The success in lung cancer therapy with programmed death (PD)-1 blockade suggests that immune escape mechanisms contribute to lung tumor pathogenesis. We identified a correlation between EGFR receptor (EGFR) pathway activation and a signature of immune suppression manifested by upregulation of PD-1, PD-L1, CTL antigen-4 (CTLA-4), and multiple tumor-promoting inflammatory cytokines. We observed decreased CTLs and increased markers of T-cell exhaustion in mouse models of EGFR-driven lung cancer. PD-1 antibody blockade improved the survival of mice with EGFR-driven adenocarcinomas by enhancing effector T-cell function and lowering the levels of tumor-promoting cytokines. Expression of mutant EGFR in bronchial epithelial cells induced PD-L1, and PD-L1 expression was reduced by EGFR inhibitors in non–small cell lung cancer cell lines with activated EGFR. These data suggest that oncogenic EGFR signaling remodels the tumor microenvironment to trigger immune escape and mechanistically link treatment response to PD-1 inhibition.

SIGNIFICANCE: We show that autochthonous EGFR-driven lung tumors inhibit antitumor immunity by activating the PD-1/PD-L1 pathway to suppress T-cell function and increase levels of proinflammatory cytokines. These findings indicate that EGFR functions as an oncogene through non–cell-autonomous mechanisms and raise the possibility that other oncogenes may drive immune escape.

INTRODUCTION

Although genomic alterations that provide growth advantages to cancer cells are widely recognized to be essential for malignant transformation, discoveries made over the past decade suggest that evading immune destruction may also be critical for tumorigenesis (1). Mice lacking particular components of innate or adaptive immunity are more susceptible to spontaneous and carcinogen-induced tumors as compared with wild-type (WT) mice. Similarly, immunosuppressed patients...
develop both virus-induced and non-pathogen-associated tumors more frequently than immunocompetent individuals (2). Although these observations support the idea that immune mechanisms may suppress tumor development, tumor formation implies successful escape from immune control.

To generate efficient antitumor immune responses while maintaining self-tolerance, host reactions are tightly regulated through a combination of stimulatory and inhibitory signals. As T lymphocytes can recognize antigens derived from all cellular compartments presented in the context of surface MHC molecules, these antitumor effector cells have been the principal focus of cancer immunotherapy (3). CTL antigen-4 (CTLA-4) is a critical negative immune checkpoint that limits the induction of potent CTL responses. Extensive clinical testing of human blocking anti–CTLA-4 monoclonal antibodies (mAb) demonstrated an increase in antitumor immunity, with approximately 20% of patients with metastatic melanoma achieving long-term survival; these substantive clinical benefits resulted in U.S. Food and Drug Administration (FDA) approval of ipilimumab as first- or second-line therapy for advanced melanoma (4). On the basis of these important results, a second negative immune checkpoint mediated through interactions of programmed death (PD)-1 with its ligands PD-L1 and PD-L2 has been investigated as a target for cancer immunotherapy (5). Blocking antibodies against PD-1 or PD-L1 have demonstrated substantial clinical activity in patients with metastatic melanoma, renal cell carcinoma, non-small cell lung cancer (NSCLC), and other tumors (6, 7). Preliminary findings raise the possibility that PD-1 blockade might be less toxic than ipilimumab, although more detailed testing is required.

In the NSCLC clinical trials, only a subset of patients responded to PD-1 blockade, and early studies suggested that PD-L1 (CD274) expression may be a biomarker for therapeutic response to anti–PD-1 antibodies. Although FTEN loss has been associated with increased PD-L1 expression in gliomas (8), it is unknown whether specific genomic subsets of lung tumors use the PD-1 pathway as a mechanism of immune escape. One of the most commonly mutated oncoproteins in patients with NSCLC is EGFR. Previous studies have shown that activation of the EGF receptor (EGFR) pathway may be involved in suppressing the immune response in murine melanoma models either through activating regulatory T cells (Treg; ref. 9) or reducing the levels of the T-cell chemokorepressor CCL27 (10).

Mutations in EGFR frequently arise in the kinase domain, rendering tumor cells sensitive to EGFR tyrosine kinase inhibitors (TKI). However, despite the initial response, tumors invariably become resistant by acquiring either a secondary point mutation in EGFR (T790M) or additional alterations in other genes that bypass the need for ongoing signaling from the mutated EGFR (11). A major focus in the therapy for EGFR-driven lung cancers is the development of therapeutic strategies that either delay acquired resistance or are effective in the setting of acquired resistance, though success in these areas has been limited to date. On the basis of the findings in the melanoma models and given that EGFR is one of the most commonly mutated oncogenes in NSCLC (12), we analyzed the immune microenvironment and a set of immunosuppressive pathways in EGFR-driven mouse lung tumors.

RESULTS

Activation of the EGFR Pathway in Murine Bronchial Epithelial Cells Leads to an Immunosuppressive Lung Microenvironment

The two most frequently detected EGFR mutations in patients with NSCLC are in the kinase domain: L858R substitution in exon 21 and deletions in a specific amino acid motif in exon 19 (Del19; ref. 11). Similar to the patients carrying these mutations, mouse lung tumors carrying EGFR L858R or Del19 mutations initially respond to treatment with erlotinib (EGFR TKI; ref. 13), followed by the development of resistance through acquired second site mutations (T790M). Separate mouse models carrying both T790M and L858R or Del19 have been characterized (14, 15); although these do not respond to erlotinib therapy, they do respond to the mutant-specific irreversible EGFR inhibitor WZ4002 for several weeks before they acquire resistance through other mechanisms (16). Microarray expression profiling of the mice T790M/L858R (TL) tumors as compared with controls revealed increased levels of Pd-1 (Pdcd1), Pd-L1 (Cd274), Cda4, Il-6, Tgf-b1, and granulin (Grn) along with ligands for the EGFR (EGFR-mutant vs. WT for the gene set shown $P = 3 \times 10^{-20}$; Fig. 1A). Analysis of microarray data from previously reported datasets showed no significant differences in Pd-H1 and Pd-I2 (Pdcd1l2) expression among tumors derived from multiple models of EGFR-driven lung adenocarcinoma [L858R, L858R/T790M (TL) and exon 19 deletion/T790M (TD); refs. 17, 18], indicating that EGFR-driven tumors of a variety of EGFR mutations display elevated Pd-H1 and Pd-I2 expression as compared with normal lung (data not shown). We next confirmed the expression of PD-L1 on tumor (CD45 human EGFR$^+$) and associated hematopoietic cells by flow cytometry and immunohistochemistry (IHC) in EGFR-driven mouse lung adenocarcinomas (Fig. 1B and Supplementary Fig. S1).

As an initial step to understanding the basis for compromised antitumor immunity in mice carrying EGFR-driven tumors, we analyzed the tumor microenvironment in comparison with the lungs from littermate controls to characterize the alterations associated with oncogene expression. Tumor-infiltrating T cells displayed a significantly lower CD8$^+$/CD4$^+$ and CD8$^+$Foxp3$^+$ ratio and elevated expression of PD-1 and Foxp3 as compared with T cells in the normal lung (Fig. 1C). We next analyzed immune cell populations in whole lungs and detected a significant increase in the absolute number of PD-1$^+$ and Foxp3$^+$ T cells in the tumor-bearing lungs, with a majority of Foxp3$^+$ T cells expressing PD-1 (Fig. 1D and E). To assess whether other T-cell inhibitory pathways were also induced in these tumors, we analyzed expression of CTLA-4, Lag-3, and Tim-3 (3). CTLA-4 was dominantly expressed by Tregs, and Lag-3 and Tim-3 were expressed by only a small percentage of PD-1$^+$ positive T cells (Fig. 1E and Supplementary Fig. S2A). These results suggest that the PD-1 pathway and Foxp3$^+$ Tregs may be dominantly involved in suppressing effector T-cell function in this setting. PD-1$^+$ positive T cells exhibited a memory and activation phenotype (ref. 19; Supplementary Fig. S2B), raising the possibility that EGFR-driven tumors may be characterized by host T-cell exhaustion, specifically through upregulation of the PD-1 and PD-L1 interactions. Interestingly, these antitumor immune changes were also detected in the mildly sick (based on tumor burden – lung
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**Figure 1.** Activation of the EGFR pathway in bronchial epithelial cells leads to an immunosuppressive lung microenvironment. **A,** microarray expression profiling analysis of lung tumors from mice with EGFR T790M/L858R (TL), or control lungs focusing on PD-1, CTLA-4, PD-L1, and other receptors involved in inhibition of immune responses. **B,** expression levels of immune checkpoint receptors were significantly higher in bronchoalveolar lavage fluid (BALF) from tumor-bearing lungs compared with those from normal lungs (**Fig. 1F** and Supplementary Fig. S5A), which correlated with their mRNA expression levels in tumor-bearing lungs (**Fig. 1A**). Because soluble factors in BALFs can be produced by tumor cells as well as tumor-infiltrating immune cells, we also compared the immune cell populations between normal and tumor-bearing lungs by flow cytometry (gating strategy described in Supplementary Methods). Among major immune cell types, the numbers of alveolar macrophages were significantly increased in tumor-bearing animals, whereas natural killer (NK) cells were significantly decreased (**Fig. 1G**) and showed a functionally impaired phenotype (Supplementary Fig. SSB).

**In Vivo Efficacy of PD-1 Antibody Blockade in Mutant EGFR-Driven Murine Lung Cancer Models**

To confirm our findings that EGFR-mutant tumors display elevated PD-L1 levels and a T-cell exhaustion phenotype, and to explore whether this upregulation drives escape from immune surveillance, we tested a rat monoclonal blocking anti-PD-1 antibody in NSCLC mouse models in which lung adenocarcinomas are driven by EGFR mutation. We generated cohorts of Del 19, TL, and TD mice and induced tumor growth with doxycycline. Upon administration of clinically
relevant doses of anti–PD-1 mAb [200 μg (~8–10 mg/kg) three times a week], we detected a reduction in tumor growth in all of the EGFR-mutant mouse models by MRI (Fig. 2A and B) and increased apoptosis measured by terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL) and cleaved caspase-3 staining in TD mice (Fig. 2C and D). Del19 mice showed the greatest tumor volume reductions (50%–60% of the baseline tumor volume after 4 weeks of therapy; Fig. 2B). TL mice showed a modest tumor shrinkage response but exhibited slowed tumor growth as compared with untreated mice (Fig. 2B). Unlike mice with EGFR-driven tumors, transgenic mice with KRAS-driven tumors did not show any significant response to the treatment with anti–PD-1 antibody (Supplementary Fig. S6A–S6C), despite elevated PD-L1 expression (Supplementary Fig. S7A and S7C), suggesting that factors in addition to PD-L1 influence the therapeutic activity of PD-1 antibody blockade. We also observed significantly increased survival with treatment in all three of the EGFR-mutant mouse models (median survival treated vs. untreated, respectively: Del19 16.5 vs. 9 weeks, P < 0.0001; TD 23.5 vs. 16, P = 0.0005; TL 23.5 vs. 16, P < 0.0001; Fig. 2E).

**Figure 2.** In vivo efficacy of PD-1 antibody blockade in EGFR-mutant murine lung cancer models. The antitumor effects of anti–PD-1 antibodies in mouse models of EGFR-driven lung cancers (A–E). A, tumor volume changes by MRI at varying time points; baseline, 2, and 4 weeks after treatment of the indicated genotypes of mice. “H” indicates location of the heart. B, quantification of tumor volume changes as compared with baseline tumor volumes in the mice that were treated with anti–PD-1 antibody (aPD-1 t.) or left untreated (Unt.). C, representative images of lung sections from tumor-bearing mice (TD) that were either treated with anti–PD-1 antibody for 1 week or left untreated. Sections were stained for H&E, TUNEL, and cleaved caspase-3. D, quantification of TUNEL and caspase-3 staining, respectively. Data points indicate total positive signal per tumor field. For TUNEL, n = 3 for untreated and n = 4 for PD-1–treated mice; for cleaved caspase-3, n = 6 for untreated and n = 3 for PD-1–treated mice. E, Kaplan-Meier survival analysis of the anti–PD-1 antibody treated or untreated mice bearing EGFR-driven tumors. Treatments were started after tumors were confirmed with MRI at the time points indicated by arrows for each of the mouse lines. TUNEL, terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling.

Anti–PD-1 Antibody Binds to Activated T Cells and Improves Effector Function

On the basis of these findings, we explored how PD-1 blockade impacts the characteristics of host T cells and other immunosuppressive factors, including cytokine production and accumulation of tumor-associated macrophages in EGFR-driven lung adenocarcinomas. Severely sick mice (based on tumor burden as determined by right lobe weights) from the two EGFR models, Del19 and TD, which showed more dramatic responses to PD-1 blockade treatment, were treated with a PD-1–blocking antibody for 1 week, and then tumor-bearing lungs were harvested along with lungs from untreated severely sick mice (Fig. 3A). Given that we used a rat immunoglobulin G 2a (IgG2a) therapeutic antibody (clone 29F.1A12), we stained lung T cells with a secondary anti-rat IgG2a antibody as well as the same anti-PD-1 antibody used for treatment to differentiate the T-cell population bound or unbound by the therapeutic antibody. The therapeutic antibody was bound to almost all of the CD4+ and CD8+ T cells (Fig. 3B and Supplementary Fig. S8A). After confirming efficient target engagement, we next analyzed the phenotypic changes in CD4+ and CD8+ T cells (Fig. 3C and Supplementary Fig. S8B).
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**Figure 3.** Anti-PD-1 antibody binds to activated T cells and improves effector function. A, schematic of the short-term in vivo treatment of mice with anti–PD-1 antibodies after tumor burden was confirmed by MRI imaging. Each group was treated either with isotype control (untreated) or anti–PD-1 antibody on days 0, 3, 5, and 8 (four doses), and then at day 9 mice were sacrificed for analysis. B, representative flow cytometry results of PD-1−/ or RetigG2a+ (therapeutic anti–PD-1 antibody binding) in CD4+ and CD8+ T cells, anti–PD-1 antibody-treated mouse (+ aPD-1), control antibody-treated mouse (− aPD-1). C, changes in total T-cell (CD3+), CD8+ T-cells, and Tregs, and ratios of CD8+/CD4+ and CD8+/Treg after PD-1 blockade. D, enhancement of effector T-cell function (IFN-γ production) by PD-1 antibody blockade E, CD3 IHC (top) and quantification of intratumoral CD3+ T cells upon PD-1 antibody blockade. Lung T cells in the treatment group showed a significantly higher CD8+/CD4+ ratio and increased numbers of total CD8+ T cells as compared with those in the untreated group (Fig. 3C). Although previous studies have shown that PD-L1 induces Tregs (22), PD-1 blockade did not change the numbers of Tregs (Fig. 3C). T-cell function was also significantly improved in terms of IFN-γ but not interleukin (IL)-2 production in treated lungs (Fig. 3D and Supplementary Fig. S2B). Consequently, IFN-γ-producing CD8+ T cells were significantly increased in the treatment group (Fig. 3D). Histologic analysis revealed increased infiltration of CD3+ T cells into the tumor nodules after anti–PD-1 antibody treatment (Fig. 3E), suggesting that PD-1 blockade may revive exhausted T cells, particularly cytotoxic CD8+ T cells, to accomplish tumor cell killing in EGFR-driven tumor models. We also explored how PD-1 blockade altered the immune microenvironment in addition to enhancing tumor apoptosis (Fig. 2C and D). Among the cytokines elevated in BALFs before therapy, IL-6, TGF-β1, and progranulin (PGRN) showed a significant decrease after treatment in both of the EGFR-driven tumor models (Del19 and TD; Fig. 3F and Supplementary Fig. S9A). Interestingly, the IFN-γ-inducible chemokine CXCL10 was significantly elevated after treatment, whereas its receptor, CXCR3, was more highly expressed in CD8+ than CD4+ T cells (Supplementary Fig. S9B and S9C). Among the immune cell populations, the total numbers of alveolar macrophages were significantly reduced in the Del19 model (Fig. 3G and Supplementary Fig. S10). We sorted the tumor-associated alveolar macrophages from these EGFR-driven tumor models and confirmed that they expressed Il6, Tgfβ1, and Gm1 (data not shown).

**EGFR Pathway Activation in Human Bronchial Epithelial Cells Induces PD-L1 Expression**

To broaden our findings that Pd-l1/2 expression is upregulated in response to EGFR-driven oncogenic signals in mice, we compared PD-L1 and PD-L2 expression in patient-derived established NSCLC cell lines (23), with a particular focus on lines with EGFR and KRAS mutations. EGFR and KRAS...
mutations are the two most prevalent drivers of lung adenocarcinomas, and tumors of these genotypes display distinct natural histories and treatment response. We observed a significant correlation among PD-L1 expression with expression of EGFR and its ligands, markers of EGFR pathway activation (P values for individual genes are shown; combined P < 10<sup>-15</sup>; Fig. 4A). We observed a nonsignificant trend toward increased levels of PD-L1 in EGFR-mutant lines compared with KRAS-mutant lines, though the number of available cell lines with an EGFR mutation for this comparison was small (Supplementary Fig. S11A). High PD-L1 expression at the protein level was confirmed in the six EGFR-mutant lines by flow cytometry (Fig. 4 and Supplementary Fig. S11B). We also observed a similar result in an analysis of previously reported microarray data from patients with lung adenocarcinoma (24), in which there was a significant correlation among expression of EGFR and its ligands and PD-L1 expression (P < 10<sup>-15</sup>; data not shown).

To test whether ectopic expression of mutant EGFR is able to induce PD-L1 expression, we stably expressed mutated EGFR (TD) in immortalized bronchial epithelial cells (BEAS2B). Expression of the mutated EGFR caused an increase in PD-L1 levels by both real-time PCR and flow cytometry in contrast to expression of KRAS<sup>G12V</sup>, which did not induce PD-L1 (Fig. 4B).

This suggests that oncogenic EGFR signaling can drive PD-L1 upregulation. Given that expression profiling of tumors suggested that the EGFR signaling pathway may positively regulate expression of PD-L1 ligands, we next tested the EGFR pathway dependency of PD-L1 expression across NSCLC cell lines. First, we evaluated the levels of PD-L1 in EGFR-mutant cell lines after treatment with sublethal doses of the EGFR TKI gefitinib. Flow cytometry analysis showed a clear reduction of PD-L1 protein (Fig. 4C) independent of effects on cell viability. In addition to the gefitinib-sensitive EGFR-mutated lines, we also treated the gefitinib-resistant H1975 and PC-9R cell lines, which harbor an EGFR T790M mutation, with the irreversible mutant-selective EGFR TKI WZ4002 (15). WZ4002, but not gefitinib, decreased PD-L1 levels in H1975 and PC-9R cell lines (Fig. 4D and Supplementary Fig. S11C), confirming a correlation among PD-L1 levels and dependence on EGFR signaling. Although EGFR mutations predict EGFR TKI sensitivity, some EGFR WT cell lines also are sensitive to EGFR TKIs due to activation of the EGFR pathway by overexpression of EGFR or by increased production of EGFR ligands. Treatment of H358 cells, which have been previously shown to display increased EGFR signaling (25), with gefitinib resulted in PD-L1 downregulation (Fig. 4E). These findings suggest that EGFR pathway activation independent of EGFR

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**Figure 4.** EGFR pathway activation in human bronchial epithelial cells induces PD-L1 expression. A, microarray expression profiling analysis of established cell lines from human patients with NSCLC. Black and red bars indicate identified KRAS or EGFR mutations, respectively. B, PD-L1 upregulation in BEAS-2B bronchial epithelial cell lines transduced with vectors encoding KRAS<sup>G12V</sup> or EGFR mutation (T790M-Del19), as assessed by quantitative PCR (qPCR) and flow cytometry (C-E). Reduction of PD-L1 expression in NSCLC cell lines 72 hours after EGFR TKI treatment at the indicated concentrations (in the absence of drug-induced apoptosis). C, EGFR-del19 mutant PC-9 and HCC827 NSCLCs. D, gefitinib-resistant H1975 NSCLC. E, EGFR WT KRAS-mutant H358 NSCLC. Representative results from three independent experiments are shown. F, sections of formalin-fixed patient tumors carrying EGFR mutations stained with H&E or PD-L1. Top, high expression on tumor cell membrane; middle, low expression on membrane; bottom, expression on macrophages. Scale bars show 100 μm. MFI, median fluorescence intensity; iso, isotype control; DMSO, dimethyl sulfoxide.
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Mutation may also induce the expression of PD-L1. In addition to these studies of cell lines, we confirmed PD-L1 expression at the protein level by IHC on tumor biopsy samples obtained from patients; of the 12 EGFR-mutant lung tumors we studied, nine stained positive for PD-L1 in the tumor and/or myeloid cells (Fig. 4F and Supplementary Table S1).

**DISCUSSION**

We have demonstrated that activation of the EGFR pathway induces PD-L1 expression and other immunosuppressive factors to accomplish evasion of the host antitumor immune response. This role of EGFR signaling seems to be independent of its effects on cell proliferation and survival, suggesting an active role for the EGFR oncogene in remodeling the immune microenvironment. Pharmacologic blockade of the PD-1 pathway in murine lung tumors we studied, nine stained positive for PD-L1 in the tumor and/or myeloid cells.

**Microarray Data Analysis**

For gene expression analysis of NSCLC cell lines, Robust Multi-chip Average normalized expression data were downloaded from the cancer cell line encyclopedia (www.broadinstitute.org/ccle). Expression data from WT and EGFR transgenic mice were obtained from a previous study (18) and converted into log2 values. Pearson correlation coefficients were calculated by comparing expression values for each transcript over all samples to either PD-L1 or PD-1 expression.

**Cell Line Experiments**

BEAS2B cells (ATTC # CRL9609) were grown in bronchiolar epithelial cell basal medium (Lonza; #CC-3170) and maintained with HEPES buffer solution, trypsin, and trypsin-neutralizing solution (Lonza; #CC-5034). Mutations in EGFR or KRAS were introduced and cloned into the PLCPX vector (Addgene). Clones stably expressing the mutant EGFR or KRAS were selected with puromycin (2 μg/mL) for 3 days. Other cell lines were purchased from the American Type Culture Collection. Genotypes of the patient-derived NSCLC cells are as follows: PC9-del 19, HCC827-del 19, H1975-L858R/T790M, PC9R-del 19/T790M. All cell lines were cultured in RPMI-1640 (Corning) supplemented with 10% heat-inactivated FBS, 100 U/mL penicillin, 100 mg/mL streptomycin and 10 mmol/L HEPES. For PD-L1 expression analysis, untreated cells and gefitinib or WZ4002-treated cells were stained with anti-PD-L1 antibody (29E.2.A3) and isotype control (BioLegend) and then stained with Annexin V and 7-aminooxycinomycin D (7-AAD; eBioscience); PD-L1 levels were determined for the Annexin V and 7-AAD double-negative population using a BD FACSCanto II flow cytometer equipped with Diva software (BD Biosciences). The final analysis and graphical output were performed using FlowJo (TreeStar). Treatment doses that did not compromise cell survival were determined with a CellTiter-Glo Luminescence Cell Viability Assay (Promega) after 72 hours.

**Real-Time PCR**

Total RNA was extracted using TRIzol (Invitrogen; #15596018) followed by RNA cleanup (Qiagen; #74204). cDNA were prepared from total RNA preps using the High-Capacity cDNA Kit (Invitrogen; #4377474). Real-time assays were conducted using TaqMan real-time probes (Invitrogen) for human PD-L1/CD274 (Hs01125301_m1) and GUSB (Hs00939627_m1) using 40 ng cDNA.
Triplet cases were run for each sample. GUSB was used as internal control and ΔCt method was used for relative mRNA calculations.

**Mouse Husbandry and Breeding**

All EGRF transgenic mice carrying tetracycline-inducible human EGFR cDNA were previously generated, crossed with CC10-RTTA mice expressing reverse tetracycline activator from lung Clara cell CC10 promoter as previously described (13–15), and maintained in mixed (C57Bl/6, FVB, and S129) background. Double-positive progeny were fed with doxycycline diet starting at 5 to 6 weeks of age for the induction of tumors and maintained on doxycycline throughout the study. All breedings and in vivo experiments were performed with the approval of the Dana-Farber Cancer Institute (Boston, MA) Animal Care and Use Committee.

**Antibody Dosing**

Mice received rat anti–PD-1 mAb (clone 29F.1A12) by intraperitoneal injections [200 μg in PBS per dose (8-10 mg/kg), three times a week], as described previously (36). Control mice received similar injections of 200 μg of rat IgG2a isotype control in PBS (BioXcell).

**MRI Tumor Volume Quantification and Survival**

Tumor volume quantifications were performed using the 3D-Slicer software as described in detail in Supplementary Methods. Survival curves were generated by pooling animals that were sacrificed because of heavy tumor burden or were otherwise found dead.

**BALF Collection and Cytokine Measurement**

One milliliter of PBS was injected into the trachea to inflame the lungs, which were then aspirated and frozen. Cytokine concentrations in serum and BALFs were measured with ELISA kits for mouse IL-2, IL-4, IL-10, IFN-γ, TNF-α, TGF-β1, iNOS, VEGF, GM-CSF (granulocyte macrophage colony-stimulating factor), MFG-E8, CCL17 (R&D Systems), CCL2, CCL5, and CXCL10 (eBioscience).

**Histology and IHC**

Mice were classified at euthanasia into mild or severe pulmonary pathology based on lung weights: severe (s), total right lung weight ≥650 mg; mild (m), total right lung weight <650 mg. Lungs were inflated with 10% formalin and embedded in paraffin. Sections (5 μm) were cut for hematoxylin and eosin (H&E) staining and IHC. Anti-cleaved caspase-3 mAb (Abcam; #2302) and anti-CD3 mAb were used at 1:20 and 1:50 dilutions respectively (Dako; #A0452). TUNEL assay was performed as per the manufacturer’s instructions (Millipore; #17-141). Cells stained positive for the indicated markers were counted on the 20X (objective) images of tumor nodules of similar size. Comparisons of treatment groups were performed using the unpaired two-tailed Student’s t test. P values for the survival curves have been calculated using a log-rank test.

**Disclosure of Potential Conflicts of Interest**

M.D. Wilkerson is employed as a consultant at Cancer Therapeutics Innovation Group and GenetecCentric. P.A. Janne is a consultant/advisory board member of Boehringer-Ingelheim, Roche, Abbott, AstraZeneca, Pfizer, Sanofi, Chugai Pharmaceuticals, and Clovis Oncology, and has given expert testimony for LabCorp. G.J. Freeman has ownership interest (including patents) in Bristol-Myers Squibb, Roche, Merck, EMD-Serono, Boehringer-Ingelheim, Amplimmune, and CoStim Pharmaceuticals, and is a consultant/advisory board member of CoStim Pharmaceuticals. G. Dranoff has received commercial research grants from Bristol-Myers Squibb and Novartis, and is a consultant/advisory board member of Novartis, Merck, and Genentech. No potential conflicts of interest were disclosed by the other authors.

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