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A tumor-intrinsic PD-L1/NLRP3 inflammasome signaling pathway drives resistance to anti–PD-1 immunotherapy

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An in-depth understanding of immune escape mechanisms in cancer is likely to lead to innovative advances in immunotherapeutic strategies. However, much remains unknown regarding these mechanisms and how they impact immunotherapy resistance. Using several preclinical tumor models as well as clinical specimens, we identified a mechanism whereby CD8⁺ T cell activation in response to programmed cell death 1 (PD-1) blockade induced a programmed death ligand 1/NOD-, LRR-, and pyrin domain–containing protein 3 (PD-L1/NLRP3) inflammasome signaling cascade that ultimately led to the recruitment of granulocytic myeloid-derived suppressor cells (PMN-MDSCs) into tumor tissues, thereby dampening the resulting antitumor immune response. The genetic and pharmacologic inhibition of NLRP3 suppressed PMN–MDSC tumor infiltration and significantly augmented the efficacy of anti–PD-1 antibody immunotherapy. This pathway therefore represents a tumor-intrinsic mechanism of adaptive resistance to anti–PD-1 checkpoint inhibitor immunotherapy and is a promising target for future translational research.

Introduction

Despite the significant impact that checkpoint inhibitor immunotherapies have generated in clinical oncology, the majority of patients with cancer still do not benefit from this treatment modality (1). It is widely believed that a more intimate understanding of the underlying mechanisms driving cancer immunotherapy resistance will lead to the discovery and development of innovative strategies to augment the efficacy of immunotherapy, while expanding the patient population capable of benefitting from these agents (2, 3). However, our understanding of the mechanisms driving both primary and secondary immunotherapy resistance remains incomplete.

There is an extensive body of literature describing the inhibitory role of myeloid-derived suppressor cells (MDSCs) in the generation of adaptive T cell immunity (4, 5). These data are consistent with additional studies that have correlated elevated circulating MDSC levels with poor clinical responses to both anticytotoxic T lymphocyte antigen 4 (anti–CTLA-4) and anti–programmed cell death 1 (anti–PD-1) antibody (Ab) immunotherapy in patients with advanced melanoma (6, 7). MDSCs have been shown to undergo chemotaxis toward tumor beds via chemokine gradients generated by the developing tumor. In particular, migration of the granulocytic subset of MDSCs (PMN-MDSCs) relies primarily on the chemokine receptor CXCR2 and several of its cognate ligands, including CXCL5 (8). Additional work has shown that CXCR2 blockade enhances the efficacy of anti–PD-1 Ab immunotherapy in models of both pancreatic cancer and sarcoma (8–10). These findings suggest that this immunosuppressive cell population plays a critical role in determining the outcome for patients with cancer undergoing anti–PD-1 Ab therapy. However, the exact mechanism by which MDSCs interfere with the development of antitumor immunity in response to checkpoint inhibitor immunotherapy remains unclear.

It is well known that the immune system is composed of many negative feedback inhibitory pathways that serve to suppress the development of overzealous immune responses to avoid autoimmune pathology. Similar mechanisms are likely to serve as the molecular underpinnings for the development of adaptive resistance to anti–PD-1 Ab immunotherapy and represent key pathways of interest for the future development of improved combinatorial immunotherapy strategies (11). Indeed, recent studies have demonstrated that both CD8⁺ T cell–dependent and IFN-depen-
dent upregulation of CSF1 in melanoma and CD38 in lung cancer promote adaptive resistance to anti–PD-1 checkpoint blockade (12, 13). These observations are reminiscent of IFN-dependent upregulation of the immunoregulatory enzyme indoleamine 2,3-dioxygenase (IDO), which serves to reestablish immune tolerance in response to cytolytic T cell activity (14, 15). Although a recent study has implicated tumor expression of CXCL1 and the recruitment of PMN-MDSCs as key factors that mediate against tumor T cell infiltration, a role for CXCR2-dependent chemokines in the generation of adaptive resistance to anti–PD-1 Ab immunotherapy has not been described (16).

Previous work, including our own, has demonstrated the Wnt5a ligand to be associated with tumor progression, immune evasion, and immunotherapist resistance (17–19). Interestingly, TLR4 signaling regulates Wnt5a expression in myeloid cells and has also been associated with tumor progression in a variety of cancer types (20, 21).

Reports of tumor-intrinsic signaling pathways induced by programmed death ligand 1 (PD-L1) have emerged, linking PD-L1 to the promotion of epithelial-to-mesenchymal transition (EMT), stimulation of the mTOR/AKT antiapoptotic pathway, as well as inhibition of IFN-dependent apoptosis (22–24). Whereas each of these pathways may be protumorigenic, there are no known associations between PD-L1 and the induction of adaptive resistance to anti–PD-1 Ab immunotherapy via the stimulation of tumor-intrinsic signaling pathways. Many groups have described the role of NOD-, LRR-, and pyrin domain–containing protein 3 (NLRP3) as a sensor for pathogen-derived danger signals by antigen-presenting cells in the innate immune system, however, relatively little is known about the contribution of NLRP3 to tumorigenesis, and its role in modulating tumor responses to immunotherapy has not been explored (25).

Here, we describe a pathway that mechanistically links the upregulation of PD-L1 with the promotion of PMN-MDSC recruitment to the tumor bed in response to anti–PD-1 blockade and demonstrate that the inhibition of this process substantially enhances responses to checkpoint inhibitor immunotherapy (Figure 1A). We provide further evidence to support the existence of this pathway in patients with cancer.

Results

Anti–PD-1 Ab immunotherapy induces the recruitment of PMN-MDSCs. We have found that the autochthonous BRAFV600E PTEN–/– melanoma model exhibits a transient response to anti–PD-1 Ab immunotherapy followed by eventual escape and progression. We harvested these melanoma tissues following anti–PD-1 Ab escape as well as after IgG isotype control Ab therapy and performed differential whole transcriptomic sequencing analysis. This study revealed the upregulation of 51 genes in anti–PD-1 Ab–treated tumor tissues using a fold-change cutoff of 2.0 (P < 0.05). Of these genes, two CXCR2 ligands, Cxcl5 (3.75-fold, P = 8.88 × 10⁻⁴) and Cxcl3 (3.49-fold, P = 0.0002), were found in the top 7 upregulated genes, whereas Cxcl2 was also noted to be upregulated by 3.63-fold (P = 0.146). These gene expression changes occurred concurrently with enhanced expression of the proinflammatory proteins S100a8 (2.27-fold, P = 1.61 × 10⁻⁶) and S100a9 (2.27-fold, P = 3.37 × 10⁻⁶) as well as Arg1 (1.45-fold, P = 1.95 × 10⁻⁴) (Figure 1B). We repeated the above experiment using a serial tissue biopsy approach coupled with quantitative real-time PCR (qRT-PCR) gene expression analysis, which confirmed a time-dependent increase in the expression of Cxcl2, Cxcl5, Cxcr2, Ly6g and the myeloid marker S100a9 during the course of anti–PD-1 Ab therapy relative to those tumors treated with an IgG isotype Ab (Figure 1C and Supplemental Figure 1A; supplemental material available online with this article; https://doi.org/10.1172/JCI133055DS1).

Together, these data suggest that immunosuppressive PMN-MDSC recruitment may correlate with suppression of cytolytic T cell activity along with anti–PD-1 Ab escape (Supplemental Figure 1A). To investigate this hypothesis, we evaluated resected melanoma tissue based on Gr-1 IHC as well as multiparameter flow cytometry, both of which confirmed a significant increase in infiltrating Gr-1⁺ and CD45⁺CD11b⁺Ly6G⁻Ly6C⁺F4/80⁻ cell populations (PMN-MDSCs), respectively, with progression through anti–PD-1 Ab therapy (Figure 1, D and E). These findings were recapitulated in the Lewis lung carcinoma (LLC) lung cancer model, an orthotopic p53 Kras pancreatic cancer model, as well as in a humanized autologous patient-derived xenograft model of renal cell carcinoma (Supplemental Figure 1B). However, we did not observe any evidence of this effect following anti–CTLA-4–Ab therapy (Supplemental Figure 1C). qRT-PCR analysis of FACS-sorted PMN-MDSCs from anti–PD-1 Ab–treated BRAFV600E PTEN–/– melanoma tissue confirmed that these cells expressed high levels of Cxcr2, Tnfa, S100a8, and S100a9 (Supplemental Figure 1D). Although we observed an increase in the expression of several CXCR2-dependent ligands following escape from anti–PD-1 Ab therapy, CD8⁺ T cell ablation studies demonstrated the CXCL5 chemokine to be particularly responsive to the induction of CD8⁺ T cell activation (Figure 1F). In addition, CXCL5 has previously been implicated in melanoma pathogenesis (26). Thus, we genetically silenced CXCL5 expression in a BRAFV600E PTEN–/– melanoma cell line, which effectively eliminated PMN-MDSC recruitment, enhanced tumor CD8⁺ T cell infiltration, and significantly increased the sensitivity of BRAFV600E PTEN–/– melanomas to anti–PD-1 Ab immunotherapy (Figure 1G and Supplemental Figure 2). Further in vivo tumor studies using a pharmacological CXCR2 inhibitor (AZD5069) also significantly suppressed PMN-MDSC recruitment in response to anti–PD-1 Ab therapy, enhanced CD8⁺ T cell tumor infiltration, and suppressed tumor progression in the autochthonous BRAFV600E PTEN–/– melanoma model (Figure 1H).

Notably, we found the impact of AZD5069 to be more significant at later time points correlating with the period of PMN-MDSC influx into the tumor (Supplemental Figure 2D). Together, these data indicate that tumors exhibit an increase in CXCR2 ligand–mediated PMN-MDSC recruitment to the tumor bed during their progression through anti–PD-1 Ab immunotherapy.

Wnt5a promotes CXCR2 ligand expression in response to anti–PD-1 immunotherapy. The differential whole transcriptomic analysis of the autochthonous BRAFV600E PTEN–/– melanoma model subjected to anti–PD-1 Ab versus IgG isotype control Ab therapy demonstrated several genetic changes suggestive of enhanced Wnt ligand signaling during anti–PD-1 Ab escape (Supplemental Figure 3A). Additional analysis of transcriptomic data for patients with metastatic melanoma in the The Cancer Genome Atlas–SKCM (TCGA-SKCM) database also revealed a statistical-
Figure 1. PMN-MDSC accumulation contributes to tumor progression following anti–PD-1 Ab immunotherapy. (A) Schematic overview of the adaptive resistance pathway. (B) RNA-Seq differential gene expression analysis of tumor tissues following treatment of the autochthonous BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma model with anti–PD-1 Ab therapy versus IgG isotype control (Ctrl) (n = 3). (C) qRT-PCR analysis of target genes of interest in serial tumor fine-needle aspiration (FNA) biopsy specimens harvested from the transgenic BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma model treated with anti–PD-1 Ab versus IgG isotype control (n = 5). (D) Gr-1 immunohistochemical analysis of transgenic BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma tissues following treatment with anti–PD-1 Ab versus IgG isotype control. Original magnification, ×40. Gr-1 staining is shown in red. Images are representative of 3 tumors per group. (E) PMN-MDSC flow cytometric analysis of transgenic BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma tissues following treatment with anti–PD-1 Ab versus IgG isotype control. PMN-MDSCs were defined as live+CD45+CD11b+Ly6G+Ly6C<sup>int</sup>F4/80<sup>−</sup> cells. Shown are a representative flow dot plot and quantification graph of PMN-MDSC flow cytometric data (n = 5). (F) qRT-PCR analysis of CXCR2 ligands in BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma tissues treated with anti–PD-1 Ab following CD8<sup>+</sup> T cell ablation in vivo (n = 3). (G) In vivo tumor study of BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma genetically silenced for CXCL5. Quantitation of tumor-infiltrating PMN-MDSCs by flow cytometry is shown along with an in vivo tumor growth curve of CXCL5-silenced BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma versus BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> NTC melanoma control tumors treated with anti–PD-1 Ab. Data were normalized to tumors treated with IgG isotype control (n = 5). (H) Combination treatment with anti–PD-1 Ab and CXCR2 inhibitor (CXCR2i) in an in vivo BRAF<sup>V600E</sup> PTEN<sup>−/−</sup> melanoma study (n = 5). Graphs show flow cytometric analysis of tumor-infiltrating PMN-MDSCs and live CD45<sup>+</sup>CD3<sup>+</sup>CD8<sup>+</sup> T cells. *P < 0.05, **P < 0.005, and ***P < 0.0005, by Student’s t test with Holm-Sidak post hoc correction for multiple comparisons (B, C, and F). Student’s t test (E and G), or 1-way ANOVA with Sidak’s post hoc multiple comparisons test (H). See also Supplemental Figures 1, 2, and 5C.
ly significant association between WNT5A and CXCL2, CXCL5, and CXCR2 gene expression (Figure 2A). Previous studies have shown that noncanonical Wnt ligands activate Yes-associated protein–dependent (YAP-dependent) signaling pathways, whereas YAP signaling has also been implicated in the migration of PMN-MDSCs into tumor tissues (27, 28). Consistent with these data, we performed whole-tissue Western blot analysis and found that resected melanoma tissues derived from the autochthonous BRAFV600E PTEN–/– model had enhanced Wnt5a expression, YAP stabilization, and increased CXCL5 expression in response to anti–PD-1 Ab therapy (Figure 2B). This enhanced level of CXCL5 expression by the tumor was also reflected by increased circulating plasma CXCL5 levels as determined by ELISA (Figure 2C).

We performed further in vitro studies using qRT-PCR, which confirmed that recombinant Wnt5a (rWnt5a) induced Cxcl2, Cxcl5, and Cxcl1 gene expression in the BRAFV600E PTEN–/– melanoma cell line (Figure 2D). Given these findings, we hypothesized that upregulation of Wnt5a results in enhanced CXCR2-dependent chemokine expression by triggering the YAP signaling pathway. Further experiments using the BRAFV600E PTEN–/– melanoma cell line indeed showed that rWnt5a induced YAP stabilization, while also stimulating CXCL5 expression in a YAP-dependent manner (Figure 2E). To confirm the role of Wnt5a in the upregulation of CXCL5 in the BRAFV600E PTEN–/– melanoma cell line, qRT-PCR further revealed diminished CXCL5 expression in a Wnt5a-knockdown (Wnt5aKD) BRAFV600E PTEN–/– melanoma cell line (BRAFV600E PTEN–/– Wnt5aKD), an effect that could be rescued with the addition of rWnt5a (Figure 2F and Supplemental Figure 3B). Additional studies using flow cytometry and IHC showed that BRAFV600E PTEN–/– Wnt5aKD tumors had reduced CXCL5 expression and an associated decrease in intratumoral PMN-MDSCs, respectively (Figure 2, G and H). On the basis of these data, we hypothesized that the previously observed recruitment of PMN-MDSCs to the tumor bed in response to anti–PD-1 Ab therapy would be eliminated in tumors silenced for Wnt5a expression. Indeed, PMN-MDSC recruitment to BRAFV600E PTEN–/– Wnt5aKD tumors was significantly diminished relative to control BRAFV600E PTEN–/– tumors in response to anti–PD-1 Ab therapy (Figure 2I). Consistent with an important role for PMN-MDSCs in driving immunotherapy resistance, we also found BRAFV600E PTEN–/– Wnt5aKD tumors to be associated with increased CD8+ T cell infiltration and to respond more favorably to anti–PD-1 Ab therapy relative to control BRAFV600E PTEN–/– tumors (Figure 2I and Supplemental Figure 3C). Altogether, these findings support a role for tumor-derived Wnt5a as an important mediator of CXCL5-dependent PMN-MDSC recruitment to the tumor bed in response to anti–PD-1 Ab checkpoint inhibitor immunotherapy.

An autocrine HSP70/TLR4 signaling pathway stimulates tumor Wnt5a release in response to anti–PD-1 immunotherapy. Given our previous data, we then investigated the underlying mechanism for Wnt5a upregulation in response to anti–PD-1 Ab therapy in the BRAFV600E PTEN–/– melanoma model. Prior studies have shown that TLR signaling modulates Wnt5a expression in macrophages (20). Heat shock proteins (HSPs) are known to bind and induce the activation of TLR signaling pathways (29). A review of the previous whole transcriptomic data analysis performed in the autochthonous BRAFV600E PTEN–/– melanoma model showed that anti–PD-1 Ab therapy results in increased expression of several genes associated with cellular stress, including a subset of HSPs (Figure 3A) (30). To investigate this further, we analyzed the secretome of resected BRAFV600E PTEN–/– melanoma tissues following escape from anti–PD-1 Ab immunotherapy, using liquid chromatography-tandem mass spectrometry (LC-MS/MS) and the stable isotope labeling with amino acids in cell culture (SILAC) technique coupled with azidohomoalanine (AHA) labeling (31). This work showed further evidence of increased release of HSPs, including HSP70, in those tumors that had escaped anti–PD-1 Ab immunotherapy relative to IgG isotype Ab control-treated tumors (Figure 3B). Consistent with these data, we also found that melanoma-bearing mice undergoing anti–PD-1 Ab treatment had increased circulating plasma HSP70 levels relative to levels in mice treated with an IgG isotype control Ab (Figure 3C). A qRT-PCR–based screen identified elevated levels of Tlr2 and Tlr4 expression by BRAFV600E PTEN–/– melanoma cells relative to other TLRs, and an analysis of TCGA database also revealed a compelling relationship between Wnt5a and TLR2 and TLR4 expression in human melanoma (Figure 3D and Supplemental Figure 4A). Consistent with this, we found that HSP70 stimulation of the BRAFV600E PTEN–/– melanoma cell line induced upregulation of Wnt5a expression in a dose-dependent manner, whereas pharmacologic inhibition of HSP70 suppressed autocrine stimulation of Wnt5a expression (Figure 3, E and F). Subsequent pharmacologic inhibitor and genetic silencing studies using a shRNA-expressing lentiviral vector revealed that HSP70 stimulation of melanoma Wnt5a expression was TLR4 dependent (Figure 3G and Supplemental Figure 4, B and C). Interestingly, these BRAFV600E PTEN–/– melanoma cells genetically silenced for Tlr4 did not generate tumors in vivo following their implantation. Even with modest TLR4 silencing using siRNA oligonucleotides, these melanomas exhibited diminished tumor growth, reduced Wnt5a and CXCL5 expression based on whole-tissue Western blot analysis, and a lower level of tumor-infiltrating PMN-MDSCs along with enhanced numbers of CD8+ T cells compared with control BRAFV600E PTEN–/– melanomas (Figure 3, H–J, and Supplemental Figure 4, D and E). To verify that HSP70 induction of the Wnt5a/CXCL5 signaling axis is not a specific phenomenon related to melanoma, we also repeated these experiments in a murine lung epithelial cell line with similar results (Supplemental Figure 4F). In summary, these data suggest that tumor HSP70 release in response to anti–PD-1 Ab treatment induces Wnt5a-mediated upregulation of CXCR2-dependent chemokine expression in tumor tissues.

CD8+ T cells drive the HSP70/TLR4/Wnt5a/CXCL5 signaling axis in tumors. Since our data indicated that PMN-MDSC recruitment was induced by anti–PD-1 Ab therapy, we hypothesized that CD8+ T cells play an important role in triggering the HSP70/TLR4/Wnt5a/CXCL5 signaling cascade. We therefore co cultured increasing numbers of OT-1 K b-SIINFEKL–specific CD8+ T cells with a BRAFV600E PTEN–/– melanoma cell line engineered to express the OVA xenotoxin (BRAFV600E OVA) and measured the soluble production of HSP70 (Supplemental Figure 5A). This approach showed a direct correlation between antigen-specific CD8+ T cells, tumor HSP70 secretion, and the induction of Wnt5a expression in vitro (Figure 4A). Further flow cytometric analysis of resected BRAFV600E PTEN–/– melanoma tissues also revealed...
anoma. Although dacarbazine was capable of inducing BRAF V600E simply to tumor cell death, we inquired whether cytotoxic chemotherapy involves tumor-dependent secretion of HSP70.

Prior studies have implicated ATP as a stimulator of HSP70 release by tumors could be interpreted to be due to the apoptosis-associated speck-like protein containing a caspase recruitment domain (ASC) adaptor protein, while also promoting ASC polymerization, both of which were necessary to generate the inflammasome macro- molecular complex (Figure 5, B and C). We then verified that PD-1 blockade promotes CD8+ T cell-mediated HSP70 release and the observed stimulation of PMN-MDSC recruitment.

We then incubated BRAFV600E PTEN+/- melanoma cells indeed induced activation of the NLRP3 inflammasome, concurrent release of HSP70, and upregulation of Wnt5a (Figure 5A). This effect was also observed in the LLC cell line, indicating that this phenomenon is not restricted to the BRAF V600E PTEN–/– melanoma model (Supplemental Figure 6A). To further confirm the sequence of this signaling pathway, we genetically silenced HSP70 using a CRISPR/Cas9 approach in the BRAFV600E PTEN+/- melanoma cell line and stimulated the upstream NLRP3 inflammasome in these BRAFV600E PTEN+/-:HSP70−/- cells along with their nontarget control (NTC) cell line. These experiments showed that HSP70 ablation eliminated the ability of the NLRP3 inflammasome to stimulate the upregulation of Wnt5a in both an autocrine and paracrine manner (Supplemental Figure 6B). Further experiments demonstrated that tumor cell PD-L1 cross-linking induced NLRP3 binding to the apoptosis-associated speck-like protein containing a caspase recruitment domain (ASC) adaptor protein, while also promoting ASC polymerization, both of which were necessary to generate the inflammasome macromolecular complex (Figure 5, B and C). We then verified that PD-1 blockade promotes CD8+ T cell induction of NLRP3 activation and tumor HSP70 release in an IFN-γ-dependent manner in further OT-1 CD8+ T cell:BRAFV600E OVA melanoma coculture experiments (Figure 5D). Notably, this induction of NLRP3 activation by CD8+ T cells was found to be antigen specific, as CD8+ T cells that recognize an irrelevant control peptide do not induce caspase-1 activation (Supplemental Figure 6C). Furthermore, this phenomenon required T cell–tumor cell contact or close proximity, as Transwell assays failed to induce caspase-1 cleavage and HSP70 release, consistent with an important role for physical PD-1–PD-L1 interactions (Supplemental Figure 6D). Importantly, both the pharmacologic inhibition and genetic silencing of Nlrp3 effectively suppressed HSP70 release and subsequent Wnt5a upregulation in response to anti-PD-1 Ab activation of tumor antigen–specific CD8+ T cells (Figure 5, E and F). We observed a similar effect with genetic silencing of
Pdl1 in the BRAFV600E PTEN−/− melanoma cell line, which resulted in elimination of ASC polymerization, caspase-1 activation, HSP70 secretion, and Wnt5a upregulation (Figure 3, C and F, and Supplemental Figure 6E).

On the basis of these data, we examined the mechanism mediating PD-L1−dependent NLRP3 activation. dsRNA-dependent protein kinase R (PKR) is a known activator of all inflammasome proteins, including NLRP3, and has been shown to regulate cer-
Recent studies have shown that tumor-intrinsic PD-L1 signaling inhibits STAT3 activation (23). Previous work has also shown that cytosolic STAT3 inhibits PKR kinase activity and suppresses activation of the NLRP3 inflammasome (35, 36). We therefore hypothesized that tumor PD-L1 promotes PKR-NLRP3 activation by suppressing STAT3 levels. Indeed, we found that Pd1 silencing upregulated total STAT3 levels concurrently with diminished PKR activity (34). Indeed, PKR inhibition suppressed caspase-1 cleavage in the BRAF V600E PTEN−/− melanoma cell line in response to anti–PD-L1 Ab treatment (Supplemental Figure 6F). Consistent with these studies, further treatment of BRAF V600E PTEN−/− melanoma cells with anti–PD-L1 Ab and IFN-γ induced PKR-NLRP3 binding, whereas genetic silencing of Pd1 also suppressed PKR phosphorylation (Figure 5, G and H). A recent report has shown that tumor-intrinsic PD-L1 signaling inhibits STAT3 activation (23). Previous work has also shown that cytosolic STAT3 inhibits PKR kinase activity and suppresses activation of the NLRP3 inflammasome (35, 36). We therefore hypothesized that tumor PD-L1 promotes PKR-NLRP3 activation by suppressing STAT3 levels. Indeed, we found that Pd1 silencing upregulated total STAT3 levels concurrently with diminished PKR.
Genetic and pharmacologic inhibition of NLRP3 blocks PMN-MDSC recruitment and enhances the efficacy of anti–PD-1 Ab immunotherapy. Given the central role of the NLRP3 inflammasome in mediating PMN-MDSC recruitment to the tumor bed in response to anti–PD-1 Ab therapy, we hypothesized that inhibiting NLRP3 activation would promote antitumor immunity and suppress tumor progression. Using a shRNA-expressing lentiviral vector, we silenced Nlrp3 in BRAFV600E PTEN-/- melanoma cells and transplanted this cell line into syngeneic hosts (Supplemental Figure 7A). After 20 days of tumor growth, Nlrp3-silenced BRAFV600E phosphorylation (Figure 5I). Consistent with a suppressive role for STAT3 in this pathway, we found that constitutive activation of STAT3 (STAT3CA) suppressed NLRP3 activation, as indicated by the diminished caspase-1 cleavage and Wnt5a expression levels (Figure 5J). These data indicate that PD-L1 triggers PKR-dependent activation of the NLRP3 inflammasome in tumors by repressing STAT3 (Figure 5K). In summary, we have elucidated a mechanistic link between PD-L1 and the tumor-intrinsic NLRP3 inflammasome and showed that this pathway drives adaptive immune evasion by promoting the recruitment of PMN-MDSCs.
PTEN\(^{-/-}\) melanomas were associated with reduced plasma HSP70 levels, decreased levels of CXCR2 ligand expression, and diminished PMN-MDSC infiltration relative to control BRAF\(^{V600E}\) PTEN\(^{-/-}\) melanomas (Figure 6, A–C). Although Nlrp3 silencing did not influence tumor cell proliferation in vitro, it increased the levels of tumor-infiltrating CD\(^{8+}\) T cells and suppressed the growth of BRAF\(^{V600E}\) PTEN\(^{-/-}\) melanomas in vivo. (Figure 6, C and D, and Supplemental Figure 7, B and C). NLRP3-dependent regulation of the antitumor immune response was further confirmed by additional in vivo tumor experiments, in which CD\(^{8+}\) T cell ablation reversed tumor growth suppression in Nlrp3-silenced BRAF\(^{V600E}\) PTEN\(^{-/-}\) melanomas (Supplemental Figure 7D).

We performed additional studies to determine whether systemic pharmacological inhibition of NLRP3 could also suppress tumor growth and augment anti–PD-1 Ab immunotherapy in the BRAF\(^{V600E}\) PTEN\(^{-/-}\) melanoma model. Using the NLRP3 inhibitor MCC950, we also found that systemic NLRP3 inhibition diminished PMN-MDSC recruitment in response to anti–PD-1 Ab therapy, enhanced levels of tumor-infiltrating CD\(^{8+}\) T cells, and suppressed tumor progression in vivo beyond what was observed with anti–PD-1 Ab monotherapy (Figure 6, E and F) (37). Whole-tissue Western blot analysis, plasma ELISAs, and tumor qRT-PCR studies further showed that these effects correlated with suppressed caspase-1 cleavage, Wnt5a expression, Cxcl5 levels, and HSP70 release and enhanced expression of the cytolytic T cell marker Gzmb (Figure 6, G and H, and Supplemental Figure 7E). Notably, neither pharmacologic inhibition of NLRP3 nor genetic silencing of Nlrp3 had any impact on tumor cell proliferation in vitro (Supplemental Figure 7C). Altogether, these data are consistent with our previous studies supporting the critical role of the NLRP3 inflammasome in driving PMN-MDSC recruitment as an adaptive response to CD\(^{8+}\) T cell activation and suggest that NLRP3 is a viable pharmacologic target for enhancing the efficacy of anti–PD-1 Ab therapy.

**PMN-MDSC recruitment as a mechanism of adaptive resistance to anti–PD-1 Ab therapy in human melanoma.** In order to determine whether PD-L1 can trigger NLRP3 activation and HSP70 release in human melanoma, we performed in vitro experiments using the WM266 human melanoma cell line. Similar to our previous observations, tumor PD-L1 cross-linking following IFN-\(\gamma\) stimulation induced caspase-1 cleavage and HSP70 release (Figure 7A). Further studies using the WM266 human melanoma cell line also showed that HSP70 induced Wnt5a upregulation in a TLR4-dependent manner and that pharmacologic NLRP3 inhibition suppressed ATP-mediated HSP70 release (Figure 7, B and C). These data were consistent with a significant correlation between expression of the myeloid markers ITGAM and CD33 as well as NLRP3 and the cytolytic T cell markers CD8A, GZMB, and PRF1 in human metastatic melanoma specimens, based on RNA expression data in TCGA-SKCM database (Figure 7D). These data are consistent with our previous observations in the autothorhous murine melanoma model and suggest that CD8\(^{+}\) T cell activation results in tumor release of HSP70, Wnt5a upregulation, and recruitment of infiltrating myeloid cells (Figure 1A). To further study this mechanism, we harvested human melanoma tissue specimens at baseline and during disease progression following nivolumab anti–PD-1 Ab immunotherapy and performed RNA-Seq differential whole transcriptomic sequencing analysis. Consistent with our preclinical studies, these studies revealed elevated expression of several myeloid markers including CXCL1, CD33, ITGAM, CXCR2, S100A8, and S100A9 following disease progression through checkpoint inhibitor immunotherapy (Figure 7E).

Our previous work showed that tumors release HSP70 in response to CD\(^{8+}\) T cell responses and that this increase in HSP70 levels can be measured in the plasma of mice undergoing anti–PD-1 Ab immunotherapy (Figure 3C and Supplemental Figure 7E). On the basis of these data, we conducted a plasma-based ELISA to quantify HSP70 levels at baseline and at week 12 of anti–PD-1 Ab immunotherapy in patients with advanced melanoma undergoing anti–PD-1 Ab immunotherapy. This study revealed that HSP70 levels increased in patients who progressed on anti–PD-1 Ab therapy, but these changes were seldom observed in responders (Figure 7F). Indeed, mean changes in plasma HSP70 levels with anti–PD-1 Ab therapy were significantly greater in nonresponding melanoma patients relative to responders (Figure 7G). This relationship was also observed after normalizing quantitative HSP70 levels to tumor burden based on CT imaging, indicating that this finding was not strictly due to disease progression. These observations suggest that the process leading to HSP70 release correlates with resistance to checkpoint inhibitor therapy, providing further support for the key role of the NLRP3 inflammasome in the evolution of adaptive resistance to anti–PD-1 Ab immunotherapy.

**Discussion**

Using several preclinical models in addition to clinical specimens, we have characterized a PD-L1-dependent, tumor-intrinsic signaling pathway that directly links CD\(^{8+}\) T cell activity with the recruitment of PMN-MDSCs to the tumor bed in response to anti–PD-1 Ab immunotherapy. We propose that this signaling cascade constitutes an adaptive resistance pathway that, when blocked, can enhance the efficacy of anti–PD-1 Ab checkpoint inhibitor immunotherapy. After recognizing a consistent increase in PMN-MDSCs in tumor tissues following anti–PD-1 Ab escape in several tumor models, we traced the underlying mechanism of this phenomenon to a process that involves PD-L1-dependent activation of the NLRP3 inflammasome in tumor tissues. Together, these data highlight several potential pharmacologic targets that may be capable of enhancing immunotherapy efficacy, as well as promising candidate biomarkers that may contribute to improved patient selection and management of patients with cancer undergoing immunotherapy.

Prior studies demonstrating that noncanonical Wnt ligands can induce the activation of YAP-dependent signaling pathways, coupled with data showing that YAP signaling can regulate the expression of several CXCR2-dependent chemokines, prompted us to explore a role for Wnt5a in mediating the observed influx of PMN-MDSCs in response to checkpoint inhibitor therapy (27, 28). These studies demonstrated that tumor Wnt5a expression was induced in response to anti–PD-1 Ab therapy and that the genetic silencing of tumor Wnt5a expression eliminated adaptive recruitment of PMN-MDSCs in response to checkpoint inhibitor immunotherapy. A recent RNA-Seq-based study found Wnt5a to be significantly upregulated in PD–1–refractory melanoma tissues, whereas other studies identified Wnt5a as a marker of dedifferentiation, disease aggressiveness, and therapeutic resistance (17,
The release of HSP70 was further confirmed by Western blot analysis and ELISA in response to cytolytic CD8+ T cell activity in vitro and in vivo, respectively. This finding was of interest since previous studies have demonstrated that HSP70 can promote cancer progression and that TLRs both mediate HSP70 signaling and have been implicated in the regulation of Wnt5a expression in macrophages (20, 29, 41, 42). We subsequently demonstrated that HSP70 is capable of stimulating Wnt5a expression in various cell lines and that genetic silencing and pharmacologic inhibition of tumor TLR4 blocked tumor Wnt5a and CXCL5 expression, while also inhibiting PMN-MDSC recruitment to developing tumors. Notably, the release of HSP70 was not found to be due simply to a cell death–dependent mechanism, as dacarbazine chemotherapy readily induced tumor apoptosis in the BRAFV600E melanoma model but did not induce significant levels of HSP70 release. Although HSP70 has been identified within tumor-derived exosomes, prior studies have also suggested that soluble HSP70 may be released...
derived IL-1β does not contribute to MDSC recruitment in response to checkpoint inhibitor immunotherapy (Supplemental Figure 7, F–H) (45). This finding is also consistent with additional studies demonstrating that genetic knockout of HSP70 eliminated stimulation of Wnt5a in response to NLRP3 activation (Supplementary Figure 6B). Whether NLRP3-dependent IL-18 secretion contributes to the overall mechanism by promoting IFN-γ expression is unclear and is currently being explored.

Using in vitro coculture assays and in vivo ablation experiments, these studies identified CD8+ T cell activity as an important driver for this tumor-intrinsic signaling pathway. This finding further prompted experiments which showed that tumor-derived IL-1β does not contribute to MDSC recruitment in response to checkpoint inhibitor immunotherapy (Supplemental Figure 7, F–H) (45). This finding is also consistent with additional studies demonstrating that genetic knockout of HSP70 eliminated stimulation of Wnt5a in response to NLRP3 activation (Supplementary Figure 6B). Whether NLRP3-dependent IL-18 secretion contributes to the overall mechanism by promoting IFN-γ expression is unclear and is currently being explored.
IFN-γ stimulation also serves to facilitate NLRP3 priming by an alternative mechanism in tumor cells is currently being investigated. Interestingly, HSP70/TLR4 signaling, as described above, may also provide a positive feed-forward priming pathway capable of perpetuating NLRP3 activation in tumors (46). These studies reveal that NLRP3 inhibition phenocopied downstream TLR4 and CXCR2 inhibition, suppressing the recruitment of PMN-MDSCs as an adaptive resistance mechanism initiated by local CD8+ T cell activity. This finding is in line with a previous study showing that NLRP3 can mitigate against DC vaccine therapies by promoting the migration of MDSCs into tumors (47).

Given the role of PD-L1 in the induction of this pathway as well as reports describing downstream signaling effects of PD-L1, we also conducted studies to better understand the underlying mechanism of NLRP3 activation in tumor cells (48). The previously described role of PKR in the regulation of inflammasome activation and its modulation by STAT3 led to a series of experiments culminating in our finding that PD-L1 induced PKR-mediated activation and its modulation by STAT3 led to a series of experiments, suggesting that the PD-L1/NLRP3 signaling axis may play a role in several inflammatory and autoimmune conditions, thus reducing the risk of systemic toxicity such as neutropenia. NLRP3 activation is inexorably linked to tumor PD-L1 and drives the recruitment of PMN-MDSCs to the tumor bed in response to anti-PD-1 checkpoint inhibitor therapy. This process extinguishes local cytotoxic antitumor T cell activity and serves as a rheostat for modulating effector T cell responses, thus making this signaling axis a promising target for immunotherapeutic intervention.

Methods

Clinical samples. All plasma samples were collected from 17 patients with advanced melanoma who were undergoing anti-PD-1 Ab immunotherapy at week 0 and week 12 on an ongoing tissue acquisition protocol investigating checkpoint inhibitor resistance at Duke Cancer Institute (NCT02694965). Three paired tumor specimens obtained from the patients at week 0 and at the time of disease progression while they were undergoing anti-PD-1 Ab immunotherapy were collected at Vanderbilt University Medical Center (institutional protocol no. 100178). Treatment responses were evaluated on the basis of RECIST (Response Evaluation Criteria in Solid Tumors, version 1.1).

In vivo animal studies. C57BL/6j (C57, H-2b) (stock no. 000664), B6.CgBRAFV600E PTEN+/−;Tg(129S7-β-Acte-deg)1Lav (Tyr-Cre/ERT2) B6; Bosj (BRAFV600E PTEN+/−, H-2b) (stock no. 012328), and C57Bl/6 Tg(Tacr1Tcrb)1100Mjb/J (OT-1, H-2b) (stock no. 003831) mice were obtained from The Jackson Laboratory. All experimental groups included randomly chosen 6- to 8-week-old littermate mice of both sexes and of the same strain.

Cell lines and culture conditions. BRAFV600E PTEN+/−: (male, BP6d) (40), BRAFV600E PTEN+/−; Wnt5aex (40), BRAFV600E PTEN+/−; CXCL5ex, BRAFV600E PTEN+/−; PDL1ex, BraFV600E PTEN+/−; NLRP3ex, and BRAFV600E PTEN+/−; NTC (40) cell lines were generated using shRNA-expressing lentiviral vectors and cultured as previously described (40). The shRNA-expressing lentiviral vectors were as follows: shNLRP3 (MilliporeSigma, SHCLN-NM_145827), shPD-L1 (MilliporeSigma, SHCLN-NM_021893), shWnt5a (MilliporeSigma, SHCLN-NM_009524), shTLR4 (MilliporeSigma, SHCLN-NM_025817), and pLKO.1-puro empty vector control (NTC) (MilliporeSigma, SHC001). The pEFS.TAT.CUb.GFP lentiviral expression plasmid (a gift from Kris Wood, Duke University) was used with the pMD2.G envelope vector and the psPAX2 packaging vector to produce lentiviral particles for generation of the BRAFV600E PTEN+/−; STAT3ex stable cell line. Stable cell lines were selected by puromycin resistance (MilliporeSigma, P8835). The OVA-expressing BRAFV600E PTEN+/− cell line was generated by transfecting the parental cell line with the pcI-neo-COVA plasmid and selecting with 3 mg/mL G418. The murine LLC cell line was from the American Type Culture Collection (ATCC) (T1704526). All cell lines were tested by the Duke University Cell Culture Facility shared services to ensure they were Mycoplasma free. All BRAFV600E PTEN+/− cell lines and the LLC cell line were maintained at 37°C in DMEM (In-vitrogen, Thermo Fisher Scientific) with 2 mM L-glutamine, supplemented with 10% FBS and 100 U/mL penicillin. Depending on the experiment, cells were treated with Wnt5a (100-200 ng/mL, R&D Systems, Bio-Techne, 645-90-01), IFN-γ (100 ng/mL, BioAbChem, 42-IFNg), anti-PD-L1 Ab (1-2 μg/mL), HSP70 (1-10 μM, Enzo, ADI-ESP-302-D), HSP70 inhibitor (Thermo Fisher Scientific, VER155008), CLI-095 TLR4 inhibitor (3-10 μM, Invivogen, tlr-cl95), TLR2-IN-C99 TLR2 inhibitor (1-10 μM, Glixix, GLXC-06203), MBL TLR4 agonist (10 μM, Enzo, ALX-581-205-C100), LPS (10 ng, MilliporeSigma, L4391-1MG), recombinant IL-1β (100-200 ng, BioLegend,
Alkylation of methylglyoxal (MGO) with N-acetyl-L-cysteine (NAC) was performed by incubating isolated splenocytes from OT-1–transgenic mice. Tumor growth was monitored by caliper measurement every 2-3 days from 3 days after s.c. injection into the base of the tail of syngeneic C57BL/6 mice. Tumor growth was monitored by caliper measurement at the Duke Cell Culture Facility in hollow fiber cartridges; 10 million cells were dispensed daily for the first 3 days and then every 7 days thereafter by treatment with RBC lysis buffer (MilliporeSigma). The hybridoma clone 53-6.7 was expanded at the Duke Cell Culture Facility in hollow fiber cartridges; 10 million cells were dispensed daily for the first 3 days and then every 7 days thereafter by treatment with RBC lysis buffer (MilliporeSigma).

**In vivo CD8 depletion.** The hybridoma clone 53-6.7 was expanded at the Duke Cell Culture Facility in hollow fiber cartridges; 10 million cells were dispensed daily for the first 3 days and then every 7 days thereafter by treatment with RBC lysis buffer (MilliporeSigma). The hybridoma clone 53-6.7 was expanded at the Duke Cell Culture Facility in hollow fiber cartridges; 10 million cells were dispensed daily for the first 3 days and then every 7 days thereafter by treatment with RBC lysis buffer (MilliporeSigma). The hybridoma clone 53-6.7 was expanded at the Duke Cell Culture Facility in hollow fiber cartridges; 10 million cells were dispensed daily for the first 3 days and then every 7 days thereafter by treatment with RBC lysis buffer (MilliporeSigma).
RNA-Seq assays. RNA-Seq on tumor tissue derived from the BRAF
V600E PTEN−/−transgenic murine model was performed by the Duke Sequencing and Genomic Technologies Shared Resource and the results previously published (30). A complementary DNA library was prepared via oligo-dT–directed reverse transcription (Ambion, Thermo Fisher Scientific) and subjected to deep sequencing on an Illumina HiSeq 4000 (50-bp single-read sequencing; Anti–PD-1 Resistance Study RNA-Seq, accession no. SAMN09878780). These data were processed by the Duke Center for Genomic and Computational Biology with the Trim Galore tool kit, which uses Cutadapt to trim low-quality bases and Illumina sequencing adapters from the 3′ end of the reads. Only reads that were 20 nt or longer after trimming were kept for further analysis. Reads were mapped to the GRCh38 reference genome, and transcriptome reads were processed by the STAR RNA-Seq alignment tool (https://code.google.com/archive/p/rna-star/). Reads were kept for subsequent analysis if they mapped to a single genomic location. Gene counts were compiled using the HTSeq tool (https://pypi.org/project/HTSeq/). Only genes that had at least 10 reads in any given library were used in subsequent analyses. Normalization and differential expression were carried out using the DESeq2 Bioconductor package with the R statistical programming environment (https://bioconductor.org/packages/packages/release/bioc/html/DESeq.html). The FDR was calculated to control for multiple hypotheses testing. Gene set enrichment analysis (GSEA) was performed to identify differentially regulated pathways and Gene Ontology (GO) terms for each of the comparisons performed. Human melanoma tissues obtained from Vanderbilt University were also subjected to RNA-Seq analysis, and these data were previously published and deposited at https://prod.tbi.lab.org/balko_lab/LAG3_JCI_Insight (53).

ELISA. Levels of CXCL5 and HSP70 (R&D Systems, DY663-2) in mouse plasma were evaluated using an ELISA kit according to the manufacturer’s instructions (R&D Systems). IL-1β (BioLegend, 432601) levels in cell lysate, tumor lysate, and supernatant were measured using the BioLegend ELISA kit according to the manufacturer’s instructions.

Human plasma ELISA. Human plasma HSP70 concentrations were measured using the human DuoSet Assay (R&D Systems, catalog DY1663) according to the manufacturer’s protocol. Human melanoma plasma samples were obtained from the Duke Cancer Institute.

Secretome assays. Single-cell suspensions were prepared by enzymatic and mechanical digestion. Cells (2 × 10^4) were plated in 2 mL 1% dialyzed FBS containing light or heavy amino acids without l-methionine in 6-well plates and then incubated in CO_2 for 30 minutes. l-Methionine or AHA, an azide-bearing analog of methionine, was added to the plates and incubated in 5% CO_2 at 37°C overnight. Culture supernatants were collected for a secretome assay. Cell supernatants were enriched for AHA-labeled proteins by incubating with dibenzocyclooctyne (DBCO) aqarose overnight. Resins were washed, followed by reduction and alkylation of cysteine (Cys) residues, and peptides were recovered after using validated primers and SsoAdvanced Universal Probes Supermix (Bio-Rad, 1725271) or SsoAdvanced Universal Probes Supermix (Bio-Rad, 1725281). All data were normalized to Actb expression, and relative gene expression was quantitated using the 2ΔΔCt method.

RNA isolation and qRT-PCR analysis. Total RNA was isolated using the RNeasy Plus Mini Kit (QIAGEN, 74134). RNA (1000 ng) was used for cDNA synthesis (iScript Reverse Transcription Supermix, Bio-Rad, 1708841). qRT-PCR was performed using an ABI7500 Real-Time PCR system (Life Technologies, Thermo Fisher Scientific). The primers used are listed in Supplemental Table 1. Data analysis was performed using PrimePCR Analysis Software (Bio-Rad). Conventional qRT-PCR was performed using validated primers and SsoAdvanced Universal SYBR Green
overnight digestion with trypsin. Samples were analyzed by quantitative 1-dimensional LC-MS/MS. Using Proteome Discoverer 2.3, the data were searched against the SwissPro Mouse database with semitrypsin specificity, fixed modification on Cys, and variable modifications on Met (oxidation), Gln/Asn (deamidation), Pro (hydroxylation), and Arg/Lys (15N-13C).

TCGA data analysis. TCGA skin cancer melanoma (TCGA-SKCM) annotated RNA expression files were extracted from the GDC portal (https://portal.gdc.cancer.gov/) for 376 cases of metastatic melanoma. Data preprocessing was performed using HTSeq counts from TCGA, and raw counts were normalized using the relative log expression method implanted in R and its extension package DESeq2. Coexpression of genes of interest were tested using the χ² statistic of sample quantile–based contingency (SQUAC) table, and scatter plots were generated using normalized counts and Bonferroni’s corrections on the group P values to account for multiple testing.

Statistics. GraphPad Prism 8 for Windows (GraphPad Software) was used for all statistical analyses. An unpaired, 2-tailed Student’s t test was used to compare mean differences between the control and treatment groups. Univariate 1-way ANOVA followed by Sidak’s post hoc multiple comparisons test was performed to analyze data containing 3 or more groups. Data correlation analyses were conducted using either Kendall Tau or Spearman calculations. A P value of less than 0.05 was considered significant. All quantitative data are presented as the mean ± SEM.

Study approval. Mouse tumor experiments were performed according to a protocol approved by the IACUC of Duke University Medical Center. All patients provided written informed consent under approval from the IRBs of Duke University (NCT02694965) and Vanderbilt University Medical Center (protocol 100178). Human melanoma tissues were obtained from Vanderbilt University with IRB approval (protocol 100178). Human melanoma plasma samples were obtained from the Duke Cancer Institute with IRB approval (protocol Pro00059349, Clinicaltrials.gov: NCT02694965).

Author contributions

BT and BAH conceptualized the project, designed all experiments, and analyzed all data. KSE, M. Sturdivant, M. Starr, LPW, YK, and DH provided technical support. AKSS, JMB, and DBJ provided clinical resources for the Duke University Health Scholar Award (to BAH); the Ross Bierkan Melanoma Fund (to BAH and AKSS); a Duke University Health Scholar Award (to BAH); a Merck & Co. Pre-Clinical Award (to BAH); and an AstraZeneca Pre-Clinical Award (to BAH).

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