

Reimagining IDO Pathway Inhibition in Cancer Immunotherapy via Downstream Focus on the Tryptophan–Kynurenine–Aryl Hydrocarbon Axis



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Abstract

Significant progress has been made in cancer immunotherapy with checkpoint inhibitors targeting programmed cell death protein 1 (PD-1)–programmed death-ligand 1 signaling pathways. Tumors from patients showing sustained treatment response predominately demonstrate a T cell–inflamed tumor microenvironment prior to, or early on, treatment. Not all tumors with this phenotype respond, however, and one mediator of immunosuppression in T cell–inflamed tumors is the tryptophan–kynurenine–aryl hydrocarbon receptor (Trp–Kyn–AhR) pathway. Multiple mechanisms of immunosuppression may be mediated by this pathway including depletion of tryptophan, direct immunosuppression of Kyn, and activity of Kyn-bound AhR. Indoleamine 2,3-dioxygenase 1 (IDO1), a principle enzyme in Trp catabolism, is the target of small-molecule inhibitors in clinical development in combi-

nation with PD-1 checkpoint inhibitors. Despite promising results in early-phase clinical trials in a range of tumor types, a phase III study of the IDO1-selective inhibitor epacadostat in combination with pembrolizumab showed no difference between the epacadostat-treated group versus placebo in patients with metastatic melanoma. This has led to a diminution of interest in IDO1 inhibitors; however, other approaches to inhibit this pathway continue to be considered. Novel Trp–Kyn–AhR pathway inhibitors, such as Kyn-degrading enzymes, direct AhR antagonists, and tryptophan mimetics are advancing in early-stage or preclinical development. Despite uncertainty surrounding IDO1 inhibition, ample preclinical evidence supports continued development of Trp–Kyn–AhR pathway inhibitors to augment immune-checkpoint and other cancer therapies.

Introduction

It has long been understood that cancer cells express antigens that are recognized and prompt elimination by the immune system. Despite clinical trial evidence that cancer vaccines led to efficient antigen presentation with subsequent priming and infiltration of cytotoxic T cells into tumors, regression of tumors only occurred in a small subset of patients (1). This finding led to the prediction that important barriers downstream of initial T-cell priming must exist that limit meaningful tumor elimination (2). It is now appreciated that evasion of immune-mediated elimination occurs through multiple mechanisms, including immunoeediting, decreased antigen presentation, and importantly, local immunosuppression in the tumor microenvironment (TME; refs. 3, 4).

Tumor analysis from patients with metastatic melanoma receiving vaccine and cytokine therapies suggested a paradigm

of two broad phenotypes characterized by the presence or absence of a T cell–inflamed tumor. T cell–inflamed tumors are characterized by tumor-infiltrating lymphocytes, a type I/II IFN transcriptional profile, and high degree of expression of immunosuppressive mechanisms. In contrast, a non-T cell–inflamed tumor is observed to have a low inflammatory signature and the absence of tumor-infiltrating lymphocytes (5–7).

Immunotherapy in the treatment of solid malignancies has evolved significantly over the past decade with the emergence of mAbs against programmed cell death protein 1 (PD-1)–PD-L1 and cytotoxic T-lymphocyte associated antigen 4 (CTLA-4), delivering meaningful clinical benefit across multiple solid tumors. Patients more likely to benefit from checkpoint immunotherapy include those with tumors demonstrating a high density of somatic mutations, elevated PD-L1 expression, and/or are enriched with IFN γ transcriptional profiles (8–13). However, a subset of tumors identified as having a T cell–inflamed tumor phenotype do not respond to checkpoint immunotherapy, suggesting other immunosuppressive mechanisms contribute to limiting immune-mediated tumor regression besides the PD-1/L1 axis. Preclinical studies have identified multiple immunosuppressive mechanisms that are present in the T-cell–inflamed tumors, including, but not limited to, extrinsic inhibition by regulatory cell populations such as forkhead box P3 (FoxP3)–positive regulatory T cells (Treg) and metabolic mechanisms of immunosuppression such as the tryptophan–kynurenine–aryl hydrocarbon receptor (Trp–Kyn–AhR) pathway (14, 15).

Specific clinical focus has increasingly centered on the immunosuppressive actions of tryptophan catabolism as regulated by indoleamine 2,3-dioxygenase 1 and 2 (IDO1/IDO2), tryptophan

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2–3-dioxygenase (TDO) and kynureninase as well as downstream signaling of tryptophan catabolites as agonists of AhR. In pre-clinical models, heightened activity of the Trp–Kyn–AhR pathway has been linked to impairment of antitumor immunity and tumor growth (16, 17). More recent characterization AhR has demonstrated multiple mechanisms by which it facilitates a tolerogenic immune environment (18). Inhibition of the Trp–Kyn–AhR pathway has become an attractive therapeutic target and the focus of substantial biotechnology and pharmaceutical effort. Currently, several IDO1, combination IDO1/TDO inhibitors, AhR inhibitors as well as a recombinant kynureninase are in clinical development or late preclinical testing.

Immunomodulatory Role of the Trp–Kyn–AhR Pathway

The Trp–Kyn–AhR pathway, in which the essential amino acid tryptophan is converted to Kyn and other secondary metabolites, is the primary route of tryptophan catabolism (19). Three enzymes catalyze the rate-limiting step of tryptophan catabolism to kynurenines: IDO1, IDO2, and TDO. The enzyme kynureninase hydrolyzes 3-hydroxykynurenine to 3-hydroxyanthranilic acid in the production of nicotinamide adenine dinucleotide. Regulation of these enzymes is notably divergent, with IDO1 being influenced by the interplay of IFN γ and IL6 as compared with TDO being regulated by tryptophan, cholesterol, and prostaglandin E2 (20, 21). The regulation and role of IDO2 is uncertain. Immunosuppression associated with Kyn was first described in experiments that demonstrated increased tryptophan catabolism limits allogeneic fetal rejection in mice (22).

In tumors, IDO1 is expressed by stromal cells of the TME and is induced by IFN γ as a result of CD8⁺ T-cell infiltration and activation of other immunosuppressive pathways (7, 23, 24). TDO is ectopically expressed by tumor cells in certain malignancies (25). Kynurenines act as potent agonists of AhR, a ligand-gated transcription factor that is expressed in many immune cells and mediates a wide range of immunomodulatory effects (26, 27). Elevated IDO1 and TDO activity and Kyn levels are associated with increased tumor grade and poor prognosis in many cancers (28).

Several mechanisms have been proposed to explain the role of the Trp–Kyn–AhR pathway in tumor-associated immunosuppression. T cells are exquisitely sensitive to local depletion of tryptophan in which low tryptophan levels suppress mTORC pathways and activate general control nondepressible 2 (GCN2) kinase leading to cell-cycle arrest and anergy of infiltrating T cells via eIF-2-dependent pathways (Fig. 1; refs. 29–31). However, recent studies have questioned the significance of this mechanism (32, 33). Accumulation of kynurenines induce effector T-cell arrest and lead to binding of AhR. This results in nuclear translocation and promotion of FoxP3 transcripts and IL10, eventually producing Treg populations (18, 34–37). *In vitro* studies of AhR-deficient lung dendritic cells demonstrate failure to promote Treg development and an increase in Th2 cell differentiation and proinflammatory responses to allergen exposure (38). AhR suppresses innate immunogenicity of antigen-presenting cells and promotes IL10 production by natural killer cells (Fig. 2; refs. 39–41). In addition, the Kyn–AhR interaction has been shown to upregulate PD-1 expression by CD8⁺

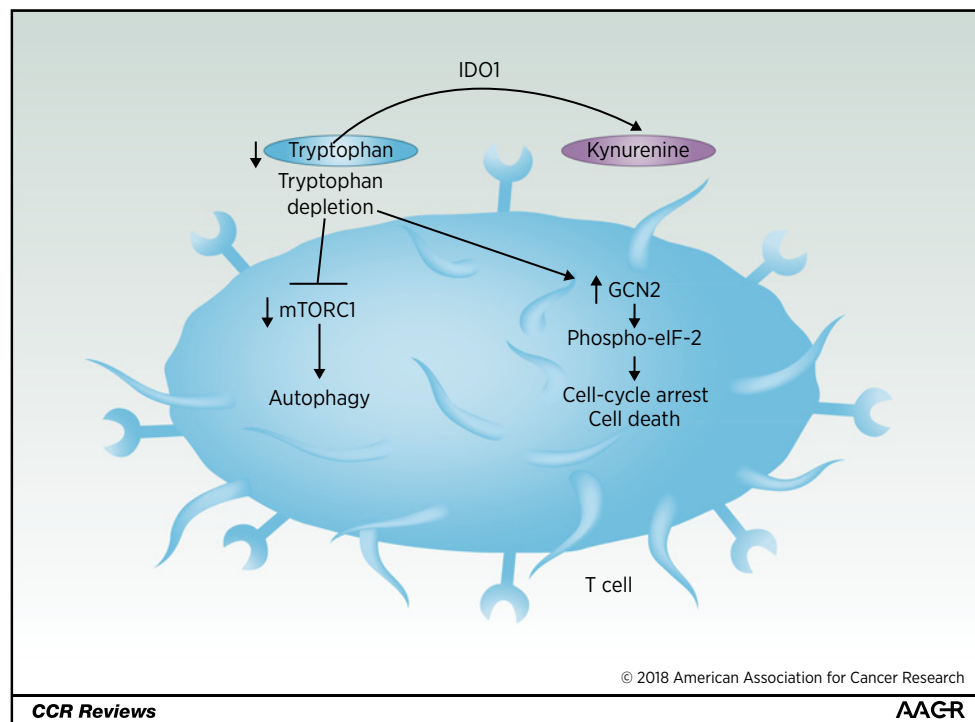


Figure 1.

Tryptophan depletion–dependent signaling. Depletion of tryptophan suppresses activity in the mTORC1 signaling pathway, leading to autophagy in T cells, and releases GCN2-mediated phosphorylation of eIF-2, inducing cell-cycle arrest and death in T cells.

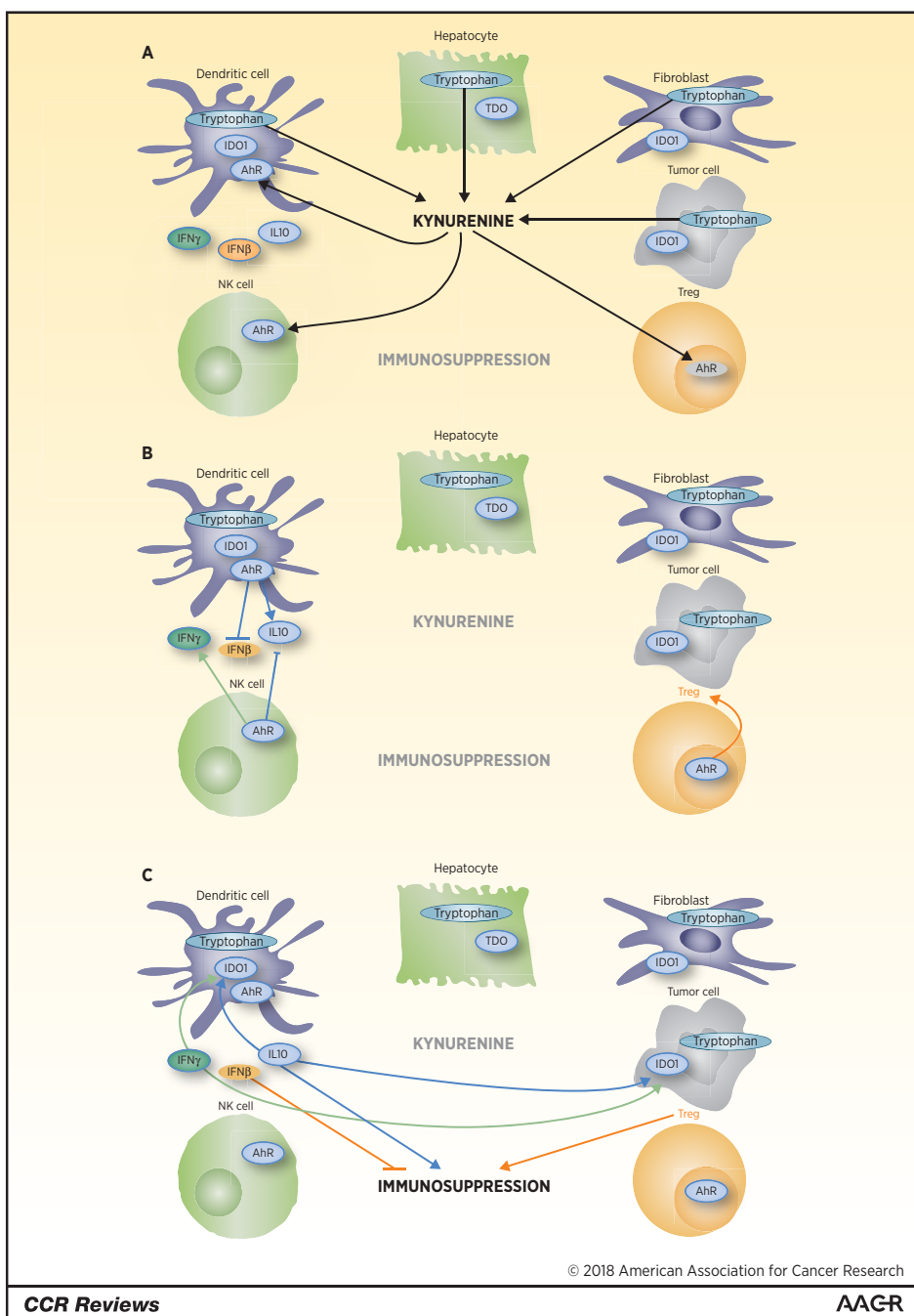


Figure 2.

IDO1-kynurenine-AhR signaling in TME immunosuppression. **A**, IDO1 in tumor cells, dendritic cells, and fibroblasts. TDO in hepatocytes are the rate-limiting enzymes in the conversion of tryptophan to kynurenine and kynurenine derivatives. Kynurenine binds to and activates the AhR, a ligand-activated transcription factor, in Tregs, natural killer (NK) cells, and dendritic cells. **B**, Activation and nuclear translocation of the AhR (1) in dendritic cells induces synthesis and release of IL10 and inhibits IFN β signaling, (2) in NK cells induces synthesis and release of IL10 and IFN γ , and (3) in Tregs promotes Treg development. **C**, Tregs and IL10 promote immunosuppression within the TME, whereas inhibition of IFN β by AhR releases regulation of immunosuppression from inhibitory IFN β signaling. In addition, both IL10 and IFN γ promote IDO1 activity, establishing a positive feedback loop for IDO1-kynurenine-AhR signaling.

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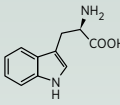
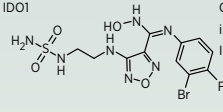
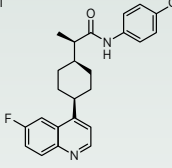
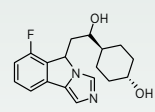
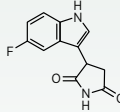
T cells via transcellular signaling mechanism in the tumor microenvironment (42).

Prominent IDO1/TDO Inhibitors and Trp-Kyn Pathway Inhibitors in Clinical Development

Several biochemical strategies exist to inhibit the Trp-Kyn-AhR pathway. IDO1 knockout mice demonstrate no clinical phenotype, in contrast to the inflammatory phenotype observed for knockouts of the immune checkpoints CTLA-4 and PD-1, and

thus, IDO1 inhibitors have predominantly been used in combination with other treatment modalities (43, 44). Selective IDO1 enzyme inhibitors such as epacadostat, NLG-919, and BMS-986205 either compete with tryptophan for the catalytic site of IDO1 or bind the enzyme with very high affinity (44–47). In contrast, the tryptophan mimetic indoximod appears to have pleiotropic effects on downstream Kyn-AhR pathway signaling and has been shown to relieve immunosuppressive signaling normally induced by tryptophan depletion (48, 49). AhR inhibitors and recombinant kynureninase have more recently entered clinical development and will be discussed below.

Figure 3.
Trp-Kyn pathway inhibitors in current or prior clinical development. BID, twice a day; DC, dendritic cell; QD, every day.

| Drug | Company | Target | Structure | Mechanism | Dosing | Human IDO1 enzymatic assay (IC ₅₀) | Human IDO1 cell-based assay (IC ₅₀) | Human TDO enzymatic activity | Phase of development |
|--------------------|-----------------------|--------------------|--|--|---------------------|--|---|------------------------------|----------------------|
| Indoximod | NewLink | Tryptophan mimetic |  | Stimulates mTOR kinase to reduce T-cell autophagy (49) | 1200 mg BID (77) | >2.5 mM (HeLa cells) (46) | -30 uM (Human DCs) | Nonselective | III |
| Epacadostat | Incyte | IDO1 |  | Competitive inhibition of IDO1 (46) | 100 mg BID (59) | 72 nM (46) | 7-23 nM (46) | >100-fold (46) | III |
| BMS986205 | Bristol-Meyers Squibb | IDO1 |  | Irreversible inhibition of IDO1 (78) | 150 mg QD (79) | 1 nM (HEK293 cells) | >2 uM in HEK293 cells (44) | >100-fold (44) | III |
| Navoximod | NewLink | IDO1 |  | Noncompetitive inhibition of IDO1 | 50-800 mg BID (80) | 28 nM (82) | 75 nM (81) | 10-20-fold (78) | IIb |
| PF-06840003 | iTeos | IDO1 |  | Noncompetitive inhibition of IDO1 (82) | 250-500 mg BID (83) | 120 nM (82) | 1100 nM (82) | >100-fold (82) | I |
| KHK2455 | Kyowa Hakko Kirin | IDO1 | Not available | Competitive inhibition, apo-conformation (84) | 1 mg QD (85) | | 14 nM (84) | >100-fold (84) | I |
| RG70099 | Roche | IDO1/TDO | Not available | Competitive inhibition | Unspecified | 16 nM (69) | 12 nM (69) | 6-fold (69) | Preclinical |
| IOM-E | Merck | IDO1 | Not available | Unknown | Unspecified | | 100 nM (70) | >100-fold (70) | Preclinical |
| IOM-D | Merck | IDO1/TDO | Not available | Unknown | Unspecified | | 365 (70) | 10 nM (70) | Preclinical |

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A primary pharmacodynamic measure reported for selective IDO1 inhibitors in clinical trials was reduction in peripheral blood Kyn levels. Initial peripheral blood Kyn suppression data demonstrated approximately 50% reduction, suggesting other enzymes contribute to the production of systemic kynurenine, such as TDO. To date, assessment of intratumoral Kyn has not been consistently collected or reported in clinical trials (50, 51). Figure 3 describes the prominent IDO, TDO inhibitors, and Trp-Kyn pathway inhibitors currently in clinical development.

IDO1, TDO, and Trp-Kyn-AhR Inhibition in Combination Treatment

Association between the Trp-Kyn-AhR pathway and PD-1/L1 was suggested by the observation that both pathways are induced by IFN γ signaling in the TME (7, 14). Indeed, across 30 human solid tumors from The Cancer Genome Atlas (TCGA) database, we have observed that the gene expression of *IDO1* was strongly correlated with the expression of

PD-1 across increasing level of IFN γ -responsive gene expression from non-T cell-inflamed to highly T cell-inflamed tumors (Fig. 4A). In contrast, expression of *IDO2*, *TDO2*, *KYNU*, *AHR*, and *GCN2* (alias *EIF2AK4*) does not appear to correlate with *PD-1* expression or demonstrate IFN γ responsiveness on a transcriptional level as strongly as *IDO1* (Fig. 4B).

Despite early observations for lack of monotherapy activity of selective IDO1 inhibitors (52), combination strategies utilizing IDO1 inhibitors were quickly advanced. Indeed, IDO1 and PD-1/L1 inhibitor combinations appeared to show great promise in early-phase clinical trials across multiple tumor types (Supplementary Tables S1 and S2).

A substantial literature also supports the potential utility of inhibition of the IDO pathway in conjunction with other anti-cancer modalities. Studies of IDO pathway blockade with radiation, chemotherapy, and tumor vaccines suggest an improvement relative to those treatments alone (53, 54). Several clinical trials evaluating combinations across these modalities are ongoing (Supplementary Table S1).

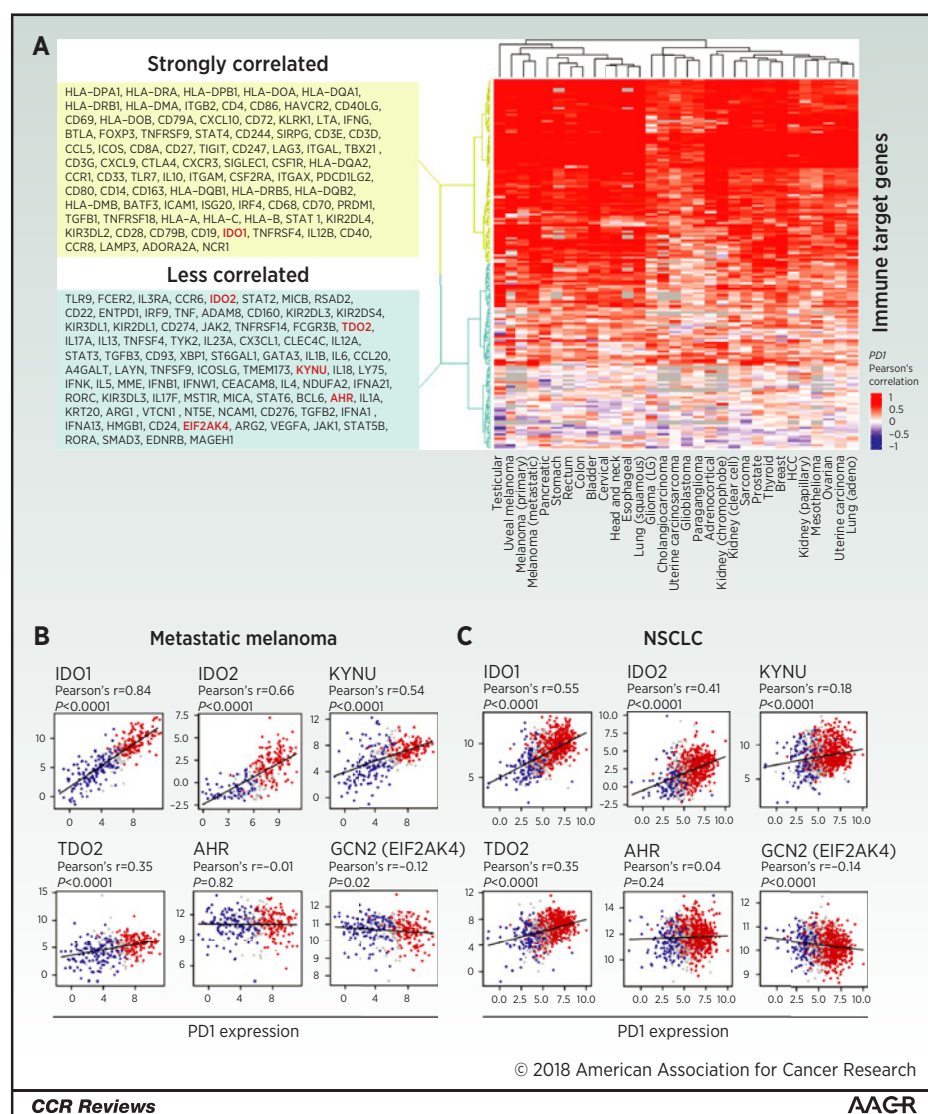


Figure 4. Expression of *PD1* is positively correlated with immunotherapy-relevant target genes across solid tumors from TCGA. **A**, Heatmap of Pearson product-moment correlation coefficient r between *PD1* and immune target genes by tumor type. Immune target genes were separated into those strongly or less correlated with *PD1* expression. Methods: level 3 RNA-seq data (release date February 4, 2015) were downloaded for 30 solid tumor types from TCGA and processed as described previously (86). Acute myeloid leukemia, diffuse large B-cell lymphoma, and thymoma were excluded because of high tumor-intrinsic immune cell transcripts. Skin cutaneous melanoma had both primary and metastatic samples available, whereas the other 29 cancers had only primary tumors available. A noncomprehensive list of 171 immune molecules representative of the interactions between tumor cells and immune cells in the TME were selected and correlated with *PD1* (alias *PDCD1*) gene expression. For each tumor type, Pearson r was computed between each immune molecule and *PD1* and used for clustering the genes by hierarchical unsupervised clustering with Euclidean distance. Two distinct groups are shown, consisting of (1) strongly correlated genes and (2) less correlated genes. Glioma (LG), low-grade glioma; HCC, hepatocellular carcinoma; Lung (adeno), lung adenocarcinoma. **B** and **C**, Correlation plots of *PD1* versus *IDO1*, *IDO2*, *KYN*, *TDO2*, *AHR*, and *GCN2* (alias *EIF2AK4*; highlighted in red in **A**) in metastatic melanoma (**B**) and NSCLC (**C**). Patients were categorized into T cell-inflamed (red), non-T cell-inflamed (blue), and intermediate groups using a defined T cell-inflamed gene signature (86). Each data point represents one patient. NSCLC, non-small cell lung carcinoma.

Epacadostat

Epacadostat, a competitive, selective inhibitor of IDO1, reached the most advanced stage of development, with the recent early termination of ECHO-301/Keynote-252; a phase III clinical trial in combination with pembrolizumab in metastatic melanoma. At median follow-up of 14 months, patients treated with epacadostat plus pembrolizumab demonstrated a progression-free survival of 4.7 months versus 4.9 months in those treated with pembrolizumab plus placebo (HR = 1.00; CI, 0.83–1.21; $P = 0.517$.) The overall response rate was 34.2% versus 31.5% in the epacadostat plus pembrolizumab and placebo plus pembrolizumab groups, respectively. Treatment-related adverse events occurred in 79.3% of patients receiving epacadostat plus pembrolizumab versus 81.0% receiving placebo plus pembrolizumab and grade ≥ 3 treatment-related adverse events occurred in 21.8% versus 17.0%, respectively (55). These negative results were unexpected as preclinical studies and early-phase clinical trials of this combination in as many as 14 different solid tumors showed

encouraging results (Supplementary Table S1). Multiple hypotheses have been advanced to explain the seeming discrepancy between early-phase clinical trial success of epacadostat and the failure of the late-phase ECHO-301 trial. A nonexhaustive list of possible explanations to differentiate early- versus late-phase results could include differences between the treatment populations, inappropriately low dosing of epacadostat, and incomplete suppression of intratumoral Kyn.

Regarding the patient populations for these studies, the patient characteristics appeared to be relatively similar from the early- (ECHO-202) to late-phase (ECHO-301) melanoma studies across multiple variables including but not limited to performance status of zero (77% vs. 76%), M1c staging (55% vs. 61%), elevated lactate dehydrogenase (37% vs. 32%), and no prior therapy (71 vs. 89%), respectively (55, 56). As IDO1 expression is intimately linked to IFN γ gene expression, the baseline quality of the T cell-inflamed TME may be of relevance to the results. To date, this is not well characterized in either study. In ECHO-301, IDO1 expression was not an

inclusion criterion (although PD-L1 expression was a randomization stratification factor) with only PD-L1 status as a surrogate from the early-phase studies. Given the seeming complete lack of activity between epacadostat and placebo in ECHO-301, some have wondered whether further study should be given to the patients treated in the early-phase study. Despite the lack of obvious clinical differentiators, perhaps the tumors from these patients were disproportionately T cell-inflamed and thus much more likely to respond to pembrolizumab and possibly epacadostat.

Other less commonly controlled for differences of potential clinical significance could exist between the early- to late-phase trial populations also however. One of these would be to note that the early-phase trial was conducted at a select number of sites in the United States, whereas the late-phase study was predominately international (Australia, Europe, Asia, South America) with a lesser accrual in the United States. It has been observed in previous trials of melanoma that outcomes appeared to be substantially different between these populations in the phase III setting (57). Consideration might be given to whether dietary or environmental exposures could be variable in these different localities especially given the canonical role of AhR as a xenobiotic sensor that is responsive to signals from the gut microbiome (18). With an evolving literature supporting the microbiome as a potential influencer of PD-1 antibody response (58), focus on diet, medication use, and microbiome contents may be important variables to track in clinical trials moving forward.

Regarding dosing of epacadostat, 100 mg was taken forward out of the phase I study despite higher dose levels being tolerable and no MTD being established (59). This dose was chosen by Incyte as it was deemed that maximal inhibition of IDO1 activity was observed at doses of ≥ 100 mg with a relative plateau in decrease of kynurenine level in peripheral blood at higher doses. This point of the most appropriate dose is debated however particularly given that published modeling of IDO inhibition only reaches approximately 50% to 70% at the 100 mg dose (60). It is somewhat notable that an early-phase study of epacadostat with nivolumab was simultaneously pursued using 300 mg of epacadostat (61) and published modeling implies a higher likelihood of IDO1 inhibition at this dose (60). The optimal dose of epacadostat continues to be explored in ongoing clinical trials.

Perhaps of most relevance to the failure of ECHO-301 however is the open question of intratumoral pharmacodynamics. Although peripheral blood monitoring of kynurenine was reported for epacadostat in phase I, to date, no intratumoral data have been released from any clinical trial. Given the lack of consensus surrounding whether limiting tryptophan depletion versus suppression of Kyn acts as a primary mechanism of immunosuppression, these data are essential to inform the field surrounding next steps. Even very low levels of canonical AhR ligands, such as Kyn and dioxin, can activate AhR-associated gene expression and recent preclinical studies have suggested kynureninase and direct AhR inhibitors have higher potency relative to IDO1-selective inhibitors (62–64). If suppression of Kyn is indeed the dominant mechanism, it is very possible that IDO1 inhibition alone may be inadequate to drive intratumoral levels consistently low enough to alleviate the immunosuppressive effects of Kyn-activated AhR, including production of IL10 and suppression of type I IFN (41).

Other Selective IDO1 Inhibitors

Pivotal studies of BMS-986205, an irreversible IDO1 inhibitor developed by Flexus Biosciences and Bristol-Myers Squibb, have been predominately scaled back in the wake of epacadostat's late-stage trial failure, although a randomized study in bladder cancer is still planned. Relative to epacadostat, BMS-986205 demonstrates higher potency based on IC_{50} in IDO1-expressing cell lines. In contrast to the lack of such data for epacadostat, analysis of 39 paired pre- versus on-treatment tumor samples across various tumor types from the phase I trial of BMS-986205 plus nivolumab demonstrated decreased Kyn levels (and mostly near zero levels on-treatment) and increased the percentage of proliferating CD8⁺ T cells (65).

Genentech has recently terminated rights to NewLink's NLG-919 (navoximod/GDC-0919), another selective inhibitor of IDO1.

Tryptophan Mimetics

Indoximod, the D-enantiomer of 1-methyl-tryptophan, has demonstrated inhibition of the IDO pathway as a tryptophan mimetic. Indoximod limits IDO-mediated immunosuppression by at least two mechanisms including (i) serving as an artificial Trp-sufficiency signal that prevents activation of GCN2 and inhibition of mTORC1 and (ii) modulation of AhR-dependent transcriptional activity (66). Indoximod increased activity and proliferation of CD8⁺ T cells by limiting tryptophan depletion-mediated mTORC1 suppression (66). mTORC1 activation has been associated with ICOS expression, a T-cell coregulatory receptor seen on tumor-infiltrating T cells that has been associated with clinical response (67). In an AhR-dependent manner, indoximod was shown to stimulate CD4⁺ T-cell differentiation to Th17⁺ helper T cells, inhibit FoxP3 Tregs, and downregulate expression of IDO in dendritic cells (66).

Data from a single-arm phase II trial of indoximod plus anti-PD-1 in advanced melanoma achieved an ORR of 56% and CR in 19% with low rates of high-grade immune-related adverse events (68). Multiple phase II and III trials combining indoximod with other current modalities of treatment, including chemotherapy, cancer vaccines, and checkpoint immunotherapy are ongoing (Supplementary Tables S1 and S2).

Dual IDO1/TDO Inhibitors

Analysis of tumor and immune cells by IHC revealed differences in the expression of IDO1 and TDO among tumor types, suggesting the potential for a possible advantage with dual IDO and TDO inhibitors in certain tumors (69). Dual IDO/TDO inhibitors such as RG70099 decrease serum Kyn levels by approximately 90%. IOM-E and IOM-D are selective IDO1 and dual IDO1 and TDO inhibitors, respectively. Preclinical studies have revealed a promising pharmacokinetic profile. Significant *in vivo* efficacy was observed in mouse pancreatic adenocarcinoma cells treated with IOM-E, the selective IDO1 inhibitor, in combination with gemcitabine and Abraxane. Particular efficacy in preclinical lung cancer models has also been seen (70). Several companies have disclosed preclinical programs surrounding the development of dual IDO/TDO inhibitors, although the current status of these programs is in flux in the wake of ECHO-301. It is worth pointing out however that in murine models, complete IDO/TDO inhibition results in significant alteration of Trp metabolism,

which has raised concern over potential neurologic toxicity (seizures) from dual IDO1/TDO inhibition (71).

AhR Inhibitors

Inhibition of AhR signaling with small-molecule antagonists interferes with the downstream immunomodulatory effects irrespective of the source of Kyn production. Early inhibitors in this class have been shown to block nuclear translocation of AhR and enhanced production of IFN γ , TNF α , IL2, and reduction in tumor-associated M2-like macrophages. In mouse models, AhR inhibitors have demonstrated activity as monotherapy, a notable contrast to IDO1 inhibitors. Furthermore, enhanced activity is seen with AhRi combination with anti-PD-1 (63). Several biotechnology companies including Hercules Pharmaceuticals, Ideaya Biosciences, and KYN Therapeutics have disclosed the development of AhR inhibitors.

Kynurenine-Degrading Enzymes

Recombinant Kyn-degrading enzymes, kynureninase or KYNase, have been shown to reduce Kyn levels in IDO1, TDO, and IDO1/TDO dual positive cancer cells without impact on systemic tryptophan levels. Preclinical studies of a recombinant PEG-KYNase in established tumor models have demonstrated inhibition of tumor growth and increase in tumor-infiltrating effector T cells as monotherapy. Synergistic activity with anti-PD-1 has also been demonstrated (72, 73). An ongoing development program of recombinant kynureninase has been disclosed by KYN Therapeutics. Intratumoral injection of engineered *E. coli* strains that metabolize kynurenine have demonstrated reduction in *in vivo* kynurenine levels and generation of antitumor response (74).

Conclusions and Future Directions

The degree of tumor inflammation, as assessed by the presence of type I/II IFN signaling and infiltrating effector T cells, is associated with an improved response to checkpoint immunotherapy (8–11, 13). However, despite robust T-cell inflammation, a considerable percentage of tumors progress by virtue of multiple immunosuppressive mechanisms (14, 15). Upregulation of the Trp–Kyn–AhR pathway has been identified as one such mechanism. The immunosuppressive effect of this pathway is believed to be mediated by Trp depletion, T-cell cycle arrest mediated by Kyn cytotoxicity and activation of immune-tolerogenic AhR.

Recent studies have cast doubt on the Trp-depletion mechanisms (32, 33) and highlighted the potent immunosuppressive activity of intratumoral Kyn and AhR signaling. To this end, in the evaluation of Trp–Kyn–AhR inhibitors, reduction of extracellular Kyn within the TME or downstream AhR transcriptional programs should be emphasized as major pharmacodynamic endpoints. Indeed, a major concern pertaining to the clinical evaluation of selective IDO1 inhibitor epacadostat was the absence of intratumoral Kyn biomarker analysis. Prior studies have demonstrated serum Kyn:Trp correlate with response to anti-PD-1 (75, 76); however, it is unclear whether serum kynurenine is a surrogate for intratumoral Kyn.

Despite the failed experience of epacadostat in unselected melanoma patients, a strong translational rationale still exists for targeting of the Trp–Kyn–AhR pathway in conjunction with immunotherapy. Alternative mechanisms to achieve intratu-

moral Kyn reduction are currently being investigated. Comprehensive inhibition of kynurenine production by dual IDO1/TDO inhibitors and/or degradation of Kyn molecules by recombinant kynurenine-degrading enzymes may provide more robust intratumoral Kyn reduction. Alternatively, inhibition of AhR may serve to alleviate the immunosuppressive TME regardless of the source of Kyn production. Novel agents in each of these classes are approaching phase I studies, and preclinical experiments have shown promising results (63, 72–74).

A contrarian view to acknowledge surrounding this pathway would be that in a T cell–inflamed tumor, inhibition of Trp–Kyn–AhR may be insufficient to elicit further antitumor immune response due to the presence of further escape mechanisms (6, 7, 15). In these settings, this pathway may fail to make an inflamed environment even more inflamed. However, it may be that targeting downstream in the pathway could mediate the induction of the T cell–inflamed TME in previously noninflamed tumors given studies suggesting regulation of type I IFN response by AhR (41). This concept awaits further investigation and biospecimens from phase I studies of AhR antagonists will be especially interesting in this regard.

Cancer immunotherapy has advanced significantly with the development of CTLA-4 and PD-1–PD-L1 inhibitors. Progress in understanding the biology underlying the T cell–inflamed tumor microenvironment suggests that the Trp–Kyn–AhR pathway and PD-1–PD-L1 signaling are both associated with IFN γ response, but mediate independent mechanisms of immunosuppression. Combinatorial therapies may thus benefit a subset of patients. Despite uncertainty surrounding selective IDO1 inhibition, ample preclinical evidence supports continued development of Trp–Kyn–AhR pathway inhibitors to augment immune-checkpoint and other cancer therapies. Novel Trp–Kyn–AhR inhibitors have demonstrated promising preclinical activity and as new candidates undergo lead optimization and early evaluation, lessons learned from recent IDO1 inhibitor failure must guide the field moving forward.

Disclosure of Potential Conflicts of Interest

J.J. Luke reports receiving commercial research grants from Array, CheckMate, Evelo, and Palleon, holds ownership interest (including patents) in Actym and Alphamab Oncology, and is a consultant/advisory board member for Actym, Aduro, Alphamab Oncology, Array, Astellas, AstraZeneca, BeneVir, Bristol-Myers Squibb, Castle, CheckMate, Compugen, EMD Serono, Ideaya, Janssen, Merck, NewLink, Novartis, RefleXion, 7 Hills, Spring Bank, Syndax, Tempest, TTC Oncology, Vividion, and WntRx. No potential conflicts of interest were disclosed by the other authors.

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