Page 1 of 5

Innate immune checkpoints for cancer immunotherapy: expanding the scope of non T cell targets

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With the recent progresses in the field of immunooncology, harnessing the power of the immune system to fight cancer has become one of the pillars of cancer care, together with the traditional approaches of surgery, chemotherapy, targeted oncogene pathway inhibition, and radiation therapy. Treatment with monoclonal antibodies against immune checkpoint targets on T-cells, including the programmed cell death protein 1 (PD-1) pathway, was proven clinically effective in a variety of cancers and was approved for several indications over the past few years (1). However, only a subset of patients respond to immunotherapy and complete response remains uncommon across cancer types (2). Among the mechanisms of resistance to immunotherapy, the establishment of a highly immunosuppressive tumor microenvironment (TME), composed of cells such as regulatory T cells (Tregs), myeloid-derived suppressor cells (MDSCs), cancer-associated fibroblasts and M2 macrophages (TAMs), was reported as having a major role in limiting effective antitumor immunity (3,4). Tumorassociated myeloid cells, particularly TAMs, constitute a major component of the TME and recent studies support their key contribution to the suppression of CD8⁺ T-cell function and is associated with poor prognosis in many cancers (5,6). Taking advantage of the highly plastic nature of myeloid cells, a number of strategies to reprogram the function of innate immunity towards an immunostimulatory state have been attempted to enhance

the activity of checkpoint inhibitors in cancer. Those include targeting PI3K γ (7,8), CSF-1R (9,10), IDO (11), VEGF/VEGFR (12,13) or CD40 (14-16).

Many pathways expressed by TAMs have been shown to control their phenotypic state, either by directly inhibiting effector cell activity (phagocytosis, antigen-presentation, cytokine production) or by promoting cell expansion, infiltration and activity (17). Proteins expressed on the surface of tumor cells, such as CD47, PD-L1 and VISTA, have the ability to trigger inhibitory "don't eat me" signals on TAMs and protect tumors from immunosurveillance mechanisms. Approaches pioneered by Dr. Weissman's research group at Stanford University found that disruption of the interaction between CD47 and signal-regulatory protein α (SIRP α), expressed on CD11b⁺ myeloid cells [including macrophages and dendritic cells (DCs)], effectively enhances phagocytosis toward tumor cells in vitro and reduces tumor growth in vivo (18-24). However, variations of the responsiveness to CD47-SIRPa blockade exist (21,25). In this new manuscript by Barkal et al., the authors describe CD24 as a novel don't eat me signal expressed in several cancers, particularly ovarian (OC) and triple-negative breast cancers (TNBC) (25). CD24 is a heavily glycosylated glycosylphosphatidylinositol-anchored surface protein that was shown previously to interact with the inhibitory receptor sialic-acid-binding Ig-like lectin 10 (Siglec-10), which is expressed on the surface of TAMs (26,27).

Through binding to Siglec-10, CD24 elicits an inhibitory signal by activating the phosphatases-SHP-1 and/or SHP-2. The interaction between CD24 and Siglec-10 was first identified and described to negatively regulate the Danger-associated molecular patterns (DAMPs) signaling through toll-like receptors (TLRs) in dendritic cells (DCs) (26).

Although authors in this paper mainly focused on the characterization of CD24 as a don't-eat-me signal, the functional contribution of CD24 as a sensor for the DAMPs signals certainly deserves further investigation since DAMP signals are found to be released from necrotic tumor cells upon anti-cancer therapies (28-30). Proteins that similarly act as negative regulators of TLRsignaling, such as IL-37 (31) and SIGIRR/IL-1R8 (32,33), have already been described to act in the cancer-immune crosstalk with potential implications in therapeutic efficacy. In fact, the release of certain DAMP molecules such as high mobility group box 1 (HMGB1) is a key component of an immunogenic type of cell death triggered by anticancer agents-such as some classes of chemotherapy (anthracyclines, oxaliplatin and bortezomib) and radiotherapy-which mediate their efficacy by enhancing antitumor immunity (34,35).

Barkal et al. describe CD24 initially as a highly expressed transcript across several cancer types, particularly TNBC and OC, and an association between its expression and poorer prognosis. Interestingly, CD24 expression in TNBC cells appeared substantially higher than classic immune checkpoints on tumor cells such as PD-L1 and with higher specificity than CD47, in the TNBC patient population tested. However, as opposed to PD-L1whose expression presents an inducible nature in response to inflammatory stimulus such as IFNy-no discussion regarding the potentially inducible nature of CD24 was presented. In addition, the remaining evidence presented of high CD24 expression in ovarian and breast tumor cells and Singlec-10 expression in TAMs by FCS raise questions as no comparisons with other tumor cell or immune cell populations are made. Similarly, even though the expression of Siglec-10 in macrophages is shown to be dependent on M2 macrophage-polarizing cytokines (such as IL-10, TGF-b and IL-4), the exact mechanism by which this inhibitory pathway is engaged is still unknown.

Considering the fact that Siglec-10—like other members of the Siglecs family (sialic-acid-binding immunoglobulinlike lectins) which exhibit preferential binding to sialylated proteins—binds to sialylated CD24 with higher affinity and that the sialylation of CD24 contributes to the suppression of tumor cell phagocytosis by macrophages (25), the authors highlight an important-yet not much explored-mechanism of tumor cell hyper-sialylation in the suppression of innate immunity. While heavy glycosylation is known as a tumor cell feature, aberrant sialylation is appreciated as the most consistent and prominent form of glycosylation among different tumor types (36). Therefore, if sialylation of proteins expressed on tumor cells suppress phagocytosis to a certain degree, the implication of the following should be considered. (I) Inhibition of sialyltransferase expression: Since there has been at least 9 sialyltransferases characterized to be essential in catalyzing the linkage of sialic acids onto the growing glycan structures during malignant tumor progression (36-38), blocking these sialyltransferases is likely to help reducing the sialylation and hence improving the tumor cell phagocytosis by macrophages. (II) Blockade of hexosamine biosynthesis pathway: it has been shown that tumor cells can utilize the hexosamine metabolism pathway driven by certain oncogenic stimuli to increase the production of cytosine monophosphate (CMP)-sialic acid and therefore sialylated glycoconjugates (36,39,40), the blockade of this pathway is hence worthwhile considering to reducing the surface sialvlation on tumor cells.

Further in vitro studies testing the therapeutic potential of CD24 blockade with monoclonal antibodies in order to disrupt CD24-Singlec-10 signaling demonstrated enhanced tumor cell engulfing by TAM, using for instance models of labeled human TNBC cells (MCF-7). Not surprisingly, induction of phagocytosis by anti-CD24 treatment was apparently dependent on the expression of CD24 on tumor cells and was largely increased upon addition of CD47 blocking antibodies. Interestingly, the synergy observed by the authors between anti-CD24 and anti-cancer agents (cetuximab) suggest again that studies evaluating the modulatory role of CD24 over DAMP signaling might be a promising avenue of research. In their final results, the authors explore the inhibitory role of CD24 on phagocytosis using in vivo models. The findings go along with their previous results and reinforce the assumption that the macrophage-dependent clearance of tumor cells relies on CD24 expression. It is important to note that no experiment was performed to address in a more definitive way the contribution of CD24-Singlec-10 interactions in the outcome of differential phagocytosis and tumor growth, such as by using conditional knockout mice for Siglec-G (the mouse version of Siglec-10). In addition, all mouse experiments were performed on immunodeficient

Annals of Translational Medicine, Vol 8, No 16 August 2020

TLR

L-Kvnurenine

MHC II

TCR

ΡΙ3Κγ

ido

Legend

Siglec-10 Sialylated

CD24

SIRP

CD47

CD40L

CD40

ТАМ Tumor cell ТАМ Tumor cell ΡΙ3Κγ Small molecule inhibitors IDC Blocking Abs Phagocytosis Phagocytosis Antigen-presentation Antigen-presentation T-cell suppression T-cell suppression Tumor progression Tumor progression T-cell

Figure 1 Molecular targets to enhance innate immunity in cancer therapy. Left, inhibitory checkpoints on the surface (Siglec-10, SIRP α) or cytoplasm (PI3K γ , IDO) of tumor-associated macrophages (TAMs) suppress their effector functions of phagocytosis and antigenpresentation to T-cells. To escape from immune surveillance, tumors cells evolve with multiple pathways including IDO-derived L-Kynurenine which mediates T-cell suppression and the overexpression of CD24 and/or CD47, which suppress phagocytosis by engaging to Siglec-10 and/or SIRP α expressed in macrophages. Proposed mechanisms regarding Siglec-10 in down modulation of TLR-signaling is still unclear. Right, blockade of CD47 and CD24 or stimulation of CD40 using mAbs and of IDO and PI3K γ using small molecule inhibitors can potentiate the activation state of TAMs towards a pro-inflammatory antitumoral phenotype. Therapeutic strategies to enhance myeloid cell activation can result in increased adaptive immunity and tumor control and can be exploited in combination with other immunotherapies.

NSG mice, which lack adaptive immunity. Although the paper focuses on crosstalk between tumor cells and macrophages and made use of more simplified systems to address CD24 signalling through Singlec-10, it is increasingly clear how the adaptive immune system influences innate immune function, by means of cytokine/ chemokine secretion and inhibitory/stimulatory signals (CD40/CD40L, PD-1/PD-L1, VISTA) for instance (16,41,42). The net sum of signals may ultimately alter the phenotypic outcome of myeloid cell function. Therefore, the use of murine immunocompetent models would be a valuable tool to confirm CD24's value as a target for cancer immunotherapy.

In summary, overcoming immunotherapy resistance is a major focus of research in the scientific community and identifying mechanisms in myeloid cells that could be exploited to switch their function towards an immunostimulatory state has the potential to enhance antitumor immunity and generate more effective immunotherapeutic combination strategies (*Figure 1*). The results presented by Barkall and collaborators propose a novel therapeutic target with particular promise for the treatment of ovarian and breast cancers, which currently lack immunotherapy options. Recent clinical successes of CAR-T cells and immune checkpoint inhibitors have led to a T-cell centric view of tumor immunity. Given that the onset and proper maintenance of T cell responses are highly dependent on the interplay between adaptive and innate immunity, harnessing the function of myeloid cells—to either overcome suppression or enhance their effector function of phagocytosis/antigen-presentation—open up new possibilities for more durable and robust tumor control with immunotherapies.

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Page 4 of 5

Footnote

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Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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Annals of Translational Medicine, Vol 8, No 16 August 2020

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