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IMMUNE CELL INFILTRATION AND TERTIARY LYMPHOID STRUCTURES AS DETERMINANTS OF ANTI-TUMOR IMMUNITY¹

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Abstract

Limited representation of intratumoral immune cells is a major barrier to tumor control. However, simply enhancing immune responses in tumor-draining lymph nodes, or through adoptive transfer, may not overcome the limited ability of tumor vasculature to support effector infiltration. An alternative is to promote a sustained immune response intratumorally. This idea has gained traction with the observation that many tumors are associated with tertiary lymphoid structures (TLS), which organizationally resemble lymph nodes. These peri- and intra-tumoral structures are usually, but not always, associated with positive prognoses in patients. Preclinical and clinical data support a role for TLS in modulating immunity in the tumor microenvironment. However, there appear to be varied functions of TLS, potentially based on their structure or location in relation to tumor, or the origin or location of the tumor itself. Understanding more about TLS development, composition, and function may offer new therapeutic opportunities to modulate anti-tumor immunity.

Introduction

Substantial intratumoral representation of T-lymphocytes, either spontaneously, or after vaccination or adoptive therapy, is generally well-correlated with immune mediated control of human cancers (1–5). Importantly, the subset of patients who respond clinically to new generation immunotherapies are those in which an immunological infiltrate is evident prior to treatment (6–10). Thus, enhancing the representation of intratumoral immune effectors holds the promise of improving clinical outcomes. However, simply enhancing the immune response in the tumor-draining lymph node, or infusing large numbers of tumor reactive T-cells through adoptive transfer, may not overcome the limitations of the tumor vasculature

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and microenvironment to support infiltration of these effectors. The desired approach would promote a sustained increase in functional intratumoral effector cells.

An interesting alternative is to promote development of an immune response inside the tumor, circumventing the limitations of dendritic cell (DC) trafficking from tumor to lymph node (LN) and of effector cells trafficking in the reverse direction. This idea originated in studies from the early 2000's in which tumors were engineered to support naïve T-cell infiltration (11, 12). However, it has recently gained additional importance with the observation that many tumors are associated with tertiary lymphoid structures (TLS). TLS, which resemble LN, were initially described in conjunction with chronic and pathogen driven immune responses. However, they are now recognized as a common feature in juxtaposition to tumors, and are often associated with a positive prognosis in patients. Here we summarize the current state of knowledge about the significance of tumor-associated TLS. We place them in the context of immune infiltration into tumors more generally, and in the context of what is known about the development of conventional LN and inflammation-associated TLS. Finally, we point to the issues that still need to be addressed to harness them for therapeutic purposes.

Tumor-associated vasculature and control of T-cell infiltration into tumors

Infiltration of tumors by exogenously activated effectors

The entry of leukocytes, including T- and B-cells, into lymphoid and non-lymphoid tissues is controlled by sequential engagement of homing receptors (HR) (selectins, chemokine receptors, and integrins) that act with corresponding ligands on vascular endothelial cells to enable capture, rolling, firm adhesion, and extravasation (13–16). During differentiation, effector T-cells acquire the ability to enter peripheral tissues, including tumors, by upregulating HR that bind to cognate ligands expressed on inflamed vasculature. HR expression on activated CD8 T-cells is determined by the secondary lymphoid organ (SLO) in which priming occurs (17–21). Tissue-specific and inflammation-induced expression of different HR ligands, in conjunction with the patterns of HR expressed by T-cells, determines which tissues are infiltrated.

While the requirements for entry of effector T-cells and other leukocytes into inflamed peripheral tissues, particularly skin and gut, have been well-established, the requirements for entry into tumors remain inadequately defined. Several studies have unambiguously identified individual HR that mediate T-cell infiltration into some tumors (22–27), while others have shown correlations between individual HR or HR ligands and T-cell infiltrates (28–34). We recently completed a comprehensive analysis of the HR that mediate entry of CD8 T-cell effectors into B16 melanoma and Lewis lung carcinoma, and demonstrated that HR ligand expression on tumor-associated vasculature varies with anatomical location of the tumor (35). This also determines the ability of T cells activated in different SLO to enter tumors growing in different locations. Consistent with other work (25, 29, 32, 33, 36–41), we also found that HR ligand expression on tumor vasculature is often low. This is consistent with the low infiltration of adoptively transferred effector T-cells observed in several studies (42–45). Thus, one opportunity to improve cancer immunotherapy is to identify and manipulate the expression of HR and HR ligands to enhance infiltration of CD8

T-cell effectors into tumors. This approach has been explored by transducing adoptively transferred T cells to express various chemokine receptors, and has resulted in enhanced infiltration and tumor control (46–49).

Naïve T-cells enter tumors through LN-like vasculature and enhance tumor control

Naïve T-cells enter LN based on their expression of L-selectin and CCR7, which bind to peripheral node addressin (PNAd) and the chemokines CCL19/CCL21, respectively. The latter are expressed on specialized LN blood vessels called high endothelial venules (HEV). Since naïve T-cells do not generally enter peripheral tissue, it had been assumed that all intratumoral lymphocytes are effectors that differentiate in tumor-draining LN and home to the tumor thereafter. However, naïve T-cells were shown to infiltrate tumors that had been genetically modified to secrete Lymphotoxin- α (LT α) (11, 50) or LIGHT (12). Tumors expressing LT α accumulated activated T cells in the absence of SLO (50). Similar results were obtained by intratumoral injection of CCL21 or CCL21 transduced DC (51–53). It was suggested that naïve T cells infiltrated through a LN-like vasculature based on expression of CCL21 (12), or expression of CCL21, PNAd, and the accumulation of CD62L⁺ T cells (11), although this was not shown. In all of these models, the infiltration of naïve T-cells, in conjunction with their differentiation to become effectors, was shown to promote tumor destruction. These studies established that tumors could be engineered to serve as a surrogate site for naïve T cells recruitment and their activation to become mediators of improved anti-tumor immunity.

More recently, we showed that adoptively transferred naïve CD8 T-cells can enter unmanipulated tumors and subsequently differentiate into functional effectors (54, 55). This also occurs in the absence of SLO (54). We also showed directly that naïve CD8 T-cell entry into tumors was entirely dependent on L-selectin and CCR7, and on the development of tumor-associated blood vessels that express PNAd and CCL21 (55). PNAd and CCL21 were co-expressed on ~5% of blood vessels in tumors growing in multiple anatomical locations (55). The primary source of CCL21 was intratumoral gp38⁺ fibroblasts, and to a lesser extent, CD31⁺ blood endothelial cells. It was also shown that preventing this influx of naïve T-cells diminished tumor control, indicating that it represents an important component of the immune response in unmanipulated tumors.

Mechanisms driving PNAd and CCL21 expression on tumor-associated vasculature

In adult LN, HEV morphology and expression of genes required for biosynthesis of PNAd is maintained by continuous engagement of Lymphotoxin- $\alpha_1\beta_2$ (LT $\alpha_1\beta_2$) expressed on DC with the Lymphotoxin- β Receptor (LT β R) expressed on blood endothelial cells (56, 57). However, the genes for PNAd biosynthesis can also be induced in cultured endothelial cells and monocytes by TNF α (58, 59). LT β R signaling does not control expression of CCL21 in adult LN (56). Developmentally, CCL21 expression depends upon signals from LT $\alpha_1\beta_2$ or the soluble homotrimeric form of Lymphotoxin- α_3 (LT α_3), which engages Tumor Necrosis Factor Receptors 1 and 2 (TNFR) but not LT β R (60–63); TNF α (64, 65); and another TNFR family member, CD30(66). However, it is not clear whether these signals regulate the expression of CCL21 directly, or the development of CCL21 expressing cells. Overall, these results point to the central importance of LT $\alpha_1\beta_2$ - LT β R engagement in driving

development and maintenance of PNAd expression on blood endothelial cells, while control of CCL21 expression remains uncertain.

In tumors, the density of intratumoral DC (67) and regulatory T cell (Treg) depletion (68) were correlated with development of PNAd⁺ CCL21⁺ vasculature, but a cause and effect relationship was not established. Indeed, in murine models of melanoma and lung carcinoma, development of PNAd⁺ CCL21⁺ vasculature was not induced by either DC or LTβR signaling (55). Instead, induction of both molecules depended on CD8 T-cell effectors that had infiltrated tumors at an earlier point. In intraperitoneal (IP) tumors, PNAd expression depended on CD8 T-cell effectors secreting LTα₃, which acted through TNFR expressed on endothelial cells and fibroblasts. CCL21, but not PNAd, also depended on IFNγ secreted by CD8 T-cell effectors, which acted through IFNγ receptors on fibroblasts and endothelial cells. Control of PNAd and CCL21 in subcutaneous (SC) tumors was more complex, in that both CD8 T-cell effectors and NK cells could independently induce expression of these molecules. While expression depends on signaling through TNFR, IFNγ seems to act redundantly with another as yet unidentified modulator to induce CCL21. These results demonstrate that the mechanisms controlling development of PNAd⁺ CCL21⁺ vasculature in tumors are distinct from those identified in SLO, and also differ between SC and IP tumors. It remains to be determined whether these or additional mechanisms operate in human tumors growing in different anatomical locations.

Tertiary lymphoid structures

TLS are lymphoid aggregates that frequently develop at sites of chronic infection, autoimmune disease, and allograft rejection (69–78). These structures have considerable morphological, cellular, and molecular similarity to SLO, particularly LN. Inflammation-associated TLS are associated with blood vascular endothelial cells that express PNAd and CCL21, similar to that of the tumors described above, and often have a characteristic “puffy” morphology. TLS contain B-cells, T-cells, and DC, which are typically organized into distinct functional compartments: a B-cell follicle mainly composed of naïve B cells, surrounding a germinal center composed of highly proliferative B cells; and a T-cell area mainly composed of T-cells and DC (77, 79). In SLO, this microarchitecture is orchestrated by the homeostatic chemokines CCL19, CCL21, CXCL13, and CXCL12 (80–83). These chemokines are also found in TLS (84–88). Cells resembling fibroblastic reticular cells (FRC) and follicular dendritic cells (FDC) have also been reported in well-developed TLS (63, 75, 84, 85, 87), suggesting that they may be the source of these chemokines and function as organizers of TLS. However, this remains to be directly demonstrated.

Identification and categorization of tumor-associated TLS

Well-organized TLS have been described in association with several different tumor types in humans, and two recent reviews have provided comprehensive summaries of this information (89, 90). The initial description in non-small cell lung cancers (91) documented large peritumoral aggregates of immune cells containing distinct T/DC and B/FDC zones, the latter of which also contained germinal centers. This group also documented the preferential expression of several homeostatic chemokines and HR ligands in these TLS

(92), which correlated with the presence of larger numbers of CD4⁺CD62L⁺ T cells (92, 93). Subsequent studies have largely replicated these findings in a number of different tumor types in humans, although the range of cellular and molecular markers examined has been variable (67, 94–113). We and others have also identified TLS in murine tumors (55, 114, 115).

One significant consideration is how tumor-associated TLS are distinguished from otherwise localized immune cell infiltrates. In addition to the histological documentation of lymphoid aggregates, which are typically located peritumorally, most human studies have relied largely or exclusively on the presence of only some TLS-associated elements, including PNAd⁺ HEV (105, 106), mature DC (67, 91–93), B cells (99, 106), or T_{FH} cells (102). A gene signature that includes CCL19, CCL21, and CXCL13, the homeostatic chemokines that likely organize TLS, also has been used (96, 109, 106, 67, 111, 102). While it seems likely that the structures identified by all groups are indeed TLS, this points to the possibility of significant unappreciated heterogeneity in structure or composition that may arise in connection with different tumor types, anatomical locations, and primary or metastatic lesions.

In this regard, it was shown that the colorectal metastases to the lung were associated with well-developed TLS in humans, while renal cell carcinomas metastases to the same organ were associated with poorly developed TLS (110). In human melanoma, it was found that TLS frequently developed in metastatic lesions, yet were largely absent from primary tumors, despite the presence of a PNAd⁺ vasculature (95). Similarly, in the transplantable murine models that we have studied, TLS form around PNAd⁺ vasculature in all IP tumors, but not SC tumors, despite the presence of comparable LN-like vasculature (55, 116) (Fig. 1). The TLS found in these murine IP tumors also lack discreet B- and T-cell areas. Instead, T-cells and DC are distributed within large B-cell aggregates that are in turn organized within a reticular network of podoplanin⁺ fibroblasts (55, 116). In these IP tumor-associated TLS, it appears that the same podoplanin⁺ fibroblasts make both CCL21 and CXCL13, which may explain the lack of discreet B- and T-cell areas. How this difference in organization relative to more conventional SLO and TLS affects the nature of the immune response remains to be determined.

A second categorization of tumor-associated TLS is their anatomical relationship to the tumor mass. Almost all studies in humans have identified peritumoral TLS (summarized in (89)), and TLS in this location have also been described in a genetically engineered mouse model (115). A smaller number of human studies have identified tumors with intratumoral TLS, usually as a subset of the tumors with peritumoral structures, although a largely intratumoral representation has also been reported in germ cell tumors (117) (summarized in (89)). The TLS in the transplantable murine models that we have used are exclusively intratumoral (55, 116). In studies of human melanoma metastases using 7-color immunofluorescence, we have identified TLS in 38% of metastatic melanomas (Mauldin, et al, unpublished). They appear in 3 locations: stroma surrounding tumor nests [extratumoral]; at the periphery of the tumor nests [peritumoral] and intratumoral. In general, TLS are more organized with discreet B-cell and DC/T-cell zones in peritumoral and extratumoral locations (Fig. 2A–D) than within the tumor nests (Fig. 2E–F). However, some peritumoral

TLS also show an intermixing of T-cells within B-cell aggregates (Fig. 2C). FoxP3⁺ putative Tregs are prevalent in the T-cell area. We have also detected intratumoral PNA⁺ vasculature that is not associated with well-organized aggregates, although there are diffuse distributions of lymphocytes and DC in the general vicinity (Fig. 2F). An important set of questions is whether these levels of TLS organization in different locations are formed by distinct mechanisms, have distinct immunological properties, or have distinct prognostic values in relation to patient survival and response to immunotherapy.

Prognostic significance and immunological impact of tumor-associated TLS

TLS are often found in lungs in response to acute infection (77, 78), where they lead to enhanced local anti-viral immunity through activation of naïve T-cells (71, 72). In keeping with this, tumor-associated TLS are usually a favorable prognostic indicator for patient survival (reviewed in (89, 90), although there are exceptions (110, 118). Several studies have pointed to the relationship between the densities of HEV, CD4 or T_H cells, B cells, and mature DC in defining TLS, and to a relationship between the densities of TLS, levels of intratumoral T and B cells, and a T_H1/cytotoxic immune profile among tumor infiltrating lymphocytes (TIL) (92, 93, 96, 97, 99, 112, 119). These observations are most often interpreted to mean that tumor-associated TLS are sites for generating useful antitumor immune responses in newly entering naïve T and B-cells.

An alternative possibility is that TLS are simply proxies for more robust intratumoral CD8 T-cell effector activity. Since intratumoral CD8 T-cells have been implicated most often as positive prognostic factors for cancer patient survival, the prognostic value of TLS needs to be evaluated through multivariate analysis capable of distinguishing independent effects. One recent study concluded that TLS did have independent value after controlling for specific TIL variables (97). Another established that a subset of individuals with low TLS-associated DC density were at great risk of death, despite the presence of a high density of CD8 effectors (93). Interestingly, the presence of TLS in triple negative breast cancer added to the positive prognostic value of moderate levels of TIL, but had no impact if there were high levels of TIL present (105). At the other extreme, TLS had positive prognostic value in Merkel cell carcinoma, while T cell infiltration and several other immunological parameters did not (119). Similarly, neither CD8 or T_H17 TIL were associated with positive prognosis in gastric cancer patients; however, Tbet⁺ cells, CD20 B cells organized into TLS, and coordinate expression of T_H1 and B cell genes were (103). Curiously however, DC-Lamp⁺ cell density, another TLS marker, did not have prognostic value.

Conversely, a limited number of studies have shown that tumor-associated TLS are a negative prognostic factor for cancer patient survival. The presence of TLS in colorectal cancer has been associated with more advanced disease (118), while TLS in breast cancer was associated with a higher tumor grade, low representation of intratumoral immune cells, and a high frequency of LN metastasis (120). These studies are seemingly at odds with studies suggesting positive associations with patient survival in each of these diseases (67, 97, 102, 105–107, 110, 112), and remain to be fully reconciled. An intriguing study showed a negative impact of DC-Lamp and CD8 markers on survival of patient with renal cell carcinoma metastases to lung, but a positive impact on patients with colorectal cancer

metastases to the same organ (110). In murine lung adenocarcinoma, it was shown that TLS serve as a site for recruitment of Treg that restrain antitumor immune responses (115). It was also shown that TLS can function as niches for malignant hepatocellular progenitor cells (98). Interestingly, in human lung transplants, TLS have been associated with a lower probability of graft rejection, whereas some other organ transplants are more likely to be rejected when TLS are identified (121–123). Thus, both in cancers and in transplanted organs, immune rejection may be enhanced or reduced by the presence of TLS. This raises the possibility that some TLS are dominated by regulatory T cells and support tolerance, whereas others support immune rejection. It will be important to understand details of the composition and location of TLS and which are most relevant for immune rejection.

A characteristic feature of all tumor-associated TLS in both humans and mice is the presence of a large number of B-lymphocytes, often accompanied by T_{FH} cells. In recent years the consensus of the field has become that CD8 T-cells are the most important determinant of anti-tumor immunity; however, these observations suggest that intratumoral B cells may play an important role(s). On the positive side, several studies have suggested that intratumoral B-cells can capture and present tumor antigens to T cells (124–126). Perhaps even more heretical (in the current environment) have been suggestions that intratumoral antibody responses can be an effective component of anti-tumor immunity (127, 128). On the negative side, many studies have shown that B cells can play a suppressive role in anti-tumor immunity, and Breg cells have been found to accumulate in several tumor models (129–132). The differences in prognostic significance of tumor-associated TLS may lie, at least in part, to distinct functional attributes of the B-cell compartment in different tumors. However, the ways in which tumors may regulate these functional attributes remains to be discovered.

Collectively, these studies point to a complex interplay in which the prognostic value of TIL and TLS depends at the very least on tumor type. It seems likely that different tumor types may drive qualitatively distinct immune responses, distinguishable by their effector and regulatory mechanisms. Such responses may also evolve over time. In some tumors, or at certain times, these may be determined largely within conventional tumor-draining SLO, while in other circumstances, they may be determined within tumor-associated TLS. Evidence demonstrating such a temporal evolution has recently been reported (94). This suggests that TLS “quality” might also confer, or result from, distinct kinds of immunity or immune regulation. Genetically engineered mouse models (115) provide a valuable opportunity to evaluate these variables systematically.

Mechanisms that control the development of TLS

The development of conventional LN depends on interaction between $CD4^+CD3^{neg}$ lymphoid tissue inducer (LTi) cells expressing $LT\alpha_1\beta_2$ and RANKL (now known to be ILC3 cells (133)), and mesenchymal lymphoid tissue organizer (LTo) cells expressing $LT\beta R$ (134–139). This leads to expression of CCL19, CCL21, and CXCL13, which attract additional LTi cells, and the recruitment and positioning of T- and B-cells (81, 140–142). In keeping with this, mice deficient in $LT\alpha$, $LT\beta$, or $LT\beta R$ fail to develop all or most LN (143–146). The formation of FDC networks and germinal centers as an element of LN development depends

on engagement of TNFR as well as LT β R (147). LT β R signaling does not control expression of CCL21 in adult LN (56), although it does maintain CXCL13 expression in adult spleen (148) presumably through interaction of LT $\alpha_1\beta_2$ -expressing B-cells with LT β R⁺ FDC (149, 150).

A key question is whether the formation of TLS in general, and tumor-associated TLS in particular, occurs through pathways analogous to those controlling conventional LN development. Transgenic expression of LT α or LT β in various organs leads to the formation of organized lymphoid aggregates typically identified as TLS, although they are not driven by an immune response (60–63). Transgenic expression of CCL21 also leads to formation of such structures, although PNA^d expression still depends on LT β R signaling (151, 152), and this operates through mature CD4 T cells rather than LT_i cells (153). Importantly, blockade of LT β R signaling prevents immune response-driven TLS formation in thyroid, lung, salivary gland, aorta, and heart (154–156, 71, 88, 157). These studies suggest that development of LN and TLS are mechanistically similar.

On the other hand, TLS have been shown to depend on TNF α in aorta, fat, and intestine (158–160), IL22 in salivary gland (84), and IL17A in lung and meninges (161, 88, 86). IL6 and IL23 also contribute to TLS development through IL17A dependent and independent pathways (162–164). While the exact mechanisms of action remain to be fully defined, TNF α induces CCL21 (64, 65), CXCL13 (148) and enzymes necessary for PNA^d synthesis (58, 59), while IL22 and IL17A induce CXCL12 and CXCL13 in TLS-associated stromal cells (165, 166, 85, 88, 84). These cytokines sometimes induce TLS independent of LT β R signaling (158, 160), but in other instances act cooperatively, either by inducing distinct aspects of TLS structure (84, 86), or by acting at either the TLS induction or maintenance phases (88). Importantly, different pathogens can induce lung-associated TLS by distinct cellular and molecular pathways (85). The involvement of additional cytokines in formation and/or maintenance of many LT β R-dependent TLS remains to be evaluated.

Aside from the involvement of distinct molecular signaling pathways in TLS formation, a variety of different inducing cells, in lieu of LT_i cells, have been identified. This includes DC (71, 72, 167) and naïve B-cells (168), both expressing LT $\alpha_1\beta_2$; macrophages (158–160), T_H17 (161, 88, 86), NKT (158), $\gamma\delta$ T-cells (85) and multiple populations of IL22-secreting adaptive and innate lymphoid cells (84). Overall, it should be expected that distinct molecular signals, conveyed by immune cells with pleiotropic regulatory signatures, will induce TLS with important differences in the immune responses that they support.

In this context, the mechanisms driving TLS formation in tumors remain almost entirely unknown. Analogous to the overexpression models described above, transgenic expression of LT α or LIGHT in tumors (11, 169) or intratumoral administration of CCL21 (52, 53) establishes that these pathways can lead to TLS formation. In transplantable murine tumors, TLS develop in IP but not SC tumors (55, 116), suggesting that the mechanisms controlling their development depend on anatomical environmental factors, and providing an opportunity to gain insight into these mechanisms through comparative analysis. Since PNA^dCCL21⁺ vasculature develops comparably in tumors growing in both locations, this

also points to distinct mechanisms controlling these two features, and to this vasculature in providing a nucleation site for TLS formation.

Compared to SC tumors, IP tumors showed a 10-fold increase in the number of B-cells relative to CD31⁺ vascular endothelial cells, while the numbers of T cells and DC were similar (116). Interestingly, IP tumors also showed a 5-fold relative increase of podoplanin⁺ fibroblasts, and these cells formed a reticular network surrounding the PNAd⁺CCL21⁺ vasculature, which was co-extensive with the B-cells (55, 116). While perivascular podoplanin⁺ cells were evident in SC tumors, they had not expanded to form reticular networks. Also, podoplanin⁺ cells in IP tumors expressed significantly higher levels of CXCL13 and the B-cell survival factors BAFF and APRIL (Rodriguez et al, in preparation), which are important for the development and survival of B-cells (170–172) and maintaining the integrity of germinal centers (173, 174). This suggests that elements of the IP tumor microenvironment induce both proliferation and differentiation of podoplanin⁺ cells, which act as scaffolding for TLS formation. While our work establishes that CCL21 recruits naïve T-cells into IP and SC tumors (55), it remains to be directly determined whether and how these remaining molecules impact B-cell recruitment and the formation of TLS in IP tumors, and what is responsible for changes in their expression in tumor association podoplanin⁺ fibroblasts (Fig. 3).

CONCLUSIONS

Tumor-associated TLS have been frequently correlated with improved patient survival, and in murine models, have generally been associated with the development of improved immune-mediated tumor control. However, tumor-associated TLS have also been identified as a locus of Treg accumulation, and they characteristically contain large numbers of B-cells, which exert a regulatory role in several tumor models. Much remains to be done to fully understand the immune mechanisms that are activated within these structures, and whether this varies based on the origin of the tumor, the oncogenic drivers leading to its formation, or its anatomical location as a primary tumor or metastatic lesion. To do so will require application of the full range of technologies that have been applied in previous studies, together with a more comprehensive analysis of molecules that mark various immune mechanisms. Advances in multi-spectral imaging of single sections, and entire tumors after tissue clearing, and advances in small scale RNAseq combined with laser capture dissection of TLS create new opportunities for comprehensive assessment of cellular composition and functional state of individual TLS in a variety of contexts. This work is also important as a means to more clearly establish the prognostic value of TLS, independent of other immune factors.

The pathways that drive the formation of PNAd⁺CCL21⁺ vasculature have been uncovered in a limited number of murine tumor models, but the factors that drive formation and/or maintenance of tumor-associated TLS remain almost completely unknown. Studies in a variety of different inflammation-driven TLS models have pointed to a number of molecular and cellular mediators that work in collaboration with or in lieu of more classic mechanisms that underlie the formation of SLO. This heterogeneity has been shown to reflect, at least in part, the nature of the inflammatory stimulus. One might also imagine a role for anatomical

location, reflecting the extent to which peripheral tissues are invested with different subsets of myeloid derived cells, innate lymphoid cells, or tissue resident memory cells. The impact of the pre-existing or early stage microenvironment in proximity to tumors on TLS formation is clear, but the exact drivers, and how they vary based on tumor origin or location, remain to be determined. These drivers are likely to also influence the composition and function of TLS, as mentioned above. Understanding these driver mechanisms will rely heavily on appropriate transplantable and genetically-induced mouse models, where they can be directly tested through knockout or blockade approaches. Their validity in human settings will be more difficult to establish, as it will depend largely on correlative studies to establish the presence or absence of various cells or signaling molecules. However, as argued above, incisive multiparameter correlative studies are key to understand the prognostic significance of TLS in humans. Together with work in mouse models, they will provide the basis for moving forward to manipulate TLS incidence, location, composition, and function.

Based on the preponderance of evidence, it seems highly desirable in most settings to increase the number of TLS as a way to promote an ongoing immune response in immediate proximity to tumor cells, avoiding the need for two-way cellular traffic between tumor and tumor-draining SLO. One open question is whether this is best achieved via intratumoral or peritumoral TLS. Related to this is the question of whether regulatory mechanisms that often occur within the tumor microenvironment are more prevalent within, or in proximity to, TLS. A second set of questions concerns TLS functionality. It remains to be established how TLS and tumor-draining SLO compare as sites for development of tumor specific CD8 T-cells, either numerically or over time. The presence of large numbers of B-cells in TLS has brought renewed focus on the positive and negative roles that B-cells might play in anti-tumor immunity, but this has yet to be clearly tied to the activity of B-cells within TLS. Finally, but more immediately in the current clinical environment, there are open questions about whether the presence of TLS, either pre- or post-treatment, has prognostic value in responses to checkpoint blockade therapy. Does checkpoint blockade enhance TLS formation, or enhance TLS function as a site for de novo anti-tumor immune responses? As new immune therapeutic modalities (IDO inhibitors, myeloid cell depletion, etc) come into the clinical landscape, these questions will only get broader.

Overall, the work accomplished to date clearly establishes the importance of tumor-associated TLS as an aspect of immunological control of tumors. However, a substantial amount of work remains to be done to fully understand how they are important, and how to begin to use them as an element of our developing armamentarium of immunological cancer control strategies.

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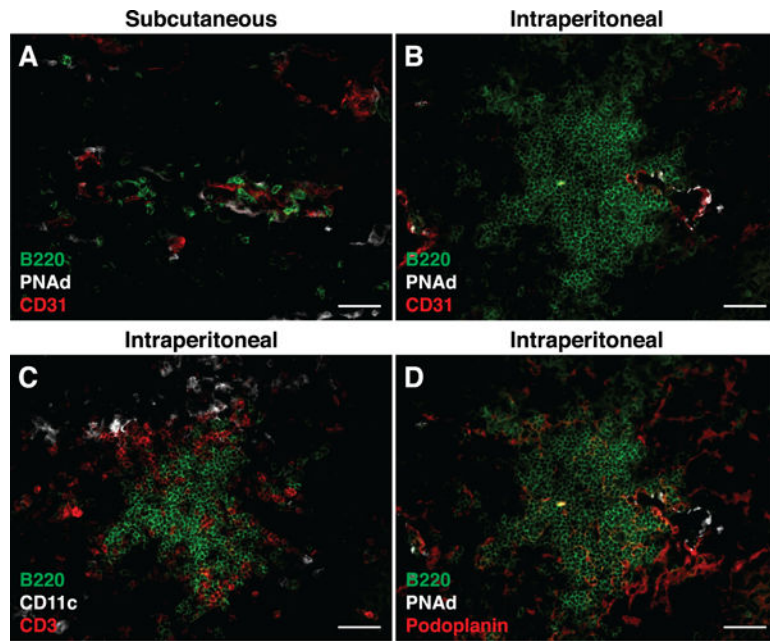


Figure 1. Intratumoral TLS with a nonclassical organization are found in association with PNAd⁺ vasculature in intraperitoneal but not subcutaneous murine B16-OVA melanoma.

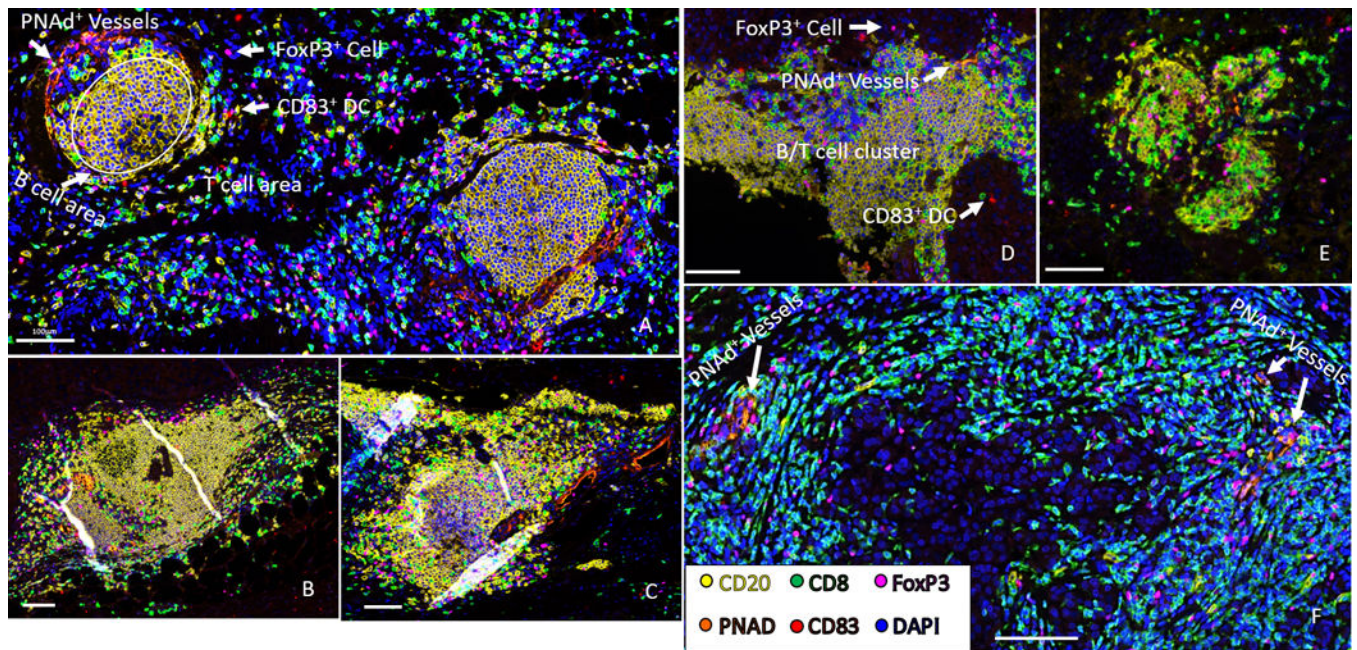


Figure 2. Multispectral imaging of TLS in human melanoma metastases localized outside the tumor area (A); peritumoral, at the peripheral edge of tumor (B–D); or intratumorally (E–F). All scale bars are equal to 100 μ m. Artefactual tissue creases due to sectioning can be seen on images B and C.

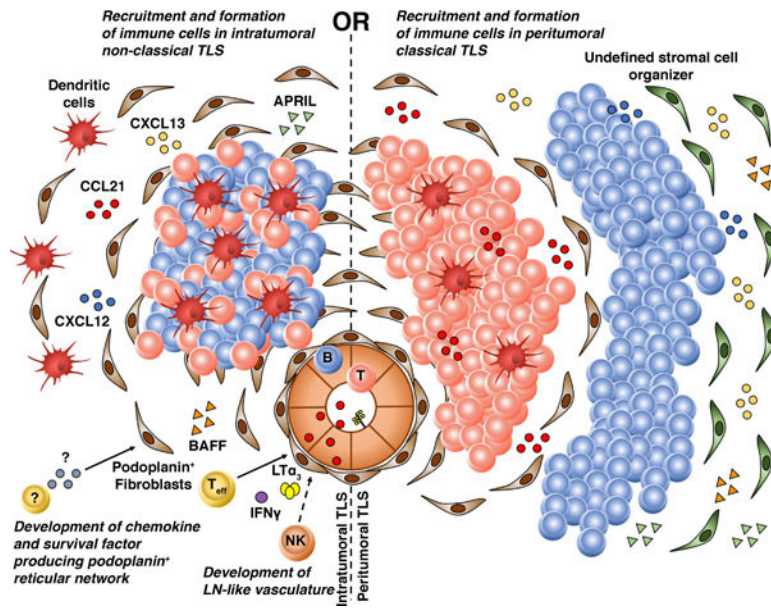


Figure 3.
Model for the formation of nonclassical and classical tumor associated TLS.

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